SEQUENCE LISTING

<110> LIFEEDIT, INC.

<120> RNA-GUIDED NUCLEASES AND ACTIVE FRAGMENTS AND VARIANTS THEREOF AND METHODS OF USE

<130> L103438 1170WO (0049.2)

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<150> 63/030,088
<151> 2020-05-26

<150> 62/901,875
<151> 2019-09-18

<150> 62/885,483
<151> 2019-08-12

<160> 742

<170> PatentIn version 3.5

<210> 1
<211> 1071
<212> PRT
<213> Bacillus sp.

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Ile Gly Trp Gly Val Ile Glu Leu Ser Trp Asn Lys Asp Arg Glu Gln
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Tyr Glu Lys Thr Arg Ile Val Asp Lys Gly Val Arg Met Phe Asp Lys
        35 40 45

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

Ala Arg Ser Ser Arg Arg Arg Leu Asn Arg Lys Ser Gln Arg Lys Lys
65 70 75 80

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Asp Ile Arg Asn Leu Leu Val Gln His Glu Ile Ile Ser Gln Lys Glu
                85                  90                  95

Leu Thr Ser Leu Tyr Pro Leu Ser Lys Ser Ser Met Asp Ile Trp Asp
            100                 105                 110

Ile Arg Leu Asp Gly Leu Asp Arg Leu Leu Asp Arg Phe Glu Trp Ala
        115                 120                 125

Arg Leu Leu Ile His Leu Ala Gln Arg Arg Gly Phe Lys Ser Asn Arg
    130                 135                 140

Lys Ser Glu Leu Lys Asp Val Glu Thr Gly Lys Val Leu Ser Ser Ile
145                 150                 155                 160

Gln Val Asn Glu Lys Arg Leu Ser Leu Tyr Arg Thr Val Gly Glu Met
                165                 170                 175

Trp Met Lys Asn Ala Asp Cys Ser Lys Tyr Gly Lys Arg Arg Asn Ser
            180                 185                 190

Pro Asn Glu Tyr Val Phe Ser Val Ser Arg Ala Asp Leu Glu Lys Glu
        195                 200                 205

Ile Val Thr Leu Phe Glu Ala Gln Arg Lys Phe His Ser Ser Tyr Ala
    210                 215                 220

Ser Val Asp Leu Gln Lys Thr Tyr Ile Gln Ile Trp Ala His Gln Leu
225                 230                 235                 240

Pro Phe Ala Ser Gly Asn Ala Ile Val Asn Lys Val Gly Tyr Cys Ser
                245                 250                 255

Leu Leu Lys Gly Lys Glu Lys Arg Val Pro Lys Ala Thr Tyr Thr Phe
            260                 265                 270

Gln Tyr Phe Asn Thr Leu Asp Gln Ile Asn Arg Thr Arg Leu Gly Pro
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        275                 280                 285

Asn Phe Gln Pro Phe Thr Lys Glu Gln Arg Asp Ile Ile Leu Asp Lys
    290                 295                 300

Met Phe Gln Arg Thr Asp Tyr Tyr Lys Lys Lys Thr Ile Pro Glu Val
305                 310                 315                 320

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

Phe Lys Gly Leu Thr Tyr Asp Pro Asn Glu Glu Leu Lys Lys Ile Glu
            340                 345                 350

Met Lys Pro Phe Ile Asn Leu Lys Pro Phe Tyr Glu Ile Lys Lys Val
        355                 360                 365

Val Thr Asn Tyr Ala Lys Lys Thr Asn Glu Val Phe Ser Ala Leu Asp
    370                 375                 380

Tyr Asp Thr Val Ala Tyr Ala Leu Thr Val Tyr Lys Thr Asp Lys Asp
385                 390                 395                 400

Ile Arg Ser Tyr Leu Lys Arg Ser Asn Asn Leu Ser Lys Arg Cys Tyr
                405                 410                 415

Asp Asp Gln Leu Ile Glu Glu Leu Leu Thr Leu Ser Tyr Thr Lys Phe
            420                 425                 430

Gly His Leu Ser Phe Lys Ala Ile Asn His Val Leu Pro Ile Met Gln
        435                 440                 445

Glu Gly Arg Thr Tyr Gln Glu Ala Ile His Gln Leu Gly Tyr Asp Thr
    450                 455                 460

Thr Asn Leu Lys Lys Glu Asn Arg Ser Met Phe Leu Pro Ile Ile Pro
465                 470                 475                 480
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Asp Glu Ile Thr Asn Pro Ile Val Lys Arg Ala Leu Thr Gln Ala Arg
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Lys Val Val Asn Ala Ile Ile Arg Arg Tyr Gly Ser Pro Asn Ser Val
            500                 505                 510

His Ile Glu Leu Ala Arg Glu Leu Ser Lys Ser His Asp Glu Arg Lys
        515                 520                 525

Lys Ile Met Thr Ala His Asp Glu Asn Tyr Lys Lys Asn Lys Gly Ala
    530                 535                 540

Ile Ser Ile Leu Ile Glu Asn Gly Ile Leu Asn Pro Thr Gly Tyr Asp
545                 550                 555                 560

Ile Val Arg Tyr Lys Leu Trp Lys Glu Gln Gly Glu Arg Cys Ala Tyr
                565                 570                 575

Ser Leu Lys Lys Ile Pro Ala Asn Thr Phe Phe Asn Glu Leu Lys Lys
            580                 585                 590

Glu Arg Ser Gly Pro Pro Val Leu Glu Val Asp His Ile Leu Pro Tyr
        595                 600                 605

Ser Gln Ser Phe Ile Asp Ser Tyr His Asn Lys Val Leu Val Tyr Gly
    610                 615                 620

Asp Glu Asn Gln Lys Lys Gly Asn Arg Ile Pro Tyr Thr Phe Phe Ser
625                 630                 635                 640

Glu Glu Asp Lys Glu Trp Glu Ser Phe Glu Ser Tyr Val Arg Ser Asn
                645                 650                 655

Ser Phe Phe Ser Lys Lys Lys Arg Gly Tyr Leu Leu Lys Lys Ala Tyr
            660                 665                 670

Leu Pro Arg Glu Ser Asn Leu Ile Lys Glu Arg His Leu Asn Asp Thr
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        675                 680                 685

Arg Tyr Ala Ser Ser Tyr Leu Lys Asn Phe Ile Glu Lys Asn Leu Lys
    690                 695                 700

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

Asn Gly Val Ile Thr Ala His Leu Arg Lys Arg Trp Gly Leu Glu Lys
                725                 730                 735

Asp Arg Gln Glu Thr Tyr Leu His His Ala Met Asp Ala Ile Ile Val
            740                 745                 750

Ala Cys Thr Asp His His Met Val Thr Lys Val Thr Glu Tyr Tyr Gln
        755                 760                 765

Ile Lys Glu Gly Asn Lys Ser Ile Lys Lys Pro Tyr Phe Pro Leu Pro
    770                 775                 780

Trp Met Gly Phe Arg Glu Glu Ile Leu Ser His Leu Glu Ser Gln Pro
785                 790                 795                 800

Ile Ala Arg Lys Ile Ser Glu Glu Leu Lys Ile Gly Tyr Gln Ser Ser
                805                 810                 815

Asp Tyr Ile Leu Val Ser Arg Met Pro Lys Arg Ser Val Thr Gly Ser
            820                 825                 830

Ala His Asp Gln Thr Val Met Lys Lys Gly Gly Ile Asp Lys Lys Gly
        835                 840                 845

Lys Thr Ile Ile Ile Lys Arg Val His Leu Lys Asp Ile Lys Phe Asp
    850                 855                 860

Glu Asn Gly Asp Phe Lys Met Val Gly Lys Glu Gln Asp Leu Ala Thr
865                 870                 875                 880
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Tyr Glu Ala Ile Lys Gln Arg Tyr Leu Glu Tyr Arg Lys Lys Ser Lys
                885                 890                 895


Lys Ala Phe Glu Thr Pro Leu Tyr Lys Pro Ser Lys Lys Gly Lys Gly
            900                 905                 910


Asn Leu Ile Lys Lys Ile Lys Val Glu Val Gln Thr Lys Ser Phe Val
        915                 920                 925


Arg Glu Ile Asn Gly Gly Val Ala Gln Asn Gly Asp Leu Val Arg Val
    930                 935                 940


Asp Leu Phe Glu Lys Asp Asn Arg Tyr Tyr Met Val Pro Ile Tyr Val
945                 950                 955                 960


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


Lys Gly Tyr Glu Gln Trp Leu Ser Ile Asp Asn Ser Phe Thr Phe Lys
            980                 985                 990


Phe Ser Leu Tyr Pro Tyr Asp Leu  Val Arg Leu Val Lys  Gly Asp Glu
        995                 1000                1005


Asp Arg  Phe Leu Tyr Phe Ser  Thr Leu Asp Ile Asn  Ser Asp Arg
    1010                1015                1020


Leu Asn  Phe Lys Asp Val Asn  Lys Pro Ser Lys Gln  Ala Glu Tyr
    1025                1030                1035


Arg Tyr  Ser Leu Lys Thr Ile  Glu Asn Leu Glu Lys  Tyr Glu Ile
    1040                1045                1050


Gly Val  Leu Gly Asp Leu Arg  Leu Val Arg Gln Glu  Thr Arg Lys
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Ile Phe  Lys
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1070

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<213> Bacillus sp.

<400> 2
gucauaguuc cauuaaagcc auugcuguuu uaug 34

<210> 3
<211> 148
<212> RNA
<213> Bacillus sp.

<400> 3
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aucgccugcc cauuuuaaug ggcuucuccc caucuauuua augagaaauu uacaaccuug 120

gcuauucuua aauagcuaag guuuuuuu 148

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<213> Artificial Sequence

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<220>
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<222> (1)..(29)
<223> a, c, u, g, unknown or other

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nnnnnnnnnn nnnnnnnnnn nnnnnnnnng ucauaguucc auuaaagcca uugcuguuuu 60

augaaagcau gauacagcaa uggcuuugau guuucuauga uaagggcuuc ggcccguggc 120

guuggggauc gccugcccau uuuaaugggc uucucccccau cuauuuaaug agaaauuuac 180

aaccuuggcu auucuuaaau agcuaagguu uuuuu 215

<210> 5
<211> 216
<212> RNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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gagcggacag cagcuuccua uaucucguac gucauaguuc cauuaaagcc auugcuguuu 60

uaugaaagca ugauacagca auggcuuuga uguuucuaug auaagggcuu cggcccgugg 120

cguuggggau cgccugccca uuuuaauggg cuucucccca ucuauuuaau gagaaauuua 180

caaccuuggc uauucuuaaa uagcuaaggu uuuuuu 216

<210> 6
<211> 216
<212> RNA
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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ccaugauaua gacguugugg cuguuguagu gucauaguuc cauuaaagcc auugcuguuu 60

uaugaaagca ugauacagca auggcuuuga uguuucuaug auaagggcuu cggcccgugg 120

cguuggggau cgccugccca uuuuaauggg cuucucccca ucuauuuaau gagaaauuua 180

caaccuuggc uauucuuaaa uagcuaaggu uuuuuu 216

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<212> DNA
<213> Artificial Sequence

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<222> (1)..(4)
<223> a, c, t, g, unknown or other

<400> 7
nnnncc 6

<210> 8
<211> 6
<212> RNA
<213> Artificial Sequence

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<223> a, c, u, g, unknown or other

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<223> a, c, u, g, unknown or other

<400> 8
unanna 6

<210> 9
<211> 1403
<212> PRT
<213> Chryseobacterium sp.

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1 5 10 15

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20 25 30

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Ile Lys Leu Gly Val Arg Val Asn Pro Leu Thr Ile Asp Glu Lys Thr
        35                  40                  45

Asn Phe Glu Lys Gly Lys Ser Ile Thr Thr Asn Ala Gly Arg Thr Ser
    50                  55                  60

Ala Arg Ser Ala Arg Arg Asn Leu Gln Arg Phe Lys Leu Arg Arg Lys
65                  70                  75                  80

Ser Leu Trp Glu Val Leu Ile Asn Tyr Lys Ile Ile Lys Asn Asp Thr
                85                  90                  95

Val Leu Ala Glu Ile Gly Lys Asn Ser Thr Phe Gln Thr Gln Tyr Leu
            100                 105                 110

Arg Ala Lys Ala Ala Lys Glu Lys Ile Glu Leu Asp Glu Leu Ala Arg
        115                 120                 125

Val Leu Phe Leu Ile Asn Lys Lys Arg Gly Tyr Lys Ser Ser Arg Lys
    130                 135                 140

Val Gln Ser Asp Asp Glu Gly Lys Ala Ile Asp Gly Met Ser Val Ala
145                 150                 155                 160

Lys Glu Leu Tyr Glu Lys Asn Tyr Thr Pro Gly Gln Tyr Val Tyr Asp
                165                 170                 175

Leu Leu Lys Asn Gly Lys Lys Gln Ile Pro Asp Phe Tyr Arg Ser Asp
            180                 185                 190

Leu Gln Asn Glu Leu Asp Arg Val Trp Glu Phe Gln Lys Gln Tyr His
        195                 200                 205

Pro Asp Ile Leu Thr Asp Glu Tyr Lys Lys Glu Leu Glu Gly Lys Gly
    210                 215                 220

Gln Arg Ala Thr Ala Ala Ile Phe Leu Asn Arg Tyr Lys Ile Tyr Thr
225                 230                 235                 240
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Ala Asp Asn Lys Gly Thr Arg Glu Glu Lys Arg Phe Gln Ala Tyr Gln
                245                 250                 255

Trp Arg Val Glu Ala Leu Ser Gln Pro Leu Asp Ile Lys Glu Val Ala
            260                 265                 270

Tyr Val Ile Thr Glu Ile Asn Asn Asn Leu Asn Asn Ser Ser Gly Tyr
        275                 280                 285

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

Thr Ile Gly Glu Tyr Leu Tyr Glu Glu Leu Ser Leu Asn Pro His Ala
305                 310                 315                 320

Arg Leu Lys Asn Gln Val Phe Tyr Arg Gln Asp Tyr Gln Asp Glu Phe
                325                 330                 335

Glu Lys Ile Trp Glu Thr Gln Ala Lys Phe His Ser Val Leu Thr Thr
            340                 345                 350

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

Leu Lys Ser Gln Lys Gly Leu Ile Ser Phe Cys Glu Phe Glu Ser Lys
    370                 375                 380

Glu Ile Val Ile Glu Glu Asn Gly Lys Lys Lys Arg Lys Lys Val Gly
385                 390                 395                 400

Leu Lys Val Val Pro Lys Ser Ser Pro Leu Phe Gln Glu Phe Lys Ile
                405                 410                 415

Trp Gln Val Leu Asn Asn Ile Glu Ile Lys Asn Glu Asp Gly Arg Arg
            420                 425                 430
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Tyr Leu Asp Gln Glu Glu Lys Glu Leu Leu Phe Asn Glu Leu Asn Cys
        435                 440                 445

Lys Gly Asn Leu Thr Ser Gln Lys Cys Leu Glu Phe Leu Gly Phe Lys
    450                 455                 460

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

Asn Glu Lys Leu Tyr Asp Ala Phe Leu Lys Ile Leu Glu Leu Lys Gly
                485                 490                 495

Tyr Asn Val Phe Glu Leu Leu Lys Ile Lys Glu Asp Arg Asp Glu Ala
            500                 505                 510

Lys Leu Ser Glu Leu Lys Ala Ser Ala Asp Glu Ile Lys Arg Met Val
        515                 520                 525

Lys Glu Ile Phe Asn Ala Asn Leu Ile Asn Thr Ser Ile Leu Asp Phe
    530                 535                 540

Asn Ala Glu Leu Glu Gly Lys Asp Phe Glu Asn Gln Ala Ser Tyr Gln
545                 550                 555                 560

Phe Trp His Leu Ile Tyr Ser Tyr Glu Gly Asp Asn Ser Pro Ser Gly
                565                 570                 575

Asn Glu Lys Leu Tyr Glu Leu Leu Glu Asn Lys Phe Gly Phe Lys Lys
            580                 585                 590

Glu His Ser Lys Ile Leu Ser Thr Ile Val Phe Pro Gln Glu Tyr Gly
        595                 600                 605

Ser Leu Ser Ala Lys Ala Met Arg Arg Ile Tyr Pro Tyr Ile Lys Asp
    610                 615                 620

Asn Lys Tyr Ser Glu Ala Cys Leu Leu Ala Gly Tyr Asn His Ser Lys
625                 630                 635                 640
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Gln Ser Leu Thr Lys Glu Glu Leu Glu Asn Arg Lys Leu Lys Glu Gln
                645                 650                 655

Leu Glu Val Leu Pro Lys Asn Ser Leu Arg Asn Pro Val Val Glu Lys
            660                 665                 670

Ile Leu Asn Gln Met Ile Asn Leu Val Asn Ala Ile Ile Ser Glu His
        675                 680                 685

Gly Lys Leu Asp Gly Val Arg Ile Glu Leu Ala Arg Glu Leu Lys Lys
    690                 695                 700

Ser Ala Gln Glu Arg Glu Asp Met Thr Lys Ser Ile Asn Glu Ala Thr
705                 710                 715                 720

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

Val Asn Pro Ser Arg Asn Asp Ile Ile Arg Tyr Lys Leu Tyr Met Glu
            740                 745                 750

Leu Ala Gly Asn Gly Tyr Lys Asp Leu Tyr Thr Asn Val Lys Ile Glu
        755                 760                 765

Lys Glu Asn Ile Phe Thr Asp Lys Tyr Asp Ile Asp His Ile Ile Pro
    770                 775                 780

Gln Ser Arg Phe Phe Asp Asp Ser Phe Ser Asn Lys Val Leu Val Pro
785                 790                 795                 800

Arg Gln Ala Asn Leu Asp Lys Gly Asn Leu Thr Gly Tyr Asp Phe Met
                805                 810                 815

Ser Asn Lys Gly Ala Glu Arg Glu Glu His Phe Leu Asn Val Ile Lys
            820                 825                 830
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Asp Leu Leu Glu Asn Gly Ser Ile Ser Lys Ala Lys Tyr Glu Lys Leu
        835                 840                 845

Lys Lys Lys Gly Ile Glu Ile Gly Asp Gly Phe Ile Glu Arg Asp Leu
    850                 855                 860

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

Ile Thr Asn Ser Val Ile Ser Thr Ser Gly Arg Ile Thr Asp Lys Leu
                885                 890                 895

Arg Glu Asp Trp Asp Leu Val Asn Thr Met Lys Glu Leu Asn Leu Asp
            900                 905                 910

Lys Tyr Arg Arg Leu Gly Leu Thr Glu Ile Val Ile Asn Ser Lys Gly
        915                 920                 925

Glu Glu Lys Glu Val Ile Pro Asp Trp Thr Lys Arg Asn Asp His Arg
    930                 935                 940

His His Ala Met Asp Ala Leu Thr Val Ala Phe Thr Thr Arg Asn His
945                 950                 955                 960

Ile Gln Tyr Leu Asn Tyr Leu Asn Ala Arg Lys Asp Glu Lys His Lys
                965                 970                 975

Glu His Gln Asn Ile Tyr Ala Ile Glu Asn Ile Ile Thr Glu Ile Ile
            980                 985                 990

Glu Lys Lys Asn Gly Ser Lys Ser  Arg Arg Phe Lys Thr  Pro Met Asn
        995                 1000                1005

Arg Phe  Arg His Glu Ala Lys  Gln His Leu Lys Glu  Val Leu Val
    1010                1015                1020

Ser His  Lys Thr Lys Asn Lys  Val Val Thr Ser Asn  Ile Asn Lys
    1025                1030                1035
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Thr Lys  Lys Lys Arg Gly Ile  His Lys Lys Ala Glu  Leu Thr Pro
    1040                1045                1050

Arg Gly  Gln Leu His Lys Glu  Thr Val Tyr Gly Ser  Lys Lys Phe
    1055                1060                1065

Leu Gln  Ser Arg Glu Glu Lys  Val Ser Ala Lys Phe  Asp Tyr Glu
    1070                1075                1080

Thr Ile  Leu Met Val Val Asn  Pro Ile His Arg Asn  Ala Leu Leu
    1085                1090                1095

Asn Arg  Leu Lys Glu Tyr Gly  Asn Asp Pro Lys Lys  Ala Phe Ser
    1100                1105                1110

Gly Lys  Asn Ala Val Asn Lys  Thr Pro Val Tyr Leu  Ser Asp Ser
    1115                1120                1125

Lys Ile  Glu Val Leu Pro Glu  Lys Val Thr Leu Ser  Trp Phe Glu
    1130                1135                1140

Thr Gly  Tyr Thr Ile Arg Lys  Ala Val Thr Pro Asp  Asn Phe Lys
    1145                1150                1155

Asp Tyr  Lys Asn Leu Glu Lys  Ile Thr Asp Met Gly  Ile Lys Lys
    1160                1165                1170

Ile Leu  Lys Glu Arg Leu Asp  Gln Phe Lys Gly Asn  Ala Lys Glu
    1175                1180                1185

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

Lys Gly  Ile Ala Ile Lys Thr  Val Thr Ile Thr Gly  Val Ser Asn
    1205                1210                1215
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Ala Glu  Ser Leu His Phe Lys  Lys Asp His Leu Gly  Lys Glu Ile
    1220                1225                1230

Leu Asp  Glu Asn Gly Asn Lys  Ile Pro Val Asp Phe  Val Ser Thr
    1235                1240                1245

Gly Asn  Asn His His Leu Ala  Ile Tyr Leu Asn Glu  Glu Glu Lys
    1250                1255                1260

Leu Asp  Asp Lys Met Val Thr  Phe Tyr Glu Ala Val  Leu Arg Val
    1265                1270                1275

Asn Gln  Gly Leu Pro Val Ile  Asp Lys Asn Tyr Asn  Arg Glu Lys
    1280                1285                1290

Gly Tyr  Lys Phe Leu Met Thr  Leu Lys Gln Asn Glu  Met Phe Val
    1295                1300                1305

Phe Pro  Asn Glu Glu Phe Asp  Pro Ser Glu Ile Asp  Leu Leu Asp
    1310                1315                1320

Glu Lys  Asn Leu Glu Gln Ile  Ser Gln Asn Leu Phe  Arg Val Gln
    1325                1330                1335

Lys Ile  Ser Lys Val Gly Tyr  Gly Asn Ser Phe Ile  Arg Asp Phe
    1340                1345                1350

Val Phe  Arg His His Leu Glu  Thr Thr Val Glu Asp  Arg Lys Glu
    1355                1360                1365

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

Arg Asn  Ile Val Lys Val Arg  Leu Asn His Leu Gly  Lys Ile Val
    1385                1390                1395

Gln Ile  Gly Glu Tyr
    1400
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<210> 10
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<212> RNA
<213> Chryseobacterium sp.

<400> 10
guugugaaau gcuuucaaaa cuua 24

<210> 11
<211> 78
<212> RNA
<213> Chryseobacterium sp.

<400> 11
auaaauuuug aaagcacuuc acaauaagga uuauuccguu gugaaaacau ucaaggcggg 60

gcaacucgcc uuuuuuuu 78

<210> 12
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<223> a, c, u, g, unknown or other

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aauuuugaaa gcacuucaca auaaggauua uuccguugug aaaacauuca aggcggggca 120

acucgccuuu uuuuu 135

<210> 13
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<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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gagcggacag cagcuuccua uaucucguac guugugaaau gcuuucaaaa cuuaaaagau 60

aaauuuugaa agcacuucac aauaaggauu auuccguugu gaaaacauuc aaggcggggc 120

aacucgccuu uuuuuu 136

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<213> Artificial Sequence

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polynucleotide"

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ccaugauaua gacguugugg cuguuguagu guugugaaau gcuuucaaaa cuuaaaagau 60

aaauuuugaa agcacuucac aauaaggauu auuccguugu gaaaacauuc aaggcggggc 120

aacucgccuu uuuuuu 136

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

<220>
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nrrttt 6

<210> 16
<211> 1404
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<213> Sphingobacterium sp.

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Met Met Lys Arg Ile Leu Gly Leu Asp Leu Gly Thr Ser Ser Ile Gly
1   5   10   15

Trp Ala Tyr Val Leu Glu Ala Gln Asp Glu Asn Glu Ile Ser Gln Ile
            20   25   30

Lys Lys Leu Gly Val Arg Val Asn Pro Leu Thr Thr Asp Glu Gln Leu
        35   40   45

Asn Phe Glu Lys Gly Lys Pro Ile Thr Thr Asn Ala Gly Arg Thr Leu
    50   55   60

Ala Arg Ser Ala Arg Arg Asn Leu Gln Arg Tyr Lys Leu Arg Arg Glu
65   70   75   80

Asn Leu Ile Glu Val Leu Lys Arg Glu Lys Trp Ile Asp Asp Lys Ser
                85   90   95

Ile Leu Ala Glu Asn Gly Asn Lys Ser Thr Phe Glu Thr Tyr Ala Leu
            100   105   110

Arg Ala Ala Ala Ala Ser Lys Glu Ile Lys Leu Glu Glu Leu Ala Arg
        115   120   125

Val Leu Leu Met Ile Asn Lys Lys Arg Gly Tyr Lys Ser Ser Arg Lys
    130   135   140

Val Asn Lys Glu Asp Asp Gly Gln Leu Val Asp Gly Met Glu Val Ala
145   150   155   160

Lys Lys Leu Tyr His Glu Asn Leu Thr Pro Gly Glu Phe Val Tyr Arg
                165   170   175

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Leu Leu Lys Glu Gly Lys Lys Lys Ile Pro Asp Phe Tyr Arg Ser Asp
            180                 185                 190

Leu Gln Arg Glu Leu Asp Leu Ile Trp Asp Phe Gln Phe Lys Tyr Tyr
        195                 200                 205

Pro Asp Leu Leu Thr Gln Asp Leu Lys Glu Glu Leu Lys Gly Lys Gly
    210                 215                 220

Leu Arg Ala Thr Ser Ala Ile Phe Trp Ser Lys Tyr Lys Phe Asn Thr
225                 230                 235                 240

Ala Glu Asn Lys Gly Thr Arg Glu Glu Lys Lys Ile Gln Ala Tyr Gln
                245                 250                 255

Trp Arg Lys Asp Gly Leu Thr Lys Gln Leu Glu Gln Glu Glu Val Ala
            260                 265                 270

Tyr Ile Ile Ala Glu Ile Asn Gly Gln Leu Ala Asn Ser Ser Gly Tyr
        275                 280                 285

Leu Gly Ala Ile Ser Asp Arg Ser Lys Glu Leu Tyr Phe Asn Lys Gln
    290                 295                 300

Thr Val Gly Gln Phe Leu Phe Asn Gln Leu Gln His Asn Thr His Ala
305                 310                 315                 320

Arg Val Lys Asn Gln Val Phe Tyr Arg Gln Asp Tyr Leu Asp Glu Phe
                325                 330                 335

Glu Lys Ile Trp Ser Val Gln Ser Gln Tyr His Gln Gly Leu Thr Glu
            340                 345                 350

Gln Leu Lys Glu Glu Ile Arg Asp Ile Ile Ile Phe Tyr Gln Arg Lys
        355                 360                 365
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Leu Lys Ser Gln Lys Gly Leu Ile Ser Phe Cys Glu Phe Glu Gln His
    370                 375                 380

Glu Val Val Ile Asn Gly Lys Asn Lys Ile Val Gly Leu Arg Val Ala
385                 390                 395                 400

Pro Lys Ser Ser Pro Ile Phe Gln Glu Phe Lys Ile Trp Gln Gln Ile
                405                 410                 415

Asn Asn Val Lys Leu Arg Asn Lys Ile Thr Lys Glu Val Tyr Asn Leu
            420                 425                 430

Ala Glu Glu Gln Lys Arg Ser Leu Phe Glu Thr Leu Asn Leu Lys Gly
        435                 440                 445

Lys Leu Ser Ala Tyr Gln Val Leu Asn Leu Ile Glu Val Lys Pro Lys
    450                 455                 460

Glu Trp Glu Leu Asn Tyr Thr Glu Leu Glu Gly Asn Ser Thr Asn Leu
465                 470                 475                 480

Ala Leu Tyr Asn Ala Tyr Leu Asp Ile Leu Asp Ile Glu Gly Tyr Asp
                485                 490                 495

Val Arg Ser Glu Leu Lys Ile Lys Leu Asn Lys Asp Glu Ile Thr Leu
            500                 505                 510

Ser Asp Leu Asp Ile Pro Val Ser Glu Ile Lys Gly Met Ile Arg Arg
        515                 520                 525

Ile Phe Gln His Leu Gly Ile Asn Thr Ser Ile Leu Asp Phe Asn Ala
    530                 535                 540

Gln Met Gln Gly Asp Asp Phe Glu Lys Gln Leu Ser Tyr Gln Leu Trp
545                 550                 555                 560

His Leu Leu Tyr Ser Tyr Glu Glu Asp Asn Ser Lys Thr Gly Met Glu
                565                 570                 575
```

```
Arg Leu Tyr Asn Gln Leu Asn Leu Lys Phe Gly Phe Ser Leu Asp Gln
            580                 585                 590

Ala Lys Ile Phe Gly Lys Ile Ala Leu Gln Glu Asp Tyr Gly Asn Leu
        595                 600                 605

Ser Thr Lys Ala Ile Arg Lys Ile Tyr Pro Tyr Ile Gln Asp Val Glu
    610                 615                 620

Tyr Ser Val Ala Cys Lys Gln Ala Gly Tyr Asn His Ser Lys Ser Ser
625                 630                 635                 640

Leu Thr Lys Glu Gln Leu Thr Asn Arg Val Leu Lys Asp His Leu Asp
                645                 650                 655

Ile Leu Pro Lys Asn Ser Leu Arg Asn Pro Val Val Glu Lys Ile Leu
            660                 665                 670

Asn Gln Met Val Asn Val Val Asn Thr Leu Ile Glu Thr Glu Asn Asp
        675                 680                 685

Lys Leu Ile Lys Glu Gly Lys Asn Ala Asp Phe Arg Phe Asp Glu Ile
    690                 695                 700

Arg Ile Glu Leu Ala Arg Glu Leu Lys Lys Asn Ala Lys Glu Arg Glu
705                 710                 715                 720

Glu Leu Thr Lys Ala Ile Asn Thr Ser Lys Ser Glu His Glu Lys Ile
                725                 730                 735

Ile Lys Ile Leu Gln Thr Glu Asp Gly Ile Lys Asn Pro Thr Arg Asn
            740                 745                 750

Asp Ile Ile Arg Phe Lys Leu Tyr Gln Glu Leu Lys Asn Asn Gly Tyr
        755                 760                 765
```

```
Lys Asn Leu Tyr Thr Asn Glu Tyr Ile Gln Arg Lys Asp Leu Phe Thr
    770                 775                 780

Asn Val Tyr Asp Ile Asp His Ile Ile Pro Gln Ser Arg Leu Phe Asp
785                 790                 795                 800

Asp Ser Phe Ser Asn Lys Val Leu Val Pro Arg Asn Ile Asn Ile Glu
                805                 810                 815

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

Asp Gly Ile Glu Ala Tyr Glu Ala Arg Val Glu Arg Leu Phe Asn Leu
        835                 840                 845

Lys Glu Glu Gly Val Ser Arg Ser Lys Tyr Lys Lys Leu Leu Met Arg
    850                 855                 860

Gly Leu Asp Ile Gly Glu Gly Phe Ile Glu Arg Asp Leu Arg Asp Ser
865                 870                 875                 880

Gln Tyr Ile Ala Lys Lys Ala Lys Ala Met Leu Phe Glu Ile Ala Pro
                885                 890                 895

Ser Val Ile Ser Thr Ser Gly Ser Val Thr Asp Arg Leu Arg Glu Asp
            900                 905                 910

Trp Gly Leu Val Ser Val Met Lys Glu Leu Asn Leu Pro Lys Phe Lys
        915                 920                 925

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

Glu Val Ile Lys Asp Trp Ser Lys Arg Asn Asp His Arg His His Ala
945                 950                 955                 960

Met Asp Ala Leu Thr Val Ala Phe Thr Lys His Ser His Ile His Tyr
                965                 970                 975
```

```
Leu Asn His Leu Asn Ala Arg Lys Asn Glu Lys Ser Glu Phe Phe Ser
            980                 985                 990

Thr Ile Lys Ala Ile Glu Ile Lys  Glu Thr Tyr Val Glu  Arg Asp Asp
        995                 1000                1005

Leu Gly  Asn Arg Lys Arg Leu  Phe Lys Glu Pro Ile  Pro His Phe
    1010                1015                1020

Arg Ser  Ile Ala Lys Glu His  Leu Glu Ser Val Leu  Val Ser His
    1025                1030                1035

Lys Ala  Lys Asn Lys Val Val  Thr Lys Asn Arg Asn  Lys Ile Asp
    1040                1045                1050

Gly Lys  Lys Gln Ala Gln Glu  Val Leu Thr Pro Arg  Gly Gln Leu
    1055                1060                1065

His Lys  Glu Ser Ile Tyr Gly  Lys Ile Leu Gln Tyr  Ala Ser Lys
    1070                1075                1080

Glu Glu  Lys Ile Ser Ala Lys  Phe Asp Ala Ala Thr  Ile Ala Met
    1085                1090                1095

Val Ser  Asn Pro Arg Tyr Arg  Ser Ala Leu Leu Asp  Arg Leu Ser
    1100                1105                1110

Ala Tyr  Gly Asn Asp Pro Lys  Lys Ala Phe Thr Gly  Lys Asn Ser
    1115                1120                1125

Pro Asn  Lys Ser Pro Ile Tyr  Leu Asp Gln Glu Lys  Gln Leu Ala
    1130                1135                1140

Val Pro  Glu Lys Val Lys Leu  Val Trp Leu Glu Glu  Asp Tyr Thr
    1145                1150                1155
```

```
Ile Arg  Lys Glu Ile Gly Pro  Asp Leu Lys Ile Glu  Lys Val Ile
    1160                1165                1170

Asp Gln  Gly Val Lys Arg Ile  Leu Glu Gln Arg Leu  Thr Glu Tyr
    1175                1180                1185

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

Ile Trp  Leu Asn Lys Glu Lys  Gly Ile Ala Ile Lys  Arg Val Thr
    1205                1210                1215

Ile Ser  Gly Val Lys Asn Ala  Glu Ala Leu His Ile  Lys Lys Asp
    1220                1225                1230

His Leu  Gly Gln Val Leu Lys  Asp Lys Asp Gly Lys  Pro Met Pro
    1235                1240                1245

Val Asp  Phe Val Ser Thr Gly  Asn Asn His His Val  Ala Ile Tyr
    1250                1255                1260

Glu Asp  Asp Asn Gly Ala Leu  Gln Glu Arg Ile Val  Pro Phe Tyr
    1265                1270                1275

Glu Ala  Val Ala Arg Val Asn  Asn Gly Phe Pro Ile  Ile Asp Lys
    1280                1285                1290

His Tyr  Asn Gln His Leu Gly  Trp Lys Phe Leu Phe  Ser Met Lys
    1295                1300                1305

Gln Asn  Glu Met Phe Leu Phe  Pro Ser Glu Glu Phe  Asp Pro Lys
    1310                1315                1320

Gln Ile  Asn Leu Leu Asp Arg  Ser Asn Tyr Arg Leu  Ile Ser Lys
    1325                1330                1335

Asn Leu  Phe Arg Val Gln Lys  Phe Gly Glu Leu Ser  Lys Ser Gly
    1340                1345                1350
```

Phe Trp Phe Arg His His Leu Glu Thr Ser Val Asp Val Asn Lys
    1355   1360   1365

Ser Leu Arg Ser Ile Ser Tyr Phe Asp Phe Tyr Ser Lys Asp Phe
    1370   1375   1380

Met Lys Asn Ile Ala Lys Val Arg Ile Asn His Leu Gly Glu Ile
    1385   1390   1395

Ile His Val Gly Glu Tyr
    1400

<210> 17
<211> 18
<212> RNA
<213> Sphingobacterium sp.

<400> 17
guugugaauu gcuuucau   18

<210> 18
<211> 72
<212> RNA
<213> Sphingobacterium sp.

<400> 18
augaaagcaa uucacaauaa ggauuauuuc cguuguguaa acauuuagcg ccucgucuau   60

cuacggggca uu   72

<210> 19
<211> 123
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<220>

<221> modified_base
<222> (1)..(29)
<223> a, c, u, g, unknown or other

<400> 19
nnnnnnnnnn nnnnnnnnnn nnnnnnnnng uugugaauug cuuucauaaa gaugaaagca 60

auucacaaua aggauuauuu ccguugugua aacauuuagc gccucgucua ucuacggggc 120

auu 123

<210> 20
<211> 124
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 20
gagcggacag cagcuuccua uaucucguac guugugaauu gcuuucauaa agaugaaagc 60

aauucacaau aaggauuauu uccguugugu aaacauuuag cgccucgucu aucuacgggg 120

cauu 124

<210> 21
<211> 124
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 21
ccaugauaua gacguugugg cuguuguagu guugugaauu gcuuucauaa agaugaaagc 60

aauucacaau aaggauuauu uccguugugu aaacauuuag cgccucgucu aucuacgggg 120

cauu 124

<210> 22
<211> 7

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<220>
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<222> (1)..(2)
<223> a, c, t, g, unknown or other

<220>
<221> modified_base
<222> (5)..(5)
<223> a, c, t, g, unknown or other

<400> 22
nnrrngg 7

<210> 23
<211> 1453
<212> PRT
<213> Chryseobacterium sp.

<400> 23
Met Met Ile Lys Asn Ile Leu Gly Leu Asp Leu Gly Thr Asn Ser Ile
1 5 10 15

Gly Trp Ala Leu Ile Lys Gln Asp Phe Glu Asn Lys Tyr Gly Glu Ile
20 25 30

Leu Gly Met Gly Ser Arg Ile Ile Pro Met Asp Gln Lys Val Leu Gly
35 40 45

Glu Phe Gly Ser Gly Asn Ser Val Ser Gln Thr Ala Asp Arg Thr Lys
50 55 60

Tyr Arg Gly Val Arg Arg Leu Arg Glu Arg Phe Leu Leu Arg Arg Glu
65 70 75 80

Arg Leu His Arg Val Leu Asn Val Leu Asn Phe Leu Pro Ile His Tyr

```
               85                  90                  95

Ala Ser Gln Ile Asp Phe Glu Lys Arg Phe Gly Lys Phe Arg Glu Glu
            100                 105                 110

Ile Glu Pro Lys Leu Val Tyr Asn Asn Asp Gly Phe Ile Phe Lys Asn
        115                 120                 125

Ser Phe Glu Glu Met Leu Ser Asp Phe Arg Lys His Gln Pro Gln Ile
    130                 135                 140

Leu Glu Asn Asp Lys Lys Ile Pro Tyr Asp Trp Thr Ile Tyr Tyr Leu
145                 150                 155                 160

Arg Lys Lys Ala Leu Thr Gln Lys Ile Glu Lys Glu Glu Leu Ala Trp
                165                 170                 175

Ile Leu Leu Asn Phe Asn Gln Lys Arg Gly Tyr Tyr Gln Leu Arg Gly
            180                 185                 190

Glu Asp Ile Glu Glu Glu Lys Asp Lys Thr Phe Val Arg Leu Lys Val
        195                 200                 205

Glu Lys Ile Val Asp Ser Gly Asp Asn Val Lys Gly Lys Ile Leu Tyr
    210                 215                 220

Asp Val Tyr Phe Asp Asn Gly Trp Lys Tyr Asp Lys Gln Ile Val Lys
225                 230                 235                 240

Thr Glu Asp Trp Ile Glu Arg Val Lys Glu Phe Ile Val Thr Glu Ser
                245                 250                 255

Phe Leu Lys Asn Gly Asp Ile Lys Arg Thr Tyr Lys Ala Val Asp Ser
            260                 265                 270

Glu Lys Asp Trp Ile Ala Ile Lys Thr Lys Thr Glu Gln Glu Ile Glu
        275                 280                 285
```

```
Lys Ser His Lys Thr Val Gly Thr Tyr Ile Tyr Glu Thr Ile Leu His
    290                 295                 300

Asn Pro Lys Gln Lys Ile Lys Gly Lys Leu Val Arg Thr Ile Glu Arg
305                 310                 315                 320

Lys Phe Tyr Lys Asp Glu Leu Arg Gln Ile Leu Glu Lys Gln Lys Glu
                325                 330                 335

Phe His Pro Glu Leu Gln Asn Asp Asp Leu Tyr Ser Asp Cys Val Arg
            340                 345                 350

Glu Leu Tyr Arg Asn Asn Glu Ala His Gln Leu Thr Leu Ser Lys Lys
        355                 360                 365

Asp Phe Val His Leu Phe Ile Glu Asp Ile Ile Phe Tyr Gln Arg Pro
    370                 375                 380

Leu Arg Ser Gln Lys Ser Ser Ile Ser Asn Cys Thr Leu Glu Tyr Arg
385                 390                 395                 400

Arg Tyr Lys Asp Lys His Gly Val Glu His Ile Gln Tyr Leu Lys Ala
                405                 410                 415

Ile Pro Lys Ser Asn Pro Tyr Tyr Gln Glu Phe Arg Ile Trp Gln Trp
            420                 425                 430

Met Tyr Asn Leu Asn Ile Tyr Lys Arg Asp Asp Asp Thr Asn Val Thr
        435                 440                 445

Lys Glu Phe Leu Asn Ser Thr Glu Asp Phe Glu Asn Leu Phe Asp Phe
    450                 455                 460

Leu Asn Asn Arg Lys Glu Val Glu Gln Lys Ala Leu Leu Lys His Phe
465                 470                 475                 480

Lys Leu Asn Glu Lys Thr His Arg Trp Asn Phe Val Glu Asn Lys Lys
```

```
                485                 490                 495

Tyr Pro Cys Asn Glu Thr Lys Thr Met Ile Ser Ser Arg Leu Asp Lys
            500                 505                 510

Val Glu Asn Ile Ser Glu Asn Phe Leu Thr Ser Glu Ile Glu His Lys
        515                 520                 525

Ile Trp His Ile Ile Tyr Ser Val Asn Asp Lys Ile Glu Tyr Glu Lys
    530                 535                 540

Ala Leu Lys Ser Phe Ala Asn Lys Asn Asn Leu Asp Glu Val Ser Phe
545                 550                 555                 560

Phe Glu Ala Phe Lys Lys Phe Pro Pro Phe Lys Asn Glu Tyr Gly Ser
                565                 570                 575

Phe Ser Glu Lys Ala Ile Lys Lys Leu Leu Pro Leu Met Arg Val Gly
            580                 585                 590

Lys Tyr Trp Asp Glu Asp Glu Ile Val Lys Asn Ser Asp Thr Tyr Phe
        595                 600                 605

Lys Asn Ile Glu Asp Leu Leu Gly Asn Ile Ala Arg Lys Glu Glu Asn
    610                 615                 620

Ile Ser Asp Asp Asp Arg Lys Lys Tyr Asn Lys Thr Val Asn Leu Lys
625                 630                 635                 640

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

Gln Lys Leu Arg Leu His Ile Ala Gln Tyr Leu Val Tyr Gly Arg His
            660                 665                 670

Ser Glu Ala Ser Ile Ile Gly Lys Trp Asn Ser Ala Asp Asp Leu Glu
        675                 680                 685
```

```
Glu Phe Leu Lys Glu Phe Lys Gln His Ser Leu Arg Asn Pro Ile Val
    690                 695                 700

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

Lys Tyr Gly Asn Gly Ala Lys Asp Phe Phe Asn Glu Ile His Ile Glu
                725                 730                 735

Leu Gly Arg Glu Met Lys Leu Pro Ala Glu Asp Arg Lys Lys Leu Thr
            740                 745                 750

Ser Gln Ile Ser Glu Asn Glu Asn Thr Asn Leu Arg Ile Lys Ala Leu
        755                 760                 765

Leu Ala Glu Met Met Asn Asp Ser Ser Val Glu Asn Val Arg Pro Phe
    770                 775                 780

Ser Pro Met Gln Gln Glu Ile Leu Lys Ile Tyr Glu Asp Gly Val Leu
785                 790                 795                 800

Asn Ser Gly Ile Glu Ile Glu Asp Glu Tyr Leu Lys Ile Ser Lys Thr
                805                 810                 815

Ala Gln Pro Ser Ser Ser Asp Leu Lys Arg Tyr Lys Leu Trp Leu Glu
            820                 825                 830

Gln Lys Tyr Lys Ser Pro Tyr Thr Gly Gln Ile Ile Pro Leu Asn Lys
        835                 840                 845

Leu Phe Thr Pro Glu Tyr Glu Ile Glu His Ile Ile Pro Lys Ser Arg
    850                 855                 860

Tyr Phe Asp Asp Ser Phe Ser Asn Lys Ile Ile Cys Glu Ser Ala Val
865                 870                 875                 880

Asn Lys Leu Lys Asp Asn Tyr Ile Gly Leu Gly Phe Ile Lys Gln Phe
```

```
               885                 890                 895

Ala Gly Ala Ile Val Glu Leu Gly Phe Gly Lys Asn Val Lys Val Phe
            900                 905                 910

Glu Ile Glu Glu Tyr Glu Asp Phe Val Lys Lys His Tyr Ala Asn Asn
        915                 920                 925

Arg Gly Lys Arg Asn Lys Leu Leu Leu Glu Glu Ile Pro Glu Lys Met
    930                 935                 940

Ile Glu Arg Gln Leu Asn Asp Thr Arg His Ile Ser Lys Tyr Ile Ser
945                 950                 955                 960

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

Val Asn Ser Lys Asn Ile Val Pro Gly Asn Gly Lys Ile Thr Ile Gln
            980                 985                 990

Leu Lys Gln Asp Trp Gly Leu Asn  Asp Val Trp Asn Asp  Leu Ile Leu
        995                 1000                1005

Pro Arg  Phe Glu Arg Met Asn  Gln Leu Thr Asn Ser  Thr Asp Phe
    1010                1015                1020

Thr Ala  Trp Asn Lys Asn His  Gln Lys Tyr Leu Pro  Thr Val Pro
    1025                1030                1035

Ile Glu  Phe Ser Lys Gly Phe  Ser Lys Lys Arg Ile  Asp His Arg
    1040                1045                1050

His His  Ala Leu Asp Ala Leu  Val Ile Ala Cys Thr  Thr Lys Asp
    1055                1060                1065

His Val  Asn Leu Leu Asn Asn  Gln Ser Ala Lys Ser  Asp Thr Lys
    1070                1075                1080
```

```
Arg Tyr  Asp Leu Lys Lys Lys  Leu Met Lys Phe Glu  Lys Val Val
    1085                1090                1095

Tyr Asn  His Thr Gln Thr Gly  Glu Lys Ile Glu Arg  Asp Ile Pro
    1100                1105                1110

Lys Gln  Phe Leu Lys Pro Trp  Glu Thr Phe Thr Ile  Asp Ala Lys
    1115                1120                1125

Asn Arg  Leu Glu Thr Ile Ile  Val Ser Phe Lys Gln  Asn Leu Arg
    1130                1135                1140

Val Ile  Asn Lys Ala Thr Asn  His Tyr Glu Lys Tyr  Val Glu Lys
    1145                1150                1155

Glu Gly  Val Lys Met Lys Glu  Arg Val Glu Gln Thr  Gly Thr Asn
    1160                1165                1170

Trp Ala  Ile Arg Lys Ser Leu  His Glu Glu Thr Val  Ser Gly Lys
    1175                1180                1185

Ile Thr  Leu Ser Trp Val Glu  Thr Ser Lys Gly Glu  Phe Ile Thr
    1190                1195                1200

Ala Thr  Arg Lys Pro Leu Asp  Ser Ser Phe Thr Phe  Glu Lys Ile
    1205                1210                1215

Asn Lys  Ile Thr Asp Thr Gly  Ile Gln Lys Ile Leu  Asn Asn Tyr
    1220                1225                1230

Leu Glu  Ala Lys Asp Asn Asn  Pro Glu Leu Ala Phe  Ser Ala Glu
    1235                1240                1245

Gly Ile  Glu Asp Leu Asn Lys  Asn Ile Glu Lys Tyr  Asn Asp Gly
    1250                1255                1260

Lys Ser  His Gln Pro Ile Ile  Lys Ile Arg Leu Tyr  Glu Lys Gly
```

```
    1265                1270                1275

Lys Gly  Arg Phe Val Leu Gly  Gln Thr Gly Asn Lys  Ile Asn Lys
    1280                1285                1290

Tyr Val  Gln Gly Ser Pro Asn  Leu Phe Phe Ala Ile  Tyr Lys Asp
    1295                1300                1305

Glu Asn  Gly Lys Lys Ile Phe  Glu Ser Ile Arg Leu  Asp Ile Val
    1310                1315                1320

Ile Glu  Arg Leu Lys Gln Gly  Leu Gln Ala Ile Pro  Glu Thr Asn
    1325                1330                1335

Gln Asn  Gly Val Ser Leu Tyr  Gln Ser Leu Ser Pro  Leu Asp Leu
    1340                1345                1350

Val Tyr  Ile Pro Thr Glu Tyr  Glu Leu Glu Ser Pro  His Ile Leu
    1355                1360                1365

Asp Phe  Ser Lys Leu Asn Lys  Thr Gln Ile Thr Arg  Leu Tyr Asn
    1370                1375                1380

Thr Asn  Asp Phe Ser Gly Val  Thr Ala Tyr Phe Ser  Gln Asn Ser
    1385                1390                1395

Phe Ala  Lys His Ile Tyr Pro  Lys Glu Met Asp Leu  Ser Trp Asn
    1400                1405                1410

Glu Lys  Lys Gln Lys Leu Ser  Gly Ser Phe Asp Ser  Lys Thr Ala
    1415                1420                1425

Ser Tyr  Asn Asn Thr Ser Ile  Lys Asp Ile Phe Ile  Lys Val Lys
    1430                1435                1440

Val Asp  Arg Leu Gly Asn Ile  Ser Lys Ala
    1445                1450
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<210> 24
<211> 29
<212> RNA
<213> Chryseobacterium sp.

<400> 24
guugugaauu gcuuucaaaa auuauuauc 29

<210> 25
<211> 83
<212> RNA
<213> Chryseobacterium sp.

<400> 25
uaauaauuuu gaaagcaauu cacaauaagg auuauuccgu ugugaaaaca uucaaggcgg 60

ggcaacucgc cuuuuuucgu uuu 83

<210> 26
<211> 145
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
<221> modified_base
<222> (1)..(29)
<223> a, c, u, g, unknown or other

<400> 26
nnnnnnnnnn nnnnnnnnnn nnnnnnnnng uugugaauug cuuucaaaaa uuauuaucaa 60

aguaauaauu uugaaagcaa uucacaauaa ggauuauucc guugugaaaa cauucaaggc 120

ggggcaacuc gccuuuuuuc guuuu 145

<210> 27
<211> 146
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 27
gagcggacag cagcuuccua uaucucguac guugugaauu gcuuucaaaa auuauuauca 60

aaguaauaau uuugaaagca auucacaaua aggauuauuc cguugugaaa acauucaagg 120

cggggcaacu cgccuuuuuu cguuuu 146

<210> 28
<211> 146
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 28
ccaugauaua gacguugugg cuguuguagu guugugaauu gcuuucaaaa auuauuauca 60

aaguaauaau uuugaaagca auucacaaua aggauuauuc cguugugaaa acauucaagg 120

cggggcaacu cgccuuuuuu cguuuu 146

<210> 29
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<220>
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<222> (1)..(2)
<223> a, c, t, g, unknown or other

<400> 29
nnraar 6

<210> 30
<211> 1093
<212> PRT
<213> Brucella sp.

<400> 30
Met Lys Thr Leu Gly Ile Asp Leu Gly Thr Ala Ser Ile Gly Trp Ala
1   5   10   15

Ile Leu Asp Glu Ala Ser Ile Ile Ala Ser Gly Val Arg Ile Phe Ser
            20   25   30

Gln Ser Glu Met Ala Gly Arg Asp Pro Gln Ser Lys Ala Ser Leu Ala
        35   40   45

Val Ala Arg Arg Asp Ala Arg Gly Ala Arg Arg Arg Arg Asp Arg Tyr
    50   55   60

Leu Lys Arg Arg Arg Arg Leu Leu Asp Leu Leu Thr Glu His Gly Leu
65   70   75   80

Ala Pro Ala Asp Glu Lys Ser Arg Lys Ala Leu Val Arg Glu Tyr Glu
                85   90   95

Asp Gly Lys Asp Gly Asp Leu Ser Asn Ser Val Tyr Ala Leu Arg Ala
            100   105   110

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

Phe Gln Leu Asn Gln Arg Arg Gly Phe Lys Ser Asn Arg Lys Thr Asp
    130   135   140

Ser Asn Asp Pro Glu Gln Gly Lys Ile Ala Thr Ala Ile His Val Leu
145   150   155   160

Asp Ala Lys Met Asp Glu Asp Lys Ala Arg Thr Phe Gly Glu Trp Leu
                165   170   175

```
His Met Arg Arg Leu Lys Gly Leu Ser Val Arg Ala Arg Met Thr Ala
            180                 185                 190

Asp Gly Asp Ser Tyr Asp Phe Tyr Pro Ser Arg Ala Ala Leu Glu Arg
        195                 200                 205

Glu Phe Asp Arg Leu Met Ala Ser Gln Lys Arg Phe His Pro Asp Leu
    210                 215                 220

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

Arg Pro Leu Lys Pro Val Gln Pro Gly Lys Cys Ser Tyr Asn His Arg
                245                 250                 255

Glu Ser Arg Leu Pro Lys Ala His Pro Leu Phe Gln Lys Phe Arg Leu
            260                 265                 270

Leu Lys Glu Val Asn Glu Leu Glu Ile Val Gly Glu Asp Gln Arg Tyr
        275                 280                 285

Val Lys Leu Thr Pro Ala Gln Arg Asp Val Leu Thr Leu Ala Leu Arg
    290                 295                 300

Thr Gly Leu Thr Lys Gln Gly Arg Leu Pro Phe Ser Lys Leu Arg Ser
305                 310                 315                 320

Ile Leu Lys Leu Gly Lys Glu Val Arg Phe Asn Lys Glu Lys Asp Asn
                325                 330                 335

Arg Thr Asp Leu Glu Gly Asp Val Ile His Phe Arg Val Ser Arg Pro
            340                 345                 350

Asp Cys Phe Gly Asn Arg Trp Ala Ala Met Pro Val Glu Glu Gln Ala
        355                 360                 365

Ala Val Thr Glu Lys Leu Arg Thr Glu Pro Asp Tyr Ser Ala Leu Leu
```

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    370                 375                 380

Asp Trp Leu Lys Asn Glu Ala Gly Leu Asp Glu Ala His Ala Arg Ala
385                 390                 395                 400

Val Ala Asp Thr Pro Val Pro Asp Gly Phe Gly Arg Met Gly Pro Ser
                405                 410                 415

Ala Leu Ser Ala Leu Ala Asp Ala Met Glu His Glu Ile Asp Ala Gln
            420                 425                 430

Gly Phe Val Ile Thr Glu Ala Glu Ala Ala Lys Arg Val Tyr Gly Arg
        435                 440                 445

Thr Asn Ser Glu Ala Asp Pro Gly Arg Lys Gly Val Asp Gln Leu Pro
    450                 455                 460

Lys Tyr Gln Glu Val Leu Gln Arg His Ile Pro Pro Gly Thr Gly Glu
465                 470                 475                 480

Pro Asp Asp Pro Tyr Asp Glu Tyr Met Gly Arg Ile Thr Asn Pro Thr
                485                 490                 495

Val His Ile Ala Leu Asn Gln Leu Arg Arg Leu Val Asn Ala Leu Ile
            500                 505                 510

Arg Lys Tyr Gly Lys Pro Asn Lys Ile Ala Ile Glu Val Gly Arg Glu
        515                 520                 525

Leu Lys Leu Asn Glu Lys Gln Arg Asn Glu Val Asn Arg Glu Ile Gly
    530                 535                 540

Gln Asn Thr Arg Ala Ala Met Ala Arg Gly Gln Gln Leu Val Glu Ile
545                 550                 555                 560

Phe Lys Gln Pro Asn Thr Gly Tyr Asn Arg Leu Arg Leu Glu Leu Trp
                565                 570                 575
```

```
Glu Asp Leu Asn Arg Glu Gln Pro Leu Lys Arg Leu Cys Thr Tyr Cys
            580                 585                 590

Gly Lys Ala Ile Ala Ala His Met Leu Phe Asn Gly Glu Thr Asp Ile
        595                 600                 605

Asp His Ile Leu Pro Tyr Ser Lys Thr Leu Asp Asp Ser Lys Ala Asn
    610                 615                 620

Arg Leu Leu Cys Cys Thr Pro Cys Asn Arg Glu Lys Lys Asn Tyr Ala
625                 630                 635                 640

Pro Ala Asn Val Leu Gln Trp Arg Asp His Tyr Gly Glu Ile Leu Ala
                645                 650                 655

Arg Ala Thr Ala Leu Pro Lys Asn Lys Gln Trp Arg Phe Ala Glu Asp
            660                 665                 670

Ala Met Thr Arg Tyr Glu Ala Glu Gly Gly Phe Leu Ala Arg Gln Leu
        675                 680                 685

Thr Asp Met Gln Tyr Ile Ser Arg Leu Ala Leu Thr Tyr Leu Ala His
    690                 695                 700

Leu Tyr Asp Tyr Glu Glu Pro Asp Leu Asp Gly Val Tyr Lys Arg His
705                 710                 715                 720

Asp Arg Val Arg Ala Leu Pro Gly Arg Met Thr Glu Met Leu Arg Arg
                725                 730                 735

Gln Trp Ala Leu Asn Glu Leu Leu His Gly His Asn Leu Ala Gly Gly
            740                 745                 750

Asp Gly Ala Lys Glu Lys Asn Arg Leu Asp His Arg His His Ala Ile
        755                 760                 765

Asp Ala Ile Val Ile Ala Cys Thr Ser Gln Ser Leu Ile Asn Arg Leu
```

```
    770                 775                 780

Ser Thr Ala Ala Gly Glu Ala Glu Glu Arg Gly Ala Ala Arg Val Val
785                 790                 795                 800

Glu Arg Ile Asp Pro Pro Trp Pro Ser Phe Arg Glu Asp Val Arg Glu
                805                 810                 815

Ala Val Asn Ala Ile Val Val Ser His Lys Pro Asp His Gly Thr Ala
            820                 825                 830

Ser Arg Ser Gly Tyr Asp Lys Gly Arg Gly Gln Thr Ala Gly Lys Leu
        835                 840                 845

His Asn Asp Thr Ala Tyr Gly Glu Thr Gly Glu Lys Asp His Asn Gly
    850                 855                 860

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

Ala Asp Ile Met Lys Ile Arg Thr Asn Ala His Gly His Ser Glu Leu
                885                 890                 895

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

Glu Gln Ala Val Thr Ala Phe Val Lys His Asp Ala Lys Phe Lys Gly
        915                 920                 925

Ile Arg His Val Arg Val Thr Glu Val Gln Asn Pro Val Trp Ile Thr
    930                 935                 940

His Gly Gly Gly Lys Tyr Lys Lys Gly Tyr Leu Pro Gly Gly Asn Asp
945                 950                 955                 960

Arg Phe Asp Val Trp Glu Leu Pro Asp Gly Lys Trp Asp Ala Glu Val
                965                 970                 975
```

```
Val Thr Thr Phe Asp Ala His Arg Pro Asp Phe Thr Pro Arg Met Arg
            980                 985                 990


Ile Glu His His Asn Ala Arg Lys  Ile Met Ser Leu Lys  Lys Gly Asp
        995                 1000                1005


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


Ile Val  Arg Lys Phe Asp Gln  Arg Asn Lys Gln Leu  Tyr Leu Asp
    1025                1030                1035


Pro His  Asn Glu Ala Gly Asn  Leu Asp Gln Arg Glu  Lys Glu Lys
    1040                1045                1050


Thr Tyr  Lys Pro Leu Arg Pro  Met Pro Asn Pro Leu  Lys Lys Tyr
    1055                1060                1065


Arg Pro  Arg Gln Val Arg Val  Asp Glu Ile Gly Gln  Val Phe Asp
    1070                1075                1080


Pro Gly  Pro Trp Trp Glu Lys  Arg Ser Asp
    1085                1090


<210> 31
<211> 27
<212> RNA
<213> Brucella sp.

<400> 31
guugcgguug gccugcgauu ucugaac                                          27


<210> 32
<211> 81
<212> RNA
<213> Brucella sp.

<400> 32
guucagaaau cgcaguccag ccguuaacaa gcugagauau gcaccaaaua aggcgcucgc       60
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uucggcgggc gcuuuuucgu u 81

<210> 33
<211> 141
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
<221> modified_base
<222> (1)..(29)
<223> a, c, u, g, unknown or other

<400> 33
nnnnnnnnnn nnnnnnnnnn nnnnnnnnng uugcgguugg ccugcgauuu cugaacaaag 60

guucagaaau cgcaguccag ccguuaacaa gcugagauau gcaccaaaua aggcgcucgc 120

uucggcgggc gcuuuuucgu u 141

<210> 34
<211> 142
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 34
gagcggacag cagcuuccua uaucucguac guugcgguug gccugcgauu ucugaacaaa 60

gguucagaaa ucgcagucca gccguuaaca agcugagaua ugcaccaaau aaggcgcucg 120

cuucggcggg cgcuuuuucg uu 142

<210> 35
<211> 142
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 35
ccaugauaua gacguugugg cuguuguagu guugcgguug gccugcgauu ucugaacaaa 60

gguucagaaa ucgcagucca gccguuaaca agcugagaua ugcaccaaau aaggcgcucg 120

cuucggcggg cgcuuuuucg uu 142

<210> 36
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<220>
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<222> (1)..(2)
<223> a, c, t, g, unknown or other

<220>
<221> modified_base
<222> (4)..(4)
<223> a, c, t, g, unknown or other

<400> 36
nnrnat 6

<210> 37
<211> 6
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<220>

<221> modified_base
<222> (2)..(2)
<223> a, c, u, g, unknown or other

<220>
<221> modified_base
<222> (4)..(5)
<223> a, c, u, g, unknown or other

<400> 37
cnanng 6

<210> 38
<211> 1054
<212> PRT
<213> Staphylococcus sp.

<400> 38
Met Lys Glu Lys Tyr Ile Leu Gly Leu Asp Leu Gly Ile Thr Ser Val
1 5 10 15

Gly Tyr Gly Ile Ile Asn Phe Glu Thr Lys Lys Ile Ile Asp Ala Gly
20 25 30

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

Ser Lys Arg Gly Ser Arg Arg Leu Lys Arg Arg Arg Ile His Arg Leu
50 55 60

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

Gln Ile Pro Thr Ser Asn Asn Pro Tyr Gln Ile Arg Val Lys Gly Leu
85 90 95

Ser Glu Ile Leu Ser Lys Asp Glu Leu Ala Ile Ala Leu Leu His Leu
100 105 110

Ala Lys Arg Arg Gly Ile His Asn Ile Asn Val Ser Ser Glu Asp Glu
115 120 125

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

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

Lys Glu Gly Gln Ile Arg Gly Glu Lys Asn Arg Phe Lys Thr Thr Asp
                165                 170                 175

Ile Leu Lys Glu Ile Asp Gln Leu Leu Lys Val Gln Lys Asp Tyr His
            180                 185                 190

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

Arg Arg Glu Tyr Phe Glu Gly Pro Gly Gln Gly Ser Pro Phe Gly Trp
    210                 215                 220

Asn Gly Asp Leu Lys Lys Trp Tyr Glu Met Leu Met Gly His Cys Thr
225                 230                 235                 240

Tyr Phe Pro Gln Glu Leu Arg Ser Val Lys Tyr Ala Tyr Ser Ala Asp
                245                 250                 255

Leu Phe Asn Ala Leu Asn Asp Leu Asn Asn Leu Ile Ile Gln Arg Asp
            260                 265                 270

Asn Ser Glu Lys Leu Glu Tyr His Glu Lys Tyr His Ile Ile Glu Asn
        275                 280                 285

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

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

Gly Thr Pro Gln Phe Thr Glu Phe Lys Leu Tyr His Asp Leu Lys Ser
```

```
                325                 330                 335

Ile Val Phe Asp Lys Ser Ile Leu Glu Asn Glu Ala Ile Leu Asp Gln
            340                 345                 350

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

Glu Leu Asn Lys Leu Pro Glu Ile Leu Asn Glu Gln Asp Lys Ala Glu
    370                 375                 380

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

Cys Ile His Leu Ile Asn Glu Glu Leu Trp Gln Thr Ser Arg Asn Gln
                405                 410                 415

Met Glu Ile Phe Asn Tyr Leu Asn Ile Lys Pro Asn Lys Val Asp Leu
            420                 425                 430

Ser Glu Gln Asn Lys Ile Pro Lys Asp Met Val Asn Asp Phe Ile Leu
        435                 440                 445

Ser Pro Val Val Lys Arg Thr Phe Ile Gln Ser Ile Asn Val Ile Asn
    450                 455                 460

Lys Val Ile Glu Lys Tyr Gly Ile Pro Glu Asp Ile Ile Ile Glu Leu
465                 470                 475                 480

Ala Arg Glu Asn Asn Ser Asp Asp Arg Lys Lys Phe Ile Asn Asn Leu
                485                 490                 495

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

Gln Thr Gly Asn Gln Asn Ala Lys Arg Ile Val Glu Lys Ile Arg Leu
        515                 520                 525
```

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

Leu Met Asp Leu Leu Asn Asn Pro Gln Asn Tyr Glu Val Asp His Ile
545                 550                 555                 560

Ile Pro Arg Ser Val Ala Phe Asp Asn Ser Ile His Asn Lys Val Leu
                565                 570                 575

Val Lys Gln Ile Glu Asn Ser Lys Lys Gly Asn Arg Thr Pro Tyr Gln
            580                 585                 590

Tyr Leu Asn Ser Ser Asp Ala Lys Leu Ser Tyr Asn Gln Phe Lys Gln
        595                 600                 605

His Ile Leu Asn Leu Ser Lys Ser Lys Asp Arg Ile Ser Lys Lys Lys
    610                 615                 620

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

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

Glu Leu Thr Ser Tyr Leu Lys Ala Tyr Phe Ser Ala Asn Asn Met Asp
            660                 665                 670

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

Val Trp Arg Phe Asp Lys Tyr Arg Asn His Gly Tyr Lys His His Ala
    690                 695                 700

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

Lys Lys Leu Gln Asn Ala Asn Lys Ile Leu Glu Lys Pro Thr Ile Glu
```

```
                725                 730                 735

Asn Asn Thr Lys Lys Val Thr Val Glu Lys Glu Glu Asp Tyr Asn Asn
            740                 745                 750

Val Phe Glu Thr Pro Lys Leu Val Glu Asp Ile Lys Gln Tyr Arg Asp
        755                 760                 765

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

Asn Asp Thr Leu Tyr Ser Thr Arg Met Lys Asp Glu His Asp Tyr Ile
785                 790                 795                 800

Val Gln Thr Ile Thr Asp Ile Tyr Gly Lys Asp Asn Thr Asn Leu Lys
                805                 810                 815

Lys Gln Phe Asn Lys Asn Pro Glu Lys Phe Leu Met Tyr Gln Asn Asp
            820                 825                 830

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

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

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

Leu Leu Gly Asn Lys Val Gly Asn His Leu Asp Val Thr Asn Lys Tyr
                885                 890                 895

Glu Asn Ser Thr Lys Lys Leu Val Lys Leu Ser Ile Lys Asn Tyr Arg
            900                 905                 910

Phe Asp Val Tyr Leu Thr Glu Lys Gly Tyr Lys Phe Val Thr Ile Ala
        915                 920                 925
```

Tyr Leu Asn Val Phe Lys Lys Asp Asn Tyr Tyr Tyr Ile Pro Lys Asp
930 935 940

Lys Tyr Gln Glu Leu Lys Glu Lys Lys Lys Ile Lys Asp Thr Asp Gln
945 950 955 960

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

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

Leu Asp Tyr Tyr Asp Ile Lys Tyr Lys Asp Tyr Cys Glu Ile Asn Asn
995 1000 1005

Ile Lys Gly Glu Pro Arg Ile Lys Lys Thr Ile Gly Lys Lys Thr
1010 1015 1020

Glu Ser Ile Glu Lys Phe Thr Thr Asp Val Leu Gly Asn Leu Tyr
1025 1030 1035

Leu His Ser Thr Glu Lys Ala Pro Gln Leu Ile Phe Lys Arg Gly
1040 1045 1050

Leu

<210> 39
<211> 28
<212> RNA
<213> Staphylococcus sp.

<400> 39
guuuuaguac ucuguaauuu uagguaug 28

<210> 40
<211> 85
<212> RNA
<213> Staphylococcus sp.

<400> 40
ucauaccuaa aauuacagaa ucuacugaaa caagacuaua ugucguguuu aucccacuaa 60

uuuauuagug ggauuuuuuu guuuu 85

<210> 41
<211> 146
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
<221> modified_base
<222> (1)..(29)
<223> a, c, u, g, unknown or other

<400> 41
nnnnnnnnnn nnnnnnnnnn nnnnnnnnng uuuuaguacu cuguaauuuu agguaugaaa 60

gucauaccua aaauuacaga aucuacugaa acaagacuau augucguguu uaucccacua 120

auuuauuagu gggauuuuuu uguuuu 146

<210> 42
<211> 147
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 42
gagcggacag cagcuuccua uaucucguac guuuuaguac ucuguaauuu uagguaugaa 60

agucauaccu aaaauuacag aaucuacuga aacaagacua uaugucgugu uuaucccacu 120

aauuuauuag ugggauuuuu uuguuuu 147

<210> 43

<211> 147
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 43
ccaugauaua gacguugugg cuguuguagu guuuuaguac ucuguaauuu uagguaugaa 60

agucauaccu aaaauuacag aaucuacuga aacaagacua uaugucgugu uuaucccacu 120

aauuuauuag ugggauuuuu uuguuuu 147

<210> 44
<211> 4
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<220>
<221> modified_base
<222> (1)..(2)
<223> a, c, t, g, unknown or other

<400> 44
nngg 4

<210> 45
<211> 6
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<220>
<221> modified_base

<222> (2)..(2)
<223> a, c, u, g, unknown or other

<220>
<221> modified_base
<222> (4)..(5)
<223> a, c, u, g, unknown or other

<400> 45
cnannu 6

<210> 46
<211> 1076
<212> PRT
<213> Bacillus sp.

<400> 46
Met Ser Glu Leu Asp Tyr Arg Ile Gly Leu Asp Ile Gly Thr Asn Ser
1 5 10 15

Ile Gly Trp Gly Val Ile Glu Leu Phe Trp Asn Lys Asp Arg Glu Arg
20 25 30

Tyr Glu Lys Val Arg Ile Val Asp Lys Gly Val Arg Met Phe Asp Lys
35 40 45

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

Ala Arg Ser Ser Arg Arg Arg Leu Asn Arg Lys Ser Gln Arg Lys Lys
65 70 75 80

Glu Ile Arg Asn Leu Leu Val Gln His Gly Val Ile Thr Gln Glu Glu
85 90 95

Leu Asp Leu Leu Tyr Pro Leu Ser Lys Lys Ser Met Asp Ile Trp Asp
100 105 110

Ile Arg Leu Asp Gly Leu Asp Arg Leu Leu Asn His Leu Glu Trp Thr
115 120 125

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Arg Leu Leu Ile His Leu Ala Gln Arg Arg Gly Phe Lys Ser Asn Arg
    130                 135                 140

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

Gln Val Asn Glu Lys Arg Leu Ser Leu Tyr Arg Thr Val Gly Glu Met
                165                 170                 175

Trp Ile Lys Asp Ala Glu Phe Ser Lys Tyr Asp Arg Arg Arg Asn Ser
            180                 185                 190

Pro Asn Glu Tyr Val Phe Ser Val Ser Arg Ala Asp Leu Glu Lys Glu
        195                 200                 205

Ile Val Thr Leu Phe Glu Ala Gln Arg Lys Phe Gln Ser Ser Tyr Ser
    210                 215                 220

Ser Lys Asn Leu Gln Glu Thr Tyr Leu Gln Ile Trp Ala His Gln Leu
225                 230                 235                 240

Pro Phe Ala Ser Gly Asn Ala Ile Leu Asn Lys Val Gly Tyr Cys Ser
                245                 250                 255

Leu Leu Lys Gly Lys Glu Arg Arg Ile Pro Lys Ala Thr Tyr Thr Phe
            260                 265                 270

Gln Tyr Phe Ser Ala Leu Asp Gln Val Asn Arg Thr Arg Leu Gly Pro
        275                 280                 285

Asp Phe Gln Pro Phe Thr Gln Glu Gln Lys Glu Ile Ile Leu Asp Lys
    290                 295                 300

Met Phe Gln Arg Thr Asp Tyr Tyr Lys Lys Lys Thr Ile Pro Glu Val
305                 310                 315                 320

Ser Tyr Tyr Asp Ile Arg Lys Trp Leu Glu Leu Asp Glu Thr Ile Gln
                325                 330                 335
```

```
Phe Lys Gly Leu Asn Tyr Asp Pro Asn Glu Glu Leu Lys Lys Ile Glu
            340                 345                 350

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

Val Ala Asn Tyr Ala Glu Arg Thr Asn Glu Ala Phe Ser Thr Leu Asp
    370                 375                 380

Tyr Asp Ala Ile Ala Tyr Ala Leu Thr Val Tyr Lys Thr Asp Lys Asp
385                 390                 395                 400

Ile Arg Ser Tyr Leu Lys Lys Ser Asn Asn Leu Ser Lys Arg Cys Tyr
                405                 410                 415

Asp Asp Gln Leu Ile Glu Glu Leu Phe Thr Leu Ser Tyr Thr Lys Phe
            420                 425                 430

Gly His Leu Ser Phe Lys Ala Ile Asn Arg Val Leu Pro Ile Met Gln
        435                 440                 445

Glu Gly Arg Thr Tyr Gln Glu Ala Ile Gln Gln Leu Gly Tyr Asp Thr
    450                 455                 460

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

Asp Glu Ile Thr Asn Pro Ile Val Lys Arg Ala Leu Thr Gln Ala Arg
                485                 490                 495

Lys Val Val Asn Ala Ile Ile Arg Arg Tyr Gly Ser Pro Asn Ser Val
            500                 505                 510

His Ile Glu Leu Ala Arg Glu Leu Ser Lys Ser His Asp Glu Arg Lys
        515                 520                 525
```

```
Lys Ile Met Thr Ala His Asp Glu Asn Tyr Lys Lys Asn Lys Gly Ala
    530                 535                 540

Ile Ser Ile Leu Ile Glu Asn Gly Ile Leu Asn Pro Thr Gly Tyr Asp
545                 550                 555                 560

Ile Val Arg Tyr Lys Leu Trp Lys Glu Gln Gly Glu Arg Cys Ala Tyr
                565                 570                 575

Ser Leu Lys Glu Ile Pro Pro Asp Thr Phe Phe Asn Glu Leu Lys Lys
            580                 585                 590

Glu Arg Asn Gly Ser Ser Ile Leu Glu Val Asp His Ile Leu Pro Tyr
        595                 600                 605

Ser Gln Ser Phe Ile Asp Ser Tyr His Asn Lys Val Leu Val Tyr Ser
    610                 615                 620

Asp Glu Asn Arg Asn Lys Gly Asn Arg Ile Pro Tyr Thr Tyr Phe Leu
625                 630                 635                 640

Glu Thr Asn Lys Asp Trp Glu Ala Phe Glu Arg Tyr Val Arg Ser Asn
                645                 650                 655

Lys Leu Phe Ser Lys Lys Lys Arg Glu Tyr Leu Leu Lys Lys Ala Tyr
            660                 665                 670

Leu Pro Arg Glu Ser Glu Leu Ile Lys Glu Arg His Leu Asn Asp Thr
        675                 680                 685

Arg Tyr Ala Ser Thr Phe Leu Lys Asn Phe Ile Glu Gln Asn Leu Gln
    690                 695                 700

Phe Lys Glu Val Glu Val Asn Leu Arg Lys Lys Arg Val Gln Thr Val
705                 710                 715                 720

Asn Gly Val Ile Thr Ala His Leu Arg Lys Arg Trp Gly Leu Glu Lys
                725                 730                 735
```

```
Asn Arg Gln Glu Thr Tyr Leu His His Ala Met Asp Ala Ile Ile Val
            740                 745                 750

Ala Cys Thr Asp His His Met Val Thr Arg Ile Thr Glu Tyr Tyr Gln
        755                 760                 765

Ile Lys Glu Ser Asn Lys Ser Val Lys Lys Pro Tyr Phe Pro Met Pro
    770                 775                 780

Trp Glu Gly Phe Arg Asp Glu Leu Leu Ser His Leu Ala Ser Gln Pro
785                 790                 795                 800

Ile Ala Lys Lys Ile Ser Glu Glu Leu Lys Ala Gly Tyr Gln Ser Ser
                805                 810                 815

Asp Tyr Ile Phe Val Ser Arg Met Pro Lys Arg Ser Val Thr Gly Ala
            820                 825                 830

Ala His Asn Gln Met Ile Arg Arg Lys Gly Gly Ile Asp Lys Lys Gly
        835                 840                 845

Lys Thr Ile Ile Ile Lys Arg Val Arg Leu Lys Asp Ile Lys Phe Asp
    850                 855                 860

Glu Asn Gly Asp Phe Lys Met Val Gly Lys Glu Gln Asp Leu Ala Thr
865                 870                 875                 880

Tyr Glu Ala Ile Lys Gln Arg Tyr Leu Asp His Gly Lys Asn Leu Lys
                885                 890                 895

Lys Ala Phe Glu Thr Pro Leu Tyr Lys Pro Ser Lys Lys Gly Thr Gly
            900                 905                 910

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

```
Arg Glu Val Asn Gly Gly Val Ala Gln Asn Ser Asp Leu Val Arg Val
    930                 935                 940

Asp Leu Phe Glu Lys Asp Asp Lys Tyr Tyr Met Val Pro Ile Tyr Val
945                 950                 955                 960

Pro Asp Thr Val Cys Ser Glu Leu Pro Lys Lys Val Val Lys Ser Gly
                965                 970                 975

Lys Gly Tyr Glu Gln Trp Leu Thr Leu Asp Asn Ser Phe Thr Phe Lys
            980                 985                 990

Phe Ser Leu Tyr Pro Tyr Asp Leu  Val Arg Leu Val Lys  Gly Asp Glu
        995                 1000                1005

Asp Arg  Phe Leu Tyr Phe Gly  Thr Leu Asp Ile Asp  Ser Asp Arg
    1010                1015                1020

Leu Asn  Phe Lys Asp Val Asn  Lys Pro Ser Lys Gln  Asn Glu Tyr
    1025                1030                1035

Arg Tyr  Ser Leu Lys Thr Ile  Glu Asp Leu Glu Lys  Tyr Glu Val
    1040                1045                1050

Gly Val  Leu Gly Asp Leu Arg  Leu Val Arg Lys Glu  Thr Arg Arg
    1055                1060                1065

Asn Phe  His Glu Ile Lys Ile  Asn
    1070                1075
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<210> 47
<211> 20
<212> RNA
<213> Bacillus sp.

<400> 47
gucauaguuc cauuaaagcc 20

<210> 48

<211> 84
<212> RNA
<213> Bacillus sp.

<400> 48
ggcuuugaug uuucuaugau aaggguuucg gcccguggcg ucggggaucg ccugcccauu 60

ccgaugggcu ucucccccauu uauu 84

<210> 49
<211> 137
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
<221> modified_base
<222> (1)..(29)
<223> a, c, u, g, unknown or other

<400> 49
nnnnnnnnnn nnnnnnnnnn nnnnnnnnng ucauaguucc auuaaagcca aagggcuuug 60

auguuucuau gauaaggguu ucggcccgug gcgucgggga ucgccugccc auuccgaugg 120

gcuucucccc auuuauu 137

<210> 50
<211> 138
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 50
gagcggacag cagcuuccua uaucucguac gucauaguuc cauuaaagcc aaagggcuuu 60

gauguuucua ugauaagggu uucggcccgu ggcgucgggg aucgccugcc cauuccgaug 120

ggcuucuccc cauuuauu 138

<210> 51
<211> 138
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 51
ccaugauaua gacguugugg cuguuguagu gucauaguuc cauuaaagcc aaagggcuuu 60

gauguuucua ugauaagggu uucggcccgu ggcgucgggg aucgccugcc cauuccgaug 120

ggcuucuccc cauuuauu 138

<210> 52
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<220>
<221> modified_base
<222> (1)..(4)
<223> a, c, t, g, unknown or other

<400> 52
nnnncc 6

<210> 53
<211> 6
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<220>
<221> modified_base
<222> (2)..(2)
<223> a, c, u, g, unknown or other

<220>
<221> modified_base
<222> (4)..(5)
<223> a, c, u, g, unknown or other

<400> 53
unanng 6

<210> 54
<211> 1108
<212> PRT
<213> Brevibacillus sp.

<400> 54
Met Ala Ile Arg Ser Ile Lys Leu Lys Leu Lys Thr Arg Thr Gly Pro
1 5 10 15

Glu Ala Gln Asn Leu Arg Lys Gly Ile Trp Arg Thr His Arg Leu Leu
20 25 30

Asn Glu Gly Val Ala Tyr Tyr Met Lys Met Leu Leu Leu Phe Arg Gln
35 40 45

Glu Ser Thr Gly Gly Gln Thr Lys Lys Glu Leu Gln Glu Glu Leu Val
50 55 60

Arg His Ile Arg Glu Gln Gln Gln Lys Asn Arg Ala Asp Lys Asn Thr
65 70 75 80

Gln Ala Leu Pro Leu Asp Lys Ala Phe Ala Ala Leu Arg Gln Leu Tyr
85 90 95

Glu Leu Leu Val Pro Ser Ser Ile Gly Gln Ser Gly Asp Ala Gln Ile
100 105 110

Ile Ser Arg Lys Phe Leu Ser Pro Leu Val Asp Pro Asn Ser Glu Gly

```
        115                 120                 125

Gly Lys Gly Thr Ser Lys Ala Gly Ala Lys Pro Thr Trp Gln Lys Lys
    130                 135                 140

Lys Glu Ala Asn Asp Pro Thr Trp Glu Gln Asp Tyr Glu Lys Trp Lys
145                 150                 155                 160

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

Glu Tyr Gly Ile Arg Pro Ile Phe Pro Leu Tyr Thr Asn Thr Val Ala
            180                 185                 190

Asp Ile Ala Trp Leu Pro Leu Gln Ser Asn Gln Phe Val Arg Thr Trp
        195                 200                 205

Asp Arg Asp Met Leu Gln Gln Ala Ile Glu Arg Leu Leu Ser Trp Glu
    210                 215                 220

Ser Trp Asn Lys Arg Val Gln Glu Glu Tyr Ser Lys Leu Gln Glu Lys
225                 230                 235                 240

Met Thr Gln Leu Asn Glu Gln Leu Glu Gly Gly Gln Glu Trp Ile Ser
                245                 250                 255

Leu Leu Glu Gln Tyr Glu Glu Gln Arg Glu Gln Glu Leu Ile Glu Asn
            260                 265                 270

Met Thr Ala Ala Asn Asp Lys Tyr Arg Ile Thr Lys Arg Gln Met Lys
        275                 280                 285

Gly Trp Asn Glu Leu Tyr Glu Gln Trp Ser Thr Val Leu Pro Asn Ala
    290                 295                 300

Ser His Glu Gln Tyr Arg Glu Ala Leu Lys Arg Val Gln Gln Arg Leu
305                 310                 315                 320
```

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Arg Gly Arg Phe Gly Asp Ala His Phe Phe Gln Tyr Leu Met Lys Glu
                325                 330                 335

Glu His His Leu Ile Trp Lys Gly Asn Pro Gln Arg Ile His Tyr Phe
            340                 345                 350

Val Ala Arg Asn Glu Leu Lys Lys Arg Leu Glu Glu Ala Lys Gln Asn
        355                 360                 365

Ala Thr Met Thr Leu Pro Asp Ala Arg Lys His Pro Leu Trp Val Arg
    370                 375                 380

Phe Asp Ala Arg Gly Gly Asn Leu Gln Asp Tyr Tyr Leu Thr Ala Glu
385                 390                 395                 400

Ala Asp Asn Pro Arg Ser Arg Arg Phe Val Thr Phe Ser Gln Leu Ile
                405                 410                 415

Trp Pro Asn Glu Ser Gly Trp Met Glu Lys Gln Asp Val Glu Val Glu
            420                 425                 430

Leu Ala Leu Ser Lys Gln Phe Tyr Gln Gln Val Thr Leu Gln Lys Asn
        435                 440                 445

Asp Lys Gly Lys Gln Glu Ile Glu Phe Lys Asp Lys Gly Ser Gly Ser
    450                 455                 460

Thr Phe Ser Gly His Leu Gly Gly Ala Lys Leu Gln Leu Glu Arg Gly
465                 470                 475                 480

Asp Leu Glu Lys Glu Glu Lys Asp Phe Glu Gly Gly Glu Ile Gly Ser
                485                 490                 495

Val Tyr Leu Asn Ile Val Ile Asp Phe Glu Pro Leu Gln Glu Val Lys
            500                 505                 510

Asn Gly Arg Leu Gln Ser Pro Tyr Gly Gln Val Leu Gln Leu Val Arg
```

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        515                 520                 525

Arg Pro Asn Glu Phe Pro Lys Val Thr Thr Tyr Lys Ser Glu Glu Leu
    530                 535                 540

Val Glu Trp Met Lys Ala Ser Gln Asn His Ser Ser Gly Val Glu Ser
545                 550                 555                 560

Leu Glu Ser Gly Phe Arg Val Met Ser Ile Asp Leu Gly Leu Arg Thr
                565                 570                 575

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

Ala Ala Gly Phe Ser Tyr Trp Ile Glu Gly Thr Pro Leu Val Ala Val
        595                 600                 605

His Lys Arg Ser Tyr Met Leu Lys Leu Pro Gly Glu Gln Val Glu Lys
    610                 615                 620

Gln Val Arg Glu Lys Arg Asp Glu Arg Gln Asp Gln Gln Arg Arg Val
625                 630                 635                 640

Arg Phe Gln Ile Arg Ile Leu Ser Gln Val Ile Arg Met Ala Lys Lys
                645                 650                 655

Gln Asn Arg Glu Arg Ala Asp Glu Leu Asp His Leu Ser Gln Ala Leu
            660                 665                 670

Glu Lys Gln Lys Ser Leu Leu Asp Gln Thr Asp Arg Thr Phe Trp Asn
        675                 680                 685

Gly Ile Val Cys Asp Leu Thr Asp Ala Leu Arg Glu Lys Glu Gly Gly
    690                 695                 700

Trp Glu Gln Ala Val Val Gln Ile His Arg Lys Ala Glu Glu His Val
705                 710                 715                 720
```

```
Gly Lys Val Val Gln Ala Trp Arg Lys Arg Phe Asp Ala Asp Glu Arg
                725                 730                 735

Lys Gly Ile Ala Gly Leu Ser Met Trp Ser Ile Glu Glu Leu Asp Ser
            740                 745                 750

Leu Arg Lys Leu Leu Ile Ser Trp Ser Arg Arg Thr Arg Asn Pro Gln
        755                 760                 765

Glu Ile Asn Arg Phe Glu Gln Gly His Thr Ser His Gln Arg Leu Leu
    770                 775                 780

Thr His Ile Gln Asn Val Lys Glu Asp Arg Leu Lys Gln Leu Ser His
785                 790                 795                 800

Ala Ile Val Met Thr Ala Leu Gly Tyr Val Tyr Asp Glu Lys Lys Leu
                805                 810                 815

Glu Trp Phe Ala Lys Tyr Pro Ala Cys Gln Val Ile Leu Phe Glu Asn
            820                 825                 830

Leu Ser Gln Tyr Arg Ser His Met Asp Arg Ser Thr Lys Glu Asn Ser
        835                 840                 845

Thr Leu Met Lys Trp Ala His Arg Ser Ile Pro Lys Tyr Val His Met
    850                 855                 860

Gln Ala Glu Pro Tyr Gly Ile Gln Ile Gly Asp Val Arg Ala Glu Tyr
865                 870                 875                 880

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

Met Val Lys Gly Gln Glu Leu Gln Gly Lys Arg Phe Glu Asn Leu Gln
            900                 905                 910

Lys Arg Leu Val Ser Glu Gln Phe Leu Thr Glu Glu Gln Val Lys Gln
```

```
        915                 920                 925

Leu Arg Pro Gly Asp Ile Val Pro Asp Asp Ser Gly Glu Trp Phe Met
    930                 935                 940

Thr Leu Ser Asp Gly Ser Glu Gly Lys Glu Val Val Phe Leu Gln Ala
945                 950                 955                 960

Asp Ile Asn Ala Ala Gln Asn Leu Gln Lys Arg Phe Trp Gln Arg Tyr
                965                 970                 975

Asn Glu Leu Phe Lys Val Ser Cys Arg Val Leu Ile Arg Gly Glu Glu
            980                 985                 990

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

Gly Leu  Phe Val Lys Lys Thr  Asp Thr Val Met Lys  Asp Val Tyr
    1010                1015                1020

Val Trp  Asp Ser Gln Ala Lys  Leu Lys Gly Lys Thr  Thr Phe Thr
    1025                1030                1035

Glu Glu  Ser Glu Ser Pro Glu  Gln Leu Glu Asp Phe  Gln Glu Ile
    1040                1045                1050

Ile Glu  Glu Ala Glu Glu Ala  Lys Gly Thr Tyr Arg  Thr Leu Phe
    1055                1060                1065

Arg Asp  Pro Ser Gly Val Phe  Phe Pro Glu Phe Val  Trp Asn Thr
    1070                1075                1080

Gln Lys  Asp Phe Trp Ser Glu  Val Lys Arg Arg Leu  Tyr Gly Lys
    1085                1090                1095

Leu Arg  Glu Arg Phe Leu Met  Lys Thr Arg
    1100                1105
```

<210> 55
<211> 22
<212> RNA
<213> Brevibacillus sp.

<400> 55
uggaaagcuu cgagguuagc ac 22

<210> 56
<211> 105
<212> RNA
<213> Brevibacillus sp.

<400> 56
cgacgguuag aggccguaug ucgauuugcu uuaauuucgu gcgugugcau ugucguccuc 60

cauuacaggg cggcuaccac gaauagucac gaaguuccac ugagu 105

<210> 57
<211> 160
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
<221> modified_base
<222> (132)..(160)
<223> a, c, u, g, unknown or other

<400> 57
cgacgguuag aggccguaug ucgauuugcu uuaauuucgu gcgugugcau ugucguccuc 60

cauuacaggg cggcuaccac gaauagucac gaaguuccac ugaguaaagu ggaaagcuuc 120

gagguuagca cnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 160

<210> 58
<211> 161
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 58
cgacgguuag aggccguaug ucgauuugcu uuaauuucgu gcgugugcau ugucguccuc 60

cauuacaggg cggcuaccac gaauagucac gaaguuccac ugaguaaagu ggaaagcuuc 120

gagguuagca cguacgagau auaggaagcu gcuguccgcu c 161

<210> 59
<211> 161
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 59
cgacgguuag aggccguaug ucgauuugcu uuaauuucgu gcgugugcau ugucguccuc 60

cauuacaggg cggcuaccac gaauagucac gaaguuccac ugaguaaagu ggaaagcuuc 120

gagguuagca cacuacaaca gccacaacgu cuauaucaug g 161

<210> 60
<211> 4
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<220>
<221> modified_base
<222> (4)..(4)
<223> a, c, t, g, unknown or other

<400> 60
dttn 4

<210> 61
<211> 1150
<212> PRT
<213> Enterococcus sp.

<400> 61
Met Tyr Ser Ile Gly Leu Asp Leu Gly Ile Ser Ser Val Gly Trp Ser
1   5   10   15

Val Ile Asp Glu Arg Thr Gly Asn Val Ile Asp Leu Gly Ile Arg Leu
            20   25   30

Phe Ser Ala Lys Asn Ser Glu Lys Asn Leu Glu Arg Arg Thr Asn Arg
        35   40   45

Gly Gly Arg Arg Leu Ile Arg Arg Lys Thr Asn Arg Leu Lys Asp Ala
    50   55   60

Lys Lys Ile Leu Ala Ala Val Gly Phe Tyr Glu Asp Lys Ser Leu Lys
65   70   75   80

Asn Ser Cys Pro Tyr Gln Leu Arg Val Lys Gly Leu Thr Glu Pro Leu
                85   90   95

Ser Lys Gly Glu Ile Tyr Lys Val Thr Leu His Ile Leu Lys Lys Arg
            100   105   110

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

Gln Asp Tyr Lys Glu Gln Val Arg Glu Asn Ala Gln Leu Leu Thr Lys
    130   135   140

Tyr Thr Pro Gly Gln Ile Gln Leu Gln Arg Leu Lys Glu Asn Asn Arg
145   150   155   160

Val Lys Thr Gly Ile Asn Ala Gln Gly Asn Tyr Gln Leu Asn Val Phe
                165   170   175

```
Lys Val Ser Ala Tyr Ala Asn Glu Leu Ala Thr Ile Leu Lys Thr Gln
            180                 185                 190

Gln Ala Phe Tyr Pro Asn Glu Leu Thr Asp Asp Trp Ile Ala Leu Phe
        195                 200                 205

Val Gln Pro Gly Ile Ala Glu Glu Ala Gly Leu Ile Tyr Arg Lys Arg
    210                 215                 220

Pro Tyr Tyr His Gly Pro Gly Asn Glu Ala Asn Asn Ser Pro Tyr Gly
225                 230                 235                 240

Arg Trp Ser Asp Phe Lys Lys Thr Gly Gln Pro Ala Thr Asn Ile Phe
                245                 250                 255

Asp Lys Leu Ile Gly Lys Asp Phe Gln Gly Glu Leu Arg Ala Ser Gly
            260                 265                 270

Leu Ser Leu Ser Ala Gln Gln Tyr Asn Leu Leu Asn Asp Leu Thr Asn
        275                 280                 285

Leu Lys Ile Asp Gly Glu Ile Pro Leu Ser Pro Glu Gln Lys Glu Tyr
    290                 295                 300

Ile Leu Ala Glu Leu Met Thr Lys Glu Phe Thr Arg Phe Gly Val Asn
305                 310                 315                 320

Asp Val Val Lys Leu Leu Gly Val Lys Lys Glu Arg Leu Ser Gly Trp
                325                 330                 335

Arg Leu Asp Lys Lys Gly Lys Pro Glu Ile His Thr Leu Lys Gly Tyr
            340                 345                 350

Arg Asn Trp Arg Lys Ile Phe Ala Glu Ser Gly Ile Asp Leu Ala Thr
        355                 360                 365

Leu Pro Thr Glu Thr Ile Asp Cys Leu Ala Lys Val Leu Thr Leu Asn
```

```
    370                 375                 380

Thr Glu Arg Glu Gly Ile Glu Asn Thr Leu Ala Phe Glu Leu Ser Glu
385                 390                 395                 400

Leu Ala Glu Ser Val Lys Leu Leu Val Leu Asp Arg Tyr Lys Glu Leu
                405                 410                 415

Ser Gln Ser Val Ser Thr Gln Ala Trp His Arg Phe Ser Leu Lys Thr
            420                 425                 430

Leu His Leu Leu Ile Pro Glu Leu Met Asn Ala Thr Ser Glu Gln Asn
        435                 440                 445

Thr Leu Leu Glu Gln Phe Gln Leu Lys Ser Asp Val Arg Lys Arg Tyr
    450                 455                 460

Ser Glu Tyr Lys Lys Leu Pro Thr Lys Asp Val Leu Thr Glu Ile Tyr
465                 470                 475                 480

Asn Pro Thr Val Asn Lys Thr Val Ser Gln Ala Phe Lys Val Ile Asp
                485                 490                 495

Ala Leu Leu Val Lys Tyr Gly Lys Glu Gln Ile Arg Tyr Ile Thr Ile
            500                 505                 510

Glu Met Pro Arg Asp Asp Asn Glu Glu Asp Glu Lys Lys Arg Ile Lys
        515                 520                 525

Glu Leu His Ala Lys Asn Ser Gln Arg Lys Asn Asp Ser Gln Ser Tyr
    530                 535                 540

Phe Met Gln Lys Ser Gly Trp Ser Gln Glu Lys Phe Gln Thr Thr Ile
545                 550                 555                 560

Gln Lys Asn Arg Arg Phe Leu Ala Lys Leu Leu Tyr Tyr Tyr Glu Gln
                565                 570                 575
```

```
Asp Gly Ile Cys Ala Tyr Thr Gly Leu Ser Ile Ser Pro Glu Leu Leu
            580                 585                 590

Val Ser Asp Ser Thr Glu Ile Asp His Ile Ile Pro Ile Ser Ile Ser
        595                 600                 605

Leu Asp Asp Ser Ile Asn Asn Lys Val Leu Val Leu Ser Lys Ala Asn
    610                 615                 620

Gln Val Lys Gly Gln Gln Thr Pro Tyr Asp Ala Trp Met Asp Gly Ser
625                 630                 635                 640

Phe Lys Lys Ile Asn Gly Lys Phe Ser Asn Trp Asp Asp Tyr Gln Lys
                645                 650                 655

Trp Val Glu Ser Cys His Phe Ser His Lys Lys Glu Asn Asn Leu Leu
            660                 665                 670

Glu Thr Arg Asn Ile Phe Asp Ser Glu Gln Val Glu Lys Phe Leu Ala
        675                 680                 685

Arg Asn Leu Asn Asp Thr Arg Tyr Ala Ser Arg Leu Val Leu Asn Thr
    690                 695                 700

Leu Gln Ser Phe Phe Ala Asn Gln Glu Thr Lys Val Arg Val Val Asn
705                 710                 715                 720

Gly Ser Phe Thr His Thr Leu Arg Lys Lys Trp Gly Ala Asp Leu Asp
                725                 730                 735

Lys Thr Arg Glu Thr His His His His Ala Val Asp Ala Thr Leu Cys
            740                 745                 750

Ala Val Thr Pro Phe Val Lys Val Ser Arg Tyr His Tyr Ala Val Lys
        755                 760                 765

Glu Glu Thr Gly Glu Lys Val Met Arg Glu Ile Asp Phe Glu Thr Gly
```

```
    770                 775                 780

Glu Ile Val Asp Glu Met Ser Tyr Arg Glu Phe Lys Lys Ser Lys Lys
785                 790                 795                 800

Tyr Glu Arg Lys Thr Tyr Gln Val Lys Trp Pro Asn Phe Arg Glu Gln
                805                 810                 815

Leu Lys Pro Val Asn Leu His Pro Arg Ile Lys Phe Ser His Gln Val
            820                 825                 830

Asp Arg Lys Ala Asn Arg Lys Leu Ser Asp Ala Thr Ile Tyr Ser Val
        835                 840                 845

Arg Glu Lys Thr Glu Val Lys Thr Leu Lys Ser Gly Lys Gln Lys Ile
    850                 855                 860

Thr Thr Asp Glu Tyr Thr Ile Gly Lys Ile Lys Asp Ile Tyr Thr Val
865                 870                 875                 880

Asp Gly Trp Glu Ala Phe Lys Lys Lys Gln Asp Lys Leu Leu Met Lys
                885                 890                 895

Asp Leu Asp Glu Lys Thr Tyr Glu Arg Leu Leu Ser Ile Ala Glu Thr
            900                 905                 910

Thr Pro Asp Phe Gln Glu Val Glu Glu Lys Asn Gly Lys Val Lys Arg
        915                 920                 925

Val Lys Arg Ser Pro Phe Ala Val Tyr Cys Glu Glu Asn Asp Ile Pro
    930                 935                 940

Ala Ile Arg Lys Tyr Ala Lys Lys Asn Asn Gly Pro Leu Ile Arg Ser
945                 950                 955                 960

Leu Lys Tyr Tyr Asp Gly Lys Leu Asn Lys His Ile Asn Ile Thr Lys
                965                 970                 975
```

```
Asp Ser Gln Gly Arg Pro Val Glu Lys Thr Lys Asn Gly Arg Lys Val
            980                 985                 990


Thr Leu Gln Ser Leu Lys Pro Tyr  Arg Tyr Asp Ile Tyr  Gln Asp Leu
        995                 1000                1005


Glu Thr  Lys Ala Tyr Tyr Thr  Val Gln Leu Tyr Tyr  Ser Asp Leu
    1010                1015                1020


Arg Phe  Val Glu Gly Lys Tyr  Gly Ile Thr Glu Lys  Glu Tyr Met
    1025                1030                1035


Lys Lys  Val Ala Glu Gln Thr  Lys Gly Gln Val Val  Arg Phe Cys
    1040                1045                1050


Phe Ser  Leu Gln Lys Asn Asp  Gly Leu Glu Ile Glu  Trp Lys Asp
    1055                1060                1065


Ser Gln  Cys Tyr Asp Val Arg  Phe Tyr Asn Phe Gln  Ser Ala Asn
    1070                1075                1080


Ser Ile  Asn Phe Lys Gly Leu  Glu Gln Glu Met Met  Pro Ala Glu
    1085                1090                1095


Asn Gln  Phe Lys Gln Lys Pro  Tyr Asn Asn Gly Ala  Ile Asn Leu
    1100                1105                1110


Asn Ile  Ala Lys Tyr Gly Lys  Glu Gly Lys Lys Leu  Arg Lys Phe
    1115                1120                1125


Asn Thr  Asp Ile Leu Gly Lys  Lys His Tyr Leu Tyr  Tyr Glu Lys
    1130                1135                1140


Glu Pro  Lys Asn Ile Ile Lys
    1145                1150


<210> 62
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<211> 19
<212> RNA
<213> Enterococcus sp.

<400> 62
guuuuuguac ucucaauaa 19

<210> 63
<211> 73
<212> RNA
<213> Enterococcus sp.

<400> 63
uuauugagaa ucuacaaaaa uaaggcauuu ugccgaauuu accgcccuac auauguaggg 60

cgguuuuuuu auu 73

<210> 64
<211> 125
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
<221> modified_base
<222> (1)..(29)
<223> a, c, u, g, unknown or other

<400> 64
nnnnnnnnnn nnnnnnnnnn nnnnnnnnng uuuuuguacu cucaauaaaa aguuauugag 60

aaucuacaaa aauaaggcau uuugccgaau uuaccgcccu acauauguag ggcgguuuuu 120

uuauu 125

<210> 65
<211> 126
<212> RNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 65
gagcggacag cagcuuccua uaucucguac guuuuuguac ucucaauaaa aaguuauuga 60

gaaucuacaa aaauaaggca uuuugccgaa uuuaccgccc uacauaugua gggcgguuuu 120

uuuauu 126

<210> 66
<211> 126
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 66
ccaugauaua gacguugugg cuguuguagu guuuuuguac ucucaauaaa aaguuauuga 60

gaaucuacaa aaauaaggca uuuugccgaa uuuaccgccc uacauaugua gggcgguuuu 120

uuuauu 126

<210> 67
<211> 5
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<220>
<221> modified_base
<222> (1)..(4)
<223> a, c, t, g, unknown or other

<400> 67
nnnna 5

<210> 68

<211> 6
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<220>
<221> modified_base
<222> (2)..(2)
<223> a, c, u, g, unknown or other

<220>
<221> modified_base
<222> (4)..(5)
<223> a, c, u, g, unknown or other

<400> 68
unannc 6

<210> 69
<211> 1408
<212> PRT
<213> Sphingobacterium sp.

<400> 69
Met Lys Arg Ile Leu Gly Leu Asp Leu Gly Thr Ser Ser Ile Gly Trp
1 5 10 15

Ala Tyr Val Leu Glu Ala Gln Asp Glu Asn Glu Ile Ser Lys Ile Glu
20 25 30

Lys Leu Gly Val Arg Val Asn Pro Leu Thr Thr Asp Glu Gln Leu Asn
35 40 45

Phe Glu Lys Gly Lys Pro Ile Thr Thr Asn Ala Gly Arg Thr Leu Ala
50 55 60

Arg Ser Ala Arg Arg Asn Leu Gln Arg Phe Lys Leu Arg Arg Asn Asn
65 70 75 80

```
Leu Ile Glu Val Leu Lys Arg Glu Lys Trp Ile Asp Asp Lys Ser Ile
                85                  90                  95

Leu Ala Glu Asn Gly Asn Lys Ser Thr Phe Glu Thr Tyr Ala Leu Arg
            100                 105                 110

Ala Ala Ala Ala Ser Lys Glu Ile Lys Leu Glu Glu Leu Ala Arg Val
        115                 120                 125

Leu Leu Met Ile Asn Lys Lys Arg Gly Tyr Lys Ser Ser Arg Lys Val
    130                 135                 140

Ile Lys Glu Asp Asp Gly Gln Leu Val Asp Gly Met Glu Val Ala Lys
145                 150                 155                 160

Lys Leu Tyr His Glu Asn Leu Thr Pro Gly Glu Phe Val Cys Arg Leu
                165                 170                 175

Leu Lys Glu Gly Lys Lys Lys Leu Pro Asp Phe Tyr Arg Ser Asp Leu
            180                 185                 190

Gln Arg Glu Leu Asp Leu Ile Trp Asp Phe Gln Phe Lys Tyr Tyr Pro
        195                 200                 205

Glu Leu Leu Thr Arg Asp Phe Lys Glu Glu Leu Lys Gly Lys Gly Leu
    210                 215                 220

Arg Ala Thr Ser Ala Ile Phe Trp Ser Lys Tyr Lys Phe Asn Thr Ala
225                 230                 235                 240

Glu Asn Lys Gly Thr Lys Glu Glu Lys Lys Ile Gln Ala Tyr Gln Trp
                245                 250                 255

Arg Lys Asp Gly Leu Thr Lys Gln Leu Ala Lys Glu Glu Val Ala Tyr
            260                 265                 270

Ile Ile Ala Glu Ile Asn Gly Gln Leu Ala Asn Ser Ser Gly Tyr Leu
        275                 280                 285
```

```
Gly Ala Ile Ser Asp Arg Ser Lys Glu Leu Tyr Phe Asn Lys Gln Thr
    290                 295                 300

Val Gly Gln Phe Leu Phe Asn Gln Leu Gln Gln Asn Thr His Ala Arg
305                 310                 315                 320

Leu Lys Asn Gln Val Phe Tyr Arg Gln Asp Tyr Leu Asp Glu Phe Glu
                325                 330                 335

Lys Ile Trp Cys Ile Gln Ser Gln Phe His Gln Ala Leu Thr Glu Gln
            340                 345                 350

Leu Lys Glu Glu Ile Arg Asp Ile Ile Ile Phe Tyr Gln Arg Lys Leu
        355                 360                 365

Lys Ser Gln Lys Gly Leu Ile Ser Phe Cys Glu Phe Glu Gln His Glu
    370                 375                 380

Val Val Val Asn Gly Lys Asn Lys Val Val Gly Leu Arg Val Ala Pro
385                 390                 395                 400

Lys Ser Ser Pro Ile Phe Gln Glu Phe Lys Ile Trp Gln Gln Leu Asn
                405                 410                 415

Asn Val Lys Leu Arg Asn Asn Ile Thr Lys Glu Val Tyr Asn Leu Ala
            420                 425                 430

Glu Glu Gln Lys Lys Leu Leu Phe Glu Thr Leu Asn Leu Lys Gly Lys
        435                 440                 445

Leu Ser Ala Tyr Gln Val Leu Ser Leu Ile Glu Gly Lys Pro Lys Glu
    450                 455                 460

Trp Glu Leu Asn Tyr Thr Glu Leu Glu Gly Asn Ser Thr Asn Ser Ala
465                 470                 475                 480
```

```
Leu Tyr Asn Ala Tyr Leu Asn Ile Leu Asp Ile Glu Gly Tyr Asp Val
                485                 490                 495

Arg Ser Glu Leu Lys Ile Lys Leu Asn Lys Asp Glu Ile Thr Leu Ser
            500                 505                 510

Asp Leu Asp Ile Pro Val Ser Glu Ile Lys Asp Met Ile Arg Arg Ile
        515                 520                 525

Phe Gln His Leu Gly Ile Asn Thr Ser Ile Leu Asp Phe Asp Ala Gln
    530                 535                 540

Met Gln Gly Asp Asp Phe Glu Lys Gln Leu Ser Tyr Gln Leu Trp His
545                 550                 555                 560

Leu Leu Tyr Ser Tyr Glu Glu Asp Asp Ser Lys Thr Gly Met Asp Arg
                565                 570                 575

Leu Tyr Asn Gln Leu Asn Leu Lys Phe Gly Phe Ser Leu Asp Gln Ala
            580                 585                 590

Lys Phe Ile Gly Lys Ile Ala Leu Gln Asp Asp Tyr Gly Asn Leu Ser
        595                 600                 605

Thr Lys Ala Ile Arg Gln Ile Tyr Pro Tyr Ile Gln Asp Ala Glu Tyr
    610                 615                 620

Ser Ala Ala Cys Lys Leu Ala Gly Tyr Asn His Ser Lys Ser Ser Leu
625                 630                 635                 640

Thr Lys Glu Gln Leu Thr Asn Arg Val Leu Lys Asp His Leu Asp Ile
                645                 650                 655

Leu Pro Lys Asn Ser Leu Arg Asn Pro Val Val Glu Lys Ile Leu Asn
            660                 665                 670

Gln Met Val Asn Val Val Asn Thr Leu Ile Asp Thr Glu Asn Asp Lys
        675                 680                 685
```

```
Leu Ile Lys Glu Gly Lys Asn Ala Asp Phe Arg Phe Asp Glu Ile Arg
    690                 695                 700

Ile Glu Leu Ala Arg Glu Leu Lys Lys Asn Ala Lys Glu Arg Glu Glu
705                 710                 715                 720

Leu Thr Lys Ala Ile Asn Thr Ser Lys Glu Gln His Glu Lys Ile Ile
                725                 730                 735

Lys Ile Leu Gln Thr Glu Asp Gly Ile Lys Asn Pro Thr Arg Asn Asp
            740                 745                 750

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

Asn Leu Tyr Thr Asn Glu Tyr Ile Gln Arg Lys Asp Leu Phe Thr Asn
    770                 775                 780

Ile Tyr Asp Ile Asp His Ile Val Pro Gln Ser Arg Leu Phe Asp Asp
785                 790                 795                 800

Ser Phe Ser Asn Lys Val Leu Val Pro Arg Asn Ile Asn Ile Glu Lys
                805                 810                 815

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

Gly Ile Glu Ala Tyr Glu Ala Arg Val Glu Arg Leu Phe Asn Leu Lys
        835                 840                 845

Glu Glu Gly Val Ser Arg Ser Lys Tyr Lys Lys Leu Leu Met Arg Gly
    850                 855                 860

Ser Asp Ile Gly Glu Gly Phe Ile Glu Arg Asp Leu Arg Asp Ser Gln
865                 870                 875                 880
```

```
Tyr Ile Ala Lys Lys Ala Lys Ala Met Leu Phe Glu Ile Thr Pro Ser
                885                 890                 895

Val Ile Ser Thr Ser Gly Ser Val Thr Asp Arg Leu Arg Glu Asp Trp
            900                 905                 910

Gly Leu Val Ser Val Met Lys Glu Leu Asn Leu Pro Lys Phe Lys Ala
        915                 920                 925

Val Gly Leu Thr Glu Tyr Leu Glu Thr Lys Asp Gly Asn Arg Lys Glu
    930                 935                 940

Val Ile Lys Asp Trp Ser Lys Arg Asn Asp His Arg His His Ala Met
945                 950                 955                 960

Asp Ala Leu Thr Val Ala Phe Thr Lys His Ser His Ile Gln Tyr Leu
                965                 970                 975

Asn His Leu Asn Ala Arg Lys Asn Glu Lys Ser Glu Phe Phe Ser Ser
            980                 985                 990

Ile Lys Ala Ile Glu Ile Lys Glu  Thr Tyr Val Glu Arg  Asp Asp Leu
        995                 1000                1005

Gly Asn  Arg Lys Arg Leu Phe  Lys Glu Pro Ile Ala  His Phe Arg
    1010                1015                1020

Thr Ile  Val Lys Glu His Leu  Glu Arg Val Leu Val  Ser His Lys
    1025                1030                1035

Ala Lys  Asn Lys Val Val Thr  Lys Asn Arg Asn Lys  Ile Asp Gly
    1040                1045                1050

Lys Lys  Glu Ala Gln Glu Val  Leu Thr Pro Arg Gly  Gln Leu His
    1055                1060                1065

Lys Glu  Thr Ile Tyr Gly Lys  Ile Leu Gln Tyr Ala  Ser Lys Glu
    1070                1075                1080
```

```
Glu Lys  Ile Ser Ala Lys Phe  Asp Ala Ala Thr Ile  Ala Met Val
    1085                1090                1095

Ser Asn  Pro Arg Tyr Arg Ser  Ala Leu Leu Asp Arg  Leu Ile Glu
    1100                1105                1110

Tyr Gly  Asn Asp Pro Lys Lys  Ala Phe Thr Gly Lys  Asn Ser Pro
    1115                1120                1125

Ser Lys  Ser Pro Ile Tyr Leu  Asp Gln Gln Arg Gln  Leu Ala Val
    1130                1135                1140

Pro Glu  Lys Val Lys Leu Val  Trp Leu Glu Ala Asp  Tyr Thr Ile
    1145                1150                1155

Arg Lys  Glu Ile Gly Pro Asp  Leu Lys Ile Glu Lys  Val Ile Asp
    1160                1165                1170

Gln Gly  Val Lys Arg Ile Leu  Lys Gln Arg Leu Ser  Val Tyr Asp
    1175                1180                1185

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

Trp Leu  Asn Glu Glu Lys Gly  Ile Ala Ile Lys Arg  Val Thr Ile
    1205                1210                1215

Ser Gly  Val Lys Asn Ala Glu  Ala Leu His Thr Lys  Lys Asp His
    1220                1225                1230

Leu Gly  Gln Val Leu Glu Asp  Lys Asp Gly Asn Thr  Met Pro Val
    1235                1240                1245

Asp Phe  Val Ser Thr Gly Asn  Asn His His Val Ala  Ile Tyr Glu
    1250                1255                1260
```

```
Asp Ser  Glu Gly Asn Leu Tyr  Asp Arg Val Val Ser  Phe Tyr Glu
    1265                1270                1275

Ala Val  Glu Arg Ile Asn Gln  Asn Leu Pro Ile Val  Asp Arg His
    1280                1285                1290

Tyr Lys  Gln Glu Glu Gly Trp  Lys Phe Leu Phe Ser  Met Lys Gln
    1295                1300                1305

Asn Glu  Leu Phe Val Phe Pro  Ser Ile Asn Phe Asp  Pro Lys Glu
    1310                1315                1320

Ile Asp  Leu Leu Asp Lys Lys  Asn Tyr Lys Glu Val  Ser Lys His
    1325                1330                1335

Leu Phe  Arg Met Gln Lys Phe  Ser Lys Val Glu Tyr  Gly Asn Ser
    1340                1345                1350

Ala Val  Arg Asp Tyr Val Phe  Arg His His Leu Glu  Thr Ser Ile
    1355                1360                1365

Ile Asp  Thr Lys Glu Leu Arg  Asp Ile Ala Tyr Lys  Val Phe Lys
    1370                1375                1380

Ser Ile  Gly Glu Phe Lys Ser  Phe Val Lys Ile Arg  Thr Asn His
    1385                1390                1395

Leu Gly  Glu Ile Val His Leu  Gly Glu Tyr
    1400                1405


<210> 70
<211> 16
<212> RNA
<213> Sphingobacterium sp.

<400> 70
guugugaauu gcuuuc                                                    16


<210> 71
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<211> 72
<212> RNA
<213> Sphingobacterium sp.

<400> 71
gaaagcaauu cacaauaagg auuauuuccg uuguguaaac auuuagcgcc ucgucuaucu 60

acggggcauu uu 72

<210> 72
<211> 121
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
<221> modified_base
<222> (1)..(29)
<223> a, c, u, g, unknown or other

<400> 72
nnnnnnnnnn nnnnnnnnnn nnnnnnnnng uugugaauug cuuucaaagg aaagcaauuc 60

acaauaagga uuauuuccgu uguguaaaca uuuagcgccu cgucuaucua cggggcauuu 120

u 121

<210> 73
<211> 122
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 73
gagcggacag cagcuuccua uaucucguac guugugaauu gcuuucaaag gaaagcaauu 60

cacaauaagg auuauuuccg uuguguaaac auuuagcgcc ucgucuaucu acggggcauu 120

uu 122

<210> 74
<211> 122
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 74
ccaugauaua gacguugugg cuguuguagu guugugaauu gcuuucaaag gaaagcaauu 60

cacaauaagg auuauuuccg uuguguaaac auuuagcgcc ucgucuaucu acggggcauu 120

uu 122

<210> 75
<211> 1429
<212> PRT
<213> Chryseobacterium sp.

<400> 75
Met Met Ile Lys His Ile Leu Gly Leu Asp Leu Gly Thr Asn Ser Ile
1 5 10 15

Gly Trp Ala Leu Ile Lys Gln Asn Phe Glu Asn Lys Tyr Gly Glu Ile
20 25 30

Leu Gly Met Gly Ser Arg Ile Ile Pro Met Ser Gln Asp Ile Leu Gly
35 40 45

Glu Phe Gly Lys Gly Asn Ser Val Ser Gln Thr Ala Ala Arg Thr Asp
50 55 60

Tyr Arg Gly Ile Arg Arg Leu Arg Glu Arg Phe Leu Leu Arg Arg Glu
65 70 75 80

Arg Leu His Arg Ile Leu Asn Val Leu Asn Phe Leu Pro Glu His Tyr
85 90 95

```
Ala Ser Gln Ile Asp Phe Asp Lys Arg Phe Gly Lys Phe Lys Val Glu
            100                 105                 110

Thr Glu Pro Lys Leu Ala Trp Lys Asn Ser Asp Gly Lys Phe Ser Phe
        115                 120                 125

Leu Phe Gln Thr Ser Phe Asn Glu Met Leu Glu Asp Phe Lys Ala His
    130                 135                 140

Gly Gln Asp Leu Lys Val Pro Tyr Asp Trp Thr Ile Tyr Tyr Leu Arg
145                 150                 155                 160

Lys Lys Ala Leu Ser Gln Lys Ile Glu Lys Glu Glu Leu Ala Trp Ile
                165                 170                 175

Leu Leu Asn Phe Asn Gln Lys Arg Gly Tyr Tyr Gln Leu Arg Gly Glu
            180                 185                 190

Glu Glu Glu Glu Asn Pro Asn Lys Leu Ile Glu Phe Tyr Ser Leu Lys
        195                 200                 205

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

Trp Tyr Ser Leu Val Leu Glu Asn Gly Trp Ile Tyr Arg Arg Ser Ser
225                 230                 235                 240

Lys Thr Ser Leu Leu Asp Trp Lys Asp Lys Ile Arg Asp Phe Ile Val
                245                 250                 255

Thr Thr Asp Leu Asn Asp Asn Gly Ser Val Lys Thr Asp Lys Glu Gly
            260                 265                 270

Asn Glu Lys Arg Ser Phe Arg Ala Pro Gly Glu Asn Asp Trp Thr Leu
        275                 280                 285

Val Lys Thr Lys Thr Glu Gln Glu Ile Asp Arg Ser Arg Lys Thr Val
    290                 295                 300
```

```
Gly Thr Tyr Ile Tyr Glu Thr Leu Leu Gln Asn Pro Lys Gln Lys Ile
305                 310                 315                 320

Lys Gly Lys Leu Val Arg Thr Ile Glu Arg Lys Phe Tyr Lys Glu Glu
                325                 330                 335

Leu Lys Gln Ile Leu Glu Lys Gln Lys Glu Phe His Tyr Glu Leu Gln
            340                 345                 350

Ser Asp Asp Leu Tyr Asp Asp Cys Ile Arg Glu Leu Tyr Arg Asn Asn
        355                 360                 365

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

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

Ser Ile Ser Asn Cys Thr Leu Glu Phe Arg Lys Tyr Lys Asp Glu Asn
                405                 410                 415

Gly Val Glu His Thr Gln Phe Leu Lys Ala Ile Pro Lys Ser Asn Pro
            420                 425                 430

Tyr Tyr Gln Glu Phe Arg Ile Trp Gln Trp Ile Phe Asn Leu Asn Ile
        435                 440                 445

Tyr Lys Lys Asp Asn Asp Asp Asn Val Thr Lys Glu Phe Leu Ser Thr
    450                 455                 460

Thr Glu Asp Phe Glu Asn Leu Phe Glu Phe Leu Asn Asn Arg Lys Glu
465                 470                 475                 480

Ile Asp Gln Lys Ala Leu Leu Lys His Phe Lys Leu Asn Glu Lys Thr
                485                 490                 495
```

```
His Arg Trp Lys Tyr Val Glu Asp Lys Lys Tyr Pro Cys Asn Glu Thr
            500                 505                 510

Lys Thr Met Ile Ser Glu Arg Leu Lys Lys Val Glu Asn Ile Ser Asp
        515                 520                 525

Asp Phe Leu Thr Arg Gly Met Glu Gln Lys Ile Trp His Ile Ile Tyr
    530                 535                 540

Ser Val Asn Asp Lys Thr Glu Tyr Glu Lys Ala Leu Lys Ser Phe Ala
545                 550                 555                 560

Glu Lys Asn Asn Leu Asp Glu Asn Ser Phe Phe Glu Ala Phe Arg Lys
                565                 570                 575

Phe Pro Pro Phe Lys Ser Glu Tyr Gly Ser Phe Ser Glu Lys Ala Ile
            580                 585                 590

Lys Lys Leu Leu Pro Leu Met Arg Leu Gly Lys Tyr Trp Ser Tyr Ala
        595                 600                 605

Asn Ile Asp Leu Tyr Ser Lys Asn Arg Ile Gln Lys Ile Ile Thr Gly
    610                 615                 620

Glu Phe Asp Glu Asn Ile Lys Asp Arg Val Arg Glu Lys Ala Ile His
625                 630                 635                 640

Leu Thr Ala Glu Asn Asp Phe Gln Gly Leu Gln Leu Trp Leu Ala Gln
                645                 650                 655

Tyr Ile Val Tyr Gly Arg His Ser Glu Ala Thr Met Ile Gly Lys Trp
            660                 665                 670

Asn Ser Ala Asp Asp Leu Glu Glu Phe Leu Lys Glu Phe Lys Gln His
        675                 680                 685

Ser Leu Arg Asn Pro Ile Val Glu Gln Val Ile Thr Glu Thr Leu Arg
    690                 695                 700
```

```
Val Val Lys Asp Ile Trp Leu Lys Tyr Gly Asn Gly Ala Lys Asp Phe
705                 710                 715                 720

Phe Asn Glu Val His Ile Glu Leu Gly Arg Glu Met Lys Gln Thr Lys
                725                 730                 735

Asp Glu Arg Ala Asn Ala Thr Lys Thr Ile Thr Glu Asn Glu Asn Thr
            740                 745                 750

Asn Leu Arg Ile Lys Ala Leu Leu Ala Glu Met Met Asn Asp His Ser
        755                 760                 765

Val Glu Asn Val Arg Pro Tyr Ser Pro Met Gln Gln Glu Ile Leu Lys
    770                 775                 780

Ile Tyr Glu Asp Gly Ile Leu Lys Ser Asp Ile Glu Ile Asp Asp Asp
785                 790                 795                 800

Ile Leu Lys Ile Ser Lys Thr Ala Gln Pro Ser Ser Ser Asp Leu Lys
                805                 810                 815

Arg Tyr Lys Leu Trp Leu Glu Gln Lys Tyr Lys Ser Pro Tyr Thr Gly
            820                 825                 830

Gln Ile Ile Pro Leu Asn Lys Leu Phe Thr Pro Glu Tyr Glu Ile Glu
        835                 840                 845

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

Ile Ile Cys Glu Ser Ala Val Asn Lys Leu Lys Asp Asn Tyr Ile Gly
865                 870                 875                 880

Leu Gly Phe Ile Lys Gln Phe Gly Gly Thr Ile Ile Glu Cys Gly Phe
                885                 890                 895
```

```
Gly Lys Arg Val Lys Val Phe Lys Ala Glu Glu Tyr Glu Glu Phe Val
            900                 905                 910

Lys Lys His Tyr Ala Asn Asn Arg Gly Lys Arg Asn Lys Leu Leu Leu
        915                 920                 925

Glu Asp Ile Pro Glu Lys Met Ile Glu Arg Gln Met Asn Asp Thr Arg
    930                 935                 940

His Ile Ser Lys Tyr Ile Ser Gly Ile Leu Ser His Ile Val Arg Val
945                 950                 955                 960

Glu Asp Gly Thr Asp Glu Gly Val Asn Ser Lys Asn Val Ile Pro Gly
                965                 970                 975

Asn Gly Lys Ile Thr Thr Gln Leu Arg Gln Asp Trp Gly Leu Asn Asp
            980                 985                 990

Val Trp Asn Glu Leu Val Leu Pro  Arg Phe Glu Arg Met  Asn Gln Leu
        995                 1000                1005

Thr Asn  Ser Thr Asp Phe Thr  Ser Trp Asn Glu Asn  His Gln Lys
    1010                1015                1020

Tyr Leu  Pro Thr Val Pro Val  Glu Phe Ser Lys Gly  Phe Ser Lys
    1025                1030                1035

Lys Arg  Ile Asp His Arg His  His Ala Leu Asp Ala  Leu Val Ile
    1040                1045                1050

Ala Cys  Ala Thr Lys Asp His  Val Asn Leu Leu Asn  Asn Gln Ser
    1055                1060                1065

Ala Lys  Ser Asp Thr Lys Arg  Tyr Asp Leu Lys Lys  Lys Leu Met
    1070                1075                1080

Lys Phe  Glu Lys Thr Val Tyr  Lys Asp Pro Gln Thr  Glu Lys Arg
    1085                1090                1095
```

```
Ile Glu  Arg Glu Val Pro Lys  Tyr Phe Leu Lys Pro  Trp Glu Thr
    1100                1105                1110

Phe Thr  Val Asp Ala Lys Asn  Lys Leu Glu Thr Ile  Ile Val Ser
    1115                1120                1125

Phe Lys  Gln Asn Leu Arg Val  Ile Asn Lys Ala Thr  Asn Tyr Tyr
    1130                1135                1140

Glu Lys  Tyr Val Asp Lys Asp  Gly Val Lys Thr Lys  Glu Arg Val
    1145                1150                1155

Glu Gln  Thr Gly Thr Asn Trp  Ala Ile Arg Lys Pro  Met His Lys
    1160                1165                1170

Glu Thr  Val Ser Gly Lys Ile  Asp Leu Pro Trp Val  Lys Val Pro
    1175                1180                1185

Lys Gly  Lys Ile Leu Thr Ala  Thr Arg Lys Ser Leu  Asp Thr Ser
    1190                1195                1200

Phe Asp  Leu Lys Ala Ile Ala  Ser Ile Thr Asp Thr  Gly Ile Gln
    1205                1210                1215

Lys Ile  Leu Lys Asn Tyr Leu  Glu Phe Lys Glu Ser  Pro Glu Leu
    1220                1225                1230

Ala Phe  Ser Pro Glu Gly Ile  Glu Asp Met Asn Lys  Asn Ile Lys
    1235                1240                1245

Lys Tyr  Asn Gly Gly Lys Pro  His Gln Pro Ile Ser  Lys Val Arg
    1250                1255                1260

Val Phe  Glu Leu Gly Ser Lys  Phe Gln Val Gly Gln  Thr Gly Asn
    1265                1270                1275
```

```
Lys Lys  Asp Lys Tyr Val Glu  Ala Ala Lys Gly Thr  Asn Leu Phe
    1280                1285                1290

Phe Ala  Ile Tyr Glu Asp Arg  Lys Gly Lys Arg Ser  Tyr Glu Thr
    1295                1300                1305

Ile Pro  Leu Asn Glu Val Ile  Glu Arg Gln Lys Gln  Gly Leu Ser
    1310                1315                1320

Val Val  Asp Leu Lys Asn Ile  Asn Asp Phe Phe Leu  Cys Pro Asn
    1325                1330                1335

Asp Leu  Val Tyr Ile Pro Ser  Gly Asp Glu Leu Glu  Asn Gly Gly
    1340                1345                1350

Ser Ile  Glu Ile Lys Asn Ile  Thr Lys Glu Lys Ser  Glu Arg Phe
    1355                1360                1365

Tyr Lys  Val Val Ser Phe Ser  Gly Ser Gln Ile Phe  Phe Val Arg
    1370                1375                1380

His Asp  Ile Ala Val Ser Ile  Val Asn Lys Gly Glu  Phe Ser Thr
    1385                1390                1395

Leu Asn  Lys Met Glu Arg Ala  Ile Asp Gly Ser Met  Val Lys Glu
    1400                1405                1410

Ser Cys  Ile Lys Leu Lys Ile  Asp Arg Leu Gly Asn  Val Leu Lys
    1415                1420                1425

Ala
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<210> 76
<211> 19
<212> RNA
<213> Chryseobacterium sp.

<400> 76

guugugaauu gcuuucaaa 19

<210> 77
<211> 75
<212> RNA
<213> Chryseobacterium sp.

<400> 77
uuugaaaagc aauucacaau aaggauuauu ccguugugaa aacauucaag gcggggcaac 60

ucgccuuuuu ucguu 75

<210> 78
<211> 127
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
<221> modified_base
<222> (1)..(29)
<223> a, c, u, g, unknown or other

<400> 78
nnnnnnnnnn nnnnnnnnnn nnnnnnnnng uugugaauug cuuucaaaaa aguuugaaaa 60

gcaauucaca auaaggauua uuccguugug aaaacauuca aggcggggca acucgccuuu 120

uuucguu 127

<210> 79
<211> 128
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 79
gagcggacag cagcuuccua uaucucguac guugugaauu gcuuucaaaa aaguuugaaa 60

agcaauucac aauaaggauu auuccguugu gaaaacauuc aaggcggggc aacucgccuu 120

uuuucguu 128

<210> 80
<211> 128
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 80
ccaugauaua gacguugugg cuguuguagu guugugaauu gcuuucaaaa aaguuugaaa 60

agcaauucac aauaaggauu auuccguugu gaaaacauuc aaggcggggc aacucgccuu 120

uuuucguu 128

<210> 81
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<220>
<221> modified_base
<222> (1)..(2)
<223> a, c, t, g, unknown or other

<400> 81
nnraat 6

<210> 82
<211> 1440
<212> PRT
<213> Chryseobacterium sp.

<400> 82

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

Ala Leu Val Lys Gln Asp Phe Lys Asn Lys Gln Gly Glu Ile Leu Gly
            20                  25                  30

Met Gly Thr Arg Ile Ile Pro Met Ser Gln Asp Ile Leu Gly Asp Phe
        35                  40                  45

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

Ser Ala Arg Arg Leu Arg Glu Arg Phe Leu Leu Arg Arg Glu Arg Leu
65                  70                  75                  80

His Arg Val Leu Asn Ile Leu Asn Phe Leu Pro Glu His Tyr Ala Ser
                85                  90                  95

Gln Ile Asp Phe Glu Lys Arg Phe Gly Lys Phe Lys Val Glu Thr Glu
            100                 105                 110

Pro Lys Leu Ala Trp Lys Asn Ile Glu Gly Gln Phe Ser Phe Leu Phe
        115                 120                 125

Gln Asn Ser Phe Asn Glu Met Leu Glu Asp Phe Lys Ala Asn Ala Gln
    130                 135                 140

Asp Leu Arg Ile Pro Tyr Asp Trp Thr Ile Tyr Tyr Leu Arg Lys Lys
145                 150                 155                 160

Ala Leu Ser Gln Lys Ile Glu Lys Glu Glu Leu Val Trp Ile Leu Leu
                165                 170                 175

Asn Phe Asn Gln Lys Arg Gly Tyr Tyr Gln Leu Arg Gly Glu Glu Glu
            180                 185                 190

Glu Glu Asn Pro Asn Lys Leu Val Glu Leu Tyr Ser Leu Lys Val Val
        195                 200                 205
```

```
Asp Val Phe Val Asp Glu Pro Gln Lys Gly Lys Ser Asp Ile Trp Tyr
    210                 215                 220

Ser Leu Val Leu Glu Asn Gly Trp Ile Tyr Arg Arg Ala Ser Lys Ile
225                 230                 235                 240

Ser Leu Phe Asp Trp Lys Asp Lys Ile Arg Asp Phe Ile Val Thr Thr
                245                 250                 255

Asp Leu Asn Asp Asp Gly Ser Val Lys Thr Asp Lys Asp Gly Asn Glu
            260                 265                 270

Lys Arg Ser Phe Arg Ala Pro Gly Glu Asn Asp Trp Thr Leu Val Lys
        275                 280                 285

Lys Lys Thr Glu Gln Glu Ile Glu Gln Ser His Lys Thr Val Gly Met
    290                 295                 300

Tyr Ile Tyr Glu Thr Leu Arg Ala Asn Pro Lys Gln Lys Ile Lys Gly
305                 310                 315                 320

Lys Leu Val Arg Thr Ile Glu Arg Lys Phe Tyr Lys Glu Glu Leu Arg
                325                 330                 335

Gln Ile Leu Glu Lys Gln Lys Glu Phe His Gln Glu Leu Gln Asn Asp
            340                 345                 350

Asp Leu Tyr Asn Asp Cys Ile Arg Glu Leu Tyr Arg Asn Asn Glu Ala
        355                 360                 365

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

Asp Ile Val Phe Tyr Gln Arg Pro Leu Arg Ser Gln Lys Ser Ser Ile
385                 390                 395                 400
```

```
Ser Asn Cys Thr Leu Glu Phe Arg Lys Tyr Lys Asp Glu Asn Gly Ala
                405                 410                 415

Glu His Thr Gln Tyr Leu Lys Ala Ile Pro Lys Ser Asn Pro Tyr Tyr
            420                 425                 430

Gln Glu Phe Arg Leu Trp Gln Trp Ile Phe Asn Leu Asn Leu Tyr Lys
        435                 440                 445

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

Asp Val Glu Asn Leu Phe Glu Phe Leu Asn Asn Arg Lys Glu Ile Asp
465                 470                 475                 480

Gln Lys Ala Leu Leu Lys His Phe Lys Leu Ser Glu Lys Thr His Arg
                485                 490                 495

Trp Asn Phe Val Glu Asp Lys Lys Tyr Pro Cys Asn Glu Thr Lys Thr
            500                 505                 510

Met Ile Ala Thr Arg Leu Glu Lys Val Glu Asn Ile Ser Asp Asp Phe
        515                 520                 525

Leu Thr Arg Glu Ile Glu Gln Lys Ile Trp His Ile Ile Tyr Ser Val
    530                 535                 540

Asn Asp Lys Ile Glu Tyr Glu Lys Ala Leu Lys Ser Phe Ala Leu Lys
545                 550                 555                 560

His Asn Leu Asp Glu Asn Ser Phe Phe Glu Ala Phe Arg Lys Phe Pro
                565                 570                 575

Pro Phe Lys Ser Glu Tyr Gly Ser Phe Ser Glu Lys Ala Ile Lys Lys
            580                 585                 590

Leu Leu Pro Leu Met Arg Leu Gly Lys Tyr Trp Asp Tyr Ala Asn Ile
        595                 600                 605
```

```
Asp Gln Phe Ser Lys Gly Arg Ile Gln Lys Ile Ile Asn Gly Glu Tyr
    610                 615                 620

Asp Glu Asn Ile Lys Asp Arg Val Arg Glu Lys Ala Val His Leu Thr
625                 630                 635                 640

Ser Glu Asn Asp Phe Gln Gly Leu Gln Leu Trp Leu Ala Gln Tyr Ile
                645                 650                 655

Val Tyr Gly Arg His Ser Glu Ala Ser Ile Ala Gly Lys Trp Asn Ser
            660                 665                 670

Ala Asp Asp Leu Glu Glu Phe Leu Lys Asp Phe Lys His His Ser Leu
        675                 680                 685

Arg Asn Pro Ile Val Glu Gln Val Ile Thr Glu Thr Leu Arg Val Val
    690                 695                 700

Lys Asp Ile Trp Leu Lys Tyr Gly Lys Gly Ala Lys Asp Phe Phe Asn
705                 710                 715                 720

Glu Ile His Ile Glu Leu Gly Arg Glu Met Lys Leu Pro Ala Asp Asp
                725                 730                 735

Arg Lys Lys Leu Thr Asn Gln Ile Thr Glu Asn Glu Asn Thr Asn Leu
            740                 745                 750

Arg Ile Lys Ala Leu Leu Ala Glu Met Met Asn Asp His Gly Val Glu
        755                 760                 765

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

Glu Asp Gly Val Leu Asn Ser Asp Ile Glu Ile Glu Asp Glu Tyr Leu
785                 790                 795                 800
```

```
Lys Ile Ser Lys Thr Ala Gln Pro Ser Pro Ser Asp Leu Lys Arg Tyr
                805                 810                 815

Lys Leu Trp Leu Glu Gln Lys Tyr Lys Ser Pro Tyr Thr Gly Gln Ile
            820                 825                 830

Ile Pro Leu Asn Lys Leu Phe Thr Pro Glu Tyr Glu Ile Glu His Ile
        835                 840                 845

Ile Pro Gln Ser Arg Tyr Phe Asp Asp Ser Phe Ser Asn Lys Ile Ile
    850                 855                 860

Cys Glu Ser Ala Val Asn Lys Leu Lys Asp Asn Tyr Ile Gly Leu Gly
865                 870                 875                 880

Phe Ile Lys Gln Phe Gly Gly Thr Ile Ile Glu Leu Gly Phe Gly Lys
                885                 890                 895

Ser Val Lys Val Phe Asp Ile Asp Glu Tyr Glu Asp Phe Val Lys Lys
            900                 905                 910

His Tyr Ala Asn Asn Arg Ser Lys Arg Asn Lys Leu Leu Leu Glu Asp
        915                 920                 925

Ile Pro Glu Lys Met Ile Glu Arg Gln Ile Asn Asp Thr Arg Tyr Ile
    930                 935                 940

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

Gly Ser Asp Glu Gly Ile Asn Ser Lys Asn Ile Val Pro Gly Asn Gly
                965                 970                 975

Lys Ile Thr Thr Gln Leu Lys Lys Asp Trp Gly Leu Asn Asp Val Trp
            980                 985                 990

Asn Asp Leu Ile Leu Pro Arg Phe  Lys Arg Met Asn Gln  Leu Thr Asn
        995                 1000                1005
```

```
Ser Thr  Asp Phe Ile Ala Trp  Asn Glu Asn Phe Gln  Lys Phe Leu
    1010                1015                1020

Pro Thr  Val Pro Ile Glu Tyr  Ser Lys Gly Phe Ser  Lys Lys Arg
    1025                1030                1035

Ile Asp  His Arg His His Ala  Leu Asp Ala Leu Val  Ile Ala Cys
    1040                1045                1050

Ala Thr  Lys Asp His Val Asn  Leu Leu Asn Asn Gln  Ser Ala Lys
    1055                1060                1065

Ser Glu  Thr Lys Arg Tyr Asp  Leu Lys Lys Lys Leu  Met Lys Phe
    1070                1075                1080

Glu Arg  Val Val Tyr Leu His  Thr Gln Thr Gly Glu  Lys Ile Glu
    1085                1090                1095

Arg Glu  Val Pro Lys His Phe  Leu Lys Pro Trp Glu  Asn Phe Thr
    1100                1105                1110

Val Asp  Val Lys His Asn Leu  Asp Thr Val Ile Val  Ser Phe Lys
    1115                1120                1125

Gln Asn  Leu Arg Val Ile Asn  Lys Ala Thr Asn Tyr  Tyr Glu Lys
    1130                1135                1140

Tyr Ala  Glu Asn Gly Gly Ala  Arg Asn Lys Ala Arg  Val Glu Gln
    1145                1150                1155

Lys Gly  Ile Asn Trp Ala Ile  Arg Lys Pro Met His  Lys Asp Thr
    1160                1165                1170

Val Ser  Gly Lys Val Asp Leu  Pro Trp Val Lys Val  Pro Lys Gly
    1175                1180                1185
```

```
Lys Ile  Leu Thr Ala Thr Arg  Lys Ser Leu Asp Thr  Ser Phe Asp
    1190                 1195                 1200

Leu Lys  Ser Ile Gly Ser Ile  Thr Asp Thr Gly Ile  Gln Lys Ile
    1205                 1210                 1215

Leu Lys  Asn Tyr Leu Met Leu  Lys Asp Gly Asn Pro  Glu Leu Ala
    1220                 1225                 1230

Phe Ser  Pro Glu Gly Ile Glu  Asp Leu Asn Lys Ser  Ile Glu Lys
    1235                 1240                 1245

Tyr Asn  Asp Gly Lys Pro His  Gln Pro Ile Asn Lys  Val Arg Val
    1250                 1255                 1260

Phe Glu  Leu Gly Ser Lys Phe  Gln Ile Gly Gln Ala  Gly Asn Lys
    1265                 1270                 1275

Lys Asp  Lys Tyr Val Glu Ala  Ala Lys Gly Thr Asn  Leu Phe Phe
    1280                 1285                 1290

Ala Val  Tyr Glu Asp Lys Asn  Gly Lys Arg Ser Tyr  Glu Thr Ile
    1295                 1300                 1305

Pro Leu  Asn Glu Val Ile Glu  Arg Gln Lys Gln Gly  Leu Pro Val
    1310                 1315                 1320

Val Asp  Leu Arg Ser Thr Asn  Asp Phe Tyr Leu Cys  Pro Asn Asp
    1325                 1330                 1335

Leu Val  Tyr Ile Leu Ser Asp  Asp Glu Arg Gly Asn  Met Thr Asn
    1340                 1345                 1350

Asn Asp  Phe Glu Asn Leu Ser  Asp Glu Gln Val Lys  Arg Ile Tyr
    1355                 1360                 1365

Lys Phe  Val Ser Cys Thr Gly  Gly Glu Gly His Phe  Ile Pro Tyr
    1370                 1375                 1380
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Ala Asn Ala Thr Glu Ile Ile Lys Asn Glu Asn Gly Thr Asn Ser
    1385   1390   1395

Lys Ser Glu Arg Met Gln Asn Phe Tyr Asp Gly Ser Cys Met Leu
    1400   1405   1410

Asp Lys Asn Ser Lys Pro Ile Met Ile Lys Glu Asn Cys Val Lys
    1415   1420   1425

Leu Lys Val Asp Arg Leu Gly Asn Ile Ser Lys Ile
    1430   1435   1440

<210> 83
<211> 20
<212> RNA
<213> Chryseobacterium sp.

<400> 83
guugugaauu gcuuucaaaa   20

<210> 84
<211> 79
<212> RNA
<213> Chryseobacterium sp.

<400> 84
uuuugaaagc aauucacaau aaggauuauu ccguugugaa aacauuuaga gccucgacua   60

ccuucggggc auuuuuauu   79

<210> 85
<211> 132
<212> RNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<220>

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<223> a, c, u, g, unknown or other

<400> 85
nnnnnnnnnn nnnnnnnnnn nnnnnnnnng uugugaauug cuuucaaaaa aaguuuugaa 60

agcaauucac aauaaggauu auuccguugu gaaaacauuu agagccucga cuaccuucgg 120

ggcauuuuua uu 132

<210> 86
<211> 133
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 86
gagcggacag cagcuuccua uaucucguac guugugaauu gcuuucaaaa aaaguuuuga 60

aagcaauuca caauaaggau uauuccguug ugaaaacauu uagagccucg acuaccuucg 120

gggcauuuuu auu 133

<210> 87
<211> 133
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 87
ccaugauaua gacguugugg cuguuguagu guugugaauu gcuuucaaaa aaaguuuuga 60

aagcaauuca caauaaggau uauuccguug ugaaaacauu uagagccucg acuaccuucg 120

gggcauuuuu auu 133

<210> 88
<211> 6

<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<220>
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<222> (1)..(2)
<223> a, c, t, g, unknown or other

<220>
<221> modified_base
<222> (5)..(5)
<223> a, c, t, g, unknown or other

<400> 88
nnrrng 6

<210> 89
<211> 1071
<212> PRT
<213> Bacillus sp.

<400> 89
Met Arg Glu Leu Asp Tyr Arg Ile Gly Leu Asp Ile Gly Thr Asn Ser
1 5 10 15

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

Tyr Glu Lys Thr Arg Ile Val Asp Lys Gly Val Arg Met Phe Asp Lys
35 40 45

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

Ala Arg Ser Ser Arg Arg Arg Leu Asn Arg Lys Ser Gln Arg Lys Lys
65 70 75 80

Asp Ile Arg Asn Leu Leu Val Gln His Glu Ile Ile Ser Gln Lys Glu

```
                85                  90                  95

Leu Thr Ser Leu Tyr Pro Leu Ser Lys Ser Ser Met Asp Ile Trp Asp
            100                 105                 110

Ile Arg Leu Asp Gly Leu Asp Arg Leu Leu Asp Arg Phe Glu Trp Ala
        115                 120                 125

Arg Leu Leu Ile His Leu Ala Gln Arg Arg Gly Phe Lys Ser Asn Arg
    130                 135                 140

Lys Ser Glu Leu Lys Asp Val Glu Thr Gly Lys Val Leu Ser Ser Ile
145                 150                 155                 160

Gln Val Asn Glu Lys Arg Leu Ser Leu Tyr Arg Thr Val Gly Glu Met
                165                 170                 175

Trp Met Lys Asn Ala Asp Phe Ser Lys Tyr Gly Lys Arg Arg Asn Ser
            180                 185                 190

Pro Asn Glu Tyr Val Phe Ser Val Ser Arg Ala Asp Leu Glu Lys Glu
        195                 200                 205

Ile Val Thr Leu Phe Glu Ala Gln Arg Lys Phe His Ser Ser Tyr Ala
    210                 215                 220

Ser Val Asp Leu Gln Lys Thr Tyr Ile Gln Ile Trp Ala His Gln Leu
225                 230                 235                 240

Pro Phe Ala Ser Gly Asn Ala Ile Val Asn Lys Val Gly Tyr Cys Ser
                245                 250                 255

Leu Leu Lys Gly Lys Glu Lys Arg Val Pro Lys Ala Thr Tyr Thr Phe
            260                 265                 270

Gln Tyr Phe Asn Thr Leu Asp Gln Ile Asn Arg Thr Arg Leu Gly Pro
        275                 280                 285
```

```
Asn Phe Gln Pro Phe Thr Lys Glu Gln Arg Asp Ile Ile Leu Asp Lys
    290                 295                 300

Met Phe Gln Arg Thr Asp Tyr Tyr Lys Lys Lys Thr Ile Pro Glu Val
305                 310                 315                 320

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

Phe Lys Gly Leu Thr Tyr Asp Pro Asn Glu Glu Leu Lys Lys Ile Glu
            340                 345                 350

Met Lys Pro Phe Ile Asn Leu Lys Pro Phe Tyr Glu Ile Lys Lys Val
        355                 360                 365

Val Thr Asn Tyr Ala Lys Lys Thr Asn Glu Val Phe Ser Ala Leu Asp
    370                 375                 380

Tyr Asp Thr Val Ala Tyr Ala Leu Thr Val Tyr Lys Thr Asp Lys Asp
385                 390                 395                 400

Ile Arg Ser Tyr Leu Lys Arg Ser Asn Asn Leu Ser Lys Arg Cys Tyr
                405                 410                 415

Asp Asp Gln Leu Ile Glu Glu Leu Leu Thr Leu Ser Tyr Thr Lys Phe
            420                 425                 430

Gly His Leu Ser Phe Lys Ala Ile Asn His Val Leu Pro Ile Met Gln
        435                 440                 445

Glu Gly Arg Thr Tyr Gln Glu Ala Ile His Gln Leu Gly Tyr Asp Thr
    450                 455                 460

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

Asp Glu Ile Thr Asn Pro Ile Val Lys Arg Ala Leu Thr Gln Ala Arg
```

```
                485                 490                 495

Lys Val Val Asn Ala Ile Ile Arg Arg Tyr Gly Ser Pro Asn Ser Val
            500                 505                 510

His Ile Glu Leu Ala Arg Glu Leu Ser Lys Ser His Asp Glu Arg Lys
        515                 520                 525

Lys Ile Met Thr Ala His Asp Glu Asn Tyr Lys Lys Asn Lys Gly Ala
    530                 535                 540

Ile Ser Ile Leu Ile Glu Asn Gly Ile Leu Asn Pro Thr Gly Tyr Asp
545                 550                 555                 560

Ile Val Arg Tyr Lys Leu Trp Lys Glu Gln Gly Glu Arg Cys Ala Tyr
                565                 570                 575

Ser Leu Lys Lys Ile Ser Ala Asn Thr Phe Phe Asn Glu Leu Lys Lys
            580                 585                 590

Glu Arg Ser Gly Pro Pro Val Leu Glu Val Asp His Ile Leu Pro Tyr
        595                 600                 605

Ser Gln Ser Phe Ile Asp Ser Tyr His Asn Lys Val Leu Val Tyr Gly
    610                 615                 620

Asp Glu Asn Gln Lys Lys Gly Asn Arg Ile Pro Tyr Thr Phe Phe Ser
625                 630                 635                 640

Glu Glu Asp Lys Glu Trp Glu Ser Phe Glu Ser Tyr Val Arg Ser Asn
                645                 650                 655

Ser Phe Phe Ser Lys Lys Lys Arg Gly Tyr Leu Leu Lys Lys Ala Tyr
            660                 665                 670

Leu Pro Arg Glu Ser Asn Leu Ile Lys Glu Arg His Leu Asn Asp Thr
        675                 680                 685
```

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Arg Tyr Ala Ser Ser Tyr Leu Lys Asn Phe Ile Glu Lys Asn Leu Lys
    690                 695                 700

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

Asn Gly Val Ile Thr Ala His Leu Arg Lys Arg Trp Gly Leu Glu Lys
                725                 730                 735

Asp Arg Gln Glu Thr Tyr Leu His His Ala Met Asp Ala Ile Ile Val
            740                 745                 750

Ala Cys Thr Asp His His Met Val Thr Lys Val Thr Glu Tyr Tyr Gln
        755                 760                 765

Ile Lys Glu Gly Asn Lys Ser Ile Lys Lys Pro Tyr Phe Pro Leu Pro
    770                 775                 780

Trp Met Gly Phe Arg Glu Glu Ile Leu Ser His Leu Glu Ser Gln Pro
785                 790                 795                 800

Ile Ala Arg Lys Ile Ser Glu Glu Leu Lys Ile Gly Tyr Gln Ser Ser
                805                 810                 815

Asp Tyr Ile Leu Val Ser Arg Met Pro Lys Arg Ser Val Thr Gly Ser
            820                 825                 830

Ala His Asp Gln Thr Val Met Lys Lys Gly Gly Ile Asp Lys Lys Gly
        835                 840                 845

Lys Thr Ile Ile Ile Lys Arg Val His Leu Lys Asp Ile Lys Phe Asp
    850                 855                 860

Glu Asn Gly Asp Phe Lys Met Val Gly Lys Glu Gln Asp Leu Ala Thr
865                 870                 875                 880

Tyr Glu Ala Ile Lys Gln Arg Tyr Leu Glu Tyr Arg Lys Glu Ser Lys
```

```
               885                 890                 895

Lys Ala Phe Glu Thr Pro Leu Tyr Lys Pro Ser Lys Lys Gly Lys Gly
            900                 905                 910

Asn Leu Ile Lys Lys Ile Lys Val Glu Val Gln Thr Lys Ser Phe Val
        915                 920                 925

Arg Glu Ile Asn Gly Gly Val Ala Gln Asn Gly Asp Leu Val Arg Val
    930                 935                 940

Asp Leu Phe Glu Lys Asp Asn Arg Tyr Tyr Met Val Pro Ile Tyr Val
945                 950                 955                 960

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

Lys Gly Tyr Glu Gln Trp Leu Ser Ile Asp Asn Ser Phe Thr Phe Lys
            980                 985                 990

Phe Ser Leu Tyr Pro Tyr Asp Leu  Val Arg Leu Val Lys  Gly Asp Glu
        995                 1000                1005

Asp Arg  Phe Leu Tyr Phe Ser  Thr Leu Asp Ile Asn  Ser Asp Arg
    1010                1015                1020

Leu Asn  Phe Lys Asp Val Asn  Lys Pro Ser Lys Gln  Ala Glu Tyr
    1025                1030                1035

Arg Tyr  Ser Leu Lys Thr Ile  Glu Asn Leu Glu Lys  Tyr Glu Ile
    1040                1045                1050

Gly Val  Leu Gly Asp Leu Arg  Leu Val Arg Gln Glu  Thr Arg Lys
    1055                1060                1065

Ile Phe  Lys
    1070
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<210> 90
<211> 24
<212> RNA
<213> Bacillus sp.

<400> 90
gucauaguuc cauuaaagcc auug 24

<210> 91
<211> 138
<212> RNA
<213> Bacillus sp.

<400> 91
caauggcuuu gauguuucua ugauaagggc uucggcccgu ggcguugggg aucgccugcc 60

cauuuuaaug ggcuucuccc caucuauuua augagaauuu uacaaccuug gcuauucuua 120

aauagcuaag guuuuuuu 138

<210> 92
<211> 195
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
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<222> (1)..(29)
<223> a, c, u, g, unknown or other

<400> 92
nnnnnnnnnn nnnnnnnnnn nnnnnnnnng ucauaguucc auuaaagcca uugaaagcaa 60

uggcuuugau guuucuauga uaagggcuuc ggcccguggc guuggggauc gccugcccau 120

uuuaaugggc uucucccccau cuauuuaaug agaauuuuac aaccuuggcu auucuuaaau 180

agcuaagguu uuuuu 195

<210> 93

<211> 196
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 93
gagcggacag cagcuuccua uaucucguac gucauaguuc cauuaaagcc auugaaagca 60

auggcuuuga uguuucuaug auaagggcuu cggcccgugg cguuggggau cgccugccca 120

uuuuaauggg cuucucccca ucuauuuaau gagaauuuua caaccuuggc uauucuuaaa 180

uagcuaaggu uuuuuu 196

<210> 94
<211> 196
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 94
ccaugauaua gacguugugg cuguuguagu gucauaguuc cauuaaagcc auugaaagca 60

auggcuuuga uguuucuaug auaagggcuu cggcccgugg cguuggggau cgccugccca 120

uuuuaauggg cuucucccca ucuauuuaau gagaauuuua caaccuuggc uauucuuaaa 180

uagcuaaggu uuuuuu 196

<210> 95
<211> 1091
<212> PRT
<213> Rhizobium sp.

<400> 95
Met Asp Ile Glu Thr Leu Phe Ala Phe Asp Ile Gly Thr Asn Ser Ile
1 5 10 15

Gly Phe Cys Val Phe Ala Leu Asp Glu Asn Gly Glu Pro Tyr Arg Ile

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            20                  25                  30

Ile Asp Ile Gly Thr Arg Ile Tyr Ala Asp Gly Arg Asp Pro Gln Ser
        35                  40                  45

Lys Ala Ser Leu Ala Val Ala Arg Arg Glu Ala Arg Ala Met Ser Arg
    50                  55                  60

Arg Arg Asp Arg Tyr Val Asn Arg Arg Lys Ala Val Leu Arg Thr Leu
65                  70                  75                  80

Thr Glu Tyr Gly Leu Met Pro Ala Glu Ala Ser Ala Arg Gln Ala Leu
                85                  90                  95

Ile Ala Glu Thr Ser Asp Arg Asn Gly Ala Ala Gly Glu Ala Ser Ala
            100                 105                 110

Asn Pro Tyr Ala Leu Arg Ala Met Ala Leu Asp Glu Lys Leu Pro Leu
        115                 120                 125

Tyr Trp Ile Gly Arg Val Leu Phe His Leu Asn Gln Arg Arg Gly Phe
    130                 135                 140

Lys Ser Asn Arg Lys Thr Asp Arg Lys Asp Asn Glu Lys Gly Val Ile
145                 150                 155                 160

Ala Leu Gly Ile Gly Glu Leu Arg Ala Ala Met His Lys Thr Lys Ala
                165                 170                 175

Arg Thr Tyr Gly Glu Trp Leu Ala Ala Arg Arg Glu Asp Gly His Val
            180                 185                 190

Thr Arg Leu Arg Ala Gly Ser Asp Ala Phe Glu Gly Asp Gly Tyr Ala
        195                 200                 205

Phe Tyr Pro Glu Arg Ser Leu Leu Glu Ala Glu Phe Arg Glu Ile Trp
    210                 215                 220
```

```
Ala Arg Gln Ser Ser Phe Tyr Pro Asp Val Leu Thr Glu Ala Arg Gly
225                 230                 235                 240

Asp His Leu Phe Gln Val Met Phe Tyr Gln Arg Pro Leu Lys Lys Pro
                245                 250                 255

Arg Val Gly Lys Cys Ala Phe Asn Pro Leu Glu Glu Arg Leu Ala Lys
            260                 265                 270

Ala His Pro Leu Phe Gln Glu Phe Arg Leu Tyr Lys Glu Val Asn Glu
        275                 280                 285

Leu Glu Leu Val Leu Pro Asp His Ser His Lys Lys Leu Asp Ile Glu
    290                 295                 300

Gln Arg Asn Ala Leu Val Ile Leu Leu Arg Ala Asn Arg Glu Val Thr
305                 310                 315                 320

Phe Lys Lys Leu Arg Thr Ala Leu Lys Leu Ala Pro Asp Ile Val Phe
                325                 330                 335

Asn Lys Glu Ser Glu Ser Arg Glu Lys Leu Arg Gly Asp Glu Val His
            340                 345                 350

Ser Val Leu Ala Asp Lys Lys Arg Phe Gly Pro Gln Trp Gly Ala Leu
        355                 360                 365

Ser Arg Glu Arg Gln Trp Gln Ile Ile Gln Thr Leu Lys Asp Glu Glu
    370                 375                 380

Asn Pro Glu Lys Leu Phe Gly Trp Leu Lys Glu Glu Phe Gly Phe Glu
385                 390                 395                 400

Gly Glu Lys Ala Asp Ala Ile Ala Asn Ala Pro Leu Pro Glu Gly Tyr
                405                 410                 415

Gly Arg Leu Gly Glu Thr Ala Leu Ser Ser Met Leu Asp Glu Met Lys
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```
            420                 425                 430

Ala Ala Val Ile Pro Glu Ala Glu Ala Ala Lys Asn Cys Gly Tyr Asp
        435                 440                 445

His Ser Lys Leu Gly Glu Asp Arg Glu Glu Gly Glu Ala Phe Leu Pro
    450                 455                 460

Pro Tyr Gln Glu Ile Leu Ser Arg Gln Ile Pro Pro Gly Thr Asn Asp
465                 470                 475                 480

Pro Ala Asp Ile Tyr Asp Ile Arg Met Gly Arg Phe Thr Asn Pro Thr
                485                 490                 495

Val His Ile Gly Leu Asn Gln Leu Arg Arg Val Val Asn Ala Leu Ile
            500                 505                 510

Ala Arg His Gly Lys Pro Gln Phe Val Ser Leu Glu Leu Ala Arg Asp
        515                 520                 525

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

Lys Asn Thr Arg Glu Ala Ala Ala Arg Ser Lys Lys Leu Gly Glu Met
545                 550                 555                 560

Gly Gln Leu Asp Thr Gly Tyr Asn Arg Leu Leu Leu Lys Leu Trp Glu
                565                 570                 575

Glu Leu Asn Pro Ser Lys Pro Glu Asp Arg Val Cys Ile Tyr Ser Gly
            580                 585                 590

Lys Pro Ile Gly Ile Asp Met Leu Phe Ser Ala Glu Val Asp Val Asp
        595                 600                 605

His Ile Leu Pro Trp Ser Lys Thr Leu Asp Asp Ser Gln Ala Asn Lys
    610                 615                 620
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Leu Leu Cys Leu Lys Ser Ala Asn Arg Gln Lys Arg Asn Arg Ala Pro
625                 630                 635                 640

Ala Asp Val Pro Glu Trp Arg Asp Arg Tyr Glu Glu Ile Leu Ala Arg
                645                 650                 655

Ala Ala Arg Leu Ala Pro Asn Lys Arg Arg Arg Phe Ala Pro Asn Ala
            660                 665                 670

Met Ala Glu Phe Glu Ala Glu Gly Gly Phe Leu Ala Arg Gln Leu Thr
        675                 680                 685

Asp Thr Gln Tyr Leu Ser Arg Met Ala Arg Glu Tyr Leu Ser Cys Leu
    690                 695                 700

Phe Pro Ser Ala Glu Ile Asp Arg Arg Gly Glu Arg Lys Lys Lys Ile
705                 710                 715                 720

Arg Val Ile Val Ser Pro Gly Arg Leu Thr Glu Met Leu Arg Arg Asn
                725                 730                 735

Trp Gly Leu Asn Asn Ile Leu Pro Asp His Asn Leu Gly Glu Met Thr
            740                 745                 750

Gln Ala Lys Asn Arg Lys Asp His Arg His His Ala Ile Asp Ala Ala
        755                 760                 765

Val Val Gly Val Thr Thr Arg Ser Leu Leu Gln Arg Ile Ala Thr Ala
    770                 775                 780

Ala Gly Arg Leu Asp Glu Ala Asp Phe Glu Asn Leu Val Arg Lys Met
785                 790                 795                 800

Val Ser Glu Asn Pro Pro Trp Pro Thr Phe Arg Glu Glu Leu Gln Ala
                805                 810                 815

Ala Val Asn Gly Ile Val Val Ser His Lys Pro Asp His Gly Thr Val
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            820                 825                 830

Ser Arg Lys Gly Tyr Ala Glu Gly Lys Gly Arg Thr Ala Gly Arg Leu
        835                 840                 845

His Asn Asp Thr Ala Tyr Gly Phe Gly Thr Asp Ala Ser Gly Asn Pro
    850                 855                 860

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

Pro Met Ile Arg Asp Pro Glu Leu Gln Ala Glu Leu Tyr Ala Ala Ile
                885                 890                 895

Asp Gly Leu Asp Asp Arg Arg Ala Leu Gln Asp Ala Leu Leu Ser Phe
            900                 905                 910

Arg Arg Thr His Pro Lys Phe Lys Gly Ile Arg Arg Val Arg Met Ala
        915                 920                 925

Glu Thr Leu Ser Phe Ile Pro Ile Arg Asp Ser Gln Gly Asn Val Tyr
    930                 935                 940

Lys Gly Tyr Lys Gly Asp Ala Asn Tyr Arg Tyr Asp Val Trp Glu Thr
945                 950                 955                 960

Leu Asp Gly Lys Trp His Ala Asp Val Val Thr Met Phe Asn Ala His
                965                 970                 975

Gln Pro Asp Trp Arg Ser Pro Val His Gln Glu His Pro Thr Ala Arg
            980                 985                 990

Arg Val Leu Arg Leu Gln Gln Asn  Asp Met Val Ala Tyr  Glu His Pro
        995                 1000                1005

Asn Asp  Gly Tyr Thr Ile Ala  Arg Val Val Lys Phe  Asn Thr Ala
    1010                1015                1020
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Gly Ile Val Tyr Phe Ala Ser His Arg Glu Ser Gly Ser Leu Lys
1025 1030 1035

Ala Arg Asp Ala Asp Lys Gln Asp Pro Phe Lys Tyr Phe Ser Lys
1040 1045 1050

Ser Ala Ala Gly Leu Lys Asp Ile Gln Cys Arg Gln Ile Arg Ile
1055 1060 1065

Asp Ala Ala Gly Arg Val Phe Asp Pro Gly Pro Gln Asp Arg Ala
1070 1075 1080

Ser Lys Ser Thr Arg Lys Thr Asn
1085 1090

<210> 96
<211> 29
<212> RNA
<213> Rhizobium sp.

<400> 96
guugcggcug gaccgcguuu ucugaucug 29

<210> 97
<211> 78
<212> RNA
<213> Rhizobium sp.

<400> 97
cagaucagaa aacgcggucu ggccguuaac aagcuagaag caccaaauaa ggccguuccu 60

ucgggagcgg cuuuuucu 78

<210> 98
<211> 140
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
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<222> (1)..(29)
<223> a, c, u, g, unknown or other

<400> 98
nnnnnnnnnn nnnnnnnnnn nnnnnnnnng uugcggcugg accgcguuuu cugaucugaa 60

agcagaucag aaaacgcggu cuggccguua acaagcuaga agcaccaaau aaggccguuc 120

cuucgggagc ggcuuuuucu 140

<210> 99
<211> 141
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 99
gagcggacag cagcuuccua uaucucguac guugcggcug gaccgcguuu ucugaucuga 60

aagcagauca gaaaacgcgg ucuggccguu aacaagcuag aagcaccaaa uaaggccguu 120

ccuucgggag cggcuuuuuc u 141

<210> 100
<211> 141
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 100
ccaugauaua gacguugugg cuguuguagu guugcggcug gaccgcguuu ucugaucuga 60

aagcagauca gaaaacgcgg ucuggccguu aacaagcuag aagcaccaaa uaaggccguu 120

ccuucgggag cggcuuuuuc u 141

<210> 101
<211> 3
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<220>
<221> modified_base
<222> (1)..(1)
<223> a, c, t, g, unknown or other

<400> 101
ngg 3

<210> 102
<211> 6
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<220>
<221> modified_base
<222> (2)..(2)
<223> a, c, u, g, unknown or other

<220>
<221> modified_base
<222> (4)..(5)
<223> a, c, u, g, unknown or other

<400> 102
cnannu 6

<210> 103
<211> 1401
<212> PRT
<213> Myroides sp.

<400> 103
Met Lys Arg Ile Leu Gly Ile Asp Leu Gly Thr Thr Ser Ile Gly Trp
1   5   10   15

Ala Tyr Val His Glu Ala Glu Asn Glu Asn Glu Ile Ser Ser Ile Glu
            20   25   30

Lys Leu Gly Val Arg Val Asn Pro Leu Thr Val Asp Glu Gln Ile Asn
        35   40   45

Phe Glu Lys Gly Lys Pro Ile Thr Thr Asn Ala Thr Arg Thr Leu Phe
    50   55   60

Arg Ser Ala Arg Arg Asn Leu Gln Arg Phe Lys Leu Arg Arg Lys His
65   70   75   80

Leu Ile Glu Ile Leu Lys His Asn Asn Trp Ile Ser Lys Gln Thr Leu
                85   90   95

Leu Thr Glu Asn Gly Asn His Thr Thr Phe Glu Thr Ile Ser Leu Arg
            100   105   110

Asp Lys Ala Ala Thr Gln Lys Val Thr Leu Glu Glu Leu Ala Arg Val
        115   120   125

Leu Leu Met Ile Asn Lys Lys Arg Gly Tyr Lys Ser Ser Arg Lys Val
    130   135   140

Asn Asn Thr Glu Glu Gly Gln Leu Ile Asp Gly Met Glu Val Ala Lys
145   150   155   160

Lys Leu Tyr His Glu Gln Leu Thr Pro Gly Gln Leu Ser Leu Gln Leu
                165   170   175

Ile Lys Gln Gly Val Lys Arg Leu Pro Asp Tyr Tyr Arg Ser Asp Leu
            180   185   190

```
Asn His Glu Leu Asp Leu Ile Trp Ala Phe Gln Gln Lys Phe Tyr Pro
        195                 200                 205

His Ile Leu Thr Ser Glu Phe Lys Glu Leu Leu Lys Gly Lys Gly Leu
    210                 215                 220

Arg Ala Thr Ser Asn Gln Phe Trp Thr Asn Tyr Asn Phe Asn Thr Ala
225                 230                 235                 240

Asp Asn Lys Gly Thr Arg Glu Glu Lys Lys Leu Gln Asn Tyr Gln Trp
                245                 250                 255

Arg Ser Asp Ala Leu Ile Lys Gln Leu Asp Lys Glu Ile Val Ala Tyr
            260                 265                 270

Val Ile Ser Glu Ile Asn Gly Gln Ile Asn Asn Ser Ser Gly Tyr Leu
        275                 280                 285

Gly Ala Ile Ser Asp Arg Ser Lys Glu Leu Tyr Phe Asn Gln Leu Thr
    290                 295                 300

Val Gly Gln Tyr Leu His Arg Gln Leu Ile Ala Asn Pro His Thr Arg
305                 310                 315                 320

Leu Lys Ser Gln Val Phe Tyr Arg Gln Asp Tyr Leu Asp Glu Phe Glu
                325                 330                 335

Lys Ile Trp Glu Thr Gln Ser Lys Phe Tyr Pro Lys Glu Leu Thr Thr
            340                 345                 350

Val Leu Lys Asn Glu Ile Arg Asp Thr Val Ile Phe Tyr Gln Arg Lys
        355                 360                 365

Leu Lys Ser Gln Lys Gly Leu Ile Ser Phe Cys Glu Phe Glu Gln Glu
    370                 375                 380

Gln Lys Ile Ile Asn Gly Lys Thr Lys Thr Ile Gly His Arg Val Ile
385                 390                 395                 400
```

```
Pro Lys Ser Ser Pro Leu Phe Gln Glu Phe Lys Ile Trp Gln Gln Leu
                405                 410                 415

His Asn Val Val Leu Arg Asn Lys Lys Thr Asn Val Ile Thr Pro Leu
            420                 425                 430

Ala Glu Glu Gln Lys Ser His Leu Phe Glu Glu Leu Asn Leu Lys Gly
        435                 440                 445

Lys Leu Ser Ser Thr Gln Ile Leu Lys Leu Ile Glu Asp Lys Pro Lys
    450                 455                 460

Asp Trp Glu Leu Asn Tyr Ser Glu Leu Glu Gly Asn Asn Thr Asn Lys
465                 470                 475                 480

Ala Leu Tyr Asn Ala Tyr Leu Asp Ile Leu Asp Leu Glu Gly Tyr Asp
                485                 490                 495

Ile Arg Asp Glu Leu Lys Ile Lys Leu Asn Lys Asp Asp Ile Glu Leu
            500                 505                 510

Ser Asp Leu Asp Val Asn Ala Ser Glu Ile Lys Glu Met Ile Phe Ser
        515                 520                 525

Ile Phe Lys His Leu Gly Ile Asn Thr Glu Ile Leu Glu Phe Asp Ala
    530                 535                 540

Thr Leu Lys Asp Lys Ala Phe Glu Lys Gln Ala Ser Tyr Gln Leu Trp
545                 550                 555                 560

His Leu Leu Tyr Ser Tyr Glu Glu Asp Asn Ser Pro Thr Gly Leu Asp
                565                 570                 575

Arg Leu His Asn Leu Leu Gln Lys Lys Phe Asn Phe Thr Leu Asp Gln
            580                 585                 590
```

```
Ala Lys Leu Val Gly Asn Val Leu Phe Gln Asp Asp Tyr Gly Asn Leu
        595                 600                 605

Ser Ser Lys Ala Ile Lys Asn Ile Phe Pro Tyr Ile Thr Asp Asn Asn
    610                 615                 620

Tyr Ser Thr Ala Cys Glu Leu Ala Gly Tyr Lys His Ser Lys His Ser
625                 630                 635                 640

Leu Thr Lys Glu Glu Asn Glu Lys Arg Glu Leu Lys Ser Arg Leu Thr
                645                 650                 655

Ile Leu Thr Lys Asn Ser Leu Arg Asn Pro Val Val Glu Lys Ile Leu
            660                 665                 670

Asn Gln Met Ile Asn Val Ile Asn Thr Leu Ile Glu Ser Glu Asn Asp
        675                 680                 685

Lys Leu Val Ala Gln Gly Lys Glu Pro Asn Phe Gln Phe Asp Glu Ile
    690                 695                 700

Arg Ile Glu Leu Ala Arg Glu Leu Lys Lys Asn Ala Lys Glu Arg Glu
705                 710                 715                 720

Glu Leu Thr Lys Ser Met Thr Gln Gly Lys Thr Asn His Glu Lys Ile
                725                 730                 735

Ile Lys Ile Leu Gln Lys Glu Asp Gly Ile Lys Asn Pro Thr Arg Asn
            740                 745                 750

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

Lys Asp Leu Tyr Thr Asn Glu Tyr Ile Glu Arg Lys Asp Ile Phe Ser
    770                 775                 780

Lys Glu Tyr Asp Ile Glu His Ile Ile Pro Gln Ser Lys Leu Phe Asp
785                 790                 795                 800
```

```
Asp Ser Phe Ser Asn Lys Thr Leu Val Arg Arg Asn Val Asn Leu Lys
                805                 810                 815

Lys Gly Asn Gln Thr Ala Tyr Asp Phe Ile Leu Ser Glu Tyr Gly Gln
            820                 825                 830

Glu Lys Ala Asn Glu Phe Glu Thr Arg Ile Thr Asn Leu Tyr Ser Leu
        835                 840                 845

Gly Lys Asp Glu Gly Ile Ser Lys Ser Lys Tyr Lys Lys Leu Leu Met
    850                 855                 860

Gln Glu Ser Glu Ile Gly Lys Gly Phe Ile Glu Arg Asp Leu Arg Glu
865                 870                 875                 880

Thr Gln Tyr Ile Ala Lys Lys Ala Lys Ser Leu Leu Leu Glu Ile Thr
                885                 890                 895

Arg Asn Val Val Ser Thr Ser Gly Gly Ile Thr Asp Arg Leu Arg Glu
            900                 905                 910

Asp Trp Gly Leu Val Asn Val Met Lys Glu Leu Asn Leu Lys Lys Phe
        915                 920                 925

Arg Asp Ala Gly Leu Thr Glu Phe Val Glu Met Lys Asp Gly Asn Lys
    930                 935                 940

Lys Glu Val Ile Ile Asp Trp Thr Lys Arg Asn Asp His Arg His His
945                 950                 955                 960

Ala Met Asp Ala Leu Thr Ile Ala Phe Thr Lys His Asn His Ile Gln
                965                 970                 975

Tyr Leu Asn His Leu Asn Ala Arg Lys Asn Thr Lys Asp Glu Leu His
            980                 985                 990
```

```
Thr Asn Ile Ile Ala Ile Glu Lys  Lys Glu Thr Thr Ile  Ile Thr Asp
        995                 1000                1005


Glu Arg  Gly Asn Lys Lys Arg  Ile Phe Lys Glu Pro  Ile Pro Asn
    1010                1015                1020


Phe Arg  Asn Ile Ala Lys Ser  His Leu Glu Ala Ile  Leu Val Ser
    1025                1030                1035


His Lys  Ala Lys Asn Lys Val  Val Thr Lys Asn Ile  Asn Lys Ile
    1040                1045                1050


Ser Gly  Lys Lys Ile Gly Gln  Gln Thr Leu Thr Pro  Arg Gly Gln
    1055                1060                1065


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


Lys Glu  Glu Lys Val Gly Pro  Lys Phe Thr Lys Glu  Val Ile Glu
    1085                1090                1095


Leu Val  Ser Asn Pro Thr Tyr  Arg Asp Leu Leu Leu  Lys Arg Leu
    1100                1105                1110


Gln Glu  Asn Asn Asn Asp Pro  Lys Lys Ala Phe Gly  Gly Lys Asn
    1115                1120                1125


Ala Leu  Ser Lys Ser Pro Ile  Tyr Ile Asn Leu Glu  Lys Asn Ile
    1130                1135                1140


Ile Val  Pro Glu Val Val Lys  Leu Val Trp Leu Glu  Asp Asp Tyr
    1145                1150                1155


Thr Ile  Arg Lys Glu Ile Ser  Pro Glu Leu Lys Ile  Asp Lys Val
    1160                1165                1170


Val Asp  Glu Gly Val Lys Arg  Ile Leu Gln Asn Arg  Leu Ala Leu
    1175                1180                1185
```

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

Pro Ile  Trp Leu Ser Lys Asp  Lys Gly Ile Thr Ile  Lys Arg Val
    1205                1210                1215

Thr Leu  Ser Gly Val Lys Asn  Ala Thr Ala Leu His  Thr Lys Lys
    1220                1225                1230

Asp His  Leu Gly Gln Pro Ile  Leu Asp His Lys Gly  Gln Glu Ile
    1235                1240                1245

Pro Val  Asp Phe Ile Ser Thr  Gly Asn Asn His His  Val Ala Ile
    1250                1255                1260

Tyr Glu  Asp Lys Asn Gly Lys  Leu Gln Glu Ser Val  Val Ser His
    1265                1270                1275

Phe Glu  Ala Val Glu Arg Val  Asn Gln Gln Leu Pro  Ile Ile Asp
    1280                1285                1290

Lys Thr  Phe Asn Gln His Leu  Gly Trp Lys Phe Leu  Phe Thr Met
    1295                1300                1305

Lys Gln  Asn Glu Leu Phe Leu  Phe Pro Ser Asp Asp  Phe Asn Pro
    1310                1315                1320

Asn Glu  Ile Asp Leu Phe Asp  Thr Arg Asn Tyr Ala  Val Ile Ser
    1325                1330                1335

Lys His  Leu Phe Arg Ala Gln  Lys Leu Ser Thr Lys  Asp Tyr Ser
    1340                1345                1350

Phe Arg  His His Leu Glu Thr  Asn Val Glu Asp Ile  Lys Asp Leu
    1355                1360                1365
```

Lys Thr Ile Thr Trp Arg Arg Glu Gly Leu Asn Gly Ile Gln Asn
    1370   1375   1380

Ile Val Lys Ile Arg Thr Asn His Leu Gly Glu Ile Val His Ile
    1385   1390   1395

Gly Glu Tyr
    1400

<210> 104
<211> 21
<212> RNA
<213> Myroides sp.

<400> 104
guugugaauu gcuuucaaac a   21

<210> 105
<211> 105
<212> RNA
<213> Myroides sp.

<400> 105
ugaaagcaau ucacaauaag gauuauuccg uugugaaaac aucuaguccu cgacuaauuu   60

cggggaauaa agccuuaacu cuguuaaggc uuuuuuuagu uuuuu   105

<210> 106
<211> 159
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<220>
<221> modified_base
<222> (1)..(29)
<223> a, c, u, g, unknown or other

<400> 106
nnnnnnnnnn nnnnnnnnnn nnnnnnnnng uugugaauug cuuucaaaca aaagugaaag   60

caauucacaa uaaggauuau uccguuguga aaacaucuag uccucgacua auuucgggga 120

auaaagccuu aacucuguua aggcuuuuuu uaguuuuuu 159

<210> 107
<211> 160
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 107
gagcggacag cagcuuccua uaucucguac guugugaauu gcuuucaaac aaaagugaaa 60

gcaauucaca auaaggauua uuccguugug aaaacaucua guccucgacu aauuucgggg 120

aauaaagccu uaacucuguu aaggcuuuuu uuaguuuuuu 160

<210> 108
<211> 160
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 108
ccaugauaua gacguugugg cuguuguagu guugugaauu gcuuucaaac aaaagugaaa 60

gcaauucaca auaaggauua uuccguugug aaaacaucua guccucgacu aauuucgggg 120

aauaaagccu uaacucuguu aaggcuuuuu uuaguuuuuu 160

<210> 109
<211> 5
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

oligonucleotide"

<220>
<221> modified_base
<222> (1)..(4)
<223> a, c, t, g, unknown or other

<400> 109
nnnnc 5

<210> 110
<211> 1432
<212> PRT
<213> Chryseobacterium sp.

<400> 110
Met Ala Lys Asn Ile Leu Gly Leu Asp Leu Gly Thr Asn Ser Ile Gly
1 5 10 15

Trp Ala Leu Ile Asn Gln Asp Phe Glu Asn Lys Gln Gly Lys Ile Leu
20 25 30

Gly Met Gly Ser Arg Ile Ile Pro Met Ser Gln Asp Ile Leu Gly Asp
35 40 45

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

Arg Gly Val Arg Arg Leu Arg Glu Arg Phe Leu Leu Arg Arg Glu Arg
65 70 75 80

Leu His Arg Val Leu Asn Ile Ile Asn Phe Leu Pro Glu His Tyr Ala
85 90 95

Ser Gln Ile Asp Phe Glu Lys Arg Phe Gly Lys Phe Lys Glu Glu Thr
100 105 110

Glu Pro Lys Leu Ala Tyr Asn Lys Asp Gly Phe Val Phe Lys Asp Ser
115 120 125

```
Phe Glu Glu Met Leu Ala Asp Phe Lys Asn Tyr Gln Pro Gln Leu Leu
    130                 135                 140

Glu Asn Asp Lys Lys Ile Pro Tyr Asp Trp Thr Ile Tyr Tyr Leu Arg
145                 150                 155                 160

Lys Lys Ala Leu Ser Gln Lys Ile Glu Lys Glu Glu Leu Ala Trp Ile
                165                 170                 175

Leu Leu Asn Phe Asn Gln Lys Arg Gly Tyr Tyr Gln Leu Arg Gly Glu
            180                 185                 190

Asp Phe Glu Glu Glu Lys Asp Lys Met Phe Val Arg Leu Lys Val Glu
        195                 200                 205

Lys Ile Ile Asp Ser Gly Asp Asn Val Lys Gly Lys Ile Leu Tyr Asp
    210                 215                 220

Val Tyr Phe Glu Asn Gly Trp Lys Tyr Asp Lys Gln Ile Val Lys Thr
225                 230                 235                 240

Glu Asp Trp Ile Glu Arg Val Lys Glu Phe Ile Val Thr Glu Ser Phe
                245                 250                 255

Leu Lys Asn Gly Asp Ile Lys Arg Thr Phe Lys Ala Val Asp Ser Glu
            260                 265                 270

Lys Asp Trp Ile Ala Ile Lys Thr Lys Thr Glu Gln Glu Ile Asp Lys
        275                 280                 285

Ser His Lys Thr Val Gly Val Tyr Ile Tyr Glu Thr Leu Leu Gln Asn
    290                 295                 300

Pro Lys Gln Lys Ile Lys Gly Lys Leu Val Arg Thr Ile Glu Arg Lys
305                 310                 315                 320

Phe Tyr Lys Asp Glu Leu Lys Gln Ile Leu Glu Lys Gln Lys Glu Phe
                325                 330                 335
```

```
His Gln Glu Leu Lys Asn Asp Asp Leu Tyr Asn Asp Cys Val Arg Glu
            340                 345                 350

Leu Tyr Arg Asn Asn Glu Ala His Gln Leu Thr Leu Ser Lys Lys Glu
        355                 360                 365

Phe Val His Leu Leu Met Glu Asp Ile Ile Phe Tyr Gln Arg Pro Leu
    370                 375                 380

Arg Ser Gln Lys Ser Ser Ile Ser Asn Cys Ser Leu Glu Phe Arg Lys
385                 390                 395                 400

Tyr Lys Asp Glu Asn Gly Val Glu His Ile Gln Tyr Leu Lys Ala Val
                405                 410                 415

Pro Lys Ser Asn Pro Tyr Tyr Gln Glu Phe Arg Ile Trp Gln Trp Ile
            420                 425                 430

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

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

Leu Asn Asn Arg Lys Glu Val Asp Gln Lys Ala Leu Leu Lys His Phe
465                 470                 475                 480

Lys Leu Asn Glu Lys Thr His Arg Trp Lys Tyr Val Glu Asp Lys Lys
                485                 490                 495

Tyr Pro Cys Asn Glu Thr Lys Ser Met Ile Ser Glu Arg Leu Lys Lys
            500                 505                 510

Val Glu Asn Ile Ala Asn Asp Phe Leu Thr Arg Glu Ile Glu Gln Lys
        515                 520                 525
```

```
Ile Trp His Ile Ile Tyr Ser Val Asn Asp Lys Ile Glu Tyr Glu Lys
    530                 535                 540

Ala Leu Lys Ser Phe Ala Lys Lys Asn Asn Leu Asp Glu Asn Ser Phe
545                 550                 555                 560

Phe Glu Ala Phe Lys Lys Phe Pro Pro Phe Lys Ser Glu Tyr Gly Ser
                565                 570                 575

Phe Ser Glu Lys Ala Ile Lys Lys Leu Leu Pro Leu Met Arg Leu Gly
            580                 585                 590

Lys Tyr Trp Asn Cys Glu Asn Ile Ser Asp Asp Ser Lys Glu Arg Ile
        595                 600                 605

Gln Lys Ile Ile Asn Gly Glu Tyr Asp Glu Asn Ile Lys Asp Arg Val
    610                 615                 620

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

Gln Leu Trp Leu Ala Gln Tyr Val Val Tyr Asp Arg His Ser Glu Ala
                645                 650                 655

Ser Met Ile Gly Lys Trp Asn Ser Ala Asp Asp Leu Glu Glu Phe Leu
            660                 665                 670

Lys Glu Phe Lys Gln His Ser Leu Arg Asn Pro Ile Val Glu Gln Val
        675                 680                 685

Ile Thr Glu Thr Leu Arg Val Val Lys Asp Ile Trp Leu Lys Tyr Gly
    690                 695                 700

Asn Gly Ala Lys Asp Phe Phe Asn Glu Ile His Ile Glu Leu Gly Arg
705                 710                 715                 720

Glu Met Lys Gln Thr Lys Asp Glu Arg Leu Asp Ala Thr Lys Arg Ile
                725                 730                 735
```

```
Thr Glu Asn Glu Asn Thr Asn Leu Arg Ile Lys Ala Leu Leu Ala Glu
            740                 745                 750

Met Met Asn Asp Asn Ser Val Glu Asn Val Arg Pro Tyr Ser Pro Met
        755                 760                 765

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

Ile Glu Ile Glu Asp Glu Tyr Leu Lys Ile Ser Lys Thr Ala Gln Pro
785                 790                 795                 800

Ser Pro Ser Asp Leu Lys Arg Tyr Lys Leu Trp Leu Glu Gln Arg Tyr
                805                 810                 815

Lys Ser Pro Tyr Thr Gly Gln Ile Ile Pro Leu Asn Lys Leu Phe Thr
            820                 825                 830

Pro Glu Tyr Glu Ile Glu His Ile Ile Pro Gln Ser Arg Tyr Phe Asp
        835                 840                 845

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

Lys Asp Asn Tyr Ile Gly Leu Gly Phe Ile Lys Gln Phe Gly Gly Thr
865                 870                 875                 880

Ile Val Glu Cys Gly Leu Gly Lys Asn Val Lys Val Phe Glu Val Asn
                885                 890                 895

Glu Tyr Glu Asp Phe Val Lys Lys His Tyr Ala Asn Asn Arg Gly Lys
            900                 905                 910

Arg Asn Lys Leu Leu Leu Glu Glu Ile Pro Glu Lys Met Ile Glu Arg
        915                 920                 925
```

```
Gln Leu Asn Asp Thr Arg His Ile Ser Lys Tyr Ile Ser Gly Val Leu
    930                 935                 940

Ser Asn Ile Val Arg Val Glu Asp Gly Ser Asp Glu Gly Val Asn Ser
945                 950                 955                 960

Lys Asn Ile Val Pro Gly Asn Gly Lys Ile Thr Thr Gln Leu Lys Gln
                965                 970                 975

Asp Trp Gly Leu Asn Asp Val Trp Asn Asp Leu Ile Leu Pro Arg Phe
            980                 985                 990

Glu Arg Met Asn Gln Leu Thr Asn  Ser Thr Asp Phe Thr  Ala Trp Asn
        995                 1000                1005

Glu Asn  His Gln Lys Phe Leu  Pro Thr Val Pro Ile  Glu Phe Ser
    1010                1015                1020

Lys Gly  Phe Ser Lys Lys Arg  Ile Asp His Arg His  His Ala Leu
    1025                1030                1035

Asp Ala  Leu Val Ile Ala Cys  Ala Thr Lys Asp His  Ile Asn Leu
    1040                1045                1050

Leu Asn  Asn Gln Ser Ala Lys  Ser Asp Thr Lys Arg  Tyr Asp Leu
    1055                1060                1065

Lys Lys  Lys Leu Met Lys Phe  Glu Lys Gly Val Tyr  Asn His Pro
    1070                1075                1080

Gln Thr  Gly Glu Arg Ile Gln  Arg Asp Val Pro Lys  Gln Phe Leu
    1085                1090                1095

Lys Pro  Trp Glu Ser Phe Thr  Ile Asp Ala Lys Asn  Asn Leu Asp
    1100                1105                1110

Lys Ile  Ile Ile Ser Phe Lys  Gln Asn Leu Arg Val  Ile Asn Lys
    1115                1120                1125
```

```
Ala Thr  Asn Tyr Tyr Glu Lys  Tyr Val Glu Lys Asn  Gly Ile Lys
    1130                1135                1140

Thr Lys  Glu Arg Val Glu Gln  Thr Gly Thr Asn Trp  Ala Ile Arg
    1145                1150                1155

Lys Pro  Met His Lys Glu Thr  Val Ser Gly Ile Val  Asn Leu Pro
    1160                1165                1170

Trp Val  Lys Val Pro Lys Gly  Lys Ile Leu Thr Ala  Thr Arg Lys
    1175                1180                1185

Ser Leu  Asp Thr Thr Phe Asp  Leu Lys Ser Ile Asn  Ser Ile Thr
    1190                1195                1200

Asp Thr  Gly Ile Gln Lys Ile  Leu Arg Asn Tyr Leu  Glu Phe Lys
    1205                1210                1215

Gly Ser  Pro Glu Leu Ala Phe  Ser Pro Glu Gly Ile  Glu Asp Met
    1220                1225                1230

Asn Lys  Asn Ile Glu Lys Tyr  Asn Asp Gly Lys Leu  His Gln Pro
    1235                1240                1245

Ile Asn  Lys Val Arg Val Phe  Glu Leu Gly Ser Lys  Phe Gln Val
    1250                1255                1260

Gly Gln  Thr Gly Asn Lys Lys  Asp Lys Tyr Val Glu  Ala Ala Lys
    1265                1270                1275

Gly Thr  Asn Leu Phe Phe Ala  Val Tyr Glu Asp Lys  Asn Gly Lys
    1280                1285                1290

Arg Asn  Tyr Glu Thr Ile Pro  Leu Asn Ile Val Ile  Glu Arg Gln
    1295                1300                1305
```

```
Lys Gln  Gly Leu Leu Ala Cys  Pro Glu Ser Asn Glu  Lys Gly Glu
    1310                 1315                 1320

Lys Leu  Leu Phe Gln Leu Ser  Pro Asn Asp Phe Val  Tyr Leu Thr
    1325                 1330                 1335

Thr Glu  Glu Glu Asn Asp Asn  Ala Thr Pro Ile Asn  Phe Ser Leu
    1340                 1345                 1350

Leu Ser  Lys Glu Gln Ile Asn  Asn Leu Tyr Lys Ile  Val Ser Phe
    1355                 1360                 1365

Thr Gly  Asn Arg Leu Tyr Gly  Ile Pro Ile Cys Val  Ala Thr Thr
    1370                 1375                 1380

Ile Val  Asn Lys Ala Glu Tyr  Thr Gln Leu Asn Lys  Ile Glu Phe
    1385                 1390                 1395

Thr Lys  Glu Lys Asp Leu Leu  Leu Lys Leu Asn Val  Asn Arg Leu
    1400                 1405                 1410

Gly Asp  Val Lys Thr Phe Thr  Ala Asn Asp Ile Arg  Lys Ile Phe
    1415                 1420                 1425

Asn Arg  Gln Glu
    1430
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<210> 111
<211> 16
<212> RNA
<213> Chryseobacterium sp.

<400> 111
guugugaauu gcuuuc 16

<210> 112
<211> 73
<212> RNA
<213> Chryseobacterium sp.

<400> 112
gaaagcaauu cacaauaagg auuauuccgu ugugaaaaca uuuagcgccu cgacuaucuu 60

cggggcauuu uuu 73

<210> 113
<211> 122
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
<221> modified_base
<222> (1)..(29)
<223> a, c, u, g, unknown or other

<400> 113
nnnnnnnnnn nnnnnnnnnn nnnnnnnnng uugugaauug cuuucaaagg aaagcaauuc 60

acaauaagga uuauuccguu gugaaaacau uuagcgccuc gacuaucuuc ggggcauuuu 120

uu 122

<210> 114
<211> 123
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 114
gagcggacag cagcuuccua uaucucguac guugugaauu gcuuucaaag gaaagcaauu 60

cacaauaagg auuauuccgu ugugaaaaca uuuagcgccu cgacuaucuu cggggcauuu 120

uuu 123

<210> 115
<211> 123

<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 115
ccaugauaua gacguugugg cuguuguagu guugugaauu gcuuucaaag gaaagcaauu 60

cacaauaagg auuauuccgu ugugaaaaca uuuagcgccu cgacuaucuu cggggcauuu 120

uuu 123

<210> 116
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<220>
<221> modified_base
<222> (1)..(5)
<223> a, c, t, g, unknown or other

<400> 116
nnnnnc 6

<210> 117
<211> 1092
<212> PRT
<213> Bacillus sp.

<400> 117
Met Arg Tyr Ser Ile Gly Leu Asp Ile Gly Thr Thr Ser Ile Gly Asn
1 5 10 15

Ala Val Ile Asn Lys Asp Leu Gln Arg Phe Glu His Leu Gly Val Arg
20 25 30

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Ile Phe Asp Ala Ala Glu Asn Pro Lys Asp Gly Ser Ser Leu Ser Ala
        35                  40                  45

Pro Arg Arg Leu Ala Arg Ser Ser Arg Arg Arg Leu Arg Arg Arg Lys
    50                  55                  60

His Arg Val Glu Arg Thr Lys Gln Leu Leu Ile Asn Lys Gly Leu Leu
65                  70                  75                  80

Thr Lys Thr Gln Val Lys Asn Leu Tyr Asn Ser Lys Asn Ile Asn Leu
                85                  90                  95

Asp Ile Trp Asp Ile Arg Val Ser Gly Ile Asp Arg Lys Leu Phe Asn
            100                 105                 110

Asn Glu Phe Ala Arg Val Leu Ile His Phe Ser Lys Asn Arg Gly Phe
        115                 120                 125

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

Leu Ser Ala Val Lys Glu Asn Arg Glu Leu Met Asp Glu Lys Gly Tyr
145                 150                 155                 160

Arg Thr Ile Ala Glu Met Leu Val Ser Asp Glu Lys Tyr Glu Gly Thr
                165                 170                 175

Lys Arg Asn Lys Gly Gly Asp Tyr Ser His Val Val Ala Arg Ser Asp
            180                 185                 190

Ile Glu Asn Glu Ile Cys Leu Leu Phe Gln Lys Gln Arg Glu Tyr Gly
        195                 200                 205

His Pro Phe Ala Thr Glu Glu Asn Glu Glu Ala Phe Leu Ser Ile Trp
    210                 215                 220

Ser Ser Gln Arg Pro Phe Ser Thr Lys Asp Asp Ile Val Lys Lys Ile
225                 230                 235                 240
```

```
Gly Asn Cys Thr Leu Glu Pro Lys Glu Lys Arg Ala Pro Lys Ser Thr
                245                 250                 255

Tyr Thr Phe Glu Arg Phe Arg Ala Leu Asp Lys Leu Asn Arg Leu Arg
            260                 265                 270

Ile Leu Ser Thr Thr Ala Pro Ser Arg Pro Leu Thr Asn Glu Glu Arg
        275                 280                 285

Lys Ser Ile Leu Ser Ser Leu Phe Ser Lys Lys Glu Val Lys Tyr Lys
    290                 295                 300

Glu Leu Arg Lys Leu Leu Lys Leu Thr Asp Asp Gln Arg Phe Asn Glu
305                 310                 315                 320

Ile Tyr Tyr Ser Pro Asp Glu Thr Ile Glu Lys Thr Glu Asn Arg Thr
                325                 330                 335

Phe Leu Ser Leu Glu Ser Gln Tyr Lys Ile Lys Lys Ile Ile Glu Lys
            340                 345                 350

Thr Glu Ser Lys Asn Met Gln Ser Ser Tyr His Pro Ile Asp Tyr Asp
        355                 360                 365

Thr Ile Gly Tyr Ala Leu Thr Val Phe Lys Asp Asp Lys Asp Ile Gln
    370                 375                 380

His Tyr Leu Gln Asn Ser Tyr Ile Asp Ser Lys Gly Lys Ala Ile Pro
385                 390                 395                 400

Asn Met Ala Asn Arg Glu Tyr Asn Leu Glu Leu Ile Glu Glu Leu Leu
                405                 410                 415

Gly Leu Ser Phe Ala Lys Phe Gly His Leu Ser Leu Lys Ala Leu Asn
            420                 425                 430
```

```
Asn Ile Leu Pro Tyr Met Glu Glu Gly Glu Pro Tyr His Ile Ala Cys
        435                 440                 445

Glu Met Ala Ser Tyr Gln Phe Ser Gln Arg Leu Ser Lys Glu Lys His
    450                 455                 460

Arg Leu Leu Pro Pro Ile Pro Val Asp Glu Ile Pro Asn Pro Val Val
465                 470                 475                 480

Val Arg Ala Leu Thr Gln Val Arg Lys Val Leu Asn Ser Ile Ile Lys
                485                 490                 495

Lys Tyr Gly Pro Pro Ser Asp Ile Tyr Ile Glu Leu Ala Arg Glu Met
            500                 505                 510

Ser Lys Pro Phe Lys Glu Arg Lys Ser Leu Glu Arg Glu Phe Asn Glu
        515                 520                 525

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

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

Trp Asn Glu Gln Asn Gly Ile Cys Pro Tyr Ser Leu Lys Pro Ile Ser
                565                 570                 575

Ile Glu Tyr Leu Phe Asn Ile Gly Tyr Ala Glu Val Asp His Ile Ile
            580                 585                 590

Pro Tyr Ser Arg Ser Phe Asp Asp Ser Asn Gly Asn Lys Val Leu Val
        595                 600                 605

Leu Thr Arg Glu Asn Gln Asn Lys Leu Asn Arg Thr Pro Tyr Glu Trp
    610                 615                 620

Phe Gly His Glu Glu Asn Arg Trp Glu Asp Phe Val Ser Phe Ile Arg
625                 630                 635                 640
```

```
Thr Met Lys Val Gly Lys Lys Lys Lys Asn Met Leu Leu Lys Lys Asn
                645                 650                 655

Phe Asp Glu Glu Gln Glu Glu Gln Ile Leu Ser Arg Asn Leu Asn Asp
            660                 665                 670

Thr Arg Tyr Ile Thr Arg Tyr Ile Lys Ser Phe Ile Glu Asp Asn Leu
        675                 680                 685

Glu Phe Arg Thr Glu Glu Asn Lys Glu Gln Tyr Val His Thr Val Asn
    690                 695                 700

Gly Ala Tyr Thr Ser Leu Met Arg Lys Arg Trp Gly Leu Asn Lys Asp
705                 710                 715                 720

Arg Arg Gly Asn Asp Leu His His Ala Val Asp Ala Ala Ile Ile Ala
                725                 730                 735

Val Ser Leu Pro Phe Lys Asn Lys Val Asn Ala Tyr Phe Lys Arg Gln
            740                 745                 750

Glu Thr Gly Leu Ser Lys Leu Leu Asn Asn Lys Lys Asp Ile Phe Pro
        755                 760                 765

Glu Pro Trp Arg Asn Phe Ile Lys Glu Leu Glu Ala Arg Met Ile Gln
    770                 775                 780

Asp Pro Glu Lys Met Lys Arg Ala Leu Glu Ser Leu Glu Leu Glu Thr
785                 790                 795                 800

Tyr Gly Glu Ile Phe Leu Asn Lys Leu Lys Pro Ile Phe Val Ser Arg
                805                 810                 815

Met Pro Lys His Ser Ile Lys Gly Gln Ile His Glu Glu Thr Ile Arg
            820                 825                 830
```

```
Arg Val Arg Gly Phe Thr Glu Glu Gly Phe Leu Val Thr Val Lys Lys
        835                 840                 845

Thr Arg Leu Asp Gln Ile Pro Phe Asp Lys Asn Gly Asp Phe Pro Met
    850                 855                 860

Tyr Gly Lys Glu Thr Asp Ile Lys Thr Tyr Met Ala Ile Lys Gln Arg
865                 870                 875                 880

Tyr Leu Glu Tyr Gly Gln Asp Lys Gln Lys Ala Phe Ala Val Pro Leu
                885                 890                 895

Arg Lys Pro Ser Lys Asn Pro Lys Asn Ala Pro Ile Val Arg Ser Val
            900                 905                 910

Lys Ile Glu Gly Lys Ala Asn Arg Val Val Met Leu Asp Asp Lys Ala
        915                 920                 925

Ala Ala Asp Asn Ala Ser Ile Val Arg Thr Glu Val Phe Arg His Lys
    930                 935                 940

Lys Thr Gly Glu Tyr Tyr Leu Thr Pro Val Tyr Val Ala Asp Ile Leu
945                 950                 955                 960

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

Asp Trp Asp Arg Ile Thr Asp Glu His Glu Tyr Leu Phe Ser Leu Tyr
            980                 985                 990

Asn Asn Asp Leu Val Lys Ile Ile  Leu Pro Lys Glu Lys  Glu Thr Lys
        995                 1000                1005

Lys Tyr  Thr Gly Gly Asn His  Leu Trp Gln Glu Gly  Phe Phe Tyr
    1010                1015                1020

Phe Lys  Gly Val Asp Ser Ser  Asn Ala Gly Ile Lys  Ile Ile Asn
    1025                1030                1035
```

His Leu Asn Ser Phe Glu Ala Arg Ile Gly Thr Lys Arg Leu Ile
    1040   1045   1050

Ala Phe Glu Lys Tyr Gln Val Asn Pro Leu Gly Glu Ile Asn Lys
    1055   1060   1065

Val His Gly Glu Lys Arg Pro Gly Glu Leu Leu Asn Lys Glu Glu
    1070   1075   1080

Ile Lys Glu Asn Arg Lys Asn Ile Ser
    1085   1090

<210> 118
<211> 23
<212> RNA
<213> Bacillus sp.

<400> 118
gccauaauuc cucuguaaaa cuu   23

<210> 119
<211> 112
<212> RNA
<213> Bacillus sp.

<400> 119
aagguuuaua gaguuauuau gguaaggcaa uaugccgugg cguuggggau cgccuauguc   60

cgguuuuacc ggaucucccu aaaggugacu aacuuugguu agucaccuuu uu   112

<210> 120
<211> 168
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<220>

<221> modified_base
<222> (1)..(29)
<223> a, c, u, g, unknown or other

<400> 120
nnnnnnnnnn nnnnnnnnnn nnnnnnnnng ccauaauucc ucuguaaaac uuaaagaagg 60

uuuauagagu uauuauggua aggcaauaug ccguggcguu ggggaucgcc uauguccggu 120

uuuaccggau cucccuaaag gugacuaacu uuggguuaguc accuuuuu 168

<210> 121
<211> 169
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 121
gagcggacag cagcuuccua uaucucguac gccauaauuc cucuguaaaa cuuaaagaag 60

guuuauagag uuauuauggu aaggcaauau gccguggcgu uggggaucgc cuauguccgg 120

uuuuaccgga ucucccuaaa ggugacuaac uuugguuagu caccuuuuu 169

<210> 122
<211> 169
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 122
ccaugauaua gacguugugg cuguuguagu gccauaauuc cucuguaaaa cuuaaagaag 60

guuuauagag uuauuauggu aaggcaauau gccguggcgu uggggaucgc cuauguccgg 120

uuuuaccgga ucucccuaaa ggugacuaac uuugguuagu caccuuuuu 169

<210> 123
<211> 4

<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 123
aaag 4

<210> 124
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 124
gccgccrcca tgg 13

<210> 125
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 125
Pro Lys Lys Lys Arg Lys Val
1 5

<210> 126
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 126
Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp Tyr
1   5   10   15

Lys Asp Asp Asp Asp Lys
            20

<210> 127
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 127
Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys Lys Lys
1   5   10   15

<210> 128
<211> 1092
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 128
Met Arg Tyr Ser Ile Gly Leu Ala Ile Gly Thr Thr Ser Ile Gly Asn
1   5   10   15

Ala Val Ile Asn Lys Asp Leu Gln Arg Phe Glu His Leu Gly Val Arg
            20   25   30

Ile Phe Asp Ala Ala Glu Asn Pro Lys Asp Gly Ser Ser Leu Ser Ala
        35   40   45

Pro Arg Arg Leu Ala Arg Ser Ser Arg Arg Arg Leu Arg Arg Arg Lys
    50   55   60

```
His Arg Val Glu Arg Thr Lys Gln Leu Leu Ile Asn Lys Gly Leu Leu
65                  70                  75                  80

Thr Lys Thr Gln Val Lys Asn Leu Tyr Asn Ser Lys Asn Ile Asn Leu
                85                  90                  95

Asp Ile Trp Asp Ile Arg Val Ser Gly Ile Asp Arg Lys Leu Phe Asn
            100                 105                 110

Asn Glu Phe Ala Arg Val Leu Ile His Phe Ser Lys Asn Arg Gly Phe
        115                 120                 125

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

Leu Ser Ala Val Lys Glu Asn Arg Glu Leu Met Asp Glu Lys Gly Tyr
145                 150                 155                 160

Arg Thr Ile Ala Glu Met Leu Val Ser Asp Glu Lys Tyr Glu Gly Thr
                165                 170                 175

Lys Arg Asn Lys Gly Gly Asp Tyr Ser His Val Val Ala Arg Ser Asp
            180                 185                 190

Ile Glu Asn Glu Ile Cys Leu Leu Phe Gln Lys Gln Arg Glu Tyr Gly
        195                 200                 205

His Pro Phe Ala Thr Glu Glu Asn Glu Glu Ala Phe Leu Ser Ile Trp
    210                 215                 220

Ser Ser Gln Arg Pro Phe Ser Thr Lys Asp Asp Ile Val Lys Lys Ile
225                 230                 235                 240

Gly Asn Cys Thr Leu Glu Pro Lys Glu Lys Arg Ala Pro Lys Ser Thr
                245                 250                 255
```

```
Tyr Thr Phe Glu Arg Phe Arg Ala Leu Asp Lys Leu Asn Arg Leu Arg
            260                 265                 270

Ile Leu Ser Thr Thr Ala Pro Ser Arg Pro Leu Thr Asn Glu Glu Arg
        275                 280                 285

Lys Ser Ile Leu Ser Ser Leu Phe Ser Lys Lys Glu Val Lys Tyr Lys
    290                 295                 300

Glu Leu Arg Lys Leu Leu Lys Leu Thr Asp Asp Gln Arg Phe Asn Glu
305                 310                 315                 320

Ile Tyr Tyr Ser Pro Asp Glu Thr Ile Glu Lys Thr Glu Asn Arg Thr
                325                 330                 335

Phe Leu Ser Leu Glu Ser Gln Tyr Lys Ile Lys Lys Ile Ile Glu Lys
            340                 345                 350

Thr Glu Ser Lys Asn Met Gln Ser Ser Tyr His Pro Ile Asp Tyr Asp
        355                 360                 365

Thr Ile Gly Tyr Ala Leu Thr Val Phe Lys Asp Asp Lys Asp Ile Gln
    370                 375                 380

His Tyr Leu Gln Asn Ser Tyr Ile Asp Ser Lys Gly Lys Ala Ile Pro
385                 390                 395                 400

Asn Met Ala Asn Arg Glu Tyr Asn Leu Glu Leu Ile Glu Glu Leu Leu
                405                 410                 415

Gly Leu Ser Phe Ala Lys Phe Gly His Leu Ser Leu Lys Ala Leu Asn
            420                 425                 430

Asn Ile Leu Pro Tyr Met Glu Glu Gly Glu Pro Tyr His Ile Ala Cys
        435                 440                 445

Glu Met Ala Ser Tyr Gln Phe Ser Gln Arg Leu Ser Lys Glu Lys His
    450                 455                 460
```

```
Arg Leu Leu Pro Pro Ile Pro Val Asp Glu Ile Pro Asn Pro Val Val
465                 470                 475                 480

Val Arg Ala Leu Thr Gln Val Arg Lys Val Leu Asn Ser Ile Ile Lys
                485                 490                 495

Lys Tyr Gly Pro Pro Ser Asp Ile Tyr Ile Glu Leu Ala Arg Glu Met
            500                 505                 510

Ser Lys Pro Phe Lys Glu Arg Lys Ser Leu Glu Arg Glu Phe Asn Glu
        515                 520                 525

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

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

Trp Asn Glu Gln Asn Gly Ile Cys Pro Tyr Ser Leu Lys Pro Ile Ser
                565                 570                 575

Ile Glu Tyr Leu Phe Asn Ile Gly Tyr Ala Glu Val Asp His Ile Ile
            580                 585                 590

Pro Tyr Ser Arg Ser Phe Asp Asp Ser Asn Gly Asn Lys Val Leu Val
        595                 600                 605

Leu Thr Arg Glu Asn Gln Asn Lys Leu Asn Arg Thr Pro Tyr Glu Trp
    610                 615                 620

Phe Gly His Glu Glu Asn Arg Trp Glu Asp Phe Val Ser Phe Ile Arg
625                 630                 635                 640

Thr Met Lys Val Gly Lys Lys Lys Lys Asn Met Leu Leu Lys Lys Asn
                645                 650                 655
```

```
Phe Asp Glu Glu Gln Glu Glu Gln Ile Leu Ser Arg Asn Leu Asn Asp
            660                 665                 670

Thr Arg Tyr Ile Thr Arg Tyr Ile Lys Ser Phe Ile Glu Asp Asn Leu
        675                 680                 685

Glu Phe Arg Thr Glu Glu Asn Lys Glu Gln Tyr Val His Thr Val Asn
    690                 695                 700

Gly Ala Tyr Thr Ser Leu Met Arg Lys Arg Trp Gly Leu Asn Lys Asp
705                 710                 715                 720

Arg Arg Gly Asn Asp Leu His His Ala Val Asp Ala Ala Ile Ile Ala
                725                 730                 735

Val Ser Leu Pro Phe Lys Asn Lys Val Asn Ala Tyr Phe Lys Arg Gln
            740                 745                 750

Glu Thr Gly Leu Ser Lys Leu Leu Asn Asn Lys Lys Asp Ile Phe Pro
        755                 760                 765

Glu Pro Trp Arg Asn Phe Ile Lys Glu Leu Glu Ala Arg Met Ile Gln
    770                 775                 780

Asp Pro Glu Lys Met Lys Arg Ala Leu Glu Ser Leu Glu Leu Glu Thr
785                 790                 795                 800

Tyr Gly Glu Ile Phe Leu Asn Lys Leu Lys Pro Ile Phe Val Ser Arg
                805                 810                 815

Met Pro Lys His Ser Ile Lys Gly Gln Ile His Glu Glu Thr Ile Arg
            820                 825                 830

Arg Val Arg Gly Phe Thr Glu Glu Gly Phe Leu Val Thr Val Lys Lys
        835                 840                 845

Thr Arg Leu Asp Gln Ile Pro Phe Asp Lys Asn Gly Asp Phe Pro Met
    850                 855                 860
```

```
Tyr Gly Lys Glu Thr Asp Ile Lys Thr Tyr Met Ala Ile Lys Gln Arg
865                 870                 875                 880

Tyr Leu Glu Tyr Gly Gln Asp Lys Gln Lys Ala Phe Ala Val Pro Leu
                885                 890                 895

Arg Lys Pro Ser Lys Asn Pro Lys Asn Ala Pro Ile Val Arg Ser Val
            900                 905                 910

Lys Ile Glu Gly Lys Ala Asn Arg Val Val Met Leu Asp Asp Lys Ala
        915                 920                 925

Ala Ala Asp Asn Ala Ser Ile Val Arg Thr Glu Val Phe Arg His Lys
    930                 935                 940

Lys Thr Gly Glu Tyr Tyr Leu Thr Pro Val Tyr Val Ala Asp Ile Leu
945                 950                 955                 960

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

Asp Trp Asp Arg Ile Thr Asp Glu His Glu Tyr Leu Phe Ser Leu Tyr
            980                 985                 990

Asn Asn Asp Leu Val Lys Ile Ile  Leu Pro Lys Glu Lys  Glu Thr Lys
        995                 1000                1005

Lys Tyr  Thr Gly Gly Asn His  Leu Trp Gln Glu Gly  Phe Phe Tyr
    1010                1015                1020

Phe Lys  Gly Val Asp Ser Ser  Asn Ala Gly Ile Lys  Ile Ile Asn
    1025                1030                1035

His Leu  Asn Ser Phe Glu Ala  Arg Ile Gly Thr Lys  Arg Leu Ile
    1040                1045                1050
```

```
Ala Phe  Glu Lys Tyr Gln Val  Asn Pro Leu Gly Glu  Ile Asn Lys
    1055                1060                1065


Val His  Gly Glu Lys Arg Pro  Gly Glu Leu Leu Asn  Lys Glu Glu
    1070                1075                1080


Ile Lys  Glu Asn Arg Lys Asn  Ile Ser
    1085                1090


<210> 129
<211> 230
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
      APG09980 deaminase sequence"

<400> 129
Met Ala Ala Gly Pro Ala Pro Glu Ala Arg Ser Leu Met Asp Glu Gln
1               5                   10                  15


Thr Phe Leu Asp Asn Phe Asn Asn Leu Lys Tyr Pro Arg Lys Thr Tyr
            20                  25                  30


Leu Cys Tyr Glu Val Glu Leu Leu Val Gly Glu Asn His Ile Pro Leu
        35                  40                  45


Asp Asp Tyr Lys Gly Phe Val His Asn Glu Gly Phe Asp Met Gly Leu
    50                  55                  60


Glu Arg Cys His Ala Glu Leu Ile Phe Leu Glu Arg Met Ala Ser Trp
65                  70                  75                  80


Asn Leu Asp Thr Glu Leu Arg Tyr Arg Ile Thr Val Phe Ile Ser Trp
                85                  90                  95


Ser Pro Cys Pro Glu Cys Ala Asp Glu Leu Val Lys Phe Leu Arg Glu
            100                 105                 110
```

```
Asn Arg His Val Asn Leu Arg Ile Phe Ala Ala Arg Ile Tyr Asp Trp
        115                 120                 125


Tyr Gln Gly Tyr Glu Ala Gly Leu Arg Ala Leu Lys Ala Ala Gly Ala
    130                 135                 140


Glu Val Ala Met Met Thr Leu His Glu Phe Glu Tyr Cys Trp Asn Asn
145                 150                 155                 160


Phe Val Asp His Gln Gln Asp Glu Asp Thr Pro Phe Pro Pro Trp Asp
                165                 170                 175


Asn Leu Val Ala Arg Ser Glu Glu Leu Ser Gln Arg Leu Glu Gly Ile
            180                 185                 190


Leu Gln Pro Ser Val Leu Val Phe Cys Trp Pro Ser Gln Val Ser Val
        195                 200                 205


Thr Ala Ala His Ser Asp Ile Met Ser Gln Ala Ser Arg Ala Trp Glu
    210                 215                 220


Lys Arg Arg Asp Pro Pro
225                 230


<210> 130
<211> 182
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
      APG07386 CTD sequence"

<400> 130
Met Glu Ala Thr Tyr Pro His Ile Phe Tyr Phe His Phe Lys Asn Leu
1               5                   10                  15


Arg Lys Ala Tyr Gly Arg Asn Glu Thr Trp Leu Cys Phe Thr Met Glu
            20                  25                  30
```

```
Ile Ile Lys Gln His Ser Thr Val Phe Trp Glu Thr Gly Val Phe Arg
        35                  40                  45

Asn Gln Val Tyr Pro Glu Ser Leu Cys His Ala Glu Arg Cys Phe Leu
    50                  55                  60

Ser Trp Phe Cys Glu Asp Ile Leu Ser Pro Asn Thr Asp Tyr Arg Val
65                  70                  75                  80

Thr Trp Tyr Thr Ser Trp Ser Pro Cys Leu Asp Cys Ala Gly Glu Val
                85                  90                  95

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

Ala Arg Leu Tyr Tyr Phe Trp Asp Pro His Tyr Gln Gln Gly Leu Arg
        115                 120                 125

Ser Leu Ser Glu Lys Gly Ala Ser Val Glu Ile Met Gly Tyr Lys Asp
    130                 135                 140

Phe Lys Tyr Cys Trp Glu Asn Phe Val Tyr Asn Gly Asp Glu Pro Phe
145                 150                 155                 160

Lys Pro Trp Lys Gly Leu Lys Tyr Asn Phe Leu Phe Leu Asp Ser Lys
                165                 170                 175

Leu Gln Glu Ile Leu Gln
            180
```

<210> 131
<211> 201
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:

APG05840 deaminase sequence"

<400> 131

```
Met Glu Ala Ser Pro Ala Ser Arg Pro Arg Pro Leu Met Asp Pro His
1               5                   10                  15

Met Phe Thr Gly Asn Phe Thr Asn Asn Pro Arg Val Phe Gly Leu His
            20                  25                  30

Gln Thr Tyr Leu Cys Tyr Glu Val Lys Arg Gln Gly Pro Asp Gly Thr
        35                  40                  45

Arg Asp Leu Met Asn Glu Gln Arg Asp Phe Leu Cys Asn Gln Ala Lys
    50                  55                  60

Asn His Phe Ser Gly Ser Glu Asp His His Ala Glu Arg Cys Phe Leu
65                  70                  75                  80

Asp Arg Ile Pro Ser Trp Gln Leu Asp Pro Ala Gln Thr Tyr Arg Val
                85                  90                  95

Thr Cys Phe Ile Ser Trp Ser Pro Cys Phe Ser Cys Ala Gln Glu Val
            100                 105                 110

Ala Glu Phe Leu His Glu Asn Pro His Val Asn Leu Arg Ile Phe Ala
        115                 120                 125

Ala Arg Ile Tyr Asp Tyr Leu Pro Arg Tyr Glu Glu Gly Leu Gln Met
    130                 135                 140

Leu Gln Asn Ala Gly Ala Gln Val Ser Ile Met Thr Ser Glu Glu Phe
145                 150                 155                 160

Gly His Cys Trp Asp Thr Phe Val Asp Arg Gln Gly His Pro Phe Gln
                165                 170                 175

Pro Trp Glu Gly Leu Asp Glu His Ser Gln Ala Leu Ser Gly Arg Leu
            180                 185                 190
```

```
Gln Ala Ile Leu Gln Asn Gln Gly Asn
        195                 200


<210> 132
<211> 192
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
      APG00868 deaminase sequence"

<400> 132
Met Glu Pro Trp Arg Pro Ser Pro Arg Asn Pro Met Asp Arg Ile Asp
1               5                   10                  15


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


Arg Lys Leu Cys Tyr Leu Cys Phe Gln Val Glu Thr Gly Asp Tyr Phe
        35                  40                  45


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


Trp Ala Arg Cys His Ala Glu Gln Cys Phe Leu Ser Trp Phe Arg Asp
65                  70                  75                  80


Gln Tyr Pro Cys Arg Asp Glu Tyr Tyr Asn Val Thr Trp Phe Leu Ser
                85                  90                  95


Trp Ser Pro Cys Pro Thr Cys Ala Glu Glu Val Val Glu Phe Leu Glu
            100                 105                 110


Glu Tyr Arg Asn Leu Thr Leu Ser Ile Phe Thr Ser Arg Leu Tyr Tyr
        115                 120                 125


Phe Tyr His Pro Asn Tyr Gln Gln Gly Leu Arg Lys Leu Trp Asp Ala
    130                 135                 140
```

```
Gly Val Gln Leu Asp Ile Met Ser Cys Asp Asp Phe Glu His Cys Trp
145                 150                 155                 160


Asp Asn Phe Val Asp His Lys Gly Met Arg Phe Gln Arg Arg Asn Leu
                165                 170                 175


Leu Lys Asp Tyr Asp Phe Leu Ala Ala Glu Leu Gln Glu Ile Leu Arg
            180                 185                 190


<210> 133
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 133
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> 134
<211> 159
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 134
gggccattaa aacctctcca gccataattc ctctgtaaaa cttaaagaag gtttatagag       60

ttattatggt aaggcaatat gccgtggcgt tggggatcgc ctatgtccgg ttttaccgga      120

tctccctaaa ggtgactaac tttggttagt caccttttt                             159
```

<210> 135
<211> 159
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 135
catggcagta cattagagca gccataattc ctctgtaaaa cttaaagaag gtttatagag 60

ttattatggt aaggcaatat gccgtggcgt tggggatcgc ctatgtccgg ttttaccgga 120

tctccctaaa ggtgactaac tttggttagt caccttttt 159

<210> 136
<211> 164
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 136
agctgtttgg gaggtcagaa atagggccat aattcctctg taaaacttaa agaaggttta 60

tagagttatt atggtaaggc aatatgccgt ggcgttgggg atcgcctatg tccggtttta 120

ccggatctcc ctaaaggtga ctaactttgg ttagtcacct tttt 164

<210> 137
<211> 1151
<212> PRT
<213> Brevibacillus sp.

<400> 137
Met Ala Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys
1 5 10 15

Lys Lys Ala Ile Arg Ser Ile Lys Leu Lys Leu Lys Thr Arg Thr Gly
20 25 30

```
Pro Glu Ala Gln Asn Leu Arg Lys Gly Ile Trp Arg Thr His Arg Leu
        35                  40                  45

Leu Asn Glu Gly Val Ala Tyr Tyr Met Lys Met Leu Leu Leu Phe Arg
    50                  55                  60

Gln Glu Ser Thr Gly Gly Gln Thr Lys Lys Glu Leu Gln Glu Glu Leu
65                  70                  75                  80

Val Arg His Ile Arg Glu Gln Gln Gln Lys Asn Arg Ala Asp Lys Asn
                85                  90                  95

Thr Gln Ala Leu Pro Leu Asp Lys Ala Phe Ala Ala Leu Arg Gln Leu
            100                 105                 110

Tyr Glu Leu Leu Val Pro Ser Ser Ile Gly Gln Ser Gly Asp Ala Gln
        115                 120                 125

Ile Ile Ser Arg Lys Phe Leu Ser Pro Leu Val Asp Pro Asn Ser Glu
    130                 135                 140

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

Lys Lys Glu Ala Asn Asp Pro Thr Trp Glu Gln Asp Tyr Glu Lys Trp
                165                 170                 175

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

Glu Glu Tyr Gly Ile Arg Pro Ile Phe Pro Leu Tyr Thr Asn Thr Val
        195                 200                 205

Ala Asp Ile Ala Trp Leu Pro Leu Gln Ser Asn Gln Phe Val Arg Thr
    210                 215                 220

Trp Asp Arg Asp Met Leu Gln Gln Ala Ile Glu Arg Leu Leu Ser Trp
```

```
225                 230                 235                 240

Glu Ser Trp Asn Lys Arg Val Gln Glu Glu Tyr Ser Lys Leu Gln Glu
                245                 250                 255

Lys Met Thr Gln Leu Asn Glu Gln Leu Glu Gly Gly Gln Glu Trp Ile
            260                 265                 270

Ser Leu Leu Glu Gln Tyr Glu Glu Gln Arg Glu Gln Glu Leu Ile Glu
        275                 280                 285

Asn Met Thr Ala Ala Asn Asp Lys Tyr Arg Ile Thr Lys Arg Gln Met
    290                 295                 300

Lys Gly Trp Asn Glu Leu Tyr Glu Gln Trp Ser Thr Val Leu Pro Asn
305                 310                 315                 320

Ala Ser His Glu Gln Tyr Arg Glu Ala Leu Lys Arg Val Gln Gln Arg
                325                 330                 335

Leu Arg Gly Arg Phe Gly Asp Ala His Phe Phe Gln Tyr Leu Met Lys
            340                 345                 350

Glu Glu His His Leu Ile Trp Lys Gly Asn Pro Gln Arg Ile His Tyr
        355                 360                 365

Phe Val Ala Arg Asn Glu Leu Lys Lys Arg Leu Glu Glu Ala Lys Gln
    370                 375                 380

Asn Ala Thr Met Thr Leu Pro Asp Ala Arg Lys His Pro Leu Trp Val
385                 390                 395                 400

Arg Phe Asp Ala Arg Gly Gly Asn Leu Gln Asp Tyr Tyr Leu Thr Ala
                405                 410                 415

Glu Ala Asp Asn Pro Arg Ser Arg Arg Phe Val Thr Phe Ser Gln Leu
            420                 425                 430
```

```
Ile Trp Pro Asn Glu Ser Gly Trp Met Glu Lys Gln Asp Val Glu Val
        435                 440                 445

Glu Leu Ala Leu Ser Lys Gln Phe Tyr Gln Gln Val Thr Leu Gln Lys
    450                 455                 460

Asn Asp Lys Gly Lys Gln Glu Ile Glu Phe Lys Asp Lys Gly Ser Gly
465                 470                 475                 480

Ser Thr Phe Ser Gly His Leu Gly Gly Ala Lys Leu Gln Leu Glu Arg
                485                 490                 495

Gly Asp Leu Glu Lys Glu Glu Lys Asp Phe Glu Gly Gly Glu Ile Gly
            500                 505                 510

Ser Val Tyr Leu Asn Ile Val Ile Asp Phe Glu Pro Leu Gln Glu Val
        515                 520                 525

Lys Asn Gly Arg Leu Gln Ser Pro Tyr Gly Gln Val Leu Gln Leu Val
    530                 535                 540

Arg Arg Pro Asn Glu Phe Pro Lys Val Thr Thr Tyr Lys Ser Glu Glu
545                 550                 555                 560

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

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

Thr Ala Ala Ala Thr Ser Ile Phe Ser Val Glu Glu Ser Asn Asp Ala
        595                 600                 605

Asn Ala Ala Gly Phe Ser Tyr Trp Ile Glu Gly Thr Pro Leu Val Ala
    610                 615                 620

Val His Lys Arg Ser Tyr Met Leu Lys Leu Pro Gly Glu Gln Val Glu
```

625 630 635 640

Lys Gln Val Arg Glu Lys Arg Asp Glu Arg Gln Asp Gln Gln Arg Arg
645 650 655

Val Arg Phe Gln Ile Arg Ile Leu Ser Gln Val Ile Arg Met Ala Lys
660 665 670

Lys Gln Asn Arg Glu Arg Ala Asp Glu Leu Asp His Leu Ser Gln Ala
675 680 685

Leu Glu Lys Gln Lys Ser Leu Leu Asp Gln Thr Asp Arg Thr Phe Trp
690 695 700

Asn Gly Ile Val Cys Asp Leu Thr Asp Ala Leu Arg Glu Lys Glu Gly
705 710 715 720

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

Val Gly Lys Val Val Gln Ala Trp Arg Lys Arg Phe Asp Ala Asp Glu
740 745 750

Arg Lys Gly Ile Ala Gly Leu Ser Met Trp Ser Ile Glu Glu Leu Asp
755 760 765

Ser Leu Arg Lys Leu Leu Ile Ser Trp Ser Arg Arg Thr Arg Asn Pro
770 775 780

Arg Glu Ile Asn Cys Phe Glu Gln Gly His Thr Ser His Gln Arg Leu
785 790 795 800

Leu Thr His Ile Gln Asn Val Lys Glu Asp Arg Leu Lys Gln Leu Ser
805 810 815

His Ala Ile Val Met Thr Ala Leu Gly Tyr Val Tyr Asp Glu Lys Lys
820 825 830

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Leu Glu Trp Phe Ala Lys Tyr Pro Ala Cys Gln Val Ile Leu Phe Glu
        835                 840                 845

Asn Leu Ser Gln Tyr Arg Ser Asn Met Asp Arg Ser Thr Lys Glu Asn
    850                 855                 860

Ser Thr Leu Met Lys Trp Ala His Arg Ser Ile Pro Lys Tyr Val His
865                 870                 875                 880

Met Gln Ala Glu Pro Tyr Gly Ile Gln Ile Gly Asp Val Arg Ala Glu
                885                 890                 895

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

Lys Met Val Ser Gly His Asp Leu Gln Gly Arg Arg Phe Glu Asn Leu
        915                 920                 925

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

Gln Leu Arg Pro Gly Asp Ile Val Pro Asp Asp Ser Gly Glu Trp Phe
945                 950                 955                 960

Met Thr Leu Ser Asp Gly Ser Glu Gly Lys Glu Val Val Phe Leu Gln
                965                 970                 975

Ala Asp Ile Asn Ala Ala Gln Asn Leu Gln Lys Arg Phe Trp Gln Arg
            980                 985                 990

Tyr Asn Glu Leu Phe Lys Val Ser  Cys Arg Val Leu Ile  Arg Gly Glu
        995                 1000                1005

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

Gly Lys  Gly Leu Phe Val Lys  Lys Thr Asp Thr Val  Met Lys Asp
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    1025                1030                1035

Val Tyr  Val Trp Asp Ser Gln  Ala Lys Leu Lys Gly  Lys Thr Thr
    1040                1045                1050

Phe Thr  Glu Glu Ser Glu Ser  Pro Glu Gln Leu Glu  Asp Phe Gln
    1055                1060                1065

Glu Ile  Ile Glu Glu Ala Glu  Glu Ala Lys Gly Thr  Tyr Arg Thr
    1070                1075                1080

Leu Phe  Arg Asp Pro Ser Gly  Val Phe Phe Pro Glu  Phe Val Trp
    1085                1090                1095

Ser Thr  Gln Lys Asp Phe Trp  Ser Glu Val Lys Arg  Arg Leu Tyr
    1100                1105                1110

Gly Lys  Leu Arg Glu Arg Phe  Leu Met Lys Thr Arg  Pro Lys Lys
    1115                1120                1125

Lys Arg  Lys Val Glu Asn Leu  Tyr Phe Gln Ser Gly  Ser His His
    1130                1135                1140

His His  His His His His His  His
    1145                1150


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<210> 139
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<211> 22
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cgagauauag gaagcugcug uc 142

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acaacagcca caacguc 137

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<210> 198
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<210> 217

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<213> Homo sapiens

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ccaattctcc atcaccaaga gagccttccg aaagaggccc ccctgggcaa acggccaccg 180

atggagaggt ctgccagtcc tcttctaccc cacccacgcc cccaccctaa tcagaggcca 240

aacccttcct ggagcctgtg ataaaagcaa ctgttagctt gcactagact agcttcaaag 300

ttgtattgac cctggtgtgt tatgtctaag agtagatgcc atatctcttt tctggcctat 360

gttattacct gtatggactt tgcactggaa tcagctatct gctcttactt atgcacacct 420

ggggcataga gccagccctg tatcgctttt cagccatctc actacagata actcccaagt 480

cctgtctagc tgccttcctt 500

<210> 221
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<213> Homo sapiens

<400> 221
tattgaccct ggtgtgttat 20

<210> 222
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<400> 222
gcttgcacta gactagcttc 20

<210> 223
<211> 20
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<213> Homo sapiens

<400> 223
cttttatcac aggctccagg 20

<210> 224
<211> 135
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<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic
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acccuggugu guuau 135

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<220>
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gctctgcccc cactcagcat cccaggggct gatttctttg gttttggatc cagctggatg 180

tctgcattgc cgaggccacc agggctggct cagcaactgt cggggaatca ccagggtctg 240

agaaatcttg tgcgcatgtg aggggctgtg ggagcagaga accactgggt gggaaattct 300

aatccccacc ctgctggaaa ctctctgggt ggccccaaca tgctaatcct ccggcaaacc 360

tctgtttcct cctcaaaagg caggaggtcg gaaagaataa acaatgagag tcacattaaa 420

aacacaaaat cctacggaaa tactgaagaa tgagtctcag cactaaggaa aagcctccag 480

cagctcctgc tttctgaggg tgaaggatag acgctgtggc tctgcatgac tcactagcac 540

tctatcacgg ccatattctg gcagggtcag tggctccaac taacatttgt ttggtacttt 600

acagtttatt aaatagatgt ttatatggag aagctctcat ttctttctca gaagagcctg 660

gctaggaagg tggatgaggc accatattca ttttgcaggt gaaattcctg agatgtaagg 720

agctgctgtg acttgctcaa ggccttatat cgagtaaacg gtagtgctgg ggcttagacg 780

caggtgttct gatttatagt tcaaaacctc tatcaatgag agagcaatct cctggtaatg 840

tgatagattt cccaacttaa tgccaacata ccataaacct cccattctgc taatgcccag 900

cctaagttgg ggagaccact ccagattcca agatgtacag tttgctttgc tgggcctttt 960

tcccatgcct gcctttactc tgccagagtt atattgctgg ggttttgaag aagatcctat 1020

taaataaaag aataagcagt attattaagt agccctgcat ttcaggtttc cttgagtggc 1080

aggccaggcc tggccgtgaa cgttcactga aatcatggcc tcttggccaa gattgatagc 1140

ttgtgcctgt ccctgagtcc cagtccatca cgagcagctg gtttctaaga tgctatttcc 1200

cgtataaagc atgagaccgt gacttgccag ccccacagag ccccgccctt gtccatcact 1260

ggcatctgga ctccagcctg ggttggggca aagagggaaa tgagatcatg tcctaaccct 1320

gatcctcttg tcccacagat atccagaacc ctgaccctgc cgtgtaccag ctgagagact 1380

ctaaatccag tgacaagtct gtctgcctat tcaccgattt tgattctcaa acaaatgtgt 1440

cacaaagtaa ggattctgat gtgtatatca cagacaaaac tgtgctagac atgaggtcta 1500

tggacttcaa gagcaacagt gctgtggcct ggagcaacaa atctgacttt gcatgtgcaa 1560

acgccttcaa caacagcatt attccagaag acaccttctt ccccagccca ggtaagggca 1620

gctttggtgc cttcgcaggc tgtttccttg cttcaggaat ggccaggttc tgcccagagc 1680

tctggtcaat gatgtctaaa actcctctga ttggtggtct cggccttatc cattgccacc 1740

aaaaccctct ttttactaag aaacagtgag ccttgttctg gcagtccaga gaatgacacg 1800

ggaaaaaagc agatgaagag aaggtggcag gagagggcac gtggcccagc ctcagtctct 1860

ccaactgagt tcctgcctgc ctgcctttgc tcagactgtt tgccccttac tgctcttcta 1920

ggcctcattc taagcccctt ctccaagttg cctctcctta tttctccctg tctgcca 1977

<210> 226
<211> 566
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 226

tcgtcggcag cgtcagatgt gtataagaga cagtttgggt tttgccagac tccacagtgc 60

atacgtgggc tccaacaggt cctcttccct cccagtcact gactaacccc ggaaccacac 120

agcttcccgt tctcagctcc acaaacttgg tgccaaattc ttctcccctg ggaagcatcc 180

ctggacactt cccaaaggac cccagtcact ccagcctgtt ggctgccgct cactttgatg 240

tctgcaggcc agatgagggc tccagatggc acattgtcag agggacacac tgtggcccct 300

gtgcccagcc ctgggctctc tgtacatgaa gcaactccag tcccaaatat gtagctgttt 360

gggaggtcag aaataggggg tccaggagca aactcccccc acccccttтc caaagcccat 420

tccctcttta gccagagccg gggtgtgcag acggcagtca ctagggggcg ctcggccacc 480

acagggaagc tgggtgaatg gagcgagcag cgtcttcgag agtgaggacg tgctgtctct 540

tatacacatc tccgagccca cgagac 566

<210> 227
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 227
gaaaggggt ggggggagtt tgctc 25

<210> 228
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 228
tcgtcggcag cgtcagatgt gtataagaga cagtttgggt tttgccagac tcc 53

<210> 229

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

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 229
gtctcgtggg ctcggagatg tgtataagag acagcctctg acaatgtgcc atct 54

<210> 230
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 230
cccgtataaa gcatgagacc 20

<210> 231
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 231
caagcatgag gagggaagta g 21

<210> 232
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 232
tggcagacag ggagaaataa g 21

<210> 233
<211> 137
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 233
ggcgacgguu agaggccgua ugucgauuug cuuuaauuuc gugcgugugc auugucgucc 60

uccauuacag ggcggcuacc acgaauagcc acgaaguaaa agcuucgugg cuagcacgaa 120

aggggguggg gggaguu 137

<210> 234
<211> 137
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 234
ggcgacgguu agaggccgua ugucgauuug cuuuaauuuc gugcgugugc auugucgucc 60

uccauuacag ggcggcuacc acgaauagcc acgaaguaaa agcuucgugg cuagcacccc 120

guauaaagca ugagacc 137

<210> 235
<211> 1071
<212> PRT
<213> Bacillus sp.

<400> 235
Met Arg Glu Leu Asp Tyr Arg Ile Gly Leu Asp Ile Gly Thr Asn Ser
1 5 10 15

```
Ile Gly Trp Gly Val Ile Glu Leu Ser Trp Asn Lys Asp Arg Glu Arg
            20                  25                  30

Tyr Glu Lys Val Arg Ile Val Asp Gln Gly Val Arg Met Phe Asp Arg
        35                  40                  45

Ala Glu Met Pro Lys Thr Gly Ala Ser Leu Ala Glu Pro Arg Arg Ile
    50                  55                  60

Ala Arg Ser Ser Arg Arg Arg Leu Asn Arg Lys Ser Gln Arg Lys Lys
65                  70                  75                  80

Asn Ile Arg Asn Leu Leu Val Gln His Gly Val Ile Thr Gln Glu Glu
                85                  90                  95

Leu Asp Ser Leu Tyr Pro Leu Ser Lys Lys Ser Met Asp Ile Trp Gly
            100                 105                 110

Ile Arg Leu Asp Gly Leu Asp Arg Leu Leu Asn His Phe Glu Trp Ala
        115                 120                 125

Arg Leu Leu Ile His Leu Ala Gln Arg Arg Gly Phe Lys Ser Asn Arg
    130                 135                 140

Lys Ser Glu Leu Lys Asp Thr Glu Thr Gly Lys Val Leu Ser Ser Ile
145                 150                 155                 160

Gln Leu Asn Glu Lys Arg Leu Ser Leu Tyr Arg Thr Val Gly Glu Met
                165                 170                 175

Trp Met Lys Asp Pro Asp Phe Ser Lys Tyr Asp Arg Lys Arg Asn Ser
            180                 185                 190

Pro Asn Glu Tyr Val Phe Ser Val Ser Arg Ala Glu Leu Glu Lys Glu
        195                 200                 205

Ile Val Thr Leu Phe Ala Ala Gln Arg Arg Phe Gln Ser Pro Tyr Ala
```

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    210                 215                 220

Ser Lys Asp Leu Gln Glu Thr Tyr Leu Gln Ile Trp Thr His Gln Leu
225                 230                 235                 240

Pro Phe Ala Ser Gly Asn Ala Ile Leu Asn Lys Val Gly Tyr Cys Ser
                245                 250                 255

Leu Leu Lys Gly Lys Glu Arg Arg Ile Pro Lys Ala Thr Tyr Thr Phe
            260                 265                 270

Gln Tyr Phe Ser Ala Leu Asp Gln Val Asn Arg Thr Arg Leu Gly Pro
        275                 280                 285

Asp Phe Gln Pro Phe Thr Lys Glu Gln Arg Glu Ile Ile Leu Asn Asn
    290                 295                 300

Met Phe Gln Arg Thr Asp Tyr Tyr Lys Lys Lys Thr Ile Pro Glu Val
305                 310                 315                 320

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

Phe Lys Gly Leu Asn Tyr Asp Pro Asn Glu Glu Leu Lys Lys Ile Glu
            340                 345                 350

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

Val Ala Asn Tyr Ser Glu Arg Thr Asn Glu Thr Phe Ser Thr Leu Asp
    370                 375                 380

Tyr Asp Gly Ile Gly Tyr Ala Leu Thr Val Tyr Lys Thr Asp Lys Asp
385                 390                 395                 400

Ile Arg Ser Tyr Leu Lys Ser Ser His Asn Leu Pro Lys Arg Cys Tyr
                405                 410                 415
```

```
Asp Asp Gln Leu Ile Glu Glu Leu Leu Ser Leu Ser Tyr Thr Lys Phe
            420                 425                 430

Gly His Leu Ser Leu Lys Ala Ile Asn His Val Leu Ser Ile Met Gln
        435                 440                 445

Lys Gly Asn Thr Tyr Lys Glu Ala Val Asp Gln Leu Gly Tyr Asp Thr
    450                 455                 460

Ser Gly Leu Lys Lys Glu Lys Arg Ser Lys Phe Leu Pro Pro Ile Ser
465                 470                 475                 480

Asp Glu Ile Thr Asn Pro Ile Val Lys Arg Ala Leu Thr Gln Ala Arg
                485                 490                 495

Lys Val Val Asn Ala Ile Ile Arg Arg His Gly Ser Pro His Ser Val
            500                 505                 510

His Ile Glu Leu Ala Arg Glu Leu Ser Lys Asn His Asp Glu Arg Thr
        515                 520                 525

Lys Ile Val Ser Ala Gln Asp Glu Asn Tyr Lys Lys Asn Lys Gly Ala
    530                 535                 540

Ile Ser Ile Leu Ser Glu His Gly Ile Leu Asn Pro Thr Gly Tyr Asp
545                 550                 555                 560

Ile Val Arg Tyr Lys Leu Trp Lys Glu Gln Gly Glu Arg Cys Ala Tyr
                565                 570                 575

Ser Leu Lys Glu Ile Pro Ala Asp Thr Phe Phe Asn Glu Leu Lys Lys
            580                 585                 590

Glu Arg Asn Gly Ala Pro Ile Leu Glu Val Asp His Ile Leu Pro Tyr
        595                 600                 605

Ser Gln Ser Phe Ile Asp Ser Tyr His Asn Lys Val Leu Val Tyr Ser
```

```
    610                 615                 620

Asp Glu Asn Arg Lys Lys Gly Asn Arg Ile Pro Tyr Thr Tyr Phe Leu
625                 630                 635                 640

Glu Thr Asn Lys Asp Trp Glu Ala Phe Glu Arg Tyr Val Arg Ser Asn
                645                 650                 655

Lys Phe Phe Ser Lys Lys Lys Arg Glu Tyr Leu Leu Lys Arg Ala Tyr
            660                 665                 670

Leu Pro Arg Glu Ser Glu Leu Ile Lys Glu Arg His Leu Asn Asp Thr
        675                 680                 685

Arg Tyr Ala Ser Thr Phe Leu Lys Asn Phe Ile Glu Gln Asn Leu Gln
    690                 695                 700

Phe Lys Glu Ala Glu Asp Asn Pro Arg Lys Arg Arg Val Gln Thr Val
705                 710                 715                 720

Asn Gly Val Ile Thr Ala His Phe Arg Lys Arg Trp Gly Leu Glu Lys
                725                 730                 735

Asp Arg Gln Glu Thr Tyr Leu His His Ala Met Asp Ala Ile Ile Val
            740                 745                 750

Ala Cys Thr Asp His His Met Val Thr Arg Val Thr Glu Tyr Tyr Gln
        755                 760                 765

Ile Lys Glu Ser Asn Lys Ser Val Lys Lys Pro Tyr Phe Pro Met Pro
    770                 775                 780

Trp Glu Gly Phe Arg Asp Glu Leu Leu Ser His Leu Ala Ser Gln Pro
785                 790                 795                 800

Ile Ala Lys Lys Ile Ser Glu Glu Leu Lys Ala Gly Tyr Gln Ser Leu
                805                 810                 815
```

```
Asp Tyr Ile Phe Val Ser Arg Met Pro Lys Arg Ser Ile Thr Gly Ala
            820                 825                 830

Ala His Lys Gln Thr Ile Met Arg Lys Gly Gly Ile Asp Lys Lys Gly
        835                 840                 845

Lys Thr Ile Ile Ile Glu Arg Leu His Leu Lys Asp Ile Lys Phe Asp
    850                 855                 860

Glu Asn Gly Asp Phe Lys Met Val Gly Lys Glu Gln Asp Met Ala Thr
865                 870                 875                 880

Tyr Glu Ala Ile Lys Gln Arg Tyr Leu Glu His Gly Lys Asn Ser Lys
                885                 890                 895

Lys Ala Phe Glu Thr Pro Leu Tyr Lys Pro Ser Lys Lys Gly Thr Gly
            900                 905                 910

Asn Leu Ile Lys Arg Val Lys Val Glu Gly Gln Ala Lys Ser Phe Val
        915                 920                 925

Arg Glu Val Asn Gly Gly Val Ala Gln Asn Gly Asp Leu Val Arg Val
    930                 935                 940

Asp Leu Phe Glu Lys Asp Asp Lys Tyr Tyr Met Val Pro Ile Tyr Val
945                 950                 955                 960

Pro Asp Thr Val Cys Ser Glu Leu Pro Lys Lys Val Val Ala Ser Ser
                965                 970                 975

Lys Gly Tyr Glu Gln Trp Leu Thr Leu Asp Asn Ser Phe Thr Phe Lys
            980                 985                 990

Phe Ser Leu Tyr Pro Tyr Asp Leu  Val Arg Leu Val Lys  Gly Asp Glu
        995                 1000                1005

Asp Arg  Phe Leu Tyr Phe Gly  Thr Leu Asp Ile Asp  Ser Asp Arg
```

```
    1010                1015                1020

Leu Asn  Phe Lys Asp Val Asn  Lys Pro Ser Lys Lys  Asn Glu Tyr
    1025                1030                1035

Arg Tyr  Ser Leu Lys Thr Ile  Glu Asp Leu Glu Lys  Tyr Glu Val
    1040                1045                1050

Gly Val  Leu Gly Asp Leu Arg  Leu Val Arg Lys Glu  Thr Arg Arg
    1055                1060                1065

Asn Phe  His
    1070
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<210> 236
<211> 46
<212> RNA
<213> Bacillus sp.

<400> 236
gacagcagcu uccuauaucu cguacgucau aguuccauua aagcca 46

<210> 237
<211> 85
<212> RNA
<213> Bacillus sp.

<400> 237
uggcuuugau guuucuauga uaaggguuuc gacccguggc gucggggauc gccugcccau 60

ugaaaugggc uucuccccau uuauu 85

<210> 238
<211> 32
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 238

gacagcagcu uccuauaucu cguacgucau ag 32

<210> 239
<211> 71
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 239
cuaugauaag gguuucgacc cguggcgucg gggaucgccu gcccauugaa augggcuucu 60

ccccauuuau u 71

<210> 240
<211> 36
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 240
gacagcagcu uccuauaucu cguacgucau agccau 36

<210> 241
<211> 75
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 241
augucuauga uaaggguuuc gacccguggc gucggggauc gccugcccau ugaaaugggc 60

uucuccccau uuauu 75

<210> 242

<211> 40
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 242
gacagcagcu uccuauaucu cguacgucau aguuccauua 40

<210> 243
<211> 79
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 243
ugauguuucu augauaaggg uuucgacccg uggcgucggg gaucgccugc ccauugaaau 60

gggcuucucc ccauuuauu 79

<210> 244
<211> 46
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 244
gacagcagcu uccuauaucu cguacgucau aguuccauua aagcca 46

<210> 245
<211> 78
<212> RNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 245
uggcuuugau guuucuauga uaaggguuuc gacccguggc gucggggauc gccugcccau 60

ugaaaugggc uucucccc 78

<210> 246
<211> 46
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 246
gacagcagcu uccuauaucu cguacgucau aguuccauua aagcca 46

<210> 247
<211> 75
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 247
uggcuuugau guuucuauga uaaggguuuc gacccguggc gucggggacc gcccauugaa 60

augggccucc ccuuu 75

<210> 248
<211> 46
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 248

gacagcagcu uccuauaucu cguacgucau aguuccauua aagcca 46

<210> 249
<211> 71
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 249
uggcuuugau guuucuauga uaaggguuuc gacccguggc gucgggaccg ccauugaaau 60

ggccucccuu u 71

<210> 250
<211> 38
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 250
gacagcagcu uccuauaucu cguacgucau aguuccau 38

<210> 251
<211> 77
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 251
auguuucuau gauaaggguu ucgacccgug gcgucgggga ucgccugccc auugaaaugg 60

gcuucucccc auuuauu 77

<210> 252

<211> 38
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 252
gacagcagcu uccuauaucu cguacgucau aguuccau 38

<210> 253
<211> 70
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 253
auguuucuau gauaaggguu ucgacccgug gcgucgggga ucgccugccc auugaaaugg 60

gcuucucccc 70

<210> 254
<211> 46
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 254
gacagcagcu uccuauaucu cguacgucau aguuccauua aagcca 46

<210> 255
<211> 76
<212> RNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 255
uggcuuugau guuucuauga uaaggguuuc gacccguggc gucggggauc gccugcccau 60

ugaaaugggc uucucc 76

<210> 256
<211> 39
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 256
gcuuccuaua ucucguacgu cauaguucca uuaaagcca 39

<210> 257
<211> 85
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 257
uggcuuugau guuucuauga uaaggguuuc gacccguggc gucggggauc gccugcccau 60

ugaaaugggc uucucccccau uuauu 85

<210> 258
<211> 38
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 258

gacagcagcu uccuauaucu cguacgucau aguuccau 38

<210> 259
<211> 71
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 259
uggcuuugau guuucuauga uaaggguuuc gacccguggc gucgggaccg ccauugaaau 60

ggccucccuu u 71

<210> 260
<211> 682
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 260
ttgtctcatg agcggataca tatttgaatg tatttagaaa aataaacaaa taggggttcc 60

gcgcacattt ccccgaaaag tgccagatac ctgaaacaaa acccatcgta cggccaagga 120

agtctccaat aactgtgatc caccacaagc gccagggttt tcccagtcac gacgttgtaa 180

aacgacggcc agtcatgcat aatccgcacg catctggaat aaggaagtgc cattccgcct 240

gacctgaaga ccaggctcga aagccttcac accctcagta agagctttct caatgtcgat 300

tgtgccacac accctgtcct cagtagcacc tagcggtaaa tcaaccatgt tgacggtcct 360

gtacgagata taggaagctg ctgtccgctc ctcaatttgt cacggacttc tgcactcatt 420

acttcttggt catctggatc tgaattgaac ggatcaccag aaataacttt gatttcagga 480

agtaaatcta ccaaagatct aaccgtggtg gacttcccgg ttcctctatc acccattatc 540

atcacaggct aggtggaggc tcagtgatga taagtctgcg atggtggatg catgtgtcat 600

ggtcatagct gtttcctgtg tgaaattgtt atccgctcag agggcacaat cctattccgc 660

gctatccgac aatctccaag ac 682

<210> 261
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 261
Thr Asn Leu Ser Asp His Glu Lys Glu Thr Gly Lys Gln Leu Val Ile
1 5 10 15

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

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

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

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

Met Leu

<210> 262
<211> 1072
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 262
Met Ser Glu Leu Asp Tyr Arg Ile Gly Leu Ala Ile Gly Thr Asn Ser
1   5   10   15

Ile Gly Trp Gly Val Ile Glu Leu Phe Trp Asn Lys Asp Arg Glu Arg
            20   25   30

Tyr Glu Lys Val Arg Ile Val Asp Lys Gly Val Arg Met Phe Asp Lys
        35   40   45

Ala Glu Ile Pro Asn Lys Gly Ala Ser Leu Ala Glu Pro Arg Arg Ile
    50   55   60

Ala Arg Ser Ser Arg Arg Arg Leu Asn Arg Lys Ser Gln Arg Lys Lys
65   70   75   80

Glu Ile Arg Asn Leu Leu Val Gln His Gly Met Ile Thr Gln Glu Glu
                85   90   95

Leu Asp Leu Leu Tyr Pro Leu Ser Lys Lys Ser Ile Asp Ile Trp Asp
            100   105   110

Ile Arg Leu Asp Gly Leu Asp Arg Leu Leu Asn His Leu Glu Trp Ala
        115   120   125

Arg Leu Leu Ile His Leu Ala Gln Arg Arg Gly Phe Lys Ser Asn Arg
    130   135   140

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

Gln Val Asn Glu Lys Arg Leu Phe Leu Tyr Arg Thr Val Gly Glu Met
                165   170   175

Trp Ile Lys Asp Ala Glu Phe Ser Lys Tyr Asp Arg Arg Arg Asn Ser
            180   185   190

Pro Asn Glu Tyr Val Phe Ser Val Ser Arg Ala Asp Leu Glu Lys Glu

```
        195                 200                 205

Ile Val Thr Leu Phe Glu Ala Gln Arg Lys Phe Gln Ser Ser Tyr Ala
    210                 215                 220

Ser Lys Asn Leu Gln Glu Thr Tyr Leu Gln Ile Trp Ala His Gln Leu
225                 230                 235                 240

Pro Phe Ala Ser Gly Asn Ala Ile Leu Asn Lys Val Gly Tyr Cys Ser
                245                 250                 255

Leu Leu Lys Gly Lys Glu Arg Arg Ile Pro Lys Ala Thr Tyr Thr Phe
            260                 265                 270

Gln Tyr Phe Ser Ala Leu Asp Gln Val Asn Arg Thr Arg Leu Gly Pro
        275                 280                 285

Asp Phe Gln Pro Phe Thr Gln Glu Gln Lys Glu Ile Ile Leu Asp Lys
    290                 295                 300

Met Phe Gln Arg Thr Asp Tyr Tyr Lys Lys Lys Thr Ile Pro Glu Val
305                 310                 315                 320

Ser Tyr Tyr Asp Ile Arg Lys Trp Leu Glu Leu Asp Glu Thr Ile Gln
                325                 330                 335

Phe Lys Gly Leu Asn Tyr Asp Pro Asn Glu Glu Leu Lys Lys Ile Glu
            340                 345                 350

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

Val Ala Asn Tyr Ala Glu Arg Thr Asn Glu Ala Phe Ser Thr Leu Asp
    370                 375                 380

Tyr Asp Ala Ile Ala Tyr Ala Leu Thr Val Tyr Lys Thr Asp Lys Asp
385                 390                 395                 400
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Ile Arg Ser Tyr Leu Lys Lys Ser Asn Asn Leu Ser Lys Arg Cys Tyr
                405                 410                 415

Asp Asp Gln Leu Ile Glu Glu Leu Phe Thr Leu Ser Tyr Thr Lys Phe
            420                 425                 430

Gly His Leu Ser Phe Lys Ala Ile Asn His Val Leu Pro Ile Met Gln
        435                 440                 445

Glu Gly Arg Thr Tyr Gln Glu Ala Ile His Gln Leu Gly Tyr Asp Thr
    450                 455                 460

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

Asp Glu Ile Thr Asn Pro Ile Val Lys Arg Ala Ile Thr Gln Ala Arg
                485                 490                 495

Lys Val Val Asn Ala Ile Ile Arg Arg Tyr Gly Ser Pro Asn Ser Val
            500                 505                 510

His Ile Glu Leu Ala Arg Glu Leu Ser Lys Ser His Asp Glu Arg Lys
        515                 520                 525

Lys Ile Met Thr Ala His Asp Glu Asn Tyr Lys Lys Asn Lys Gly Ala
    530                 535                 540

Ile Ser Ile Leu Ile Glu Asn Gly Ile Leu Asn Pro Thr Gly Tyr Asp
545                 550                 555                 560

Ile Val Arg Tyr Lys Leu Trp Lys Glu Gln Gly Glu Arg Cys Ala Tyr
                565                 570                 575

Ser Leu Lys Glu Ile Pro Pro Asp Thr Phe Phe Asn Glu Leu Lys Lys
            580                 585                 590

Glu Arg Asn Gly Ser Pro Ile Leu Glu Val Asp His Ile Leu Pro Tyr
```

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        595                 600                 605

Ser Gln Ser Phe Ile Asp Ser Tyr His Asn Lys Val Leu Val Tyr Ser
    610                 615                 620

Asp Glu Asn Arg Asn Lys Gly Asn Arg Ile Pro Tyr Thr Tyr Phe Leu
625                 630                 635                 640

Glu Thr Asn Lys Asp Trp Glu Ala Phe Glu Arg Tyr Val Arg Ser Asn
                645                 650                 655

Lys Leu Phe Ser Lys Lys Lys Arg Glu Tyr Leu Leu Lys Lys Thr Tyr
            660                 665                 670

Leu Pro Arg Glu Ser Glu Leu Ile Lys Glu Arg His Leu Asn Asp Thr
        675                 680                 685

Arg Tyr Ala Ser Thr Phe Leu Lys Asn Phe Ile Glu Gln Asn Leu Gln
    690                 695                 700

Phe Lys Glu Val Glu Val Asn Leu Arg Lys Lys Arg Val Gln Thr Val
705                 710                 715                 720

Asn Gly Val Ile Thr Ala His Leu Arg Lys Arg Trp Gly Leu Glu Lys
                725                 730                 735

Asn Arg Gln Glu Thr Tyr Leu His His Ala Met Asp Ala Ile Ile Val
            740                 745                 750

Ala Cys Thr Asp His His Met Val Thr Arg Ile Thr Glu Tyr Tyr Gln
        755                 760                 765

Ile Lys Glu Ser Asn Lys Ser Val Lys Lys Pro Tyr Phe Pro Met Pro
    770                 775                 780

Trp Glu Gly Phe Arg Asp Glu Leu Leu Ser His Leu Ala Ser Gln Pro
785                 790                 795                 800
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```
Ile Ala Lys Lys Ile Ser Glu Glu Leu Lys Ala Gly Tyr Gln Ser Ser
                805                 810                 815

Asp Tyr Ile Phe Val Ser Arg Met Pro Lys Arg Ser Val Thr Gly Ala
            820                 825                 830

Ala His Asp Gln Thr Ile Arg Arg Lys Gly Gly Ile Asp Lys Lys Gly
        835                 840                 845

Lys Thr Ile Ile Ile Lys Arg Val Arg Leu Lys Asp Ile Lys Phe Asp
    850                 855                 860

Glu Asn Gly Asp Phe Lys Met Val Gly Lys Glu Gln Asp Leu Ala Thr
865                 870                 875                 880

Tyr Glu Ala Ile Lys Gln Arg Tyr Leu Glu His Arg Lys Asn Ser Lys
                885                 890                 895

Lys Ala Phe Glu Thr Pro Leu Tyr Lys Pro Ser Lys Lys Gly Thr Gly
            900                 905                 910

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

Arg Glu Val Asn Gly Gly Val Ala Gln Asn Ser Asp Leu Val Arg Val
    930                 935                 940

Asp Leu Phe Glu Lys Asp Asp Lys Tyr Tyr Met Val Pro Ile Tyr Val
945                 950                 955                 960

Pro Asp Thr Val Cys Ser Glu Leu Pro Lys Lys Val Val Lys Ser Gly
                965                 970                 975

Lys Gly Tyr Glu Gln Trp Leu Thr Leu Asp Asn Ser Phe Thr Phe Lys
            980                 985                 990

Ser Ser Leu Tyr Pro Tyr Asp Leu  Val Arg Leu Val Lys  Gly Asn Glu
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995 1000 1005

Asp Arg Phe Leu Tyr Phe Gly Thr Leu Asp Ile Asp Ser Asp Arg
1010 1015 1020

Leu Asn Phe Lys Asp Val Asn Lys Pro Ser Lys Gln Asn Glu Tyr
1025 1030 1035

Arg Tyr Ser Leu Lys Thr Ile Glu Asn Leu Glu Lys Tyr Glu Val
1040 1045 1050

Gly Val Leu Gly Asp Leu Arg Leu Val Lys Gln Glu Thr Arg Arg
1055 1060 1065

Ile Phe Asn Arg
1070

<210> 263
<211> 130
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 263
catggcagta cattagagca gtcatagttc cattaaagcc aaaagtggct ttgatgtttc 60

tatgataagg gtttcgaccc gtggcgtcgg ggatcgcctg cccattgaaa tgggcttctc 120

cccatttatt 130

<210> 264
<211> 130
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 264
cacatctcga gcaagacgtt gtcatagttc cattaaagcc aaaagtggct ttgatgtttc 60

tatgataagg gtttcgaccc gtggcgtcgg ggatcgcctg cccattgaaa tgggcttctc 120

cccatttatt 130

<210> 265
<211> 130
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 265
cttctatagc ctccttcccc gtcatagttc cattaaagcc aaaagtggct ttgatgtttc 60

tatgataagg gtttcgaccc gtggcgtcgg ggatcgcctg cccattgaaa tgggcttctc 120

cccatttatt 130

<210> 266
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 266
caggtcgact ctagaggatc ccatgatata gacgttgtgg ctgttgtagt 50

<210> 267
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<220>
<221> modified_base
<222> (19)..(23)
<223> a, c, t, g, unknown or other

<400> 267
aacgacggcc agtgaattnn nnnactacaa cagccacaac gtctatatca tgg 53

<210> 268
<211> 1493
<212> PRT
<213> Homo sapiens

<400> 268
Met Pro Asn Glu Gly Ile Pro His Ser Ser Gln Thr Gln Glu Gln Asp
1 5 10 15

Cys Leu Gln Ser Gln Pro Val Ser Asn Asn Glu Glu Met Ala Ile Lys
20 25 30

Gln Glu Ser Gly Gly Asp Gly Glu Val Glu Glu Tyr Leu Ser Phe Arg
35 40 45

Ser Val Gly Asp Gly Leu Ser Thr Ser Ala Val Gly Cys Ala Ser Ala
50 55 60

Ala Pro Arg Arg Gly Pro Ala Leu Leu His Ile Asp Arg His Gln Ile
65 70 75 80

Gln Ala Val Glu Pro Ser Ala Gln Ala Leu Glu Leu Gln Gly Leu Gly
85 90 95

Val Asp Val Tyr Asp Gln Asp Val Leu Glu Gln Gly Val Leu Gln Gln
100 105 110

Val Asp Asn Ala Ile His Glu Ala Ser Arg Ala Ser Gln Leu Val Asp
115 120 125

Val Glu Lys Glu Tyr Arg Ser Val Leu Asp Asp Leu Thr Ser Cys Thr

```
    130                 135                 140

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

Ala Ala Thr Ser Arg Asp Ile Asn Arg Lys Leu Asp Ser Val Lys Arg
                165                 170                 175

Gln Lys Tyr Asn Lys Glu Gln Gln Leu Lys Lys Ile Thr Ala Lys Gln
            180                 185                 190

Lys His Leu Gln Ala Ile Leu Gly Gly Ala Glu Val Lys Ile Glu Leu
        195                 200                 205

Asp His Ala Ser Leu Glu Glu Asp Ala Glu Pro Gly Pro Ser Ser Leu
    210                 215                 220

Gly Ser Met Leu Met Pro Val Gln Glu Thr Ala Trp Glu Glu Leu Ile
225                 230                 235                 240

Arg Thr Gly Gln Met Thr Pro Phe Gly Thr Gln Ile Pro Gln Lys Gln
                245                 250                 255

Glu Lys Lys Pro Arg Lys Ile Met Leu Asn Glu Ala Ser Gly Phe Glu
            260                 265                 270

Lys Tyr Leu Ala Asp Gln Ala Lys Leu Ser Phe Glu Arg Lys Lys Gln
        275                 280                 285

Gly Cys Asn Lys Arg Ala Ala Arg Lys Ala Pro Ala Pro Val Thr Pro
    290                 295                 300

Pro Ala Pro Val Gln Asn Lys Asn Lys Pro Asn Lys Lys Ala Arg Val
305                 310                 315                 320

Leu Ser Lys Lys Glu Glu Arg Leu Lys Lys His Ile Lys Lys Leu Gln
                325                 330                 335
```

```
Lys Arg Ala Leu Gln Phe Gln Gly Lys Val Gly Leu Pro Lys Ala Arg
            340                 345                 350

Arg Pro Trp Glu Ser Asp Met Arg Pro Glu Ala Glu Gly Asp Ser Glu
        355                 360                 365

Gly Glu Glu Ser Glu Tyr Phe Pro Thr Glu Glu Glu Glu Glu Glu Glu
    370                 375                 380

Asp Asp Glu Val Glu Gly Ala Glu Ala Asp Leu Ser Gly Asp Gly Thr
385                 390                 395                 400

Asp Tyr Glu Leu Lys Pro Leu Pro Lys Gly Gly Lys Arg Gln Lys Lys
                405                 410                 415

Val Pro Val Gln Glu Ile Asp Asp Asp Phe Phe Pro Ser Ser Gly Glu
            420                 425                 430

Glu Ala Glu Ala Ala Ser Val Gly Glu Gly Gly Gly Gly Gly Arg Lys
        435                 440                 445

Val Gly Arg Tyr Arg Asp Asp Gly Asp Glu Asp Tyr Tyr Lys Gln Arg
    450                 455                 460

Leu Arg Arg Trp Asn Lys Leu Arg Leu Gln Asp Lys Glu Lys Arg Leu
465                 470                 475                 480

Lys Leu Glu Asp Asp Ser Glu Glu Ser Asp Ala Glu Phe Asp Glu Gly
                485                 490                 495

Phe Lys Val Pro Gly Phe Leu Phe Lys Lys Leu Phe Lys Tyr Gln Gln
            500                 505                 510

Thr Gly Val Arg Trp Leu Trp Glu Leu His Cys Gln Gln Ala Gly Gly
        515                 520                 525

Ile Leu Gly Asp Glu Met Gly Leu Gly Lys Thr Ile Gln Ile Ile Ala
```

```
    530                 535                 540

Phe Leu Ala Gly Leu Ser Tyr Ser Lys Ile Arg Thr Arg Gly Ser Asn
545                 550                 555                 560

Tyr Arg Phe Glu Gly Leu Gly Pro Thr Val Ile Val Cys Pro Thr Thr
                565                 570                 575

Val Met His Gln Trp Val Lys Glu Phe His Thr Trp Trp Pro Pro Phe
            580                 585                 590

Arg Val Ala Ile Leu His Glu Thr Gly Ser Tyr Thr His Lys Lys Glu
        595                 600                 605

Lys Leu Ile Arg Asp Val Ala His Cys His Gly Ile Leu Ile Thr Ser
    610                 615                 620

Tyr Ser Tyr Ile Arg Leu Met Gln Asp Asp Ile Ser Arg Tyr Asp Trp
625                 630                 635                 640

His Tyr Val Ile Leu Asp Glu Gly His Lys Ile Arg Asn Pro Asn Ala
                645                 650                 655

Ala Val Thr Leu Ala Cys Lys Gln Phe Arg Thr Pro His Arg Ile Ile
            660                 665                 670

Leu Ser Gly Ser Pro Met Gln Asn Asn Leu Arg Glu Leu Trp Ser Leu
        675                 680                 685

Phe Asp Phe Ile Phe Pro Gly Lys Leu Gly Thr Leu Pro Val Phe Met
    690                 695                 700

Glu Gln Phe Ser Val Pro Ile Thr Met Gly Gly Tyr Ser Asn Ala Ser
705                 710                 715                 720

Pro Val Gln Val Lys Thr Ala Tyr Lys Cys Ala Cys Val Leu Arg Asp
                725                 730                 735
```

```
Thr Ile Asn Pro Tyr Leu Leu Arg Arg Met Lys Ser Asp Val Lys Met
            740                 745                 750

Ser Leu Ser Leu Pro Asp Lys Asn Glu Gln Val Leu Phe Cys Arg Leu
        755                 760                 765

Thr Asp Glu Gln His Lys Val Tyr Gln Asn Phe Val Asp Ser Lys Glu
    770                 775                 780

Val Tyr Arg Ile Leu Asn Gly Glu Met Gln Ile Phe Ser Gly Leu Ile
785                 790                 795                 800

Ala Leu Arg Lys Ile Cys Asn His Pro Asp Leu Phe Ser Gly Gly Pro
                805                 810                 815

Lys Asn Leu Lys Gly Leu Pro Asp Asp Glu Leu Glu Glu Asp Gln Phe
            820                 825                 830

Gly Tyr Trp Lys Arg Ser Gly Lys Met Ile Val Val Glu Ser Leu Leu
        835                 840                 845

Lys Ile Trp His Lys Gln Gly Gln Arg Val Leu Leu Phe Ser Gln Ser
    850                 855                 860

Arg Gln Met Leu Asp Ile Leu Glu Val Phe Leu Arg Ala Gln Lys Tyr
865                 870                 875                 880

Thr Tyr Leu Lys Met Asp Gly Thr Thr Thr Ile Ala Ser Arg Gln Pro
                885                 890                 895

Leu Ile Thr Arg Tyr Asn Glu Asp Thr Ser Ile Phe Val Phe Leu Leu
            900                 905                 910

Thr Thr Arg Val Gly Gly Leu Gly Val Asn Leu Thr Gly Ala Asn Arg
        915                 920                 925

Val Val Ile Tyr Asp Pro Asp Trp Asn Pro Ser Thr Asp Thr Gln Ala
```

```
    930                 935                 940

Arg Glu Arg Ala Trp Arg Ile Gly Gln Lys Lys Gln Val Thr Val Tyr
945                 950                 955                 960

Arg Leu Leu Thr Ala Gly Thr Ile Glu Glu Lys Ile Tyr His Arg Gln
                965                 970                 975

Ile Phe Lys Gln Phe Leu Thr Asn Arg Val Leu Lys Asp Pro Lys Gln
            980                 985                 990

Arg Arg Phe Phe Lys Ser Asn Asp  Leu Tyr Glu Leu Phe  Thr Leu Thr
        995                 1000                1005

Ser Pro  Asp Ala Ser Gln Ser  Thr Glu Thr Ser Ala  Ile Phe Ala
    1010                1015                1020

Gly Thr  Gly Ser Asp Val Gln  Thr Pro Lys Cys His  Leu Lys Arg
    1025                1030                1035

Arg Ile  Gln Pro Ala Phe Gly  Ala Asp His Asp Val  Pro Lys Arg
    1040                1045                1050

Lys Lys  Phe Pro Ala Ser Asn  Ile Ser Val Asn Asp  Ala Thr Ser
    1055                1060                1065

Ser Glu  Glu Lys Ser Glu Ala  Lys Gly Ala Glu Val  Asn Ala Val
    1070                1075                1080

Thr Ser  Asn Arg Ser Asp Pro  Leu Lys Asp Asp Pro  His Met Ser
    1085                1090                1095

Ser Asn  Val Thr Ser Asn Asp  Arg Leu Gly Glu Glu  Thr Asn Ala
    1100                1105                1110

Val Ser  Gly Pro Glu Glu Leu  Ser Val Ile Ser Gly  Asn Gly Glu
    1115                1120                1125
```

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Cys Ser  Asn Ser Ser Gly Thr  Gly Lys Thr Ser Met  Pro Ser Gly
    1130                1135                1140

Asp Glu  Ser Ile Asp Glu Lys  Leu Gly Leu Ser Tyr  Lys Arg Glu
    1145                1150                1155

Arg Pro  Ser Gln Ala Gln Thr  Glu Ala Phe Trp Glu  Asn Lys Gln
    1160                1165                1170

Met Glu  Asn Asn Phe Tyr Lys  His Lys Ser Lys Thr  Lys His His
    1175                1180                1185

Ser Val  Ala Glu Glu Glu Thr  Leu Glu Lys His Leu  Arg Pro Lys
    1190                1195                1200

Gln Lys  Pro Lys Asn Ser Lys  His Cys Arg Asp Ala  Lys Phe Glu
    1205                1210                1215

Gly Thr  Arg Ile Pro His Leu  Val Lys Lys Arg Arg  Tyr Gln Lys
    1220                1225                1230

Gln Asp  Ser Glu Asn Lys Ser  Glu Ala Lys Glu Gln  Ser Asn Asp
    1235                1240                1245

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

Ser Val  Met Lys His Asp Ala  Ile Met Asp Gly Ala  Ser Pro Asp
    1265                1270                1275

Tyr Val  Leu Val Glu Ala Glu  Ala Asn Arg Val Ala  Gln Asp Ala
    1280                1285                1290

Leu Lys  Ala Leu Arg Leu Ser  Arg Gln Arg Cys Leu  Gly Ala Val
    1295                1300                1305

Ser Gly  Val Pro Thr Trp Thr  Gly His Arg Gly Ile  Ser Gly Ala
```

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    1310                1315                1320

Pro Ala  Gly Lys Lys Ser Arg  Phe Gly Lys Lys Arg  Asn Ser Asn
    1325                1330                1335

Phe Ser  Val Gln His Pro Ser  Ser Thr Ser Pro Thr  Glu Lys Cys
    1340                1345                1350

Gln Asp  Gly Ile Met Lys Lys  Glu Gly Lys Asp Asn  Val Pro Glu
    1355                1360                1365

His Phe  Ser Gly Arg Ala Glu  Asp Ala Asp Ser Ser  Ser Gly Pro
    1370                1375                1380

Leu Ala  Ser Ser Ser Leu Leu  Ala Lys Met Arg Ala  Arg Asn His
    1385                1390                1395

Leu Ile  Leu Pro Glu Arg Leu  Glu Ser Glu Ser Gly  His Leu Gln
    1400                1405                1410

Glu Ala  Ser Ala Leu Leu Pro  Thr Thr Glu His Asp  Asp Leu Leu
    1415                1420                1425

Val Glu  Met Arg Asn Phe Ile  Ala Phe Gln Ala His  Thr Asp Gly
    1430                1435                1440

Gln Ala  Ser Thr Arg Glu Ile  Leu Gln Glu Phe Glu  Ser Lys Leu
    1445                1450                1455

Ser Ala  Ser Gln Ser Cys Val  Phe Arg Glu Leu Leu  Arg Asn Leu
    1460                1465                1470

Cys Thr  Phe His Arg Thr Ser  Gly Gly Glu Gly Ile  Trp Lys Leu
    1475                1480                1485

Lys Pro  Glu Tyr Cys
    1490
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<210> 269
<211> 135
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 269
cgacgguuag aggccguaug ucgauuugcu uuaauuucgu gcgugugcau ugucguccuc 60

cauuacaggg cggcuaccac gaauagccac gaaguaaaag cuucguggcu agcacgcuug 120

cacuagacua gcuuc 135

<210> 270
<211> 135
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 270
cgacgguuag aggccguaug ucgauuugcu uuaauuucgu gcgugugcau ugucguccuc 60

cauuacaggg cggcuaccac gaauagccac gaaguaaaag cuucguggcu agcaccuuuu 120

aucacaggcu ccagg 135

<210> 271
<211> 25
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 271
gacagcagcu uccuauaucu cguac 25

<210> 272
<211> 18
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 272
gcuuccuaua ucucguac 18

<210> 273
<211> 22
<212> RNA
<213> Brevibacillus sp.

<400> 273
uggaaagcuu cgagguuagc ac 22

<210> 274
<211> 95
<212> RNA
<213> Brevibacillus sp.

<400> 274
cgacgguuag aggccguaug ucgauuugcu uuaauuucgu gcgugugcau ugucguccuc 60

cauuacaggg cggcuaccac gaauagccac gaagu 95

<210> 275
<211> 151
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
<221> modified_base
<222> (132)..(151)
<223> a, c, u, g, unknown or other

<400> 275
cgacgguuag aggccguaug ucgauuugcu uuaauuucgu gcgugugcau ugucguccuc 60

cauuacaggg cggcuaccac gaauagucac gaaguuccac ugaguaaagu ggaaagcuuc 120

gagguuagca cnnnnnnnnn nnnnnnnnnn n 151

<210> 276
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
6xHis tag"

<400> 276
His His His His His His
1 5

<210> 277
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
10xHis tag"

<400> 277
His His His His His His His His His His
1 5 10

<210> 278
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 278

cccgtataaa gcatgagacc gtgac 25

<210> 279
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 279
ctcagactgt ttgcccctta ctgct 25

<210> 280
<211> 135
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 280
cgacgguuag aggccguaug ucgauuugcu uuaauuucgu gcgugugcau ugucguccuc 60

cauuacaggg cggcuaccac gaauagccac gaaguaaaag cuucguggcu agcaccccgu 120

auaaagcaug agacc 135

<210> 281
<211> 135
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 281
cgacgguuag aggccguaug ucgauuugcu uuaauuucgu gcgugugcau ugucguccuc 60

cauuacaggg cggcuaccac gaauagccac gaaguaaaag cuucguggcu agcaccucag 120

acuguuugcc ccuua 135

<210> 282
<211> 156
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 282
cgacgguuag aggccguaug ucgauuugcu uuaauuucgu gcgugugcau ugucguccuc 60

cauuacaggg cggcuaccac gaauagucac gaaguuccac ugaguaaagu ggaaagcuuc 120

gagguuagca ccccguauaa agcaugagac cgugac 156

<210> 283
<211> 156
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 283
cgacgguuag aggccguaug ucgauuugcu uuaauuucgu gcgugugcau ugucguccuc 60

cauuacaggg cggcuaccac gaauagucac gaaguuccac ugaguaaagu ggaaagcuuc 120

gagguuagca ccucagacug uuugccccuu acugcu 156

<210> 284
<211> 4
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 284

aaaa 4

<210> 285
<211> 135
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
<221> modified_base
<222> (116)..(135)
<223> a, c, u, g, unknown or other

<400> 285
cgacgguuag aggccguaug ucgauuugcu uuaauuucgu gcgugugcau ugucguccuc 60

cauuacaggg cggcuaccac gaauagccac gaaguaaaag cuucguggcu agcacnnnnn 120

nnnnnnnnnn nnnnn 135

<210> 286
<211> 95
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 286
cgacgguuag aggccguaug ucgauuugcu uuaauuucgu gcgugugcau ugucguccuc 60

cauuacaggg cggcuaccac gaauagccac gaagu 95

<210> 287
<211> 16
<212> RNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 287
gcuucguggc uagcac 16

<210> 288
<211> 151
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
<221> modified_base
<222> (132)..(151)
<223> a, c, u, g, unknown or other

<400> 288
cgacgguuag aggccguaug ucgauuugcu uuaauuucgu gcgugugcau ugucguccuc 60

cauuacaggg cggcuaccac gaauagucac gaaguuccac ugaguaaagu ggaaagcuuc 120

gagguuagca cnnnnnnnnn nnnnnnnnnn n 151

<210> 289
<211> 135
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
<221> modified_base
<222> (116)..(135)
<223> a, c, u, g, unknown or other

<400> 289
cgacgguuag aggccguaug ucgauuugcu uuaauuucgu gcgugugcau ugucguccuc 60

cauuacaggg cggcuaccac gaauagucac gaaguaaaag cuucgagguu agcacnnnnn 120

nnnnnnnnnn nnnnn 135

<210> 290
<211> 144
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
<221> modified_base
<222> (125)..(144)
<223> a, c, u, g, unknown or other

<400> 290
cgacgguuag aggccguaug ucgauuugcu uuaauuucgu gcgugugcau ugucguccuc 60

cauuacaggg cggcuaccac gaauagccac gaaguuccaa aauggaaagc uucguggcua 120

gcacnnnnnn nnnnnnnnnn nnnn 144

<210> 291
<211> 135
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
<221> modified_base
<222> (116)..(135)
<223> a, c, u, g, unknown or other

<400> 291
cgacgguuag aggccguaug ucgauuugcu uuaauuucgu gcgugugcau ugucguccuc 60

cauuacaggg cggcuaccac gaauagccac gaaguaaaag cuucguggcu agcacnnnnn 120

nnnnnnnnnn nnnnn 135

<210> 292
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 292
gtacgagata taggaagctg ctgtccgctc 30

<210> 293
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 293
actacaacag ccacaacgtc tatatcatg 29

<210> 294
<211> 149
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 294
cgacgguuag aggccguaug ucgauuugcu uuaauuucgu gcgugugcau ugucguccuc 60

cauuacaggg cggcuaccac gaauagucac gaaguuccac ugaguaaagu ggaaagcuuc 120

gagguuagca cacuacaaca gccacaacg 149

<210> 295

<211> 151
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 295
cgacgguuag aggccguaug ucgauuugcu uuaauuucgu gcgugugcau ugucguccuc 60

cauuacaggg cggcuaccac gaauagucac gaaguuccac ugaguaaagu ggaaagcuuc 120

gagguuagca cguacgagau auaggaagcu g 151

<210> 296
<211> 151
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 296
cgacgguuag aggccguaug ucgauuugcu uuaauuucgu gcgugugcau ugucguccuc 60

cauuacaggg cggcuaccac gaauagucac gaaguuccac ugaguaaagu ggaaagcuuc 120

gagguuagca cacuacaaca gccacaacgu c 151

<210> 297
<211> 156
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 297
cgacgguuag aggccguaug ucgauuugcu uuaauuucgu gcgugugcau ugucguccuc 60

cauuacaggg cggcuaccac gaauagucac gaaguuccac ugaguaaagu ggaaagcuuc 120

gagguuagca cguacgagau auaggaagcu gcuguc 156

<210> 298
<211> 156
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 298
cgacgguuag aggccguaug ucgauuugcu uuaauuucgu gcgugugcau ugucguccuc 60

cauuacaggg cggcuaccac gaauagucac gaaguuccac ugaguaaagu ggaaagcuuc 120

gagguuagca cacuacaaca gccacaacgu cuauau 156

<210> 299
<211> 140
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 299
cgacgguuag aggccguaug ucgauuugcu uuaauuucgu gcgugugcau ugucguccuc 60

cauuacaggg cggcuaccac gaauagucac gaaguaaaag cuucgagguu agcacacuac 120

aacagccaca acgucuauau 140

<210> 300
<211> 149
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 300

cgacgguuag aggccguaug ucgauuugcu uuaauuucgu gcgugugcau ugucguccuc 60

cauuacaggg cggcuaccac gaauagccac gaaguuccaa aauggaaagc uucguggcua 120

gcacacuaca acagccacaa cgucuauau 149

<210> 301
<211> 140
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 301
cgacgguuag aggccguaug ucgauuugcu uuaauuucgu gcgugugcau ugucguccuc 60

cauuacaggg cggcuaccac gaauagccac gaaguaaaag cuucguggcu agcacacuac 120

aacagccaca acgucuauau 140

<210> 302
<211> 135
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 302
cgacgguuag aggccguaug ucgauuugcu uuaauuucgu gcgugugcau ugucguccuc 60

cauuacaggg cggcuaccac gaauagccac gaaguaaaag cuucguggcu agcacacuac 120

aacagccaca acguc 135

<210> 303
<211> 140
<212> RNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 303
cgacgguuag aggccguaug ucgauuugcu uuaauuucgu gcgugugcau ugucguccuc 60

cauuacaggg cggcuaccac gaauagccac gaaguaaaag cuucguggcu agcacguacg 120

agauauagga agcugcuguc 140

<210> 304
<211> 3324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 304
atggccattc ggagcatcaa gctcaagctg aagaccagaa ccggtcctga ggctcagaac 60

ctgcggaagg gcatctggag aacccaccgg ctgctgaacg agggcgtggc ctactacatg 120

aagatgctgc tgctcttccg gcaggaatcc actggcggcc agacaaagaa ggaactgcag 180

gaggaactgg tgcggcacat ccgggagcag cagcagaaaa acagagccga caagaatacc 240

caggccctgc ctctggataa ggccttcgcc gctctgagac aactgtacga gctgctcgtg 300

ccatctagca tcggccagag cggcgatgcc cagatcatct ctagaaaatt cctgtctcct 360

ttggtggacc ctaacagcga gggcggcaag ggcactagca aggccggagc caagcccaca 420

tggcagaaaa agaaggaggc caatgaccct acatgggagc aagattacga gaagtggaaa 480

aagcgtagag aggaagatcc taccgccagt gtgataacaa ccctggaaga atatggaatt 540

agacctatct ttccactgta caccaacacc gtggccgata tcgcctggct gcctctgcag 600

tctaaccagt ttgtccggac atgggatcgg gacatgctgc agcaggccat cgagaggcta 660

ctctcttggg agtcttggaa caagcgggtg caagaggaat acagcaagct gcaggagaag 720

atgacgcaac tgaacgagca actggagggc ggacaggagt ggatcagcct gctggaacaa 780

tacgaggaac agagagagca ggagctgatc gaaaacatga ccgccgcaaa cgataaatac 840

cgcatcacca agcggcagat gaagggctgg aatgagctgt atgagcagtg gtctaccgtg 900

ctgcccaatg ccagccacga gcagtacaga gaggcactga aaagagtgca acagcggctg 960

aggggcagat tcggcgacgc tcatttcttc cagtatctga tgaaagaaga acaccacctg 1020

atctggaagg ggaaccctca gagaatccac tacttcgtgg ccagaaacga gctgaagaaa 1080

agactggaag aagccaagca gaacgccacc atgaccctgc ctgatgccag aaagcaccct 1140

ctgtgggtca gatttgacgc cagaggcggc aacctgcaag actactacct gacggccgaa 1200

gccgacaacc ccagaagcag aaggttcgtg accttcagcc aactgatctg gcctaacgag 1260

agcggctgga tggaaaaaca ggacgtggaa gttgaactgg ccctgagcaa gcagttctac 1320

cagcaagtga cactgcagaa aaacgacaag gggaagcagg aaatcgagtt caaagacaag 1380

ggcagtggca gcaccttcag cggccacctg ggcggggcca agctgcaact ggagagagga 1440

gatctggaga aggaagaaaa agactttgaa ggcggcgaaa tcggcagcgt gtacctgaac 1500

atcgtgatcg acttcgagcc actgcaggag gtgaagaacg gccgactgca atctccttac 1560

ggccaggtgc tgcaactggt cagaaggcct aatgagttcc ccaaggtgac cacctacaag 1620

tctgaggaac tggtcgagtg gatcaagagc agcaccaagg acagcgccgg cgtggagtcc 1680

ttagagagcg gttttagagt gatgagcatc gacctgggac tgcggaccgc cgccgcaaca 1740

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gagggaactc ctctggttgc cgttcataag cggtcatata tgctgaaact gcccggagag 1860

caagtcgaaa agcaggtgcg agagaagcgg gacgagcggc aggatcagca gagaagagtg 1920

aggttccaaa tcagaatcct gagccaggtg atccggatgg ccaagaagca gaaccgggag 1980

cgggctgatg agctggacca cctgtcccag gccctggaga agcaaaaatc tctgctggac 2040

cagaccgatc ggacctttg gaacggcatc gtgtgcgacc tgacagacgc tctgagagag 2100

aaagagggcg gatgggaaca ggccgtggtc cagatccaca ggaaggccga ggagcacgtg 2160

ggcaaggtgg tgcaagcctg gcggaaacgg ttcgacgccg atgaacgcaa gggcatcgcc 2220

ggcctgtcta tgtggtctat cgaggagctg gacagcctgc ggaagctgct gatctcttgg 2280

agcagaagaa caagaaaccc cagagaaatc aactgcttcg agcagggcca caccagccac 2340

cagcggctgc tgacacacat ccagaacgtg aaggaggacc ggctgaagca actgagccac 2400

gccattgtga tgacagcctt gggctacgtg tacgacgaga agaaattgga atggtttgcc 2460

aagtaccctg cttgtcaggt gatcctgttc gagaacctgt cccagtaccg gtccaacatg 2520

gacagaagca ccaaagagaa tagcaccctg atgaaatggg cccacaggag catccctaag 2580

tacgtgcaca tgcaggccga gccttacggc atccagatcg gcgatgtgcg ggccgagtac 2640

tccagcagat tccacgccaa gacaggcaca cctggcatcc ggtgcaagat ggtgtccgga 2700

cacgacctgc aaggcaggcg cttcgagaac ctgcagaagc ggttaatctc tgaacagttc 2760

ctgacagagg agcaagtgaa gcagctcaga cccggcgaca tcgtgcccga cgactccggc 2820

gagtggttca tgaccctgag cgacggcagc gaaggcaaag aggttgtgtt cctccaagcc 2880

gacatcaacg ccgcccaaaa tctgcaaaag agattctggc agcggtacaa cgagctgttt 2940

aaggtctcct gcagagtgct gatccgagga gaagaggaat acctgatccc caagacaaag 3000

tccgtgcaag ccaagctggg caaaggcctg ttcgtgaaaa aaaccgacac cgtgatgaag 3060

gacgtgtacg tgtgggacag ccaggctaag ctgaagggca aaaccacatt caccgaggag 3120

tccgaaagcc ctgagcaact ggaggatttt caggagatca tcgaagaagc cgaagaagct 3180

aagggcacat acagaacact gtttagagac cccagcggag tgttcttccc tgagttcgtg 3240

tggtccaccc agaaagattt ctggtccgag gtgaagagac ggctgtacgg caagctgaga 3300

gagcggttcc tgatgaagac cagg 3324

<210> 305
<211> 3324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 305
atggccatca gatctatcaa gctgaagctc aagaccagaa caggtcctga ggcccagaac 60

ctgcggaagg gcatttggcg gacacaccgc ctcctcaacg agggcgtcgc ctattatatg 120

aaaatgctgc tgctgttcag acaggagagc acaggcggcc agaccaagaa agagctgcag 180

gaagaactgg tccggcacat cagagagcag cagcagaaga atcgggccga caagaacacc 240

caggccctgc ctctggacaa ggcttttgcc gctctgcggc agctctacga gctgctggtg 300

ccttcttcta tcggccagag cggagacgcg cagatcatca gcagaaagtt cctgtcccct 360

ctcgtggacc ccaacagcga gggcggcaag ggcacatcta aagctggcgc caagcctaca 420

tggcagaaaa agaaggaggc caacgacccc acctgggaac aggattacga gaaatggaag 480

aagcggagag aggaggaccc taccgccagc gtgattacca ccctggaaga atacggcatc 540

agaccaatct tcccactgta caccaacacc gtggccgaca tcgcctggct gcctctgcag 600

tccaaccagt tcgtgcggac atgggacaga gacatgctgc agcaggctat cgagagactg 660

ctgagctggg aaagctggaa caagagagtg caagaggaat acagcaagct gcaagagaag 720

atgacacagc tcaacgagca actggagggc ggccaggagt ggatcagcct gctggaacag 780

tacgaggagc aacgggagca ggagctgatc gagaacatga ccgccgctaa cgacaaatat 840

agaataacaa agcggcagat gaagggctgg aacgagctgt acgagcagtg gagcaccgtg 900

ctgcccaatg cctctcacga gcagtaccgg gaagccctta agcgggtcca gcaaagactg 960

cggggcagat tcggcgacgc tcatttcttc cagtatctga tgaaggaaga gcaccacctg 1020

atttggaagg gcaaccccca gagaatccac tactttgtgg ccagaaacga gctgaagaaa 1080

agactggaag aggccaagca gaacgccact atgaccctgc cagacgccag aaagcacccc 1140

ctgtgggtgc ggttcgacgc cagaggcgga aatctgcagg actactacct gaccgccgag 1200

gccgataacc ccagatctag aagattcgtt acctttagcc agttgatctg gcctaacgag 1260

tccggctgga tggaaaagca ggacgtggaa gtggaactcg ccctgagcaa gcagttctac 1320

cagcaagtga ccctgcagaa gaacgataag gggaaacagg agatcgagtt taaggacaag 1380

ggctccggat ctacgttcag tggccatctg ggcggggcta agctgcaact ggagcgaggc 1440

gacctggaga aagaagagaa ggactttgag ggcggagaaa tcggaagcgt gtacctgaac 1500

atcgtgatcg acttcgagcc cttgcaggag gtgaaaaacg gcagactgca gagcccatac 1560

ggccaggtgc tgcagctcgt tcggagacct aatgagttcc ctaaggtgac cacatacaag 1620

tctgaagaac ttgttgagtg gatgaaggcc agccagaatc acagcagcgg cgtggagtct 1680

ctggagtcgg gcttcagagt gatgagcatc gatctgggac tgaggacagc cgctgccacc 1740

agcattttct ctgtggaaga aagcaacgat gccaacgccg ctggcttcag ctactggatc 1800

gagggcaccc ctctggtcgc cgtgcacaag agaagctaca tgctgaagct gccaggcgaa 1860

caagtggaaa aacaggtgcg ggaaaagaga gatgagagac aagaccagca gaggcgcgtc 1920

agatttcaga tcagaatcct gagccaggtg atcaggatgg ccaagaaaca aaacagagaa 1980

agagctgacg aactggacca cctgagccag gcactggaga agcagaagtc cctgctcgat 2040

cagaccgata gaaccttctg gaacggcatc gtttgtgacc tgaccgatgc gctgcgcgaa 2100

aaggagggag gctgggagca agccgtggtc caaatccaca gaaaggccga ggaacacgtg 2160

ggcaaggtgg tgcaagcctg gcggaaaaga tttgacgccg atgagcggaa gggcatcgcc 2220

ggcctgagca tgtggtccat agaagagctg gacagcctcc ggaagctgct cattagctgg 2280

agcagaagga caagaaaccc tcaggagatc aacagattcg agcagggcca cacctctcac 2340

cagcggctgc tgacacatat ccagaacgtg aaggaagata gactgaagca actgagccac 2400

gccatcgtga tgaccgccct gggctacgtg tacgacgaga agaagctgga gtggttcgcc 2460

aaataccccg cctgccaggt gatcctgttc gagaatctgt ctcagtacag aagccacatg 2520

gacagatcca cgaaggaaaa tagcaccctg atgaaatggg cccacagaag catccctaag 2580

tacgtccaca tgcaggccga gccttacgga atccagatcg gagatgtgag agccgaatat 2640

agcagcaggt tccacgccaa gacagggaca cctggcatcc gttgcaagat ggtgaaggga 2700

caagaactgc aaggcaagcg attcgagaac ctgcaaaaga gactggtgtc cgaacagttt 2760

ctgaccgagg aacaggtgaa gcagcttcgg cctggagata tcgtgccaga tgacagcgga 2820

gagtggttca tgaccctgag tgatggcagc gaaggcaagg aagtggtgtt cctgcaagcc 2880

gacatcaacg ccgcccagaa ccttcagaaa cgattctggc agagatacaa cgaactgttc 2940

aaggtgtcat gcagagtgct gatcagaggc gaggaagagt acctgatccc caaggccaag 3000

agcgtgcaag ccaaactcgg caagggactg ttcgtgaaga aaaccgacac cgtgatgaag 3060

gacgtgtacg tgtgggatag ccaggccaaa ctgaagggca aaacaacctt caccgaggaa 3120

agcgagagcc ctgagcaact ggaggacttc caggagatca tcgaagaagc cgaggaagcc 3180

aagggcacct acagaacact gtttagagat cctagcggcg ttttcttccc cgagttcgtg 3240

tggaataccc agaaagactt ctggtccgag gtgaagagaa ggctgtacgg caagctgcgc 3300

gagagattcc tgatgaagac ccgg 3324

<210> 306
<211> 203
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 306
tgatgcggtt ttggcagtac atcaatgggc gtggatagcg gtttgactca cggggatttc 60

caagtctcca ccccattgac gtcaatggga gtttgttttg gcaccaaaat caacgggact 120

ttccaaaatg tcgtaacaac tccgccccat tgacgcaaat gggcggtagg cgtgtacggt 180

gggaggtcta tataagcaga gct 203

<210> 307
<211> 304
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 307
cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc cccgcccatt 60

gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc attgacgtca 120

atgggtggag tatttacggt aaactgccca cttggcagta catcaagtgt atcatatgcc 180

aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt atgcccagta 240

catgacctta tgggactttc ctacttggca gtacatctac gtattagtca tcgctattac 300

catg 304

<210> 308
<211> 318
<212> DNA
<213> Homo sapiens

<400> 308
tgtacaaaaa agcaggcttt aaaggaacca attcagtcga ctggatccgg taccaaggtc 60

gggcaggaag agggcctatt tcccatgatt ccttcatatt tgcatatacg atacaaggct 120

gttagagaga taattagaat taatttgact gtaaacacaa agatattagt acaaaatacg 180

tgacgtagaa agtaataatt tcttgggtag tttgcagttt taaaattatg ttttaaaatg 240

gactatcata tgcttaccgt aacttgaaag tatttcgatt tcttggcttt atatatcttg 300

tggaaaggac gaaacacc 318

<210> 309
<211> 3324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 309
atggccatca gatctatcaa gctgaagctc aagaccagaa caggtcctga ggcccagaac 60

ctgcggaagg gcatttggcg gacacaccgc ctcctcaacg agggcgtcgc ctattatatg 120

aaaatgctgc tgctgttcag acaggagagc acaggcggcc agaccaagaa agagctgcag 180

gaagaactgg tccggcacat cagagagcag cagcagaaga atcgggccga caagaacacc 240

caggccctgc ctctggacaa ggcttttgcc gctctgcggc agctctacga gctgctggtg 300

ccttcttcta tcggccagag cggagacgcg cagatcatca gcagaaagtt cctgtcccct 360

ctcgtggacc ccaacagcga gggcggcaag ggcacatcta aagctggcgc caagcctaca 420

tggcagaaaa agaaggaggc caacgacccc acctgggaac aggattacga gaaatggaag 480

aagcggagag aggaggaccc taccgccagc gtgattacca ccctggaaga atacggcatc 540

agaccaatct tcccactgta caccaacacc gtggccgaca tcgcctggct gcctctgcag 600

tccaaccagt tcgtgcggac atgggacaga gacatgctgc agcaggctat cgagagactg 660

ctgagctggg aaagctggaa caagagagtg caagaggaat acagcaagct gcaagagaag 720

atgacacagc tcaacgagca actggagggc ggccaggagt ggatcagcct gctggaacag 780

tacgaggagc aacgggagca ggagctgatc gagaacatga ccgccgctaa cgacaaatat 840

agaataacaa agcggcagat gaagggctgg aacgagctgt acgagcagtg gagcaccgtg 900

ctgcccaatg cctctcacga gcagtaccgg gaagccctta agcgggtcca gcaaagactg 960

cggggcagat tcggcgacgc tcatttcttc cagtatctga tgaaggaaga gcaccacctg 1020

atttggaagg gcaaccccca gagaatccac tactttgtgg ccagaaacga gctgaagaaa 1080

agactggaag aggccaagca gaacgccact atgaccctgc cagacgccag aaagcacccc 1140

ctgtgggtgc ggttcgacgc cagaggcgga aatctgcagg actactacct gaccgccgag 1200

gccgataacc ccagatctag aagattcgtt acctttagcc agttgatctg gcctaacgag 1260

tccggctgga tggaaaagca ggacgtggaa gtggaactcg ccctgagcaa gcagttctac 1320

cagcaagtga ccctgcagaa gaacgataag gggaaacagg agatcgagtt taaggacaag 1380

ggctccggat ctacgttcag tggccatctg ggcggggcta agctgcaact ggagcgaggc 1440

gacctggaga aagaagagaa ggactttgag ggcggagaaa tcggaagcgt gtacctgaac 1500

atcgtgatcg acttcgagcc cttgcaggag gtgaaaaacg gcagactgca gagcccatac 1560

ggccaggtgc tgcagctcgt tcggagacct aatgagttcc ctaaggtgac cacatacaag 1620

tctgaagaac ttgttgagtg gatgaaggcc agccagaatc acagcagcgg cgtggagtct 1680

ctggagtcgg gcttcagagt gatgagcatc gatctgggac tgaggacagc cgctgccacc 1740

agcattttct ctgtggaaga aagcaacgat gccaacgccg ctggcttcag ctactggatc 1800

gagggcaccc ctctggtcgc cgtgcacaag agaagctaca tgctgaagct gccaggcgaa 1860

caagtggaaa aacaggtgcg ggaaaagaga gatgagagac aagaccagca gaggcgcgtc 1920

agatttcaga tcagaatcct gagccaggtg atcaggatgg ccaagaaaca aaacagagaa 1980

agagctgacg aactggacca cctgagccag gcactggaga agcagaagtc cctgctcgat 2040

cagaccgata gaaccttctg gaacggcatc gtttgtgacc tgaccgatgc gctgcgcgaa 2100

aaggagggag gctgggagca agccgtggtc caaatccaca gaaaggccga ggaacacgtg 2160

ggcaaggtgg tgcaagcctg gcggaaaaga tttgacgccg atgagcggaa gggcatcgcc 2220

ggcctgagca tgtggtccat agaagagctg gacagcctcc ggaagctgct cattagctgg 2280

agcagaagga caagaaaccc tcaggagatc aacagattcg agcagggcca cacctctcac 2340

cagcggctgc tgacacatat ccagaacgtg aaggaagata gactgaagca actgagccac 2400

gccatcgtga tgaccgccct gggctacgtg tacgacgaga agaagctgga gtggttcgcc 2460

aaataccccg cctgccaggt gatcctgttc gagaatctgt ctcagtacag aagccacatg 2520

gacagatcca cgaaggaaaa tagccgcctg atgaaatggg cccacagaag catccctaag 2580

tacgtccaca tgcaggccga gccttacgga atccagatcg gagatgtgag agccgaatat 2640

agcagcaggt tccacgccaa gacagggaca cctggcatcc gttgcaagat ggtgaaggga 2700

caagaactgc aaggcaagcg attcgagaac ctgcaaaaga gactggtgtc cgaacagttt 2760

ctgaccgagg aacaggtgaa gcagcttcgg cctggagata tcgtgccaga tgacagcgga 2820

gagtggttca tgaccctgag tgatggcagc gaaggcaagg aagtggtgtt cctgcaagcc 2880

gacatcaacg ccgcccagaa ccttcagaaa cgattctggc agagatacaa cgaactgttc 2940

aaggtgtcat gcagagtgct gatcagaggc gaggaagagt acctgatccc caaggccaag 3000

agcgtgcaag ccaaactcgg caagggactg ttcgtgaaga aaaccgacac cgtgatgaag 3060

gacgtgtacg tgtgggatag ccaggccaaa ctgaagggca aaacaacctt caccgaggaa 3120

agcgagagcc ctgagcaact ggaggacttc caggagatca tcgaagaagc cgaggaagcc 3180

aagggcacct acagaacact gtttagagat cctagcggcg ttttcttccc cgagttcgtg 3240

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<210> 310
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<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 310
cccagcccta ggttgtttat t 21

<210> 311
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 311
ctggctacat cttccttgac tac 23

<210> 312
<211> 140
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 312
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cauuacaggg cggcuaccac gaauagccac gaaguaaaag cuucguggcu agcacccuug 120

gcuagucuug aauuccuagg 140

<210> 313
<211> 25
<212> DNA
<213> Homo sapiens

<400> 313
ccaacagtcc tacttccctg tttca 25

<210> 314
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide"

<400> 314
gagatgtccc cagtgaactc caaat 25

<210> 315
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 315
cctgtcgttg cccctcccag atcat 25

<210> 316
<211> 49
<212> RNA
<213> Artificial Sequence

<220>
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oligonucleotide"

<400> 316
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<210> 317
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

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<210> 318
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 318
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gttggcaga 69

<210> 319
<211> 39
<212> DNA
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

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<210> 320
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 320
gtctgattgc ctgtcgttgc ccctcccaga tcggaggagt tggcaga 47

<210> 321
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 321
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<210> 322
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 322
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<210> 323
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 323
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<210> 324
<211> 23
<212> DNA
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<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

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<210> 325
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

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

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 326
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<211> 34
<212> DNA
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

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<210> 328

<211> 42
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 328
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<210> 329
<211> 43
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 329
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<210> 330
<211> 33
<212> DNA
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

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<210> 331
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

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<210> 332
<211> 43
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 332
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<210> 333
<211> 35
<212> DNA
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 333
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<210> 334
<211> 42
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 334
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<210> 335
<211> 25
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<213> Homo sapiens

<400> 335
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<210> 336
<211> 25
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<400> 336
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<210> 337
<211> 25
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<213> Homo sapiens

<400> 337
ctgccacaat accttggccc ttctc 25

<210> 338
<211> 25
<212> DNA
<213> Homo sapiens

<400> 338
gctgcgaccc atacacccaa aggat 25

<210> 339
<211> 25
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<400> 339
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<210> 340
<211> 25
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<210> 341
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<400> 341
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<210> 342
<211> 25
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<400> 342
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<210> 343
<211> 25
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<213> Homo sapiens

<400> 343
cacaggtcct caagggcaga agagt 25

<210> 344
<211> 25
<212> DNA
<213> Homo sapiens

<400> 344
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<210> 345
<211> 25
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<213> Homo sapiens

<400> 345
tccttcacca ttatcaccac ccagt 25

<210> 346
<211> 25
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<213> Homo sapiens

<400> 346
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<210> 347
<211> 25
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<213> Homo sapiens

<400> 347
ggctcagggt tactgaagag gggcc 25

<210> 348
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<213> Homo sapiens

<400> 348
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<213> Homo sapiens

<400> 349
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<213> Homo sapiens

<400> 350
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<211> 25
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<213> Homo sapiens

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<210> 353
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<213> Homo sapiens

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<213> Homo sapiens

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<400> 356
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<210> 357
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<400> 357
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<400> 358
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<210> 359
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<213> Homo sapiens

<400> 359
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<210> 360
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<400> 360
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<210> 361
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<400> 361
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<400> 362
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<210> 363

<211> 25
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<400> 363
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<210> 364
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<400> 364
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<400> 365
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<210> 368
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<400> 368

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<210> 370
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<400> 370
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<210> 371
<211> 25
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<400> 371
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<210> 373
<211> 25
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<400> 373
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<210> 374
<211> 25

<212> DNA
<213> Homo sapiens

<400> 374
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<210> 375
<211> 25
<212> DNA
<213> Homo sapiens

<400> 375
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<210> 376
<211> 25
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<400> 376
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<210> 377
<211> 25
<212> DNA
<213> Homo sapiens

<400> 377
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<210> 378
<211> 25
<212> DNA
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<400> 378
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<210> 379
<211> 25
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<400> 379
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<400> 380
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<210> 381
<211> 25
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<400> 381
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<400> 382
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<210> 383
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<400> 383
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<210> 384
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<400> 384
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<210> 385
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<213> Homo sapiens

<400> 385
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<210> 386
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<400> 386
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<210> 387
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<400> 387
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<210> 388
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<400> 388
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<210> 389
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<400> 389
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<210> 390
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<213> Homo sapiens

<400> 390
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<210> 391
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<400> 391
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<400> 396
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<210> 397
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<400> 397
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acagatgaac actggtcagc 20

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<210> 400
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<210> 401
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<220>
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oligonucleotide"

<400> 401
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<210> 402
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 402
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<210> 403
<211> 20
<212> DNA
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<220>
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oligonucleotide"

<400> 403
gccgggcgtg gtgtcgcgcg 20

<210> 404
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 404
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<210> 405
<211> 135
<212> RNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 405
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cauuacaggg cggcuaccac gaauagccac gaaguaaaag cuucguggcu agcacaagac 120

uaaccuggcc aacau 135

<210> 406
<211> 135
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 406
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cauuacaggg cggcuaccac gaauagccac gaaguaaaag cuucguggcu agcacgucuu 120

gaacuccgga ccuca 135

<210> 407
<211> 135
<212> RNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 407
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cauuacaggg cggcuaccac gaauagccac gaaguaaaag cuucguggcu agcacgccgg 120

gcgugguguc gcgcg 135

<210> 408
<211> 135
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 408
cgacgguuag aggccguaug ucgauuugcu uuaauuucgu gcgugugcau ugucguccuc 60

cauuacaggg cggcuaccac gaauagccac gaaguaaaag cuucguggcu agcacuccug 120

ccgcagccuc uggag 135

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<211> 3324
<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 409
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ctgcggaagg gcatctggag aacccaccgg ctgctgaacg agggcgtggc ctactacatg 120

aagatgctgc tgctcttccg gcaggaatcc actggcggcc agacaaagaa ggaactgcag 180

gaggaactgg tgcggcacat ccgggagcag cagcagaaaa acagagccga caagaatacc 240

caggccctgc ctctggataa ggccttcgcc gctctgagac aactgtacga gctgctcgtg 300

ccatctagca tcggccagag cggcgatgcc cagatcatct ctagaaaatt cctgtctcct 360

ttggtggacc ctaacagcga gggcggcaag ggcactagca aggccggagc caagcccaca 420

tggcagaaaa agaaggaggc caatgaccct acatgggagc aagattacga gaagtggaaa 480

aagcgtagag aggaagatcc taccgccagt gtgataacaa ccctggaaga atatggaatt 540

agacctatct ttccactgta caccaacacc gtggccgata tcgcctggct gcctctgcag 600

tctaaccagt ttgtccggac atgggatcgg gacatgctgc agcaggccat cgagaggcta 660

ctctcttggg agtcttggaa caagcgggtg caagaggaat acagcaagct gcaggagaag 720

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ctgcccaatg ccagccacga gcagtacaga gaggcactga aaagagtgca acagcggctg 960

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gccgacaacc ccagaagcag aaggttcgtg accttcagcc aactgatctg gcctaacgag 1260

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atcgtgatcg acttcgagcc actgcaggag gtgaagaacg gccgactgca atctccttac 1560

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<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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<211> 3279
<212> DNA
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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gctccagccg atgagaaaag ccggaaggcc ctggtgcggg aatacgagga tggcaaagat 300

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<211> 3162
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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gtggacaaca atgagggaag acggagcaag agaggcagca gaaggctgaa gagaagaaga 180

attcacagac tggaaagagt gaagctgctg ctgaccgagt acgacctgat taacaaggaa 240

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<211> 3213
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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gaggtgcaga ccaagagctt cgtgagggag atcaacggcg gcgtggccca gaacggcgac 2820

ctggtgaggg tggacctgtt cgagaaggac aacaggtact acatggtgcc catctacgtg 2880

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agcgacaggc tgaacttcaa ggacgtgaac aagcccagca agcaggccga gtacaggtac 3120

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ctggtgaggc aggagaccag gaagatcttc aag 3213

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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
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cctagaagaa tcgccagaag cagcagaagg agacttaata gaaagagcca gagaaaaaag 240

gagatcagaa acctgctggt gcaacacggc gtgatcaccc aggaagagct ggacctgctg 300

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caggtgaacg agaaaagact gagcctgtat agaaccgtgg gcgaaatgtg gatcaaggac 540

gccgaattct caaaatacga tagacggaga aatagcccta acgaatacgt ctttagcgtg 600

tccagagccg acctggagaa ggaaatcgtt accctcttcg aggcccagcg gaaattccag 660

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<210> 415
<211> 3276
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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cggagaagaa agcaccgggt cgagcggacc aaacaactgc tgatcaacaa gggtctgctg 240

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aatggcgcta tcctgagcgc cgtcaaggaa aacagagagc tgatggacga gaagggctac 480

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<210> 416
<211> 3450
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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<211> 4287
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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aaggttttca aggccgagga atacgaggaa ttcgtgaaga agcactacgc caacaaccgg 2760

ggcaagagaa acaagctgct gctggaagac atcccagaga agatgatcga gcggcagatg 2820

aacgacaccc ggcatatctc taagtacatc agcggcattc tgtcccacat cgtccgggtg 2880

gaagacggca ccgacgaggg cgttaacagc aaaaatgtga tccccggcaa cggcaaaatc 2940

accacacaac tgagacagga ctggggactg aatgatgtgt ggaacgagct tgtgctgccg 3000

cgattcgaga gaatgaacca actgaccaac agcacagatt ttacaagctg gaacgagaac 3060

caccagaagt acctgcctac agtgcctgtg gagtttagca agggattctc taagaaaaga 3120

atcgaccacc ggcaccacgc cctggacgcc ctggtgatcg cctgcgccac caaggatcat 3180

gtgaacctgc tgaacaatca gagcgccaag agcgacacga agcgatacga tctgaagaag 3240

aagctgatga agttcgagaa gacagtgtac aaggaccccc agaccgagaa gcgaatcgag 3300

cgagaagtgc caaagtactt tctgaagcct tgggagactt ttaccgtgga cgccaagaac 3360

aagctggaaa ccatcatcgt gtccttcaaa cagaacctca gagtcatcaa caaggccaca 3420

aactactacg agaagtacgt ggacaaggac ggcgtgaaga cgaaggagcg ggttgagcag 3480

actggaacaa actgggccat cagaaaacct atgcacaagg aaaccgtgtc cggcaaaatt 3540

gacctgcctt gggtgaaagt gcccaagggc aagatcctga ccgccaccag aaagagcctg 3600

gacaccagct tcgacctcaa ggctatcgcc agcatcacgg acaccggcat ccagaagatc 3660

ctgaagaact acctggagtt caaggaatcc cctgagctgg ccttcagccc tgagggcatc 3720

gaggacatga acaagaacat caaaaagtac aacggcggaa agccccacca gcctatctct 3780

aaggtgcgcg tctttgagct gggcagcaag ttccaagtgg gccagaccgg caataagaag 3840

gacaagtacg tggaagccgc caagggaacc aacctgttct tcgccatcta tgaggacaga 3900

aagggcaagc gctcctacga gaccatccct ctgaacgagg tgatcgagag acagaagcag 3960

ggtctgtctg tggtggacct gaagaacatt aacgacttct tcctgtgtcc taacgacctg 4020

gtgtacattc ccagcggcga cgagttggaa aacggcggct ccatagagat caaaaacatc 4080

accaaagaaa agtccgaaag attttataag gtggtctctt tttctggcag ccaaatcttc 4140

ttcgtgcggc acgacattgc cgtgtccatc gtgaacaagg gggaattctc caccctaaac 4200

aagatggaac gcgccatcga tggctctatg gtgaaggaat cttgtatcaa gctgaagatc 4260

gacagactgg gcaacgtgct gaaagcg 4287

<210> 418
<211> 4296
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 418
atggccaaga atatcctcgg cctggacctg ggcaccaaca gcatcggctg ggcccttatc 60

aaccaagact tcgagaacaa gcagggtaag atcctcggaa tgggcagccg gatcattcca 120

atgagccaag atatcctggg cgacttcggc aagggcaact ctgtgtccca gaccgccgct 180

agaaccggct accggggcgt gcggagactc agagagcggt ttctgctgag aagagagaga 240

ctgcaccggg tgctgaatat aatcaacttc ctgcccgaac attacgcctc tcagatcgac 300

tttgagaaaa gattcggcaa gttcaaggaa gaaaccgagc ctaagctggc ctacaacaaa 360

gacggcttcg tgttcaagga tagctttgag gaaatgctgg ccgattttaa gaactaccag 420

cctcaactgc tggaaaacga caagaaaatt ccctacgact ggaccatcta ctacctgaga 480

aagaaggccc tgtcccagaa aatcgagaag gaagagttgg cctggattct gctcaatttc 540

aaccagaaga gaggctatta ccaactgagg ggcgaagact tcgaggaaga gaaggacaaa 600

atgttcgtcc gcctgaaggt ggagaagatc atcgatagcg gcgacaacgt gaagggtaag 660

attctgtacg acgtctactt cgagaacggc tggaaatacg acaaacagat cgttaagacc 720

gaggactgga tcgaaagagt gaaggaattc atcgtcaccg aatctttcct gaagaatggc 780

gacatcaaga gaacatttaa ggccgtggac tccgagaagg attggatcgc catcaaaaca 840

aaaacagaac aagagattga caagtcccac aagaccgtgg gcgtgtacat ctacgaaaca 900

ctgctccaga accctaagca gaagattaag ggcaagctgg tgagaacaat cgagcgcaag 960

ttttacaagg acgaactgaa gcagatcttg gagaagcaga aagagttcca ccaggagctg 1020

aagaacgatg acctgtataa cgactgcgtg agagaactgt acagaaacaa tgaagctcat 1080

caactgaccc tctctaagaa ggagtttgtg cacctgctga tggaagatat cattttctac 1140

caaagacccc tgaggtccca gaagagcagc atcagcaatt gcagcctgga attcagaaag 1200

tacaaggacg agaacggcgt ggagcatatc caatatctga aagccgtgcc taagagcaat 1260

ccttactacc aggagtttcg gatctggcag tggatcttta acctgaacat ctacaagcgg 1320

gacgatgagc aaaaccccgt gaccacagag ttcctgaaca ccaccaccga tattgaaaac 1380

ctcttcgagt tcctcaacaa ccggaaggaa gtggatcaga aagccctgct gaaacatttc 1440

aagctgaacg agaagaccca cagatggaag tacgtggagg ataagaaata cccctgcaac 1500

gaaaccaaga gcatgatttc cgagcggctg aagaaggtgg agaacatagc taacgacttc 1560

ctgaccagag agattgagca gaaaatctgg catatcatct attctgtgaa cgacaaaatc 1620

gaatacgaaa aagccctgaa gagttttgcc aagaagaaca acctggacga gaactccttt 1680

ttcgaggctt tcaagaaatt ccccccccttc aaaagcgagt acggcagttt cagcgaaaag 1740

gccatcaaga agctgctgcc tctgatgcgg cttggcaagt actggaactg cgagaacatc 1800

agcgacgaca gcaaggaaag aatccagaag attatcaacg gcgagtacga cgagaatatc 1860

aaggatagag tgcgcgagaa agccattcac ctgaccagcg aaaacaactt ccagggcctg 1920

cagctctggc tggcccagta cgtggtgtac gacagacatt cggaagccag catgatcggc 1980

aagtggaata gcgccgacga cctcgaagaa ttcctgaagg agttcaaaca gcacagcctt 2040

agaaacccta ttgtggagca ggtgatcaca gagacactgc gggtggtgaa ggacatctgg 2100

ctgaagtacg gcaatggagc caaagatttc ttcaatgaga ttcacatcga actgggaaga 2160

gagatgaagc aaaccaaaga cgagcgcctc gatgctacga agcggatcac cgagaacgag 2220

aataccaatc tgagaatcaa ggctctgctg gctgagatga tgaatgataa cagcgtggaa 2280

aacgtccggc cttacagccc tatgcagcag gagatcctga agatctacga ggatggcgtg 2340

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agcccttctg acctcaagcg gtacaagctg tggctggaac agagatacaa gagcccatac 2460

accggccaga tcattcccct gaacaagctg tttacccctg aatacgagat tgagcacatc 2520

atccctcaga gcagatactt cgacgacagc ttcagcaaca agatcatctg tgaaagcgcc 2580

gtgaacaagc tgaaggacaa ctatatcgga ctgggcttca tcaagcagtt cggcggaacc 2640

atcgtggagt gcggcctggg aaaaaacgtg aaggtgtttg aagtgaacga gtacgaggac 2700

ttcgtgaaga aacactacgc caacaacaga ggaaagagga ataagctgct cctggaggaa 2760

atccctgaga aaatgatcga gaggcaactg aacgacacca ggcatatcag caagtacatc 2820

tccggcgtgc tgagcaacat cgtgcgggtg gaagacggct ctgacgaggg agtgaacagc 2880

aaaaacatcg tgccaggcaa tggcaagatc accacccaac tgaagcagga ttggggactg 2940

aacgatgtgt ggaacgacct gatcctgcct agattcgaga gaatgaacca actgaccaat 3000

tcaacagact tcaccgcctg gaacgaaaat caccagaagt ttctccctac agtgcccatc 3060

gaatttagca agggatttag caagaaaaga atcgaccaca gacaccacgc cctggacgcc 3120

ctcgtgatcg cctgtgccac caaggaccac atcaatctgc tgaacaatca gtctgccaaa 3180

agcgacacca aacggtacga cctgaagaaa aagctcatga aattcgagaa gggcgtgtac 3240

aaccaccctc agaccggcga gagaatccag cgggacgtgc cgaagcaatt tctgaagcct 3300

tgggagagct tcaccatcga cgctaagaac aacctggaca agatcatcat cagcttcaag 3360

cagaacttga gggtgatcaa caaagccaca aactactacg agaagtatgt ggaaaagaac 3420

ggcatcaaga caaaagagag agtcgaacag acaggcacaa actgggccat ccggaagccc 3480

atgcacaagg aaaccgtgtc tggcatcgtt aacctgcctt gggtgaaagt gcctaaaggc 3540

aaaatcctga ccgccacccg gaaaagcctg gacaccacat ttgacctgaa aagcatcaac 3600

tccataacag ataccggcat tcagaagatc ttgagaaact acctggaatt caaaggcagt 3660

cctgaactgg ccttcagccc agagggcatc gaggacatga acaagaacat cgagaaatac 3720

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ttccaagtgg gacagaccgg caacaagaag gacaagtacg tggaggccgc caagggcacc 3840

aacctgttct tcgccgtcta cgaggacaag aacggcaaaa gaaactacga aacaatccct 3900

ctgaacatag tgatcgagag acagaagcag ggcctcctgg cctgccccga gagtaatgaa 3960

aaaggcgaga agctgctgtt ccaactgagc ccaaacgact tcgtgtatct cacgacagag 4020

gaagaaaatg ataacgccac acctatcaat ttctctctgc tgagcaagga acagattaac 4080

aacctgtaca aaatcgtgtc ctttaccggc aacagactgt acggcatccc tatctgcgtg 4140

gccaccacaa tcgtgaacaa agccgagtac acccaactga acaagatcga gttcaccaaa 4200

gagaaagatc tgctgctgaa gctcaatgtc aatagactgg gcgacgtgaa gacctttaca 4260

gccaatgaca tcagaaagat tttcaaccgg caggag 4296

<210> 419
<211> 137
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 419
aagugggaga guacugaaug ggcacguugc gguuggccug cgauuucuga acaaagguuc 60

agaaaucgca guccagccgu uaacaagcug agauaugcac caaauaaggc gcucgcuucg 120

gcgggcgcuu uuucguu 137

<210> 420
<211> 137
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 420
accuucuucc cauggcagua cauuaguugc gguuggccug cgauuucuga acaaagguuc 60

agaaaucgca guccagccgu uaacaagcug agauaugcac caaauaaggc gcucgcuucg 120

gcgggcgcuu uuucguu 137

<210> 421
<211> 137
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 421
gcccacaacu gcgauaauga cucuaguugc gguuggccug cgauuucuga acaaagguuc 60

agaaaucgca guccagccgu uaacaagcug agauaugcac caaauaaggc gcucgcuucg 120

gcgggcgcuu uuucguu 137

<210> 422
<211> 137
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 422
ugggggcgcu caguuuccag aaccuguugc gguuggccug cgauuucuga acaaagguuc 60

agaaaucgca guccagccgu uaacaagcug agauaugcac caaauaaggc gcucgcuucg 120

gcgggcgcuu uuucguu 137

<210> 423
<211> 133
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 423
acagugcgca ucucccuggu caccguuuua guacucugua auuuuaggua ugaaagucau 60

accuaaaauu acagaaucua cugaaacaag acuauauguc guguuuaucc cacuaauuua 120

uuaguggggau uuu 133

<210> 424

<211> 131
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 424
auuuacagcc uggccuuugg ggguuuuagu acucuguaau uuuagguaug aaagucauac 60

cuaaaauuac agaaucuacu gaaacaagac uauaugucgu guuuauccca cuaauuuauu 120

agugggauuu u 131

<210> 425
<211> 134
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 425
ccuuggggcc cagacugagc acgugguuuu aguacucugu aauuuuaggu augaaaguca 60

uaccuaaaau uacagaaucu acugaaacaa gacuauaugu cguguuuauc ccacuaauuu 120

auuaguggga uuuu 134

<210> 426
<211> 134
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 426
cuucuccuca ggagucagau gcaccguuuu aguacucugu aauuuuaggu augaaaguca 60

uaccuaaaau uacagaaucu acugaaacaa gacuauaugu cguguuuauc ccacuaauuu 120

auuaguggga uuuu 134

<210> 427
<211> 132
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 427
gaugauauuu ucuuuaaugg ugcguuuuag uacucuguaa uuuuagguau gaaagucaua 60

ccuaaaauua cagaaucuac ugaaacaaga cuauaugucg uguuuauccc acuaauuuau 120

uaguggggauu uu 132

<210> 428
<211> 133
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 428
ggcugggcca uuaaaaccuc uccaguuuua guacucugua auuuuaggua ugaaagucau 60

accuaaaauu acagaaucua cugaaacaag acuauauguc guguuuaucc cacuaauuua 120

uuaguggggau uuu 133

<210> 429
<211> 206
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 429

cacaucucga gcaagacguu gucauaguuc cauuaaagcc auugcuguuu uaugaaagca 60

ugauacagca auggcuuuga uguuucuaug auaagggcuu cggcccgugg cguuggggau 120

cgccugccca uuuuaauggg cuucucccca ucuauuuaau gagaaauuua caaccuuggc 180

uauucuuaaa uagcuaaggu uuuuuu 206

<210> 430
<211> 206
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 430
cauggcagua cauuagagca gucauaguuc cauuaaagcc auugcuguuu uaugaaagca 60

ugauacagca auggcuuuga uguuucuaug auaagggcuu cggcccgugg cguuggggau 120

cgccugccca uuuuaauggg cuucucccca ucuauuuaau gagaaauuua caaccuuggc 180

uauucuuaaa uagcuaaggu uuuuuu 206

<210> 431
<211> 206
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 431
ccugaaugcu gugcggcucu gucauaguuc cauuaaagcc auugcuguuu uaugaaagca 60

ugauacagca auggcuuuga uguuucuaug auaagggcuu cggcccgugg cguuggggau 120

cgccugccca uuuuaauggg cuucucccca ucuauuuaau gagaaauuua caaccuuggc 180

uauucuuaaa uagcuaaggu uuuuuu 206

<210> 432

<211> 206
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 432
cuucuauagc cuccuucccc gucauaguuc cauuaaagcc auugcuguuu uaugaaagca 60

ugauacagca auggcuuuga uguuucuaug auaagggcuu cggcccgugg cguuggggau 120

cgccugccca uuuuaauggg cuucucccca ucuauuuaau gagaaauuua caaccuuggc 180

uauucuuaaa uagcuaaggu uuuuuu 206

<210> 433
<211> 206
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 433
ggacagugcg caucucccug gucauaguuc cauuaaagcc auugcuguuu uaugaaagca 60

ugauacagca auggcuuuga uguuucuaug auaagggcuu cggcccgugg cguuggggau 120

cgccugccca uuuuaauggg cuucucccca ucuauuuaau gagaaauuua caaccuuggc 180

uauucuuaaa uagcuaaggu uuuuuu 206

<210> 434
<211> 133
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 434

aagacauuac acucauauua cacccgucau aguuccauua aagccaaagg gcuuugaugu 60

uucuaugaua aggguuucgg cccguggcgu cggggaucgc cugcccauuc cgaugggcuu 120

cuccccauuu auu 133

<210> 435
<211> 133
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 435
agagccauca ccaucacauc ccuaagucau aguuccauua aagccaaagg gcuuugaugu 60

uucuaugaua aggguuucgg cccguggcgu cggggaucgc cugcccauuc cgaugggcuu 120

cuccccauuu auu 133

<210> 436
<211> 133
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 436
aucuggaggg aacuuacagc auauggucau aguuccauua aagccaaagg gcuuugaugu 60

uucuaugaua aggguuucgg cccguggcgu cggggaucgc cugcccauuc cgaugggcuu 120

cuccccauuu auu 133

<210> 437
<211> 133
<212> RNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 437
ccacccagcc ugcucugccu ugggggucau aguuccauua aagccaaagg gcuuugaugu 60

uucuaugaua aggguuucgg cccguggcgu cggggaucgc cugcccauuc cgaugggcuu 120

cuccccauuu auu 133

<210> 438
<211> 133
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 438
gaacaacuca aauggaaaug aauaugucau aguuccauua aagccaaagg gcuuugaugu 60

uucuaugaua aggguuucgg cccguggcgu cggggaucgc cugcccauuc cgaugggcuu 120

cuccccauuu auu 133

<210> 439
<211> 133
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 439
gcuucuacuc uuggcuuaca acccagucau aguuccauua aagccaaagg gcuuugaugu 60

uucuaugaua aggguuucgg cccguggcgu cggggaucgc cugcccauuc cgaugggcuu 120

cuccccauuu auu 133

<210> 440
<211> 133
<212> RNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 440
ggccaaaauc cagcugccuu ccuuggucau aguuccauua aagccaaagg gcuuugaugu 60

uucuaugaua aggguuucgg cccguggcgu cggggaucgc cugcccauuc cgaugggcuu 120

cuccccauuu auu 133

<210> 441
<211> 133
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 441
uaaaaugauu uggaagagca gagacgucau aguuccauua aagccaaagg gcuuugaugu 60

uucuaugaua aggguuucgg cccguggcgu cggggaucgc cugcccauuc cgaugggcuu 120

cuccccauuu auu 133

<210> 442
<211> 133
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 442
uccuguucca ucaccaucaa aaaaagucau aguuccauua aagccaaagg gcuuugaugu 60

uucuaugaua aggguuucgg cccguggcgu cggggaucgc cugcccauuc cgaugggcuu 120

cuccccauuu auu 133

<210> 443
<211> 164
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 443
aagacauuac acucauauua cacccgccau aauuccucug uaaaacuuaa agaagguuua 60

uagaguuauu augguaaggc aauaugccgu ggcguuuggg aucgccuaug uccgguuuua 120

ccggaucucc cuaaagguga cuaacuuugg uuagucaccu uuuu 164

<210> 444
<211> 164
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 444
agcuguuugg gaggucagaa auagggccau aauuccucug uaaaacuuaa agaagguuua 60

uagaguuauu augguaaggc aauaugccgu ggcguuuggg aucgccuaug uccgguuuua 120

ccggaucucc cuaaagguga cuaacuuugg uuagucaccu uuuu 164

<210> 445
<211> 159
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 445
agguuuuaau ggcccagccu gccauaauuc cucuguaaaa cuuaaagaag guuuauagag 60

uuauuauggu aaggcaauau gccguggcgu uggggaucgc cuauguccgg uuuuaccgga 120

ucucccuaaa ggugacuaac uuugguuagu caccuuuuu 159

<210> 446
<211> 164
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 446
auguacugcc augggaagaa ggugagccau aauuccucug uaaaacuuaa agaagguuua 60

uagaguuauu augguaaggc aauaugccgu ggcguuggggg aucgccuaug uccgguuuua 120

ccggaucucc cuaaagguga cuaacuuugg uuagucaccu uuuu 164

<210> 447
<211> 164
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 447
cagaagucag gcuggacacu gaggagccau aauuccucug uaaaacuuaa agaagguuua 60

uagaguuauu augguaaggc aauaugccgu ggcguuggggg aucgccuaug uccgguuuua 120

ccggaucucc cuaaagguga cuaacuuugg uuagucaccu uuuu 164

<210> 448
<211> 164
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 448
cagggccucg auaaugagau aauuugccau aauuccucug uaaaacuuaa agaagguuua 60

uagaguuauu augguaaggc aauaugccgu ggcguuggggg aucgccuaug uccgguuuua 120

ccggaucucc cuaaagguga cuaacuuugg uuagucaccu uuuu 164

<210> 449
<211> 164
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 449
caucuacuaa uuucuuccca cucccgccau aauuccucug uaaaacuuaa agaagguuua 60

uagaguuauu augguaaggc aauaugccgu ggcguuggggg aucgccuaug uccgguuuua 120

ccggaucucc cuaaagguga cuaacuuugg uuagucaccu uuuu 164

<210> 450
<211> 159
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 450
cauggcagua cauuagagca gccauaauuc cucuguaaaa cuuaaagaag guuuauagag 60

uuauuauggu aaggcaauau gccguggcgu uggggaucgc cuauguccgg uuuuaccgga 120

ucucccuaaa ggugacuaac uuugguuagu caccuuuuu 159

<210> 451
<211> 164
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 451
cccuggcugu gcacauuccc uccuggccau aauuccucug uaaaacuuaa agaagguuua 60

uagaguuauu augguaaggc aauaugccgu ggcguuuggg aucgccuaug uccgguuuua 120

ccggaucucc cuaaagguga cuaacuuugg uuagucaccu uuuu 164

<210> 452
<211> 164
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 452
ccgcuguuuc cauuccucau cauucgccau aauuccucug uaaaacuuaa agaagguuua 60

uagaguuauu augguaaggc aauaugccgu ggcguuuggg aucgccuaug uccgguuuua 120

ccggaucucc cuaaagguga cuaacuuugg uuagucaccu uuuu 164

<210> 453
<211> 164
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 453
ccuagagccc aagagaaccc acugagccau aauuccucug uaaaacuuaa agaagguuua 60

uagaguuauu augguaaggc aauaugccgu ggcguuuggg aucgccuaug uccgguuuua 120

ccggaucucc cuaaagguga cuaacuuugg uuagucaccu uuuu 164

<210> 454

<211> 164
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 454
cgcacagcau ucaggucgua gucccgccau aauuccucug uaaaacuuaa agaagguuua 60

uagaguuauu augguaaggc aauaugccgu ggcguugggg aucgccuaug uccgguuuua 120

ccggaucucc cuaaagguga cuaacuuugg uuagucaccu uuuu 164

<210> 455
<211> 164
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 455
cggcacuauc auugacucag cugcugccau aauuccucug uaaaacuuaa agaagguuua 60

uagaguuauu augguaaggc aauaugccgu ggcguugggg aucgccuaug uccgguuuua 120

ccggaucucc cuaaagguga cuaacuuugg uuagucaccu uuuu 164

<210> 456
<211> 164
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 456
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uagaguuauu augguaaggc aauaugccgu ggcguugggg aucgccuaug uccgguuuua 120

ccggaucucc cuaaagguga cuaacuuugg uuagucaccu uuuu 164

<210> 457
<211> 164
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 457
gaaugcugug cggcucugcu uccaggccau aauuccucug uaaaacuuaa agaagguuua 60

uagaguuauu augguaaggc aauaugccgu ggcguugggg aucgccuaug uccgguuuua 120

ccggaucucc cuaaagguga cuaacuuugg uuagucaccu uuuu 164

<210> 458
<211> 164
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 458
gcuaccaccu cugugccccc ccggcgccau aauuccucug uaaaacuuaa agaagguuua 60

uagaguuauu augguaaggc aauaugccgu ggcguugggg aucgccuaug uccgguuuua 120

ccggaucucc cuaaagguga cuaacuuugg uuagucaccu uuuu 164

<210> 459
<211> 164
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 459

ggaggccugc agcuccugca ccuccgccau aauuccucug uaaaacuuaa agaagguuua 60

uagaguuauu augguaaggc aauaugccgu ggcguuuggg aucgccuaug uccgguuuua 120

ccggaucucc cuaaagguga cuaacuuugg uuagucaccu uuuu 164

<210> 460
<211> 159
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 460
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uuauuauggu aaggcaauau gccguggcgu uggggaucgc cuauguccgg uuuuaccgga 120

ucucccuaaa ggugacuaac uuugguuagu caccuuuuu 159

<210> 461
<211> 164
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 461
gggccauuaa aaccucucca ggggcgccau aauuccucug uaaaacuuaa agaagguuua 60

uagaguuauu augguaaggc aauaugccgu ggcguuuggg aucgccuaug uccgguuuua 120

ccggaucucc cuaaagguga cuaacuuugg uuagucaccu uuuu 164

<210> 462
<211> 164
<212> RNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 462
guuuuaaugg cccagccuca cacccgccau aauuccucug uaaaacuuaa agaagguuua 60

uagaguuauu augguaaggc aauaugccgu ggcguuuggg aucgccuaug uccgguuuua 120

ccggaucucc cuaaagguga cuaacuuugg uuagucaccu uuuu 164

<210> 463
<211> 164
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 463
uaaaaugauu uggaagagca gagacgccau aauuccucug uaaaacuuaa agaagguuua 60

uagaguuauu augguaaggc aauaugccgu ggcguuuggg aucgccuaug uccgguuuua 120

ccggaucucc cuaaagguga cuaacuuugg uuagucaccu uuuu 164

<210> 464
<211> 164
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 464
uccuguucca ucaccaucaa aaaaagccau aauuccucug uaaaacuuaa agaagguuua 60

uagaguuauu augguaaggc aauaugccgu ggcguuuggg aucgccuaug uccgguuuua 120

ccggaucucc cuaaagguga cuaacuuugg uuagucaccu uuuu 164

<210> 465
<211> 164
<212> RNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 465
ugucucaaau aauaaaaaaa auaaggccau aauuccucug uaaaacuuaa agaagguuua 60

uagaguuauu augguaaggc aauaugccgu ggcguuuggg aucgccuaug uccgguuuua 120

ccggaucucc cuaaagguga cuaacuuugg uuagucaccu uuuu 164

<210> 466
<211> 164
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 466
uguugguuac cucccugcca ccaccgccau aauuccucug uaaaacuuaa agaagguuua 60

uagaguuauu augguaaggc aauaugccgu ggcguuuggg aucgccuaug uccgguuuua 120

ccggaucucc cuaaagguga cuaacuuugg uuagucaccu uuuu 164

<210> 467
<211> 164
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 467
uuuagguucg uaucuguaaa accaagccau aauuccucug uaaaacuuaa agaagguuua 60

uagaguuauu augguaaggc aauaugccgu ggcguuuggg aucgccuaug uccgguuuua 120

ccggaucucc cuaaagguga cuaacuuugg uuagucaccu uuuu 164

<210> 468
<211> 118
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 468
aagugggaga guacugaaug ggcacguuuu uguacucuca auaaaaaguu auugagaauc 60

uacaaaaaua aggcauuuug ccgaauuuac cgcccuacau auguagggcg guuuuuuu 118

<210> 469
<211> 113
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 469
accggaggac aaaguacaaa guuuuuguac ucucaauaaa aaguuauuga gaaucuacaa 60

aaauaaggca uuuugccgaa uuuaccgccc uacauaugua gggcgguuuu uuu 113

<210> 470
<211> 113
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 470
ccacggcucc uccgaagcga guuuuuguac ucucaauaaa aaguuauuga gaaucuacaa 60

aaauaaggca uuuugccgaa uuuaccgccc uacauaugua gggcgguuuu uuu 113

<210> 471

<211> 113
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 471
cccugauccu cuugucccac guuuuuguac ucucaauaaa aaguuauuga gaaucuacaa 60

aaauaaggca uuuugccgaa uuuaccgccc uacauaugua gggcgguuuu uuu 113

<210> 472
<211> 113
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 472
cuggagcaac aaaucugacu guuuuuguac ucucaauaaa aaguuauuga gaaucuacaa 60

aaauaaggca uuuugccgaa uuuaccgccc uacauaugua gggcgguuuu uuu 113

<210> 473
<211> 113
<212> RNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 473
gggggucggg gcucgcggcg guuuuuguac ucucaauaaa aaguuauuga gaaucuacaa 60

aaauaaggca uuuugccgaa uuuaccgccc uacauaugua gggcgguuuu uuu 113

<210> 474
<211> 113
<212> RNA

<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 474
uggauuuaga gucucucagc guuuuuguac ucucaauaaa aaguuauuga gaaucuacaa 60

aaauaaggca uuuugccgaa uuuaccgccc uacauaugua gggcgguuuu uuu 113

<210> 475
<211> 123
<212> RNA
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 475
aagugggaga guacugaaug ggcacguugu gaauugcuuu caaaaaaguu ugaaaagcaa 60

uucacaauaa ggauuauucc guugugaaaa cauucaaggc ggggcaacuc gccuuuuuuc 120

guu 123

<210> 476
<211> 123
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 476
aggugauuca cagagacaua aagccguugu gaauugcuuu caaaaaaguu ugaaaagcaa 60

uucacaauaa ggauuauucc guugugaaaa cauucaaggc ggggcaacuc gccuuuuuuc 120

guu 123

<210> 477

<211> 123
<212> RNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 477
auuuagcucu uaguccuggc aagccguugu gaauugcuuu caaaaaaguu ugaaaagcaa 60

uucacaauaa ggauuauucc guugugaaaa cauucaaggc ggggcaacuc gccuuuuuuc 120

guu 123

<210> 478
<211> 123
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<213> Artificial Sequence

<220>
<221> source
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polynucleotide"

<400> 478
cugggagguc aagacugcaa ugagaguugu gaauugcuuu caaaaaaguu ugaaaagcaa 60

uucacaauaa ggauuauucc guugugaaaa cauucaaggc ggggcaacuc gccuuuuuuc 120

guu 123

<210> 479
<211> 123
<212> RNA
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<220>
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polynucleotide"

<400> 479
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uucacaauaa ggauuauucc guugugaaaa cauucaaggc ggggcaacuc gccuuuuuuc 120

guu 123

<210> 480
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 480
aagcaacucu ccugucucag ccuccguugu gaauugcuuu caaaggaaag caauucacaa 60

uaaggauuau uccguuguga aaacauuuag cgccucgacu aucuucgggg cauuuuuu 118

<210> 481
<211> 118
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 481
gggaagaagg ugauucacag agacaguugu gaauugcuuu caaaggaaag caauucacaa 60

uaaggauuau uccguuguga aaacauuuag cgccucgacu aucuucgggg cauuuuuu 118

<210> 482
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 482
aagtgggaga gtactgaatg ggcac 25

<210> 483

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

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 483
accttcttcc catggcagta catta 25

<210> 484
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 484
gcccacaact gcgataatga ctcta 25

<210> 485
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 485
tgggggcgct cagtttccag aacct 25

<210> 486
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 486
acagtgcgca tctccctggt cacc 24

<210> 487
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 487
atttacagcc tggcctttgg gg 22

<210> 488
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 488
ccttggggcc cagactgagc acgtg 25

<210> 489
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 489
cttctcctca ggagtcagat gcacc 25

<210> 490
<211> 23
<212> DNA

<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 490
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<210> 491
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 491
ggctgggcca ttaaaacctc tcca 24

<210> 492
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 492
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<210> 493
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 493

catggcagta cattagagca 20

<210> 494
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 494
cctgaatgct gtgcggctct 20

<210> 495
<211> 20
<212> DNA
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 495
cttctatagc ctccttcccc 20

<210> 496
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 496
ggacagtgcg catctccctg 20

<210> 497
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 497
aagacattac actcatatta caccc 25

<210> 498
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 498
agagccatca ccatcacatc cctaa 25

<210> 499
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 499
atctggaggg aacttacagc atatg 25

<210> 500
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 500
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<210> 501
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 501
gaacaactca aatggaaatg aatat 25

<210> 502
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 502
gcttctactc ttggcttaca accca 25

<210> 503
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 503
ggccaaaatc cagctgcctt ccttg 25

<210> 504
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 504
taaaatgatt tggaagagca gagac 25

<210> 505
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 505
tcctgttcca tcaccatcaa aaaaa 25

<210> 506
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 506
agctgtttgg gaggtcagaa atagg 25

<210> 507
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 507
aggttttaat ggcccagcct 20

<210> 508

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

<220>
<221> source
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oligonucleotide"

<400> 508
atgtactgcc atgggaagaa ggtga 25

<210> 509
<211> 25
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 509
cagaagtcag gctggacact gagga 25

<210> 510
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 510
cagggcctcg ataatgagat aattt 25

<210> 511
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 511
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<210> 512
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 512
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<210> 513
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 513
ccgctgtttc cattcctcat cattc 25

<210> 514
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 514
cctagagccc aagagaaccc actga 25

<210> 515
<211> 25
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 515
cgcacagcat tcaggtcgta gtccc 25

<210> 516
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 516
cggcactatc attgactcag ctgct 25

<210> 517
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 517
ctcaacattc cagggctcaa gcgat 25

<210> 518
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 518

gaatgctgtg cggctctgct tccag 25

<210> 519
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 519
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<210> 520
<211> 25
<212> DNA
<213> Artificial Sequence

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uuauuauggu aaggcaauau gccguggcgu uggggaucgc cuauguccgg uuuuaccgga 120

ucucccuaaa ggugacuaac uuugguuagu caccuuuuu 159

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ucucccuaaa ggugacuaac uuugguuagu caccuuuuu 159

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ucucccuaaa ggugacuaac uuugguuagu caccuuuuu 159

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ucucccuaaa ggugacuaac uuugguuagu caccuuuuu 159

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<210> 738
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<210> 739
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<210> 740
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uuauuauggu aaggcaauau gccguggcgu uggggaucgc cuauguccgg uuuuaccgga 120

ucucccuaaa ggugacuaac uuugguuagu caccuuuuu 159

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ucucccuaaa ggugacuaac uuugguuagu caccuuuuu 159

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polynucleotide"

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ucucccuaaa ggugacuaac uuugguuagu caccuuuuu 159