SEQUENCE LISTING

<110> SMITH, JULIANNE
SCHARENBERG, ANDREW
MANNIOUI, CECILE
EYQUEM, JUSTIN
CELLECTIS

<120> MULTI-CHAIN CHIMERIC ANTIGEN RECEPTORS AND USES THEREOF

<130> 421394WO-59

<160> 232

<170> PatentIn version 3.5

<210> 1

<211> 49
<212> DNA
<213> Artificial sequence

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

<220>
<223> GRex2

<400> 1
tattcactga tggactccaa agaatcatta actcctggta gagaagaaa 49

<210> 2

<211> 49
<212> DNA
<213> Artificial sequence

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

<220>
<223> GRex3T2

<400> 2
tgcctggtgt gctctgatga agcttcagga tgtcattatg gagtcttaa 49

<210> 3

<211> 49
<212> DNA
<213> Artificial sequence

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

<220>
<223> GRex3T4

<400> 3
tgctctgatg aagcttcagg atgtcattat ggagtcttaa cttgtggaa 49

<210> 4

<211> 49
<212> DNA

<213> Artificial sequence

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

<220>
<223> GRex5T1

<400> 4
tggtgtcact gttggaggtt attgaacctg aagtgttata tgcaggata 49

<210> 5

<211> 49
<212> DNA
<213> Artificial sequence

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

<220>
<223> GRex5T2

<400> 5
tatgatagct ctgttccaga ctcaacttgg aggatcatga ctacgctca 49

<210> 6

<211> 49
<212> DNA
<213> Artificial sequence

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

<220>
<223> GRex5T3

<400> 6
ttatatgcag gatatgatag ctctgttcca gactcaactt ggaggatca 49

<210> 7

<211> 530
<212> PRT
<213> Artificial sequence

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

<220>
<223> Repeat-GRex2-LPT9-L1

<400> 7
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys
1 5 10 15

Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala
20 25 30

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

```
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
    50                  55                  60

Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn
65                  70                  75                  80

Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
                85                  90                  95

Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
            100                 105                 110

Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
        115                 120                 125

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

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

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
                165                 170                 175

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

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln
        195                 200                 205

Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu
    210                 215                 220

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
225                 230                 235                 240

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala
                245                 250                 255

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly
            260                 265                 270

Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys
        275                 280                 285

Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala
    290                 295                 300

His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly
305                 310                 315                 320
```

```
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
                325                 330                 335

Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn
            340                 345                 350

Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
        355                 360                 365

Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
    370                 375                 380

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
385                 390                 395                 400

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala
                405                 410                 415

Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala
            420                 425                 430

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
        435                 440                 445

Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val
    450                 455                 460

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln
465                 470                 475                 480

Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu
                485                 490                 495

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
            500                 505                 510

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala
        515                 520                 525

Leu Glu
    530
```

<210> 8

<211> 530
<212> PRT
<213> Artificial sequence

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

<220>

<223> Repeat-GRex2-LPT9-R1

<400> 8

```
Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys
1               5                  10                  15

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
            20                  25                  30

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

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
    50                  55                  60

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

Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
                85                  90                  95

Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
            100                 105                 110

Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
        115                 120                 125

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala
    130                 135                 140

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

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
                165                 170                 175

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

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln
        195                 200                 205

Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu
    210                 215                 220

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
225                 230                 235                 240

Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala
                245                 250                 255

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly
```

260 265 270

Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys
275 280 285

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
290 295 300

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

Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys
325 330 335

Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His
340 345 350

Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
355 360 365

Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
370 375 380

Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
385 390 395 400

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala
405 410 415

Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala
420 425 430

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val
435 440 445

Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val
450 455 460

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln
465 470 475 480

Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu
485 490 495

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
500 505 510

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala
515 520 525

Leu Glu

530

<210> 9

<211> 530
<212> PRT
<213> Artificial sequence

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

<220>
<223> Repeat-GRex3T2-L1

<400> 9

```
Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
1               5                  10                  15

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
            20                  25                  30

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

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
    50                  55                  60

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

Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
                85                  90                  95

Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
            100                 105                 110

Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
        115                 120                 125

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala
    130                 135                 140

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

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val
                165                 170                 175

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

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln
        195                 200                 205
```

```
Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu
    210                 215                 220

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
225                 230                 235                 240

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala
                245                 250                 255

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly
            260                 265                 270

Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys
        275                 280                 285

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
    290                 295                 300

His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly
305                 310                 315                 320

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
                325                 330                 335

Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His
            340                 345                 350

Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
        355                 360                 365

Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
    370                 375                 380

Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
385                 390                 395                 400

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala
                405                 410                 415

Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
            420                 425                 430

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val
        435                 440                 445

Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val
    450                 455                 460

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln
465                 470                 475                 480
```

Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu
485 490 495

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
500 505 510

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala
515 520 525

Leu Glu
530

<210> 10

<211> 530
<212> PRT
<213> Artificial sequence

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

<220>
<223> Repeat-GRex3T2-R1

<400> 10
Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys
1 5 10 15

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
20 25 30

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly
35 40 45

Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys
50 55 60

Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn
65 70 75 80

Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val
85 90 95

Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
100 105 110

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
115 120 125

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

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

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
165 170 175

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

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln
195 200 205

Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu
210 215 220

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
225 230 235 240

Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala
245 250 255

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly
260 265 270

Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys
275 280 285

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
290 295 300

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

Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys
325 330 335

Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn
340 345 350

Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
355 360 365

Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
370 375 380

Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu
385 390 395 400

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala
405 410 415

Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala
420 425 430

```
Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val
        435                 440                 445

Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val
    450                 455                 460

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln
465                 470                 475                 480

Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu
                485                 490                 495

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
            500                 505                 510

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala
        515                 520                 525

Leu Glu
    530
```

<210> 11

<211> 530
<212> PRT
<213> Artificial sequence

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

<220>
<223> Repeat-GRex3T4-L1

<400> 11

```
Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
1               5                   10                  15

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
            20                  25                  30

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

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
    50                  55                  60

Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn
65                  70                  75                  80

Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
                85                  90                  95

Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
            100                 105                 110
```

```
Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
        115                 120                 125

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala
    130                 135                 140

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

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val
                165                 170                 175

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

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
        195                 200                 205

Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu
    210                 215                 220

Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
225                 230                 235                 240

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala
                245                 250                 255

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly
            260                 265                 270

Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
        275                 280                 285

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
    290                 295                 300

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

Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys
                325                 330                 335

Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn
            340                 345                 350

Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val
        355                 360                 365

Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
    370                 375                 380
```

```
Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
385                 390                 395                 400

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala
                405                 410                 415

Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
            420                 425                 430

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val
        435                 440                 445

Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val
    450                 455                 460

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln
465                 470                 475                 480

Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu
                485                 490                 495

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
            500                 505                 510

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala
        515                 520                 525

Leu Glu
    530
```

<210> 12

<211> 530
<212> PRT
<213> Artificial sequence

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

<220>
<223> Repeat-GRex3T4-R1

<400> 12

```
Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys
1               5                   10                  15

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
            20                  25                  30

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

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
```

```
    50                  55                  60

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

Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
                85                  90                  95

Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
            100                 105                 110

Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu
        115                 120                 125

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

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

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
                165                 170                 175

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

Gln Ala Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
        195                 200                 205

Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu
    210                 215                 220

Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
225                 230                 235                 240

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala
                245                 250                 255

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly
            260                 265                 270

Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys
        275                 280                 285

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
    290                 295                 300

His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly
305                 310                 315                 320

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
```

325 330 335

Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn
340 345 350

Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val
355 360 365

Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
370 375 380

Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu
385 390 395 400

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala
405 410 415

Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
420 425 430

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
435 440 445

Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val
450 455 460

Gln Ala Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
465 470 475 480

Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu
485 490 495

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
500 505 510

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala
515 520 525

Leu Glu
530

<210> 13

<211> 530
<212> PRT
<213> Artificial sequence

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

<220>
<223> Repeat-GRex5T1-LPT8-L1

<400> 13

```
Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
1               5                  10                  15

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
            20                  25                  30

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

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
    50                  55                  60

Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn
65                  70                  75                  80

Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
                85                  90                  95

Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
            100                 105                 110

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
        115                 120                 125

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala
    130                 135                 140

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

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
                165                 170                 175

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

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
        195                 200                 205

Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu
    210                 215                 220

Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
225                 230                 235                 240

Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala
                245                 250                 255

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly
            260                 265                 270
```

Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys
275 280 285

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
290 295 300

His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly
305 310 315 320

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
325 330 335

Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn
340 345 350

Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
355 360 365

Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
370 375 380

Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
385 390 395 400

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala
405 410 415

Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
420 425 430

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val
435 440 445

Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val
450 455 460

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
465 470 475 480

Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu
485 490 495

Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
500 505 510

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala
515 520 525

Leu Glu
530

<210> 14

<211> 530
<212> PRT
<213> Artificial sequence

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

<220>
<223> Repeat-GRex5T1-LPT8-R1

<400> 14

```
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys
1               5                  10                  15

Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala
            20                  25                  30

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

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
    50                  55                  60

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

Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
                85                  90                  95

Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
            100                 105                 110

Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
        115                 120                 125

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala
    130                 135                 140

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

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val
                165                 170                 175

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

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
        195                 200                 205

Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu
    210                 215                 220
```

```
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
225                 230                 235                 240

Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala
                245                 250                 255

Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala His Gly
            260                 265                 270

Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys
        275                 280                 285

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
    290                 295                 300

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

Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys
                325                 330                 335

Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn
            340                 345                 350

Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
        355                 360                 365

Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
    370                 375                 380

Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu
385                 390                 395                 400

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala
                405                 410                 415

Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala
            420                 425                 430

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
        435                 440                 445

Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val
    450                 455                 460

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
465                 470                 475                 480

Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu
                485                 490                 495
```

```
Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
            500                 505                 510

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala
        515                 520                 525

Leu Glu
    530
```

<210> 15

<211> 530
<212> PRT
<213> Artificial sequence

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

<220>
<223> Repeat-GRex5T2-L1

<400> 15

```
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys
1               5                   10                  15

Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala
            20                  25                  30

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

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
    50                  55                  60

Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn
65                  70                  75                  80

Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
                85                  90                  95

Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
            100                 105                 110

Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu
        115                 120                 125

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala
    130                 135                 140

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

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
                165                 170                 175
```

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

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

Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu
210 215 220

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
225 230 235 240

Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala
245 250 255

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly
260 265 270

Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys
275 280 285

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
290 295 300

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly
305 310 315 320

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
325 330 335

Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn
340 345 350

Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
355 360 365

Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
370 375 380

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
385 390 395 400

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala
405 410 415

Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
420 425 430

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val
435 440 445

Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val
450 455 460

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
465 470 475 480

Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu
485 490 495

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
500 505 510

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala
515 520 525

Leu Glu
530

<210> 16

<211> 530
<212> PRT
<213> Artificial sequence

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

<220>
<223> Repeat-GRex5T2-R1

<400> 16
Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
1 5 10 15

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
20 25 30

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly
35 40 45

Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys
50 55 60

Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn
65 70 75 80

Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
85 90 95

Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
100 105 110

Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu

115 120 125

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala
130 135 140

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

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val
165 170 175

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

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
195 200 205

Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu
210 215 220

Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
225 230 235 240

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala
245 250 255

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly
260 265 270

Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys
275 280 285

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
290 295 300

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly
305 310 315 320

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
325 330 335

Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn
340 345 350

Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val
355 360 365

Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
370 375 380

Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu

385 390 395 400

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala
405 410 415

Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
420 425 430

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
435 440 445

Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val
450 455 460

Gln Ala Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln
465 470 475 480

Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu
485 490 495

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
500 505 510

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala
515 520 525

Leu Glu
530

<210> 17

<211> 530
<212> PRT
<213> Artificial sequence

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

<220>
<223> Repeat-GRex5T3-L1

<400> 17
Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys
1 5 10 15

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
20 25 30

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly
35 40 45

Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys
50 55 60

```
Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn
65                  70                  75                  80

Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
                85                  90                  95

Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
            100                 105                 110

Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu
        115                 120                 125

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala
    130                 135                 140

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

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val
                165                 170                 175

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

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
        195                 200                 205

Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu
    210                 215                 220

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
225                 230                 235                 240

Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala
                245                 250                 255

Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala His Gly
            260                 265                 270

Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
        275                 280                 285

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
    290                 295                 300

His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly
305                 310                 315                 320

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
                325                 330                 335
```

```
Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn
            340                 345                 350

Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val
        355                 360                 365

Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
    370                 375                 380

Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
385                 390                 395                 400

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala
                405                 410                 415

Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala
            420                 425                 430

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val
        435                 440                 445

Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val
    450                 455                 460

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln
465                 470                 475                 480

Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu
                485                 490                 495

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
            500                 505                 510

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala
        515                 520                 525

Leu Glu
    530
```

<210> 18

<211> 530
<212> PRT
<213> Artificial sequence

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

<220>
<223> Repeat-GRex5T3-R1

<400> 18

```
Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
1               5                   10                  15
```

```
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
            20                  25                  30

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly
        35                  40                  45

Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys
    50                  55                  60

Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn
65                  70                  75                  80

Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
                85                  90                  95

Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
            100                 105                 110

Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
        115                 120                 125

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

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

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val
                165                 170                 175

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

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
        195                 200                 205

Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu
    210                 215                 220

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
225                 230                 235                 240

Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala
                245                 250                 255

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly
            260                 265                 270

Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys
        275                 280                 285
```

```
Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala
    290                 295                 300

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

Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys
                325                 330                 335

Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn
            340                 345                 350

Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
        355                 360                 365

Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
    370                 375                 380

Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
385                 390                 395                 400

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala
                405                 410                 415

Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
            420                 425                 430

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val
        435                 440                 445

Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val
    450                 455                 460

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
465                 470                 475                 480

Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu
                485                 490                 495

Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
            500                 505                 510

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala
        515                 520                 525

Leu Glu
    530
```

<210> 19

<211> 2814
<212> DNA
<213> Artificial sequence

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

<220>
<223> GRex2-L TALEN

<400> 19
atgggcgatc ctaaaaagaa acgtaaggtc atcgattacc catacgatgt tccagattac 60
gctatcgata tcgccgatct acgcacgctc ggctacagcc agcagcaaca ggagaagatc 120
aaaccgaagg ttcgttcgac agtggcgcag caccacgagg cactggtcgg ccacgggttt 180
acacacgcgc acatcgttgc gttaagccaa cacccggcag cgttagggac cgtcgctgtc 240
aagtatcagg acatgatcgc agcgttgcca gaggcgacac acgaagcgat cgttggcgtc 300
ggcaaacagt ggtccggcgc acgcgctctg gaggccttgc tcacggtggc gggagagttg 360
agaggtccac cgttacagtt ggacacaggc caacttctca agattgcaaa acgtggcggc 420
gtgaccgcag tggaggcagt gcatgcatgg cgcaatgcac tgacgggtgc cccgctcaac 480
ttgaccccgg agcaggtggt ggccatcgcc agcaatattg gtggcaagca ggcgctggag 540
acggtgcagg cgctgttgcc ggtgctgtgc caggcccacg gcttgacccc ccagcaggtg 600
gtggccatcg ccagcaatgg cggtggcaag caggcgctgg agacggtcca gcggctgttg 660
ccggtgctgt gccaggccca cggcttgacc ccccagcagg tggtggccat cgccagcaat 720
ggcggtggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 780
cacggcttga ccccggagca ggtggtggcc atcgccagcc acgatggcgg caagcaggcg 840
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccggag 900
caggtggtgg ccatcgccag caatattggt ggcaagcagg cgctggagac ggtgcaggcg 960
ctgttgccgg tgctgtgcca ggcccacggc ttgaccccgg agcaggtggt ggccatcgcc 1020
agccacgatg gcggcaagca ggcgctggag acggtccagc ggctgttgcc ggtgctgtgc 1080
caggcccacg gcttgacccc ccagcaggtg gtggccatcg ccagcaatgg cggtggcaag 1140
caggcgctgg agacggtcca gcggctgttg ccggtgctgt gccaggccca cggcttgacc 1200
ccccagcagg tggtggccat cgccagcaat aatggtggca agcaggcgct ggagacggtc 1260
cagcggctgt tgccggtgct gtgccaggcc cacggcttga ccccggagca ggtggtggcc 1320
atcgccagca atattggtgg caagcaggcg ctggagacgg tgcaggcgct gttgccggtg 1380
ctgtgccagg cccacggctt gacccccag caggtggtgg ccatcgccag caatggcggt 1440
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 1500
ttgacccccc agcaggtggt ggccatcgcc agcaataatg gtggcaagca ggcgctggag 1560
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ccagcaggtg 1620
gtggccatcg ccagcaataa tggtggcaag caggcgctgg agacggtcca gcggctgttg 1680
ccggtgctgt gccaggccca cggcttgacc ccggagcagg tggtggccat cgccagcaat 1740
attggtggca agcaggcgct ggagacggtg caggcgctgt tgccggtgct gtgccaggcc 1800
cacggcttga ccccggagca ggtggtggcc atcgccagcc acgatggcgg caagcaggcg 1860
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gacccccag 1920
caggtggtgg ccatcgccag caatggcggt ggcaagcagg cgctggagac ggtccagcgg 1980
ctgttgccgg tgctgtgcca ggcccacggc ttgacccctc agcaggtggt ggccatcgcc 2040
agcaatggcg gcggcaggcc ggcgctggag agcattgttg cccagttatc tcgccctgat 2100
ccggcgttgg ccgcgttgac caacgaccac ctcgtcgcct tggcctgcct cggcgggcgt 2160
cctgcgctgg atgcagtgaa aaagggattg ggggatccta tcagccgttc ccagctggtg 2220
aagtccgagc tggaggagaa gaaatccgag ttgaggcaca agctgaagta cgtgccccac 2280
gagtacatcg agctgatcga gatcgcccgg aacagcaccc aggaccgtat cctggagatg 2340
aaggtgatgg agttcttcat gaaggtgtac ggctacaggg gcaagcacct gggcggctcc 2400
aggaagcccg acggcgccat ctacaccgtg ggctccccca tcgactacgg cgtgatcgtg 2460
gacaccaagg cctactccgg cggctacaac ctgcccatcg gccaggccga cgaaatgcag 2520
aggtacgtgg aggagaacca gaccaggaac aagcacatca accccaacga gtggtggaag 2580
gtgtaccct ccagcgtgac cgagttcaag ttcctgttcg tgtccggcca cttcaagggc 2640
aactacaagg cccagctgac caggctgaac cacatcacca actgcaacgg cgccgtgctg 2700
tccgtggagg agctcctgat cggcggcgag atgatcaagg ccggcaccct gaccctggag 2760
gaggtgagga ggaagttcaa caacggcgag atcaacttcg cggccgactg ataa 2814

<210> 20

<211> 2832
<212> DNA
<213> Artificial sequence

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

<220>
<223> GRex2-R TALEN

<400> 20
atgggcgatc ctaaaaagaa acgtaaggtc atcgataagg agaccgccgc tgccaagttc 60
gagagacagc acatggacag catcgatatc gccgatctac gcacgctcgg ctacagccag 120
cagcaacagg agaagatcaa accgaaggtt cgttcgacag tggcgcagca ccacgaggca 180
ctggtcggcc acgggtttac acacgcgcac atcgttgcgt taagccaaca cccggcagcg 240
ttagggaccg tcgctgtcaa gtatcaggac atgatcgcag cgttgccaga ggcgacacac 300
gaagcgatcg ttggcgtcgg caaacagtgg tccggcgcac gcgctctgga ggccttgctc 360
acggtggcgg gagagttgag aggtccaccg ttacagttgg acacaggcca acttctcaag 420
attgcaaaac gtggcggcgt gaccgcagtg gaggcagtgc atgcatggcg caatgcactg 480
acgggtgccc cgctcaactt gacccccag caggtggtgg ccatcgccag caatggcggt 540
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 600
ttgacccccc agcaggtggt ggccatcgcc agcaatggcg gtggcaagca ggcgctggag 660
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ggagcaggtg 720
gtggccatcg ccagccacga tggcggcaag caggcgctgg agacggtcca gcggctgttg 780
ccggtgctgt gccaggccca cggcttgacc ccccagcagg tggtggccat cgccagcaat 840
ggcggtggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 900
cacggcttga ccccccagca ggtggtggcc atcgccagca atggcggtgg caagcaggcg 960
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccggag 1020
caggtggtgg ccatcgccag ccacgatggc ggcaagcagg cgctggagac ggtccagcgg 1080
ctgttgccgg tgctgtgcca ggcccacggc ttgacccccc agcaggtggt ggccatcgcc 1140
agcaatggcg gtggcaagca ggcgctggag acggtccagc ggctgttgcc ggtgctgtgc 1200
caggcccacg gcttgacccc ggagcaggtg gtggccatcg ccagccacga tggcggcaag 1260
caggcgctgg agacggtcca gcggctgttg ccggtgctgt gccaggccca cggcttgacc 1320
ccccagcagg tggtggccat cgccagcaat ggcggtggca agcaggcgct ggagacggtc 1380
cagcggctgt tgccggtgct gtgccaggcc cacggcttga ccccggagca ggtggtggcc 1440
atcgccagca atattggtgg caagcaggcg ctggagacgg tgcaggcgct gttgccggtg 1500
ctgtgccagg cccacggctt gaccccggag caggtggtgg ccatcgccag ccacgatggc 1560
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 1620
ttgaccccgg agcaggtggt ggccatcgcc agccacgatg gcggcaagca ggcgctggag 1680
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ggagcaggtg 1740
gtggccatcg ccagcaatat tggtggcaag caggcgctgg agacggtgca ggcgctgttg 1800
ccggtgctgt gccaggccca cggcttgacc ccccagcagg tggtggccat cgccagcaat 1860
aatggtggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 1920
cacggcttga ccccccagca ggtggtggcc atcgccagca ataatggtgg caagcaggcg 1980
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccctcag 2040
caggtggtgg ccatcgccag caatggcggc ggcaggccgg cgctggagag cattgttgcc 2100
cagttatctc gccctgatcc ggcgttggcc gcgttgacca acgaccacct cgtcgccttg 2160
gcctgcctcg gcgggcgtcc tgcgctggat gcagtgaaaa agggattggg ggatcctatc 2220
agccgttccc agctggtgaa gtccgagctg gaggagaaga aatccgagtt gaggcacaag 2280
ctgaagtacg tgccccacga gtacatcgag ctgatcgaga tcgcccggaa cagcacccag 2340
gaccgtatcc tggagatgaa ggtgatggag ttcttcatga aggtgtacgg ctacaggggc 2400
aagcacctgg gcggctccag gaagcccgac ggcgccatct acaccgtggg ctcccccatc 2460
gactacggcg tgatcgtgga caccaaggcc tactccggcg gctacaacct gcccatcggc 2520
caggccgacg aaatgcagag gtacgtggag gagaaccaga ccaggaacaa gcacatcaac 2580
cccaacgagt ggtggaaggt gtacccctcc agcgtgaccg agttcaagtt cctgttcgtg 2640
tccggccact tcaagggcaa ctacaaggcc cagctgacca ggctgaacca catcaccaac 2700
tgcaacggcg ccgtgctgtc cgtggaggag ctcctgatcg gcggcgagat gatcaaggcc 2760
ggcaccctga ccctggagga ggtgaggagg aagttcaaca acggcgagat caacttcgcg 2820
gccgactgat aa 2832

<210> 21

<211> 2814
<212> DNA
<213> Artificial sequence

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

<220>
<223> GRex3T2-L TALEN

<400> 21

atgggcgatc ctaaaaagaa acgtaaggtc atcgattacc catacgatgt tccagattac 60
gctatcgata tcgccgatct acgcacgctc ggctacagcc agcagcaaca ggagaagatc 120
aaaccgaagg ttcgttcgac agtggcgcag caccacgagg cactggtcgg ccacgggttt 180
acacacgcgc acatcgttgc gttaagccaa cacccggcag cgttagggac cgtcgctgtc 240
aagtatcagg acatgatcgc agcgttgcca gaggcgacac acgaagcgat cgttggcgtc 300
ggcaaacagt ggtccggcgc acgcgctctg gaggccttgc tcacggtggc gggagagttg 360
agaggtccac cgttacagtt ggacacaggc caacttctca agattgcaaa acgtggcggc 420
gtgaccgcag tggaggcagt gcatgcatgg cgcaatgcac tgacgggtgc cccgctcaac 480
ttgaccccc agcaggtggt ggccatcgcc agcaataatg gtggcaagca ggcgctggag 540
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ggagcaggtg 600
gtggccatcg ccagccacga tggcggcaag caggcgctgg agacggtcca gcggctgttg 660
ccggtgctgt gccaggccca cggcttgacc ccggagcagg tggtggccat cgccagccac 720
gatggcggca agcaggcgct ggagacggtc agcggctgt tgccggtgct gtgccaggcc 780
cacggcttga ccccccagca ggtggtggcc atcgccagca atggcggtgg caagcaggcg 840
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccccag 900
caggtggtgg ccatcgccag caataatggt ggcaagcagg cgctggagac ggtccagcgg 960
ctgttgccgg tgctgtgcca ggcccacggc ttgacccccc agcaggtggt ggccatcgcc 1020
agcaataatg gtggcaagca ggcgctggag acggtccagc ggctgttgcc ggtgctgtgc 1080
caggcccacg gcttgacccc ccagcaggtg gtggccatcg ccagcaatgg cggtggcaag 1140
caggcgctgg agacggtcca gcggctgttg ccggtgctgt gccaggccca cggcttgacc 1200
ccccagcagg tggtggccat cgccagcaat aatggtggca agcaggcgct ggagacggtc 1260
cagcggctgt tgccggtgct gtgccaggcc cacggcttga ccccccagca ggtggtggcc 1320
atcgccagca atggcggtgg caagcaggcg ctggagacgg tccagcggct gttgccggtg 1380
ctgtgccagg cccacggctt gaccccccag caggtggtgg ccatcgccag caataatggt 1440
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 1500
ttgaccccgg agcaggtggt ggccatcgcc agccacgatg gcggcaagca ggcgctggag 1560
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ccagcaggtg 1620
gtggccatcg ccagcaatgg cggtggcaag caggcgctgg agacggtcca gcggctgttg 1680
ccggtgctgt gccaggccca cggcttgacc ccggagcagg tggtggccat cgccagccac 1740
gatggcggca agcaggcgct ggagacggtc agcggctgt tgccggtgct gtgccaggcc 1800
cacggcttga ccccccagca ggtggtggcc atcgccagca atggcggtgg caagcaggcg 1860
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccccag 1920
caggtggtgg ccatcgccag caataatggt ggcaagcagg cgctggagac ggtccagcgg 1980
ctgttgccgg tgctgtgcca ggcccacggc ttgacccctc agcaggtggt ggccatcgcc 2040
agcaatggcg gcggcaggcc ggcgctggag agcattgttg cccagttatc tcgccctgat 2100
ccggcgttgg ccgcgttgac caacgaccac ctcgtcgcct tggcctgcct cggcgggcgt 2160
cctgcgctgg atgcagtgaa aaagggattg ggggatccta tcagccgttc ccagctggtg 2220
aagtccgagc tggaggagaa gaaatccgag ttgaggcaca agctgaagta cgtgccccac 2280
gagtacatcg agctgatcga gatcgcccgg aacagcaccc aggaccgtat cctggagatg 2340
aaggtgatgg agttcttcat gaaggtgtac ggctacaggg gcaagcacct gggcggctcc 2400
aggaagcccg acggcgccat ctacaccgtg ggctccccca tcgactacgg cgtgatcgtg 2460
gacaccaagg cctactccgg cggctacaac ctgcccatcg gccaggccga cgaaatgcag 2520
aggtacgtgg aggagaacca gaccaggaac aagcacatca accccaacga gtggtggaag 2580
gtgtacccct ccagcgtgac cgagttcaag ttcctgttcg tgtccggcca cttcaagggc 2640
aactacaagg cccagctgac caggctgaac cacatcacca actgcaacgg cgccgtgctg 2700
tccgtggagg agctcctgat cggcggcgag atgatcaagg ccggcaccct gaccctggag 2760
gaggtgagga ggaagttcaa caacggcgag atcaacttcg cggccgactg ataa 2814

<210> 22

<211> 2832
<212> DNA
<213> Artificial sequence

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

<220>
<223> GRex3T2-R TALEN

<400> 22
atgggcgatc ctaaaaagaa acgtaaggtc atcgataagg agaccgccgc tgccaagttc 60
gagagacagc acatggacag catcgatatc gccgatctac gcacgctcgg ctacagccag 120
cagcaacagg agaagatcaa accgaaggtt cgttcgacag tggcgcagca ccacgaggca 180
ctggtcggcc acgggtttac acacgcgcac atcgttgcgt taagccaaca cccggcagcg 240
ttagggaccg tcgctgtcaa gtatcaggac atgatcgcag cgttgccaga ggcgacacac 300
gaagcgatcg ttggcgtcgg caaacagtgg tccggcgcac gcgctctgga ggccttgctc 360

```
acggtggcgg gagagttgag aggtccaccg ttacagttgg acacaggcca acttctcaag    420
attgcaaaac gtggcggcgt gaccgcagtg gaggcagtgc atgcatggcg caatgcactg    480
acgggtgccc cgctcaactt gacccccag caggtggtgg ccatcgccag caatggcggt    540
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc    600
ttgaccccgg agcaggtggt ggccatcgcc agcaatattg gtggcaagca ggcgctggag    660
acggtgcagg cgctgttgcc ggtgctgtgc caggcccacg gcttgacccc ggagcaggtg    720
gtggccatcg ccagcaatat tggtggcaag caggcgctgg agacggtgca ggcgctgttg    780
ccggtgctgt gccaggccca cggcttgacc ccccagcagg tggtggccat cgccagcaat    840
aatggtggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc    900
cacggcttga ccccggagca ggtggtggcc atcgccagca atattggtgg caagcaggcg    960
ctggagacgg tgcaggcgct gttgccggtg ctgtgccagg cccacggctt gaccccggag   1020
caggtggtgg ccatcgccag ccacgatggc ggcaagcagg cgctggagac ggtccagcgg   1080
ctgttgccgg tgctgtgcca ggcccacggc ttgacccccc agcaggtggt ggccatcgcc   1140
agcaatggcg gtggcaagca ggcgctggag acggtccagc ggctgttgcc ggtgctgtgc   1200
caggcccacg gcttgacccc ggagcaggtg gtggccatcg ccagccacga tggcggcaag   1260
caggcgctgg agacggtcca gcggctgttg ccggtgctgt gccaggccca cggcttgacc   1320
ccggagcagg tggtggccat cgccagccac gatggcggca agcaggcgct ggagacggtc   1380
cagcggctgt tgccggtgct gtgccaggcc cacggcttga ccccggagca ggtggtggcc   1440
atcgccagca atattggtgg caagcaggcg ctggagacgg tgcaggcgct gttgccggtg   1500
ctgtgccagg cccacggctt gacccccag caggtggtgg ccatcgccag caatggcggt   1560
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc   1620
ttgaccccgg agcaggtggt ggccatcgcc agcaatattg gtggcaagca ggcgctggag   1680
acggtgcagg cgctgttgcc ggtgctgtgc caggcccacg gcttgacccc ggagcaggtg   1740
gtggccatcg ccagcaatat tggtggcaag caggcgctgg agacggtgca ggcgctgttg   1800
ccggtgctgt gccaggccca cggcttgacc ccccagcagg tggtggccat cgccagcaat   1860
ggcggtggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc   1920
cacggcttga ccccccagca ggtggtggcc atcgccagca ataatggtgg caagcaggcg   1980
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccctcag  2040
caggtggtgg ccatcgccag caatggcggc ggcaggccgg cgctggagag cattgttgcc   2100
cagttatctc gccctgatcc ggcgttggcc gcgttgacca acgaccacct cgtcgccttg   2160
gcctgcctcg gcgggcgtcc tgcgctggat gcagtgaaaa agggattggg ggatcctatc   2220
agccgttccc agctggtgaa gtccgagctg gaggagaaga aatccgagtt gaggcacaag   2280
ctgaagtacg tgccccacga gtacatcgag ctgatcgaga tcgcccggaa cagcacccag   2340
gaccgtatcc tggagatgaa ggtgatggag ttcttcatga aggtgtacgg ctacaggggc   2400
aagcacctgg gcggctccag gaagcccgac ggcgccatct acaccgtggg ctcccccatc   2460
gactacggcg tgatcgtgga caccaaggcc tactccggcg gctacaacct gcccatcggc   2520
caggccgacg aaatgcagag gtacgtggag gagaaccaga ccaggaacaa gcacatcaac   2580
cccaacgagt ggtggaaggt gtacccctcc agcgtgaccg agttcaagtt cctgttcgtg   2640
tccggccact tcaagggcaa ctacaaggcc cagctgacca ggctgaacca catcaccaac   2700
tgcaacggcg ccgtgctgtc cgtggaggag ctcctgatcg gcggcgagat gatcaaggcc   2760
ggcaccctga ccctggagga ggtgaggagg aagttcaaca acggcgagat caacttcgcg   2820
gccgactgat aa                                                       2832
```

<210> 23

<211> 2814
<212> DNA
<213> Artificial sequence

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

<220>
<223> GRex3T4-L TALEN

<400> 23

```
atgggcgatc ctaaaaagaa acgtaaggtc atcgattacc catacgatgt tccagattac     60
gctatcgata tcgccgatct acgcacgctc ggctacagcc agcagcaaca ggagaagatc    120
aaaccgaagg ttcgttcgac agtggcgcag caccacgagg cactggtcgg ccacgggttt    180
acacacgcgc acatcgttgc gttaagccaa cacccggcag cgttagggac cgtcgctgtc    240
aagtatcagg acatgatcgc agcgttgcca gaggcgacac acgaagcgat cgttggcgtc    300
ggcaaacagt ggtccggcgc acgcgctctg gaggccttgc tcacggtggc gggagagttg    360
agaggtccac cgttacagtt ggacacaggc caacttctca agattgcaaa acgtggcggc    420
gtgaccgcag tggaggcagt gcatgcatgg cgcaatgcac tgacgggtgc cccgctcaac    480
ttgacccccc agcaggtggt ggccatcgcc agcaataatg gtggcaagca ggcgctggag    540
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ggagcaggtg    600
gtggccatcg ccagccacga tggcggcaag caggcgctgg agacggtcca gcggctgttg    660
```

```
ccggtgctgt gccaggccca cggcttgacc ccccagcagg tggtggccat cgccagcaat    720
ggcggtggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc    780
cacggcttga ccccggagca ggtggtggcc atcgccagcc acgatggcgg caagcaggcg    840
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccccag    900
caggtggtgg ccatcgccag caatggcggt ggcaagcagg cgctggagac ggtccagcgg    960
ctgttgccgg tgctgtgcca ggcccacggc ttgacccccc agcaggtggt ggccatcgcc   1020
agcaataatg gtggcaagca ggcgctggag acggtccagc ggctgttgcc ggtgctgtgc   1080
caggcccacg gcttgacccc ggagcaggtg gtggccatcg ccagcaatat tggtggcaag   1140
caggcgctgg agacggtgca ggcgctgttg ccggtgctgt gccaggccca cggcttgacc   1200
ccccagcagg tggtggccat cgccagcaat ggcggtggca agcaggcgct ggagacggtc   1260
cagcggctgt tgccggtgct gtgccaggcc cacggcttga ccccccagca ggtggtggcc   1320
atcgccagca ataatggtgg caagcaggcg ctggagacgg tccagcggct gttgccggtg   1380
ctgtgccagg cccacggctt gaccccggag caggtggtgg ccatcgccag caatattggt   1440
ggcaagcagg cgctggagac ggtgcaggcg ctgttgccgg tgctgtgcca ggcccacggc   1500
ttgaccccgg agcaggtggt ggccatcgcc agcaatattg gtggcaagca ggcgctggag   1560
acggtgcagg cgctgttgcc ggtgctgtgc caggcccacg gcttgacccc ccagcaggtg   1620
gtggccatcg ccagcaataa tggtggcaag caggcgctgg agacggtcca gcggctgttg   1680
ccggtgctgt gccaggccca cggcttgacc ccggagcagg tggtggccat cgccagccac   1740
gatggcggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc   1800
cacggcttga ccccccagca ggtggtggcc atcgccagca atggcggtgg caagcaggcg   1860
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccccag   1920
caggtggtgg ccatcgccag caatggcggt ggcaagcagg cgctggagac ggtccagcgg   1980
ctgttgccgg tgctgtgcca ggcccacggc ttgacccctc agcaggtggt ggccatcgcc   2040
agcaatggcg gcggcaggcc ggcgctggag agcattgttg cccagttatc tcgccctgat   2100
ccggcgttgg ccgcgttgac caacgaccac ctcgtcgcct tggcctgcct cggcgggcgt   2160
cctgcgctgg atgcagtgaa aaagggattg ggggatccta tcagccgttc ccagctggtg   2220
aagtccgagc tggaggagaa gaaatccgag ttgaggcaca agctgaagta cgtgccccac   2280
gagtacatcg agctgatcga gatcgcccgg aacagcaccc aggaccgtat cctggagatg   2340
aaggtgatgg agttcttcat gaaggtgtac ggctacaggg gcaagcacct gggcggctcc   2400
aggaagcccg acggcgccat ctacaccgtg ggctccccca tcgactacgg cgtgatcgtg   2460
gacaccaagg cctactccgg cggctacaac ctgcccatcg gccaggccga cgaaatgcag   2520
aggtacgtgg aggagaacca gaccaggaac aagcacatca accccaacga gtggtggaag   2580
gtgtaccct ccagcgtgac cgagttcaag ttcctgttcg tgtccggcca cttcaagggc   2640
aactacaagg cccagctgac caggctgaac cacatcacca actgcaacgg cgccgtgctg   2700
tccgtggagg agctcctgat cggcggcgag atgatcaagg ccggcaccct gaccctggag   2760
gaggtgagga ggaagttcaa caacggcgag atcaacttcg cggccgactg ataa         2814
```

<210> 24

<211> 2832
<212> DNA
<213> Artificial sequence

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

<220>
<223> GRex3T4-R TALEN

<400> 24

```
atgggcgatc ctaaaaagaa acgtaaggtc atcgataagg agaccgccgc tgccaagttc     60
gagagacagc acatggacag catcgatatc gccgatctac gcacgctcgg ctacagccag    120
cagcaacagg agaagatcaa accgaaggtt cgttcgacag tggcgcagca ccacgaggca    180
ctggtcggcc acgggtttac acacgcgcac atcgttgcgt taagccaaca cccggcagcg    240
ttagggaccg tcgctgtcaa gtatcaggac atgatcgcag cgttgccaga ggcgacacac    300
gaagcgatcg ttggcgtcgg caaacagtgg tccggcgcac gcgctctgga ggccttgctc    360
acggtggcgg gagagttgag aggtccaccg ttacagttgg acacaggcca acttctcaag    420
attgcaaaac gtggcggcgt gaccgcagtg gaggcagtgc atgcatggcg caatgcactg    480
acgggtgccc cgctcaactt gacccccag caggtggtgg ccatcgccag caatggcggt    540
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc    600
ttgaccccgg agcaggtggt ggccatcgcc agccacgatg gcggcaagca ggcgctggag    660
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ggagcaggtg    720
gtggccatcg ccagccacga tggcggcaag caggcgctgg agacggtcca gcggctgttg    780
ccggtgctgt gccaggccca cggcttgacc ccggagcagg tggtggccat cgccagcaat    840
attggtggca agcaggcgct ggagacggtg caggcgctgt tgccggtgct gtgccaggcc    900
cacggcttga ccccggagca ggtggtggcc atcgccagcc acgatggcgg caagcaggcg    960
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccggag   1020
```

caggtggtgg ccatcgccag caatattggt ggcaagcagg cgctggagac ggtgcaggcg 1080
ctgttgccgg tgctgtgcca ggcccacggc ttgaccccgg agcaggtggt ggccatcgcc 1140
agcaatattg gtggcaagca ggcgctggag acggtgcagg cgctgttgcc ggtgctgtgc 1200
caggcccacg gcttgacccc ccagcaggtg gtggccatcg ccagcaataa tggtggcaag 1260
caggcgctgg agacggtcca gcggctgttg ccggtgctgt gccaggccca cggcttgacc 1320
ccccagcagg tggtggccat cgccagcaat ggcggtggca agcaggcgct ggagacggtc 1380
cagcggctgt tgccggtgct gtgccaggcc cacggcttga ccccccagca ggtggtggcc 1440
atcgccagca atggcggtgg caagcaggcg ctggagacgg tccagcggct gttgccggtg 1500
ctgtgccagg cccacggctt gaccccggag caggtggtgg ccatcgccag caatattggt 1560
ggcaagcagg cgctggagac ggtgcaggcg ctgttgccgg tgctgtgcca ggcccacggc 1620
ttgaccccgg agcaggtggt ggccatcgcc agcaatattg gtggcaagca ggcgctggag 1680
acggtgcagg cgctgttgcc ggtgctgtgc caggcccacg gcttgacccc ccagcaggtg 1740
gtggccatcg ccagcaataa tggtggcaag caggcgctgg agacggtcca gcggctgttg 1800
ccggtgctgt gccaggccca cggcttgacc ccggagcagg tggtggccat cgccagcaat 1860
attggtggca agcaggcgct ggagacggtg caggcgctgt tgccggtgct gtgccaggcc 1920
cacggcttga ccccggagca ggtggtggcc atcgccagcc acgatggcgg caagcaggcg 1980
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccctcag 2040
caggtggtgg ccatcgccag caatggcggc ggcaggccgg cgctggagag cattgttgcc 2100
cagttatctc gccctgatcc ggcgttggcc gcgttgacca acgaccacct cgtcgccttg 2160
gcctgcctcg gcgggcgtcc tgcgctggat gcagtgaaaa agggattggg ggatcctatc 2220
agccgttccc agctggtgaa gtccgagctg gaggagaaga aatccgagtt gaggcacaag 2280
ctgaagtacg tgccccacga gtacatcgag ctgatcgaga tcgcccggaa cagcacccag 2340
gaccgtatcc tggagatgaa ggtgatggag ttcttcatga aggtgtacgg ctacaggggc 2400
aagcacctgg gcggctccag gaagcccgac ggcgccatct acaccgtggg ctcccccatc 2460
gactacggcg tgatcgtgga caccaaggcc tactccggcg gctacaacct gcccatcggc 2520
caggccgacg aaatgcagag gtacgtggag gagaaccaga ccaggaacaa gcacatcaac 2580
cccaacgagt ggtggaaggt gtacccctcc agcgtgaccg agttcaagtt cctgttcgtg 2640
tccggccact tcaagggcaa ctacaaggcc cagctgacca ggctgaacca catcaccaac 2700
tgcaacggcg ccgtgctgtc cgtggaggag ctcctgatcg gcggcgagat gatcaaggcc 2760
ggcaccctga ccctggagga ggtgaggagg aagttcaaca acggcgagat caacttcgcg 2820
gccgactgat aa 2832

<210> 25

<211> 2814
<212> DNA
<213> Artificial sequence

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

<220>
<223> GRex5T1-L TALEN

<400> 25
atgggcgatc ctaaaaagaa acgtaaggtc atcgattacc catacgatgt tccagattac 60
gctatcgata tcgccgatct acgcacgctc ggctacagcc agcagcaaca ggagaagatc 120
aaaccgaagg ttcgttcgac agtggcgcag caccacgagg cactggtcgg ccacgggttt 180
acacacgcgc acatcgttgc gttaagccaa cacccggcag cgttagggac cgtcgctgtc 240
aagtatcagg acatgatcgc agcgttgcca gaggcgacac acgaagcgat cgttggcgtc 300
ggcaaacagt ggtccggcgc acgcgctctg gaggccttgc tcacggtggc gggagagttg 360
agaggtccac cgttacagtt ggacacaggc caacttctca agattgcaaa acgtggcggc 420
gtgaccgcag tggaggcagt gcatgcatgg cgcaatgcac tgacgggtgc cccgctcaac 480
ttgacccccc agcaggtggt ggccatcgcc agcaataatg gtggcaagca ggcgctggag 540
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ccagcaggtg 600
gtggccatcg ccagcaataa tggtggcaag caggcgctgg agacggtcca gcggctgttg 660
ccggtgctgt gccaggccca cggcttgacc ccccagcagg tggtggccat cgccagcaat 720
ggcggtggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 780
cacggcttga ccccccagca ggtggtggcc atcgccagca ataatggtgg caagcaggcg 840
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gacccccag 900
caggtggtgg ccatcgccag caatggcggt ggcaagcagg cgctggagac ggtccagcgg 960
ctgttgccgg tgctgtgcca ggcccacggc ttgaccccgg agcaggtggt ggccatcgcc 1020
agccacgatg gcggcaagca ggcgctggag acggtccagc ggctgttgcc ggtgctgtgc 1080
caggcccacg gcttgacccc ggagcaggtg gtggccatcg ccagcaatat tggtggcaag 1140
caggcgctgg agacggtgca ggcgctgttg ccggtgctgt gccaggccca cggcttgacc 1200
ccggagcagg tggtggccat cgccagccac gatggcggca agcaggcgct ggagacggtc 1260
cagcggctgt tgccggtgct gtgccaggcc cacggcttga ccccccagca ggtggtggcc 1320

atcgccagca atggcggtgg caagcaggcg ctggagacgg tccagcggct gttgccggtg 1380
ctgtgccagg cccacggctt gacccccag caggtggtgg ccatcgccag caataatggt 1440
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 1500
ttgacccccc agcaggtggt ggccatcgcc agcaatggcg gtggcaagca ggcgctggag 1560
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ccagcaggtg 1620
gtggccatcg ccagcaatgg cggtggcaag caggcgctgg agacggtcca gcggctgttg 1680
ccggtgctgt gccaggccca cggcttgacc ccccagcagg tggtggccat cgccagcaat 1740
aatggtggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 1800
cacggcttga ccccccagca ggtggtggcc atcgccagca ataatggtgg caagcaggcg 1860
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccggag 1920
caggtggtgg ccatcgccag caatattggt ggcaagcagg cgctggagac ggtgcaggcg 1980
ctgttgccgg tgctgtgcca ggcccacggc ttgacccctc agcaggtggt ggccatcgcc 2040
agcaatggcg gcggcaggcc ggcgctggag agcattgttg cccagttatc tcgccctgat 2100
ccggcgttgg ccgcgttgac caacgaccac ctcgtcgcct tggcctgcct cggcgggcgt 2160
cctgcgctgg atgcagtgaa aaagggattg ggggatccta tcagccgttc ccagctggtg 2220
aagtccgagc tggaggagaa gaaatccgag ttgaggcaca agctgaagta cgtgccccac 2280
gagtacatcg agctgatcga gatcgcccgg aacagcaccc aggaccgtat cctggagatg 2340
aaggtgatgg agttcttcat gaaggtgtac ggctacaggg gcaagcacct gggcggctcc 2400
aggaagcccg acggcgccat ctacaccgtg ggctccccca tcgactacgg cgtgatcgtg 2460
gacaccaagg cctactccgg cggctacaac ctgcccatcg gccaggccga cgaaatgcag 2520
aggtacgtgg aggagaacca gaccaggaac aagcacatca accccaacga gtggtggaag 2580
gtgtaccct ccagcgtgac cgagttcaag ttcctgttcg tgtccggcca cttcaagggc 2640
aactacaagg cccagctgac caggctgaac cacatcacca actgcaacgg cgccgtgctg 2700
tccgtggagg agctcctgat cggcggcgag atgatcaagg ccggcaccct gaccctggag 2760
gaggtgagga ggaagttcaa caacggcgag atcaacttcg cggccgactg ataa 2814

<210> 26

<211> 2832
<212> DNA
<213> Artificial sequence

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

<220>
<223> GRex5T1-R TALEN

<400> 26
atgggcgatc ctaaaaagaa acgtaaggtc atcgataagg agaccgccgc tgccaagttc 60
gagagacagc acatggacag catcgatatc gccgatctac gcacgctcgg ctacagccag 120
cagcaacagg agaagatcaa accgaaggtt cgttcgacag tggcgcagca ccacgaggca 180
ctggtcggcc acgggtttac acacgcgcac atcgttgcgt taagccaaca cccggcagcg 240
ttagggaccg tcgctgtcaa gtatcaggac atgatcgcag cgttgccaga ggcgacacac 300
gaagcgatcg ttggcgtcgg caaacagtgg tccggcgcac gcgctctgga ggccttgctc 360
acggtggcgg gagagttgag aggtccaccg ttacagttgg acacaggcca acttctcaag 420
attgcaaaac gtggcggcgt gaccgcagtg gaggcagtgc atgcatggcg caatgcactg 480
acgggtgccc cgctcaactt gaccccggag caggtggtgg ccatcgccag caatattggt 540
ggcaagcagg cgctggagac ggtgcaggcg ctgttgccgg tgctgtgcca ggcccacggc 600
ttgacccccc agcaggtggt ggccatcgcc agcaatggcg gtggcaagca ggcgctggag 660
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ggagcaggtg 720
gtggccatcg ccagccacga tggcggcaag caggcgctgg agacggtcca gcggctgttg 780
ccggtgctgt gccaggccca cggcttgacc ccggagcagg tggtggccat cgccagccac 840
gatggcggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 900
cacggcttga ccccccagca ggtggtggcc atcgccagca atggcggtgg caagcaggcg 960
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gacccccag 1020
caggtggtgg ccatcgccag caataatggt ggcaagcagg cgctggagac ggtccagcgg 1080
ctgttgccgg tgctgtgcca ggcccacggc ttgaccccgg agcaggtggt ggccatcgcc 1140
agccacgatg gcggcaagca ggcgctggag acggtccagc ggctgttgcc ggtgctgtgc 1200
caggcccacg gcttgacccc ggagcaggtg gtggccatcg ccagcaatat tggtggcaag 1260
caggcgctgg agacggtgca ggcgctgttg ccggtgctgt gccaggccca cggcttgacc 1320
ccccagcagg tggtggccat cgccagcaat ggcggtggca agcaggcgct ggagacggtc 1380
cagcggctgt tgccggtgct gtgccaggcc cacggcttga ccccggagca ggtggtggcc 1440
atcgccagca atattggtgg caagcaggcg ctggagacgg tgcaggcgct gttgccggtg 1500
ctgtgccagg cccacggctt gaccccccag caggtggtgg ccatcgccag caatggcggt 1560
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 1620
ttgaccccgg agcaggtggt ggccatcgcc agcaatattg gtggcaagca ggcgctggag 1680

acggtgcagg cgctgttgcc ggtgctgtgc caggcccacg gcttgacccc ggagcaggtg 1740
gtggccatcg ccagcaatat tggtggcaag caggcgctgg agacggtgca ggcgctgttg 1800
ccggtgctgt gccaggccca cggcttgacc ccggagcagg tggtggccat cgccagccac 1860
gatggcggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 1920
cacggcttga ccccggagca ggtggtggcc atcgccagca atattggtgg caagcaggcg 1980
ctggagacgg tgcaggcgct gttgccggtg ctgtgccagg cccacggctt gacccctcag 2040
caggtggtgg ccatcgccag caatggcggc ggcaggccgg cgctggagag cattgttgcc 2100
cagttatctc gccctgatcc ggcgttggcc gcgttgacca acgaccacct cgtcgccttg 2160
gcctgcctcg gcgggcgtcc tgcgctggat gcagtgaaaa agggattggg ggatcctatc 2220
agccgttccc agctggtgaa gtccgagctg gaggagaaga aatccgagtt gaggcacaag 2280
ctgaagtacg tgccccacga gtacatcgag ctgatcgaga tcgcccggaa cagcacccag 2340
gaccgtatcc tggagatgaa ggtgatggag ttcttcatga aggtgtacgg ctacaggggc 2400
aagcacctgg gcggctccag gaagcccgac ggcgccatct acaccgtggg ctcccccatc 2460
gactacggcg tgatcgtgga caccaaggcc tactccggcg gctacaacct gcccatcggc 2520
caggccgacg aaatgcagag gtacgtggag gagaaccaga ccaggaacaa gcacatcaac 2580
cccaacgagt ggtggaaggt gtacccctcc agcgtgaccg agttcaagtt cctgttcgtg 2640
tccggccact tcaagggcaa ctacaaggcc cagctgacca ggctgaacca catcaccaac 2700
tgcaacggcg ccgtgctgtc cgtggaggag ctcctgatcg gcggcgagat gatcaaggcc 2760
ggcaccctga ccctggagga ggtgaggagg aagttcaaca acggcgagat caacttcgcg 2820
gccgactgat aa 2832

<210> 27

<211> 2814
<212> DNA
<213> Artificial sequence

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

<220>
<223> GRex5T2-L TALEN

<400> 27
atgggcgatc ctaaaaagaa acgtaaggtc atcgattacc catacgatgt tccagattac 60
gctatcgata tcgccgatct acgcacgctc ggctacagcc agcagcaaca ggagaagatc 120
aaaccgaagg ttcgttcgac agtggcgcag caccacgagg cactggtcgg ccacgggttt 180
acacacgcgc acatcgttgc gttaagccaa cacccggcag cgttagggac cgtcgctgtc 240
aagtatcagg acatgatcgc agcgttgcca gaggcgacac acgaagcgat cgttggcgtc 300
ggcaaacagt ggtccggcgc acgcgctctg gaggccttgc tcacggtggc gggagagttg 360
agaggtccac cgttacagtt ggacacaggc caacttctca agattgcaaa acgtggcggc 420
gtgaccgcag tggaggcagt gcatgcatgg cgcaatgcac tgacgggtgc cccgctcaac 480
ttgaccccgg agcaggtggt ggccatcgcc agcaatattg gtggcaagca ggcgctggag 540
acggtgcagg cgctgttgcc ggtgctgtgc caggcccacg gcttgacccc ccagcaggtg 600
gtggccatcg ccagcaatgg cggtggcaag caggcgctgg agacggtcca gcggctgttg 660
ccggtgctgt gccaggccca cggcttgacc ccccagcagg tggtggccat cgccagcaat 720
aatggtggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 780
cacggcttga ccccggagca ggtggtggcc atcgccagca atattggtgg caagcaggcg 840
ctggagacgg tgcaggcgct gttgccggtg ctgtgccagg cccacggctt gacccccccag 900
caggtggtgg ccatcgccag caatggcggt ggcaagcagg cgctggagac ggtccagcgg 960
ctgttgccgg tgctgtgcca ggcccacggc ttgaccccgg agcaggtggt ggccatcgcc 1020
agcaatattg gtggcaagca ggcgctggag acggtgcagg cgctgttgcc ggtgctgtgc 1080
caggcccacg gcttgacccc ccagcaggtg gtggccatcg ccagcaataa tggtggcaag 1140
caggcgctgg agacggtcca gcggctgttg ccggtgctgt gccaggccca cggcttgacc 1200
ccggagcagg tggtggccat cgccagccac gatggcggca agcaggcgct ggagacggtc 1260
cagcggctgt tgccggtgct gtgccaggcc cacggcttga ccccccagca ggtggtggcc 1320
atcgccagca atggcggtgg caagcaggcg ctggagacgg tccagcggct gttgccggtg 1380
ctgtgccagg cccacggctt gaccccggag caggtggtgg ccatcgccag ccacgatggc 1440
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 1500
ttgacccccc agcaggtggt ggccatcgcc agcaatggcg gtggcaagca ggcgctggag 1560
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ccagcaggtg 1620
gtggccatcg ccagcaataa tggtggcaag caggcgctgg agacggtcca gcggctgttg 1680
ccggtgctgt gccaggccca cggcttgacc ccccagcagg tggtggccat cgccagcaat 1740
ggcggtggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 1800
cacggcttga ccccccagca ggtggtggcc atcgccagca atggcggtgg caagcaggcg 1860
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccggag 1920
caggtggtgg ccatcgccag ccacgatggc ggcaagcagg cgctggagac ggtccagcgg 1980

ctgttgccgg tgctgtgcca ggcccacggc ttgaccctc agcaggtggt ggccatcgcc 2040
agcaatggcg gcggcaggcc ggcgctggag agcattgttg cccagttatc tcgccctgat 2100
ccggcgttgg ccgcgttgac caacgaccac ctcgtcgcct tggcctgcct cggcgggcgt 2160
cctgcgctgg atgcagtgaa aaagggattg ggggatccta tcagccgttc ccagctggtg 2220
aagtccgagc tggaggagaa gaaatccgag ttgaggcaca agctgaagta cgtgccccac 2280
gagtacatcg agctgatcga gatcgcccgg aacagcaccc aggaccgtat cctggagatg 2340
aaggtgatgg agttcttcat gaaggtgtac ggctacaggg gcaagcacct gggcggctcc 2400
aggaagcccg acggcgccat ctacaccgtg ggctccccca tcgactacgg cgtgatcgtg 2460
gacaccaagg cctactccgg cggctacaac ctgcccatcg gccaggccga cgaaatgcag 2520
aggtacgtgg aggagaacca gaccaggaac aagcacatca accccaacga gtggtggaag 2580
gtgtaccct ccagcgtgac cgagttcaag ttcctgttcg tgtccggcca cttcaagggc 2640
aactacaagg cccagctgac caggctgaac cacatcacca actgcaacgg cgccgtgctg 2700
tccgtggagg agctcctgat cggcggcgag atgatcaagg ccggcaccct gaccctggag 2760
gaggtgagga ggaagttcaa caacggcgag atcaacttcg cggccgactg ataa 2814

<210> 28

<211> 2832
<212> DNA
<213> Artificial sequence

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

<220>
<223> GRex5T2-R TALEN

<400> 28
atgggcgatc ctaaaaagaa acgtaaggtc atcgataagg agaccgccgc tgccaagttc 60
gagagacagc acatggacag catcgatatc gccgatctac gcacgctcgg ctacagccag 120
cagcaacagg agaagatcaa accgaaggtt cgttcgacag tggcgcagca ccacgaggca 180
ctggtcggcc acgggtttac acacgcgcac atcgttgcgt taagccaaca cccggcagcg 240
ttagggaccg tcgctgtcaa gtatcaggac atgatcgcag cgttgccaga ggcgacacac 300
gaagcgatcg ttggcgtcgg caaacagtgg tccggcgcac gcgctctgga ggccttgctc 360
acggtggcgg gagagttgag aggtccaccg ttacagttgg acacaggcca acttctcaag 420
attgcaaaac gtggcggcgt gaccgcagtg gaggcagtgc atgcatggcg caatgcactg 480
acgggtgccc cgctcaactt gacccccag caggtggtgg ccatcgccag caataatggt 540
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 600
ttgaccccgg agcaggtggt ggccatcgcc agcaatattg gtggcaagca ggcgctggag 660
acggtgcagg cgctgttgcc ggtgctgtgc caggcccacg gcttgacccc ccagcaggtg 720
gtggccatcg ccagcaataa tggtggcaag caggcgctgg agacggtcca gcggctgttg 780
ccggtgctgt gccaggccca cggcttgacc ccggagcagg tggtggccat cgccagccac 840
gatggcggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 900
cacggcttga ccccccagca ggtggtggcc atcgccagca ataatggtgg caagcaggcg 960
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccccag 1020
caggtggtgg ccatcgccag caatggcggt ggcaagcagg cgctggagac ggtccagcgg 1080
ctgttgccgg tgctgtgcca ggcccacggc ttgaccccgg agcaggtggt ggccatcgcc 1140
agcaatattg gtggcaagca ggcgctggag acggtgcagg cgctgttgcc ggtgctgtgc 1200
caggcccacg gcttgacccc ccagcaggtg gtggccatcg ccagcaataa tggtggcaag 1260
caggcgctgg agacggtcca gcggctgttg ccggtgctgt gccaggccca cggcttgacc 1320
ccccagcagg tggtggccat cgccagcaat ggcggtggca agcaggcgct ggagacggtc 1380
cagcggctgt tgccggtgct gtgccaggcc cacggcttga ccccggagca ggtggtggcc 1440
atcgccagcc acgatggcgg caagcaggcg ctggagacgg tccagcggct gttgccggtg 1500
ctgtgccagg cccacggctt gaccccggag caggtggtgg ccatcgccag caatattggt 1560
ggcaagcagg cgctggagac ggtgcaggcg ctgttgccgg tgctgtgcca ggcccacggc 1620
ttgaccccc agcaggtggt ggccatcgcc agcaatggcg gtggcaagca ggcgctggag 1680
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ccagcaggtg 1740
gtggccatcg ccagcaataa tggtggcaag caggcgctgg agacggtcca gcggctgttg 1800
ccggtgctgt gccaggccca cggcttgacc ccggagcagg tggtggccat cgccagcaat 1860
attggtggca agcaggcgct ggagacggtg caggcgctgt tgccggtgct gtgccaggcc 1920
cacggcttga ccccccagca ggtggtggcc atcgccagca atggcggtgg caagcaggcg 1980
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccctcag 2040
caggtggtgg ccatcgccag caatggcggc ggcaggccgg cgctggagag cattgttgcc 2100
cagttatctc gccctgatcc ggcgttggcc gcgttgacca acgaccacct cgtcgccttg 2160
gcctgcctcg gcgggcgtcc tgcgctggat gcagtgaaaa agggattggg ggatcctatc 2220
agccgttccc agctggtgaa gtccgagctg gaggagaaga aatccgagtt gaggcacaag 2280
ctgaagtacg tgccccacga gtacatcgag ctgatcgaga tcgcccggaa cagcacccag 2340

gaccgtatcc tggagatgaa ggtgatggag ttcttcatga aggtgtacgg ctacaggggc 2400
aagcacctgg gcggctccag gaagcccgac ggcgccatct acaccgtggg ctcccccatc 2460
gactacggcg tgatcgtgga caccaaggcc tactccggcg gctacaacct gcccatcggc 2520
caggccgacg aaatgcagag gtacgtggag gagaaccaga ccaggaacaa gcacatcaac 2580
cccaacgagt ggtggaaggt gtacccctcc agcgtgaccg agttcaagtt cctgttcgtg 2640
tccggccact tcaagggcaa ctacaaggcc cagctgacca ggctgaacca catcaccaac 2700
tgcaacggcg ccgtgctgtc cgtggaggag ctcctgatcg gcggcgagat gatcaaggcc 2760
ggcaccctga ccctggagga ggtgaggagg aagttcaaca acggcgagat caacttcgcg 2820
gccgactgat aa 2832

<210> 29

<211> 2814
<212> DNA
<213> Artificial sequence

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

<220>
<223> GRex5T3-L TALEN

<400> 29
atgggcgatc ctaaaaagaa acgtaaggtc atcgattacc catacgatgt tccagattac 60
gctatcgata tcgccgatct acgcacgctc ggctacagcc agcagcaaca ggagaagatc 120
aaaccgaagg ttcgttcgac agtggcgcag caccacgagg cactggtcgg ccacgggttt 180
acacacgcgc acatcgttgc gttaagccaa cacccggcag cgttagggac cgtcgctgtc 240
aagtatcagg acatgatcgc agcgttgcca gaggcgacac acgaagcgat cgttggcgtc 300
ggcaaacagt ggtccggcgc acgcgctctg gaggccttgc tcacggtggc gggagagttg 360
agaggtccac cgttacagtt ggacacaggc caacttctca agattgcaaa acgtggcggc 420
gtgaccgcag tggaggcagt gcatgcatgg cgcaatgcac tgacgggtgc cccgctcaac 480
ttgacccccc agcaggtggt ggccatcgcc agcaatggcg gtggcaagca ggcgctggag 540
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ggagcaggtg 600
gtggccatcg ccagcaatat tggtggcaag caggcgctgg agacggtgca ggcgctgttg 660
ccggtgctgt gccaggccca cggcttgacc ccccagcagg tggtggccat cgccagcaat 720
ggcggtggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 780
cacggcttga ccccggagca ggtggtggcc atcgccagca atattggtgg caagcaggcg 840
ctggagacgg tgcaggcgct gttgccggtg ctgtgccagg cccacggctt gacccccag 900
caggtggtgg ccatcgccag caatggcggt ggcaagcagg cgctggagac ggtccagcgg 960
ctgttgccgg tgctgtgcca ggcccacggc ttgaccccc agcaggtggt ggccatcgcc 1020
agcaataatg gtggcaagca ggcgctggag acggtccagc ggctgttgcc ggtgctgtgc 1080
caggcccacg gcttgacccc ggagcaggtg gtggccatcg ccagccacga tggcggcaag 1140
caggcgctgg agacggtcca gcggctgttg ccggtgctgt gccaggccca cggcttgacc 1200
ccggagcagg tggtggccat cgccagcaat attggtggca agcaggcgct ggagacggtg 1260
caggcgctgt tgccggtgct gtgccaggcc cacggcttga ccccccagca ggtggtggcc 1320
atcgccagca ataatggtgg caagcaggcg ctggagacgg tccagcggct gttgccggtg 1380
ctgtgccagg cccacggctt gacccccag caggtggtgg ccatcgccag caataatggt 1440
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 1500
ttgaccccgg agcaggtggt ggccatcgcc agcaatattg gtggcaagca ggcgctggag 1560
acggtgcagg cgctgttgcc ggtgctgtgc caggcccacg gcttgacccc ccagcaggtg 1620
gtggccatcg ccagcaatgg cggtggcaag caggcgctgg agacggtcca gcggctgttg 1680
ccggtgctgt gccaggccca cggcttgacc ccggagcagg tggtggccat cgccagcaat 1740
attggtggca agcaggcgct ggagacggtg caggcgctgt tgccggtgct gtgccaggcc 1800
cacggcttga ccccccagca ggtggtggcc atcgccagca atggcggtgg caagcaggcg 1860
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gacccccag 1920
caggtggtgg ccatcgccag caataatggt ggcaagcagg cgctggagac ggtccagcgg 1980
ctgttgccgg tgctgtgcca ggcccacggc ttgaccctc agcaggtggt ggccatcgcc 2040
agcaatggcg gcggcaggcc ggcgctggag agcattgttg cccagttatc tcgccctgat 2100
ccggcgttgg ccgcgttgac caacgaccac ctcgtcgcct tggcctgcct cggcgggcgt 2160
cctgcgctgg atgcagtgaa aaagggattg ggggatccta tcagccgttc ccagctggtg 2220
aagtccgagc tggaggagaa gaaatccgag ttgaggcaca agctgaagta cgtgccccac 2280
gagtacatcg agctgatcga gatcgcccgg aacagcaccc aggaccgtat cctggagatg 2340
aaggtgatgg agttcttcat gaaggtgtac ggctacaggg gcaagcacct gggcggctcc 2400
aggaagcccg acggcgccat ctacaccgtg ggctccccca tcgactacgg cgtgatcgtg 2460
gacaccaagg cctactccgg cggctacaac ctgcccatcg gccaggccga cgaaatgcag 2520
aggtacgtgg aggagaacca gaccaggaac aagcacatca accccaacga gtggtggaag 2580
gtgtacccct ccagcgtgac cgagttcaag ttcctgttcg tgtccggcca cttcaagggc 2640

aactacaagg cccagctgac caggctgaac cacatcacca actgcaacgg cgccgtgctg 2700
tccgtggagg agctcctgat cggcggcgag atgatcaagg ccggcaccct gaccctggag 2760
gaggtgagga ggaagttcaa caacggcgag atcaacttcg cggccgactg ataa 2814

<210> 30

<211> 2832
<212> DNA
<213> Artificial sequence

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

<220>
<223> GRex5T3-R TALEN

<400> 30
atgggcgatc ctaaaaagaa acgtaaggtc atcgataagg agaccgccgc tgccaagttc 60
gagagacagc acatggacag catcgatatc gccgatctac gcacgctcgg ctacagccag 120
cagcaacagg agaagatcaa accgaaggtt cgttcgacag tggcgcagca ccacgaggca 180
ctggtcggcc acgggtttac acacgcgcac atcgttgcgt taagccaaca cccggcagcg 240
ttagggaccg tcgctgtcaa gtatcaggac atgatcgcag cgttgccaga ggcgacacac 300
gaagcgatcg ttggcgtcgg caaacagtgg tccggcgcac gcgctctgga ggccttgctc 360
acggtggcgg gagagttgag aggtccaccg ttacagttgg acacaggcca acttctcaag 420
attgcaaaac gtggcggcgt gaccgcagtg gaggcagtgc atgcatggcg caatgcactg 480
acgggtgccc cgctcaactt gacccccag caggtggtgg ccatcgccag caataatggt 540
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 600
ttgaccccgg agcaggtggt ggccatcgcc agcaatattg gtggcaagca ggcgctggag 660
acggtgcagg cgctgttgcc ggtgctgtgc caggcccacg gcttgacccc ccagcaggtg 720
gtggccatcg ccagcaatgg cggtggcaag caggcgctgg agacggtcca gcggctgttg 780
ccggtgctgt gccaggccca cggcttgacc ccggagcagg tggtggccat cgccagccac 840
gatggcggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 900
cacggcttga ccccggagca ggtggtggcc atcgccagcc acgatggcgg caagcaggcg 960
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gacccccag 1020
caggtggtgg ccatcgccag caatggcggt ggcaagcagg cgctggagac ggtccagcgg 1080
ctgttgccgg tgctgtgcca ggcccacggc ttgaccccgg agcaggtggt ggccatcgcc 1140
agccacgatg gcggcaagca ggcgctggag acggtccagc ggctgttgcc ggtgctgtgc 1200
caggcccacg gcttgacccc ggagcaggtg gtggccatcg ccagccacga tggcggcaag 1260
caggcgctgg agacggtcca gcggctgttg ccggtgctgt gccaggccca cggcttgacc 1320
ccggagcagg tggtggccat cgccagcaat attggtggca agcaggcgct ggagacggtg 1380
caggcgctgt tgccggtgct gtgccaggcc cacggcttga ccccggagca ggtggtggcc 1440
atcgccagca atattggtgg caagcaggcg ctggagacgg tgcaggcgct gttgccggtg 1500
ctgtgccagg cccacggctt gacccccag caggtggtgg ccatcgccag caataatggt 1560
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 1620
ttgacccccc agcaggtggt ggccatcgcc agcaatggcg gtggcaagca ggcgctggag 1680
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ccagcaggtg 1740
gtggccatcg ccagcaatgg cggtggcaag caggcgctgg agacggtcca gcggctgttg 1800
ccggtgctgt gccaggccca cggcttgacc ccccagcagg tggtggccat cgccagcaat 1860
aatggtggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 1920
cacggcttga ccccggagca ggtggtggcc atcgccagca atattggtgg caagcaggcg 1980
ctggagacgg tgcaggcgct gttgccggtg ctgtgccagg cccacggctt gaccctcag 2040
caggtggtgg ccatcgccag caatggcggc ggcaggccgg cgctggagag cattgttgcc 2100
cagttatctc gccctgatcc ggcgttggcc gcgttgacca acgaccacct cgtcgccttg 2160
gcctgcctcg gcgggcgtcc tgcgctggat gcagtgaaaa agggattggg ggatcctatc 2220
agccgttccc agctggtgaa gtccgagctg gaggagaaga aatccgagtt gaggcacaag 2280
ctgaagtacg tgccccacga gtacatcgag ctgatcgaga tcgcccggaa cagcacccag 2340
gaccgtatcc tggagatgaa ggtgatggag ttcttcatga aggtgtacgg ctacaggggc 2400
aagcacctgg gcggctccag gaagcccgac ggcgccatct acaccgtggg ctcccccatc 2460
gactacggcg tgatcgtgga caccaaggcc tactccggcg gctacaacct gcccatcggc 2520
caggccgacg aaatgcagag gtacgtggag gagaaccaga ccaggaacaa gcacatcaac 2580
cccaacgagt ggtggaaggt gtacccctcc agcgtgaccg agttcaagtt cctgttcgtg 2640
tccggccact tcaagggcaa ctacaaggcc cagctgacca ggctgaacca catcaccaac 2700
tgcaacggcg ccgtgctgtc cgtggaggag ctcctgatcg gcggcgagat gatcaaggcc 2760
ggcaccctga ccctggagga ggtgaggagg aagttcaaca acggcgagat caacttcgcg 2820
gccgactgat aa 2832

<210> 31

<211> 60
<212> DNA
<213> Artificial sequence

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

<220>
<223> Forward composite primer GR exon 2, including SEQ ID NO: 128, 10N and SEQ ID NO: 129

<220>
<221> modified_base
<222> (31)..(40)
<223> a or c or t or g

<400> 31
ccatctcatc cctgcgtgtc tccgactcag nnnnnnnnnn ggttcattta acaagctgcc 60

<210> 32

<211> 60
<212> DNA
<213> Artificial sequence

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

<220>
<223> Forward composite primer GR exon 3, including SEQ ID NO: 128, 10N and SEQ ID NO: 130

<220>
<221> modified_base
<222> (31)..(40)
<223> a or c or t or g

<400> 32
ccatctcatc cctgcgtgtc tccgactcag nnnnnnnnnn gcattctgac tatgaagtga 60

<210> 33

<211> 69
<212> DNA
<213> Artificial sequence

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

<220>
<223> Forward composite primer GR exon 5, including SEQ ID NO: 128, 10N and SEQ ID NO: 131

<220>
<221> modified_base
<222> (31)..(40)
<223> a or c or t or g

<400> 33
ccatctcatc cctgcgtgtc tccgactcag nnnnnnnnnn tcagcaggcc actacaggag 60
tctcacaag 69

<210> 34

<211> 50
<212> DNA
<213> Artificial sequence

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

<220>
<223> Reverse composite primer GR exon 2, including SEQ ID NO: 132 and SEQ ID NO: 133

<400> 34
cctatcccct gtgtgccttg gcagtctcag agccagtgag ggtgaagacg 50

<210> 35

<211> 50
<212> DNA
<213> Artificial sequence

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

<220>
<223> Reverse composite primer GR exon 3, including SEQ ID NO: 132 and SEQ ID NO: 134

<400> 35
cctatcccct gtgtgccttg gcagtctcag gggctttgca tataatggaa 50

<210> 36

<211> 59
<212> DNA
<213> Artificial sequence

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

<220>
<223> Reverse composite primer GR exon 5, including SEQ ID NO: 132 and SEQ ID NO: 135

<400> 36
cctatcccct gtgtgccttg gcagtctcag ctgactctcc ccttcatagt ccccagaac 59

<210> 37

<211> 49
<212> DNA
<213> Artificial sequence

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

<220>
<223> TRAC_T01

<400> 37
ttgtcccaca gatatccaga accctgaccc tgccgtgtac cagctgaga 49

<210> 38

<211> 49
<212> DNA
<213> Artificial sequence

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

<220>
<223> TRBC_T01

<400> 38
tgtgtttgag ccatcagaag cagagatctc ccacacccaa aaggccaca 49

<210> 39

<211> 50
<212> DNA
<213> Artificial sequence

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

<220>
<223> TRBC_T02

<400> 39
ttcccacccg aggtcgctgt gtttgagcca tcagaagcag agatctccca 50

<210> 40

<211> 49
<212> DNA
<213> Artificial sequence

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

<220>
<223> CD52_T02

<400> 40
ttcctcctac tcaccatcag cctcctggtt atggtacagg taagagcaa 49

<210> 41

<211> 530
<212> PRT
<213> Artificial sequence

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

<220>

<223> Repeat TRAC_T01-L

<400> 41

```
Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys
1               5                  10                  15

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
            20                  25                  30

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

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
    50                  55                  60

Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn
65                  70                  75                  80

Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
                85                  90                  95

Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
            100                 105                 110

Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
        115                 120                 125

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

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

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
                165                 170                 175

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

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
        195                 200                 205

Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu
    210                 215                 220

Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
225                 230                 235                 240

Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala
                245                 250                 255

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly
```

260 265 270

Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys
275 280 285

Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala
290 295 300

His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly
305 310 315 320

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
325 330 335

Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn
340 345 350

Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val
355 360 365

Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
370 375 380

Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
385 390 395 400

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala
405 410 415

Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala
420 425 430

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val
435 440 445

Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val
450 455 460

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
465 470 475 480

Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu
485 490 495

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
500 505 510

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala
515 520 525

Leu Glu

530

<210> 42

<211> 530
<212> PRT
<213> Artificial sequence

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

<220>
<223> Repeat TRAC_T01-R

<400> 42

Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys
1 5 10 15

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
20 25 30

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

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
50 55 60

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

Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
85 90 95

Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
100 105 110

Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu
115 120 125

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala
130 135 140

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

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
165 170 175

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

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln
195 200 205

```
Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu
    210                 215                 220

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
225                 230                 235                 240

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala
                245                 250                 255

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly
            260                 265                 270

Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
        275                 280                 285

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
    290                 295                 300

His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly
305                 310                 315                 320

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
                325                 330                 335

Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn
            340                 345                 350

Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val
        355                 360                 365

Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
    370                 375                 380

Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
385                 390                 395                 400

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala
                405                 410                 415

Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala
            420                 425                 430

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
        435                 440                 445

Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val
    450                 455                 460

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln
465                 470                 475                 480
```

Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu
485 490 495

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
500 505 510

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala
515 520 525

Leu Glu
530

<210> 43

<211> 530
<212> PRT
<213> Artificial sequence

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

<220>
<223> Repeat TRBC_T01-L

<400> 43
Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
1 5 10 15

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
20 25 30

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

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
50 55 60

Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn
65 70 75 80

Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
85 90 95

Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
100 105 110

Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
115 120 125

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala
130 135 140

Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg

145 150 155 160

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val
165 170 175

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

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln
195 200 205

Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu
210 215 220

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
225 230 235 240

Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala
245 250 255

Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala His Gly
260 265 270

Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
275 280 285

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
290 295 300

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly
305 310 315 320

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
325 330 335

Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His
340 345 350

Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
355 360 365

Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
370 375 380

Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu
385 390 395 400

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala
405 410 415

Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg

420 425 430

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
435 440 445

Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val
450 455 460

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
465 470 475 480

Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu
485 490 495

Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
500 505 510

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala
515 520 525

Leu Glu
530

<210> 44

<211> 530
<212> PRT
<213> Artificial sequence

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

<220>
<223> Repeat TRBC_T01-R

<400> 44
Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
1 5 10 15

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
20 25 30

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

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
50 55 60

Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn
65 70 75 80

Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
85 90 95

```
Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
            100                 105                 110

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
        115                 120                 125

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

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

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
                165                 170                 175

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

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln
        195                 200                 205

Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu
    210                 215                 220

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
225                 230                 235                 240

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala
                245                 250                 255

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly
            260                 265                 270

Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys
        275                 280                 285

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
    290                 295                 300

His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly
305                 310                 315                 320

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
                325                 330                 335

Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn
            340                 345                 350

Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
        355                 360                 365
```

```
Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
    370                 375                 380

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
385                 390                 395                 400

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala
                405                 410                 415

Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
            420                 425                 430

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val
        435                 440                 445

Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val
    450                 455                 460

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln
465                 470                 475                 480

Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu
                485                 490                 495

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
            500                 505                 510

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala
        515                 520                 525

Leu Glu
    530
```

<210> 45

<211> 530
<212> PRT
<213> Artificial sequence

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

<220>
<223> Repeat TRBC_T02-L

<400> 45

```
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys
1               5                   10                  15

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
            20                  25                  30

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly
```

35 40 45

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
50 55 60

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

Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
85 90 95

Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
100 105 110

Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu
115 120 125

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

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

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
165 170 175

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

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
195 200 205

Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu
210 215 220

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
225 230 235 240

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala
245 250 255

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly
260 265 270

Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys
275 280 285

Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala
290 295 300

His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly

305 310 315 320

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
325 330 335

Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn
340 345 350

Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
355 360 365

Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
370 375 380

Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
385 390 395 400

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala
405 410 415

Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
420 425 430

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val
435 440 445

Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val
450 455 460

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
465 470 475 480

Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu
485 490 495

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
500 505 510

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala
515 520 525

Leu Glu
530

<210> 46

<211> 530
<212> PRT
<213> Artificial sequence

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

<220>
<223> Repeat TRBC_T02-R

<400> 46

```
Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
1               5                  10                  15

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
            20                  25                  30

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

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
    50                  55                  60

Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn
65                  70                  75                  80

Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
                85                  90                  95

Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
            100                 105                 110

Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu
        115                 120                 125

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala
    130                 135                 140

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

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
                165                 170                 175

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

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

Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu
    210                 215                 220

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
225                 230                 235                 240

Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala
                245                 250                 255
```

```
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly
            260                 265                 270

Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys
        275                 280                 285

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
    290                 295                 300

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly
305                 310                 315                 320

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
                325                 330                 335

Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn
            340                 345                 350

Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
        355                 360                 365

Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
    370                 375                 380

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
385                 390                 395                 400

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala
                405                 410                 415

Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
            420                 425                 430

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val
        435                 440                 445

Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val
    450                 455                 460

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln
465                 470                 475                 480

Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu
                485                 490                 495

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
            500                 505                 510

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala
        515                 520                 525
```

Leu Glu
530

<210> 47

<211> 530
<212> PRT
<213> Artificial sequence

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

<220>
<223> Repeat CD52_T02-L

<400> 47
Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys
1 5 10 15

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
20 25 30

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

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
50 55 60

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

Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
85 90 95

Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
100 105 110

Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
115 120 125

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

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

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
165 170 175

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

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln

195 200 205

Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu
210 215 220

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
225 230 235 240

Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala
245 250 255

Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala His Gly
260 265 270

Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys
275 280 285

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
290 295 300

His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly
305 310 315 320

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
325 330 335

Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His
340 345 350

Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
355 360 365

Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
370 375 380

Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu
385 390 395 400

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala
405 410 415

Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
420 425 430

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
435 440 445

Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val
450 455 460

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu

465 470 475 480

Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu
485 490 495

Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
500 505 510

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala
515 520 525

Leu Glu
530

<210> 48

<211> 530
<212> PRT
<213> Artificial sequence

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

<220>
<223> Repeat CD52_T02-R

<400> 48
Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys
1 5 10 15

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
20 25 30

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

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
50 55 60

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

Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
85 90 95

Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
100 105 110

Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
115 120 125

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

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

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val
                165                 170                 175

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

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln
        195                 200                 205

Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu
    210                 215                 220

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
225                 230                 235                 240

Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala
                245                 250                 255

Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala His Gly
            260                 265                 270

Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys
        275                 280                 285

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
    290                 295                 300

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly
305                 310                 315                 320

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
                325                 330                 335

Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn
            340                 345                 350

Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
        355                 360                 365

Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
    370                 375                 380

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
385                 390                 395                 400

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala
                405                 410                 415
```

```
Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
            420                 425                 430

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
        435                 440                 445

Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val
    450                 455                 460

Gln Ala Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
465                 470                 475                 480

Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu
                485                 490                 495

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
            500                 505                 510

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala
        515                 520                 525

Leu Glu
    530
```

<210> 49

<211> 2814
<212> DNA
<213> Artificial sequence

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

<220>
<223> TRAC_T01-L TALEN

<400> 49

```
atgggcgatc ctaaaaagaa acgtaaggtc atcgattacc catacgatgt tccagattac     60
gctatcgata tcgccgatct acgcacgctc ggctacagcc agcagcaaca ggagaagatc    120
aaaccgaagg ttcgttcgac agtggcgcag caccacgagg cactggtcgg ccacgggttt    180
acacacgcgc acatcgttgc gttaagccaa cacccggcag cgttagggac cgtcgctgtc    240
aagtatcagg acatgatcgc agcgttgcca gaggcgacac acgaagcgat cgttggcgtc    300
ggcaaacagt ggtccggcgc acgcgctctg gaggccttgc tcacggtggc gggagagttg    360
agaggtccac cgttacagtt ggacacaggc caacttctca agattgcaaa acgtggcggc    420
gtgaccgcag tggaggcagt gcatgcatgg cgcaatgcac tgacgggtgc cccgctcaac    480
ttgacccccc agcaggtggt ggccatcgcc agcaatggcg gtggcaagca ggcgctggag    540
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ccagcaggtg    600
gtggccatcg ccagcaataa tggtggcaag caggcgctgg agacggtcca gcggctgttg    660
ccggtgctgt gccaggccca cggcttgacc ccccagcagg tggtggccat cgccagcaat    720
ggcggtggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc    780
cacggcttga ccccggagca ggtggtggcc atcgccagcc acgatggcgg caagcaggcg    840
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccggag    900
caggtggtgg ccatcgccag ccacgatggc ggcaagcagg cgctggagac ggtccagcgg    960
ctgttgccgg tgctgtgcca ggcccacggc ttgaccccgg agcaggtggt ggccatcgcc   1020
agccacgatg gcggcaagca ggcgctggag acggtccagc ggctgttgcc ggtgctgtgc   1080
caggcccacg gcttgacccc ggagcaggtg gtggccatcg ccagcaatat tggtggcaag   1140
caggcgctgg agacggtgca ggcgctgttg ccggtgctgt gccaggccca cggcttgacc   1200
```

ccggagcagg tggtggccat cgccagccac gatggcggca agcaggcgct ggagacggtc 1260
cagcggctgt tgccggtgct gtgccaggcc cacggcttga ccccggagca ggtggtggcc 1320
atcgccagca atattggtgg caagcaggcg ctggagacgg tgcaggcgct gttgccggtg 1380
ctgtgccagg cccacggctt gacccccag caggtggtgg ccatcgccag caataatggt 1440
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 1500
ttgaccccgg agcaggtggt ggccatcgcc agcaatattg gtggcaagca ggcgctggag 1560
acggtgcagg cgctgttgcc ggtgctgtgc caggcccacg gcttgacccc ccagcaggtg 1620
gtggccatcg ccagcaatgg cggtggcaag caggcgctgg agacggtcca gcggctgttg 1680
ccggtgctgt gccaggccca cggcttgacc ccggagcagg tggtggccat cgccagcaat 1740
attggtggca agcaggcgct ggagacggtg caggcgctgt tgccggtgct gtgccaggcc 1800
cacggcttga ccccccagca ggtggtggcc atcgccagca atggcggtgg caagcaggcg 1860
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccggag 1920
caggtggtgg ccatcgccag ccacgatggc ggcaagcagg cgctggagac ggtccagcgg 1980
ctgttgccgg tgctgtgcca ggcccacggc ttgaccccctc agcaggtggt ggccatcgcc 2040
agcaatggcg gcggcaggcc ggcgctggag agcattgttg cccagttatc tcgccctgat 2100
ccggcgttgg ccgcgttgac caacgaccac ctcgtcgcct tggcctgcct cggcgggcgt 2160
cctgcgctgg atgcagtgaa aaagggattg ggggatccta tcagccgttc ccagctggtg 2220
aagtccgagc tggaggagaa gaaatccgag ttgaggcaca agctgaagta cgtgccccac 2280
gagtacatcg agctgatcga gatcgcccgg aacagcaccc aggaccgtat cctggagatg 2340
aaggtgatgg agttcttcat gaaggtgtac ggctacaggg gcaagcacct gggcggctcc 2400
aggaagcccg acggcgccat ctacaccgtg ggctccccca tcgactacgg cgtgatcgtg 2460
gacaccaagg cctactccgg cggctacaac ctgcccatcg gccaggccga cgaaatgcag 2520
aggtacgtgg aggagaacca gaccaggaac aagcacatca accccaacga gtggtggaag 2580
gtgtaccct ccagcgtgac cgagttcaag ttcctgttcg tgtccggcca cttcaagggc 2640
aactacaagg cccagctgac caggctgaac cacatcacca actgcaacgg cgccgtgctg 2700
tccgtggagg agctcctgat cggcggcgag atgatcaagg ccggcaccct gaccctggag 2760
gaggtgagga ggaagttcaa caacggcgag atcaacttcg cggccgactg ataa 2814

<210> 50

<211> 2832
<212> DNA
<213> Artificial sequence

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

<220>
<223> TRAC_T01-R TALEN

<400> 50
atgggcgatc ctaaaaagaa acgtaaggtc atcgataagg agaccgccgc tgccaagttc 60
gagagacagc acatggacag catcgatatc gccgatctac gcacgctcgg ctacagccag 120
cagcaacagg agaagatcaa accgaaggtt cgttcgacag tggcgcagca ccacgaggca 180
ctggtcggcc acgggtttac acacgcgcac atcgttgcgt taagccaaca cccggcagcg 240
ttagggaccg tcgctgtcaa gtatcaggac atgatcgcag cgttgccaga ggcgacacac 300
gaagcgatcg ttggcgtcgg caaacagtgg tccggcgcac gcgctctgga ggccttgctc 360
acggtggcgg gagagttgag aggtccaccg ttacagttgg acacaggcca acttctcaag 420
attgcaaaac gtggcggcgt gaccgcagtg gaggcagtgc atgcatggcg caatgcactg 480
acgggtgccc cgctcaactt gaccccggag caggtggtgg ccatcgccag ccacgatggc 540
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 600
ttgaccccc agcaggtggt ggccatcgcc agcaatggcg gtggcaagca ggcgctggag 660
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ggagcaggtg 720
gtggccatcg ccagccacga tggcggcaag caggcgctgg agacggtcca gcggctgttg 780
ccggtgctgt gccaggccca cggcttgacc ccggagcagg tggtggccat cgccagcaat 840
attggtggca agcaggcgct ggagacggtg caggcgctgt tgccggtgct gtgccaggcc 900
cacggcttga ccccccagca ggtggtggcc atcgccagca ataatggtgg caagcaggcg 960
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccggag 1020
caggtggtgg ccatcgccag ccacgatggc ggcaagcagg cgctggagac ggtccagcgg 1080
ctgttgccgg tgctgtgcca ggcccacggc ttgacccccc agcaggtggt ggccatcgcc 1140
agcaatggcg gtggcaagca ggcgctggag acggtccagc ggctgttgcc ggtgctgtgc 1200
caggcccacg gcttgacccc ccagcaggtg gtggccatcg ccagcaataa tggtggcaag 1260
caggcgctgg agacggtcca gcggctgttg ccggtgctgt gccaggccca cggcttgacc 1320
ccccagcagg tggtggccat cgccagcaat aatggtggca agcaggcgct ggagacggtc 1380
cagcggctgt tgccggtgct gtgccaggcc cacggcttga ccccccagca ggtggtggcc 1440
atcgccagca atggcggtgg caagcaggcg ctggagacgg tccagcggct gttgccggtg 1500

ctgtgccagg cccacggctt gaccccggag caggtggtgg ccatcgccag caatattggt 1560
ggcaagcagg cgctggagac ggtgcaggcg ctgttgccgg tgctgtgcca ggcccacggc 1620
ttgaccccgg agcaggtggt ggccatcgcc agccacgatg gcggcaagca ggcgctggag 1680
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ggagcaggtg 1740
gtggccatcg ccagcaatat tggtggcaag caggcgctgg agacggtgca ggcgctgttg 1800
ccggtgctgt gccaggccca cggcttgacc ccggagcagg tggtggccat cgccagccac 1860
gatggcggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 1920
cacggcttga ccccccagca ggtggtggcc atcgccagca ataatggtgg caagcaggcg 1980
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gacccctcag 2040
caggtggtgg ccatcgccag caatggcggc ggcaggccgg cgctggagag cattgttgcc 2100
cagttatctc gccctgatcc ggcgttggcc gcgttgacca acgaccacct cgtcgccttg 2160
gcctgcctcg gcgggcgtcc tgcgctggat gcagtgaaaa agggattggg ggatcctatc 2220
agccgttccc agctggtgaa gtccgagctg gaggagaaga aatccgagtt gaggcacaag 2280
ctgaagtacg tgccccacga gtacatcgag ctgatcgaga tcgcccggaa cagcacccag 2340
gaccgtatcc tggagatgaa ggtgatggag ttcttcatga aggtgtacgg ctacaggggc 2400
aagcacctgg gcggctccag gaagcccgac ggcgccatct acaccgtggg ctcccccatc 2460
gactacggcg tgatcgtgga caccaaggcc tactccggcg gctacaacct gcccatcggc 2520
caggccgacg aaatgcagag gtacgtggag gagaaccaga ccaggaacaa gcacatcaac 2580
cccaacgagt ggtggaaggt gtacccctcc agcgtgaccg agttcaagtt cctgttcgtg 2640
tccggccact tcaagggcaa ctacaaggcc cagctgacca ggctgaacca catcaccaac 2700
tgcaacggcg ccgtgctgtc cgtggaggag ctcctgatcg gcggcgagat gatcaaggcc 2760
ggcaccctga ccctggagga ggtgaggagg aagttcaaca acggcgagat caacttcgcg 2820
gccgactgat aa 2832

<210> 51

<211> 2814
<212> DNA
<213> Artificial sequence

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

<220>
<223> TRBC_T01-L TALEN

<400> 51
atgggcgatc ctaaaaagaa acgtaaggtc atcgattacc catacgatgt tccagattac 60
gctatcgata tcgccgatct acgcacgctc ggctacagcc agcagcaaca ggagaagatc 120
aaaccgaagg ttcgttcgac agtggcgcag caccacgagg cactggtcgg ccacgggttt 180
acacacgcgc acatcgttgc gttaagccaa cacccggcag cgttagggac cgtcgctgtc 240
aagtatcagg acatgatcgc agcgttgcca gaggcgacac acgaagcgat cgttggcgtc 300
ggcaaacagt ggtccggcgc acgcgctctg gaggccttgc tcacggtggc gggagagttg 360
agaggtccac cgttacagtt ggacacaggc caacttctca agattgcaaa acgtggcggc 420
gtgaccgcag tggaggcagt gcatgcatgg cgcaatgcac tgacgggtgc cccgctcaac 480
ttgacccccc agcaggtggt ggccatcgcc agcaataatg gtggcaagca ggcgctggag 540
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ccagcaggtg 600
gtggccatcg ccagcaatgg cggtggcaag caggcgctgg agacggtcca gcggctgttg 660
ccggtgctgt gccaggccca cggcttgacc ccccagcagg tggtggccat cgccagcaat 720
aatggtggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 780
cacggcttga ccccccagca ggtggtggcc atcgccagca atggcggtgg caagcaggcg 840
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gacccccag 900
caggtggtgg ccatcgccag caatggcggt ggcaagcagg cgctggagac ggtccagcgg 960
ctgttgccgg tgctgtgcca ggcccacggc ttgacccccc agcaggtggt ggccatcgcc 1020
agcaatggcg gtggcaagca ggcgctggag acggtccagc ggctgttgcc ggtgctgtgc 1080
caggcccacg gcttgacccc ccagcaggtg gtggccatcg ccagcaataa tggtggcaag 1140
caggcgctgg agacggtcca gcggctgttg ccggtgctgt gccaggccca cggcttgacc 1200
ccggagcagg tggtggccat cgccagcaat attggtggca agcaggcgct ggagacggtg 1260
caggcgctgt tgccggtgct gtgccaggcc cacggcttga ccccccagca ggtggtggcc 1320
atcgccagca ataatggtgg caagcaggcg ctggagacgg tccagcggct gttgccggtg 1380
ctgtgccagg cccacggctt gaccccggag caggtggtgg ccatcgccag ccacgatggc 1440
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 1500
ttgaccccgg agcaggtggt ggccatcgcc agccacgatg gcggcaagca ggcgctggag 1560
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ggagcaggtg 1620
gtggccatcg ccagcaatat tggtggcaag caggcgctgg agacggtgca ggcgctgttg 1680
ccggtgctgt gccaggccca cggcttgacc ccccagcagg tggtggccat cgccagcaat 1740

ggcggtggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 1800
cacggcttga ccccggagca ggtggtggcc atcgccagcc acgatggcgg caagcaggcg 1860
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccggag 1920
caggtggtgg ccatcgccag caatattggt ggcaagcagg cgctggagac ggtgcaggcg 1980
ctgttgccgg tgctgtgcca ggcccacggc ttgaccctc agcaggtggt ggccatcgcc 2040
agcaatggcg gcggcaggcc ggcgctggag agcattgttg cccagttatc tcgccctgat 2100
ccggcgttgg ccgcgttgac caacgaccac ctcgtcgcct tggcctgcct cggcgggcgt 2160
cctgcgctgg atgcagtgaa aaagggattg ggggatccta tcagccgttc ccagctggtg 2220
aagtccgagc tggaggagaa gaaatccgag ttgaggcaca agctgaagta cgtgccccac 2280
gagtacatcg agctgatcga gatcgcccgg aacagcaccc aggaccgtat cctggagatg 2340
aaggtgatgg agttcttcat gaaggtgtac ggctacaggg gcaagcacct gggcggctcc 2400
aggaagcccg acggcgccat ctacaccgtg ggctccccca tcgactacgg cgtgatcgtg 2460
gacaccaagg cctactccgg cggctacaac ctgcccatcg gccaggccga cgaaatgcag 2520
aggtacgtgg aggagaacca gaccaggaac aagcacatca accccaacga gtggtggaag 2580
gtgtaccct ccagcgtgac cgagttcaag ttcctgttcg tgtccggcca cttcaagggc 2640
aactacaagg cccagctgac caggctgaac cacatcacca actgcaacgg cgccgtgctg 2700
tccgtggagg agctcctgat cggcggcgag atgatcaagg ccggcaccct gaccctggag 2760
gaggtgagga ggaagttcaa caacggcgag atcaacttcg cggccgactg ataa 2814

<210> 52

<211> 2832
<212> DNA
<213> Artificial sequence

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

<220>
<223> TRBC_T01-R TALEN

<400> 52
atgggcgatc ctaaaaagaa acgtaaggtc atcgataagg agaccgccgc tgccaagttc 60
gagagacagc acatggacag catcgatatc gccgatctac gcacgctcgg ctacagccag 120
cagcaacagg agaagatcaa accgaaggtt cgttcgacag tggcgcagca ccacgaggca 180
ctggtcggcc acgggtttac acacgcgcac atcgttgcgt taagccaaca cccggcagcg 240
ttagggaccg tcgctgtcaa gtatcaggac atgatcgcag cgttgccaga ggcgacacac 300
gaagcgatcg ttggcgtcgg caaacagtgg tccggcgcac gcgctctgga ggccttgctc 360
acggtggcgg gagagttgag aggtccaccg ttacagttgg acacaggcca acttctcaag 420
attgcaaaac gtggcggcgt gaccgcagtg gaggcagtgc atgcatggcg caatgcactg 480
acgggtgccc cgctcaactt gaccccccag caggtggtgg ccatcgccag caataatggt 540
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 600
ttgaccccc agcaggtggt ggccatcgcc agcaatggcg gtggcaagca ggcgctggag 660
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ccagcaggtg 720
gtggccatcg ccagcaataa tggtggcaag caggcgctgg agacggtcca gcggctgttg 780
ccggtgctgt gccaggccca cggcttgacc ccccagcagg tggtggccat cgccagcaat 840
aatggtggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 900
cacggcttga ccccggagca ggtggtggcc atcgccagcc acgatggcgg caagcaggcg 960
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccggag 1020
caggtggtgg ccatcgccag ccacgatggc ggcaagcagg cgctggagac ggtccagcgg 1080
ctgttgccgg tgctgtgcca ggcccacggc ttgacccccc agcaggtggt ggccatcgcc 1140
agcaatggcg gtggcaagca ggcgctggag acggtccagc ggctgttgcc ggtgctgtgc 1200
caggcccacg gcttgacccc ccagcaggtg gtggccatcg ccagcaatgg cggtggcaag 1260
caggcgctgg agacggtcca gcggctgttg ccggtgctgt gccaggccca cggcttgacc 1320
ccccagcagg tggtggccat cgccagcaat ggcggtggca agcaggcgct ggagacggtc 1380
cagcggctgt tgccggtgct gtgccaggcc cacggcttga ccccccagca ggtggtggcc 1440
atcgccagca atggcggtgg caagcaggcg ctggagacgg tccagcggct gttgccggtg 1500
ctgtgccagg cccacggctt gaccccccag caggtggtgg ccatcgccag caataatggt 1560
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 1620
ttgaccccc agcaggtggt ggccatcgcc agcaataatg gtggcaagca ggcgctggag 1680
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ccagcaggtg 1740
gtggccatcg ccagcaataa tggtggcaag caggcgctgg agacggtcca gcggctgttg 1800
ccggtgctgt gccaggccca cggcttgacc ccccagcagg tggtggccat cgccagcaat 1860
ggcggtggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 1920
cacggcttga ccccccagca ggtggtggcc atcgccagca ataatggtgg caagcaggcg 1980
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gacccctcag 2040

caggtggtgg ccatcgccag caatggcggc ggcaggccgg cgctggagag cattgttgcc 2100
cagttatctc gccctgatcc ggcgttggcc gcgttgacca acgaccacct cgtcgccttg 2160
gcctgcctcg gcgggcgtcc tgcgctggat gcagtgaaaa agggattggg ggatcctatc 2220
agccgttccc agctggtgaa gtccgagctg gaggagaaga aatccgagtt gaggcacaag 2280
ctgaagtacg tgccccacga gtacatcgag ctgatcgaga tcgcccggaa cagcacccag 2340
gaccgtatcc tggagatgaa ggtgatggag ttcttcatga aggtgtacgg ctacaggggc 2400
aagcacctgg gcggctccag gaagcccgac ggcgccatct acaccgtggg ctcccccatc 2460
gactacggcg tgatcgtgga caccaaggcc tactccggcg gctacaacct gcccatcggc 2520
caggccgacg aaatgcagag gtacgtggag gagaaccaga ccaggaacaa gcacatcaac 2580
cccaacgagt ggtggaaggt gtacccctcc agcgtgaccg agttcaagtt cctgttcgtg 2640
tccggccact tcaagggcaa ctacaaggcc cagctgacca ggctgaacca catcaccaac 2700
tgcaacggcg ccgtgctgtc cgtggaggag ctcctgatcg gcggcgagat gatcaaggcc 2760
ggcaccctga ccctggagga ggtgaggagg aagttcaaca acggcgagat caacttcgcg 2820
gccgactgat aa 2832

<210> 53

<211> 2814
<212> DNA
<213> Artificial sequence

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

<220>
<223> TRBC_T02-L TALEN

<400> 53
atgggcgatc ctaaaaagaa acgtaaggtc atcgattacc catacgatgt tccagattac 60
gctatcgata tcgccgatct acgcacgctc ggctacagcc agcagcaaca ggagaagatc 120
aaaccgaagg ttcgttcgac agtggcgcag caccacgagg cactggtcgg ccacgggttt 180
acacacgcgc acatcgttgc gttaagccaa cacccggcag cgttagggac cgtcgctgtc 240
aagtatcagg acatgatcgc agcgttgcca gaggcgacac acgaagcgat cgttggcgtc 300
ggcaaacagt ggtccggcgc acgcgctctg gaggccttgc tcacggtggc gggagagttg 360
agaggtccac cgttacagtt ggacacaggc caacttctca agattgcaaa acgtggcggc 420
gtgaccgcag tggaggcagt gcatgcatgg cgcaatgcac tgacgggtgc cccgctcaac 480
ttgaccccgg agcaggtggt ggccatcgcc agccacgatg gcggcaagca ggcgctggag 540
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ggagcaggtg 600
gtggccatcg ccagccacga tggcggcaag caggcgctgg agacggtcca gcggctgttg 660
ccggtgctgt gccaggccca cggcttgacc ccggagcagg tggtggccat cgccagccac 720
gatggcggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 780
cacggcttga ccccggagca ggtggtggcc atcgccagca atattggtgg caagcaggcg 840
ctggagacgg tgcaggcgct gttgccggtg ctgtgccagg cccacggctt gaccccggag 900
caggtggtgg ccatcgccag ccacgatggc ggcaagcagg cgctggagac ggtccagcgg 960
ctgttgccgg tgctgtgcca ggcccacggc ttgaccccgg agcaggtggt ggccatcgcc 1020
agccacgatg gcggcaagca ggcgctggag acggtccagc ggctgttgcc ggtgctgtgc 1080
caggcccacg gcttgacccc ggagcaggtg gtggccatcg ccagccacga tggcggcaag 1140
caggcgctgg agacggtcca gcggctgttg ccggtgctgt gccaggccca cggcttgacc 1200
ccccagcagg tggtggccat cgccagcaat aatggtggca agcaggcgct ggagacggtc 1260
cagcggctgt tgccggtgct gtgccaggcc cacggcttga ccccggagca ggtggtggcc 1320
atcgccagca atattggtgg caagcaggcg ctggagacgg tgcaggcgct gttgccggtg 1380
ctgtgccagg cccacggctt gacccccag caggtggtgg ccatcgccag caataatggt 1440
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 1500
ttgacccccc agcaggtggt ggccatcgcc agcaataatg gtggcaagca ggcgctggag 1560
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ccagcaggtg 1620
gtggccatcg ccagcaatgg cggtggcaag caggcgctgg agacggtcca gcggctgttg 1680
ccggtgctgt gccaggccca cggcttgacc ccggagcagg tggtggccat cgccagccac 1740
gatggcggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 1800
cacggcttga ccccccagca ggtggtggcc atcgccagca ataatggtgg caagcaggcg 1860
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccggag 1920
caggtggtgg ccatcgccag ccacgatggc ggcaagcagg cgctggagac ggtccagcgg 1980
ctgttgccgg tgctgtgcca ggcccacggc ttgaccccctc agcaggtggt ggccatcgcc 2040
agcaatggcg gcggcaggcc ggcgctggag agcattgttg cccagttatc tcgccctgat 2100
ccggcgttgg ccgcgttgac caacgaccac ctcgtcgcct tggcctgcct cggcgggcgt 2160
cctgcgctgg atgcagtgaa aaagggattg ggggatccta tcagccgttc ccagctggtg 2220
aagtccgagc tggaggagaa gaaatccgag ttgaggcaca agctgaagta cgtgccccac 2280

gagtacatcg agctgatcga gatcgcccgg aacagcaccc aggaccgtat cctggagatg 2340
aaggtgatgg agttcttcat gaaggtgtac ggctacaggg gcaagcacct gggcggctcc 2400
aggaagcccg acggcgccat ctacaccgtg ggctccccca tcgactacgg cgtgatcgtg 2460
gacaccaagg cctactccgg cggctacaac ctgcccatcg gccaggccga cgaaatgcag 2520
aggtacgtgg aggagaacca gaccaggaac aagcacatca accccaacga gtggtggaag 2580
gtgtaccccct ccagcgtgac cgagttcaag ttcctgttcg tgtccggcca cttcaagggc 2640
aactacaagg cccagctgac caggctgaac cacatcacca actgcaacgg cgccgtgctg 2700
tccgtggagg agctcctgat cggcggcgag atgatcaagg ccggcaccct gaccctggag 2760
gaggtgagga ggaagttcaa caacggcgag atcaacttcg cggccgactg ataa 2814

<210> 54

<211> 2832
<212> DNA
<213> Artificial sequence

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

<220>
<223> TRBC_T02-R TALEN

<400> 54
atgggcgatc ctaaaaagaa acgtaaggtc atcgataagg agaccgccgc tgccaagttc 60
gagagacagc acatggacag catcgatatc gccgatctac gcacgctcgg ctacagccag 120
cagcaacagg agaagatcaa accgaaggtt cgttcgacag tggcgcagca ccacgaggca 180
ctggtcggcc acgggtttac acacgcgcac atcgttgcgt taagccaaca cccggcagcg 240
ttagggaccg tcgctgtcaa gtatcaggac atgatcgcag cgttgccaga ggcgacacac 300
gaagcgatcg ttggcgtcgg caaacagtgg tccggcgcac gcgctctgga ggccttgctc 360
acggtggcgg gagagttgag aggtccaccg ttacagttgg acacaggcca acttctcaag 420
attgcaaaac gtggcggcgt gaccgcagtg gaggcagtgc atgcatggcg caatgcactg 480
acgggtgccc cgctcaactt gacccccag caggtggtgg ccatcgccag caataatggt 540
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 600
ttgacccccc agcaggtggt ggccatcgcc agcaataatg gtggcaagca ggcgctggag 660
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ccagcaggtg 720
gtggccatcg ccagcaataa tggtggcaag caggcgctgg agacggtcca gcggctgttg 780
ccggtgctgt gccaggccca cggcttgacc ccggagcagg tggtggccat cgccagcaat 840
attggtggca agcaggcgct ggagacggtg caggcgctgt tgccggtgct gtgccaggcc 900
cacggcttga ccccccagca ggtggtggcc atcgccagca ataatggtgg caagcaggcg 960
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccggag 1020
caggtggtgg ccatcgccag caatattggt ggcaagcagg cgctggagac ggtgcaggcg 1080
ctgttgccgg tgctgtgcca ggcccacggc ttgacccccc agcaggtggt ggccatcgcc 1140
agcaatggcg gtggcaagca ggcgctggag acggtccagc ggctgttgcc ggtgctgtgc 1200
caggcccacg gcttgacccc ggagcaggtg gtggccatcg ccagccacga tggcggcaag 1260
caggcgctgg agacggtcca gcggctgttg ccggtgctgt gccaggccca cggcttgacc 1320
ccccagcagg tggtggccat cgccagcaat ggcggtggca agcaggcgct ggagacggtc 1380
cagcggctgt tgccggtgct gtgccaggcc cacggcttga ccccggagca ggtggtggcc 1440
atcgccagcc acgatggcgg caagcaggcg ctggagacgg tccagcggct gttgccggtg 1500
ctgtgccagg cccacggctt gacccccag caggtggtgg ccatcgccag caatggcggt 1560
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 1620
ttgacccccc agcaggtggt ggccatcgcc agcaataatg gtggcaagca ggcgctggag 1680
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ggagcaggtg 1740
gtggccatcg ccagccacga tggcggcaag caggcgctgg agacggtcca gcggctgttg 1800
ccggtgctgt gccaggccca cggcttgacc ccccagcagg tggtggccat cgccagcaat 1860
ggcggtggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 1920
cacggcttga ccccccagca ggtggtggcc atcgccagca atggcggtgg caagcaggcg 1980
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccctcag 2040
caggtggtgg ccatcgccag caatggcggc ggcaggccgg cgctggagag cattgttgcc 2100
cagttatctc gccctgatcc ggcgttggcc gcgttgacca acgaccacct cgtcgccttg 2160
gcctgcctcg gcgggcgtcc tgcgctggat gcagtgaaaa agggattggg ggatcctatc 2220
agccgttccc agctggtgaa gtccgagctg gaggagaaga aatccgagtt gaggcacaag 2280
ctgaagtacg tgccccacga gtacatcgag ctgatcgaga tcgcccggaa cagcacccag 2340
gaccgtatcc tggagatgaa ggtgatggag ttcttcatga aggtgtacgg ctacaggggc 2400
aagcacctgg gcggctccag gaagcccgac ggcgccatct acaccgtggg ctcccccatc 2460
gactacggcg tgatcgtgga caccaaggcc tactccggcg gctacaacct gcccatcggc 2520
caggccgacg aaatgcagag gtacgtggag gagaaccaga ccaggaacaa gcacatcaac 2580

cccaacgagt ggtggaaggt gtacccctcc agcgtgaccg agttcaagtt cctgttcgtg 2640
tccggccact tcaagggcaa ctacaaggcc cagctgacca ggctgaacca catcaccaac 2700
tgcaacggcg ccgtgctgtc cgtggaggag ctcctgatcg gcggcgagat gatcaaggcc 2760
ggcaccctga ccctggagga ggtgaggagg aagttcaaca acggcgagat caacttcgcg 2820
gccgactgat aa 2832

<210> 55

<211> 2814
<212> DNA
<213> Artificial sequence

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

<220>
<223> CD52_T02-L TALEN

<400> 55
atgggcgatc ctaaaaagaa acgtaaggtc atcgattacc catacgatgt tccagattac 60
gctatcgata tcgccgatct acgcacgctc ggctacagcc agcagcaaca ggagaagatc 120
aaaccgaagg ttcgttcgac agtggcgcag caccacgagg cactggtcgg ccacgggttt 180
acacacgcgc acatcgttgc gttaagccaa cacccggcag cgttagggac cgtcgctgtc 240
aagtatcagg acatgatcgc agcgttgcca gaggcgacac acgaagcgat cgttggcgtc 300
ggcaaacagt ggtccggcgc acgcgctctg gaggccttgc tcacggtggc gggagagttg 360
agaggtccac cgttacagtt ggacacaggc caacttctca agattgcaaa acgtggcggc 420
gtgaccgcag tggaggcagt gcatgcatgg cgcaatgcac tgacgggtgc cccgctcaac 480
ttgacccccc agcaggtggt ggccatcgcc agcaatggcg gtggcaagca ggcgctggag 540
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ggagcaggtg 600
gtggccatcg ccagccacga tggcggcaag caggcgctgg agacggtcca gcggctgttg 660
ccggtgctgt gccaggccca cggcttgacc ccggagcagg tggtggccat cgccagccac 720
gatggcggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 780
cacggcttga ccccccagca ggtggtggcc atcgccagca atggcggtgg caagcaggcg 840
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccggag 900
caggtggtgg ccatcgccag ccacgatggc ggcaagcagg cgctggagac ggtccagcgg 960
ctgttgccgg tgctgtgcca ggcccacggc ttgaccccgg agcaggtggt ggccatcgcc 1020
agccacgatg gcggcaagca ggcgctggag acggtccagc ggctgttgcc ggtgctgtgc 1080
caggcccacg gcttgacccc ccagcaggtg gtggccatcg ccagcaatgg cggtggcaag 1140
caggcgctgg agacggtcca gcggctgttg ccggtgctgt gccaggccca cggcttgacc 1200
ccggagcagg tggtggccat cgccagcaat attggtggca agcaggcgct ggagacggtg 1260
caggcgctgt tgccggtgct gtgccaggcc cacggcttga ccccggagca ggtggtggcc 1320
atcgccagcc acgatggcgg caagcaggcg ctggagacgg tccagcggct gttgccggtg 1380
ctgtgccagg cccacggctt gacccccag caggtggtgg ccatcgccag caatggcggt 1440
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 1500
ttgaccccgg agcaggtggt ggccatcgcc agccacgatg gcggcaagca ggcgctggag 1560
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ggagcaggtg 1620
gtggccatcg ccagcaatat tggtggcaag caggcgctgg agacggtgca ggcgctgttg 1680
ccggtgctgt gccaggccca cggcttgacc ccggagcagg tggtggccat cgccagccac 1740
gatggcggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 1800
cacggcttga ccccggagca ggtggtggcc atcgccagcc acgatggcgg caagcaggcg 1860
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccggag 1920
caggtggtgg ccatcgccag caatattggt ggcaagcagg cgctggagac ggtgcaggcg 1980
ctgttgccgg tgctgtgcca ggcccacggc ttgaccctc agcaggtggt ggccatcgcc 2040
agcaatggcg gcggcaggcc ggcgctggag agcattgttg cccagttatc tcgccctgat 2100
ccggcgttgg ccgcgttgac caacgaccac ctcgtcgcct tggcctgcct cggcgggcgt 2160
cctgcgctgg atgcagtgaa aaagggattg ggggatccta tcagccgttc ccagctggtg 2220
aagtccgagc tggaggagaa gaaatccgag ttgaggcaca agctgaagta cgtgccccac 2280
gagtacatcg agctgatcga gatcgcccgg aacagcaccc aggaccgtat cctggagatg 2340
aaggtgatgg agttcttcat gaaggtgtac ggctacaggg gcaagcacct gggcggctcc 2400
aggaagcccg acggcgccat ctacaccgtg ggctccccca tcgactacgg cgtgatcgtg 2460
gacaccaagg cctactccgg cggctacaac ctgcccatcg gccaggccga cgaaatgcag 2520
aggtacgtgg aggagaacca gaccaggaac aagcacatca accccaacga gtggtggaag 2580
gtgtaccct ccagcgtgac cgagttcaag ttcctgttcg tgtccggcca cttcaagggc 2640
aactacaagg cccagctgac caggctgaac cacatcacca actgcaacgg cgccgtgctg 2700
tccgtggagg agctcctgat cggcggcgag atgatcaagg ccggcaccct gaccctggag 2760
gaggtgagga ggaagttcaa caacggcgag atcaacttcg cggccgactg ataa 2814

<210> 56

<211> 2832
<212> DNA
<213> Artificial sequence

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

<220>
<223> CD52_T02-R TALEN

<400> 56
atgggcgatc ctaaaaagaa acgtaaggtc atcgataagg agaccgccgc tgccaagttc 60
gagagacagc acatggacag catcgatatc gccgatctac gcacgctcgg ctacagccag 120
cagcaacagg agaagatcaa accgaaggtt cgttcgacag tggcgcagca ccacgaggca 180
ctggtcggcc acgggtttac acacgcgcac atcgttgcgt taagccaaca cccggcagcg 240
ttagggaccg tcgctgtcaa gtatcaggac atgatcgcag cgttgccaga ggcgacacac 300
gaagcgatcg ttggcgtcgg caaacagtgg tccggcgcac gcgctctgga ggccttgctc 360
acggtggcgg gagagttgag aggtccaccg ttacagttgg acacaggcca acttctcaag 420
attgcaaaac gtggcggcgt gaccgcagtg gaggcagtgc atgcatggcg caatgcactg 480
acgggtgccc cgctcaactt gacccccag caggtggtgg ccatcgccag caatggcggt 540
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 600
ttgacccccc agcaggtggt ggccatcgcc agcaataatg gtggcaagca ggcgctggag 660
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ggagcaggtg 720
gtggccatcg ccagccacga tggcggcaag caggcgctgg agacggtcca gcggctgttg 780
ccggtgctgt gccaggccca cggcttgacc ccccagcagg tggtggccat cgccagcaat 840
ggcggtggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 900
cacggcttga ccccggagca ggtggtggcc atcgccagcc acgatggcgg caagcaggcg 960
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gacccccag 1020
caggtggtgg ccatcgccag caatggcggt ggcaagcagg cgctggagac ggtccagcgg 1080
ctgttgccgg tgctgtgcca ggcccacggc ttgacccccc agcaggtggt ggccatcgcc 1140
agcaatggcg gtggcaagca ggcgctggag acggtccagc ggctgttgcc ggtgctgtgc 1200
caggcccacg gcttgacccc ggagcaggtg gtggccatcg ccagcaatat tggtggcaag 1260
caggcgctgg agacggtgca ggcgctgttg ccggtgctgt gccaggccca cggcttgacc 1320
ccggagcagg tggtggccat cgccagccac gatggcggca agcaggcgct ggagacggtc 1380
cagcggctgt tgccggtgct gtgccaggcc cacggcttga ccccggagca ggtggtggcc 1440
atcgccagcc acgatggcgg caagcaggcg ctggagacgg tccagcggct gttgccggtg 1500
ctgtgccagg cccacggctt gacccccag caggtggtgg ccatcgccag caatggcggt 1560
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 1620
ttgacccccc agcaggtggt ggccatcgcc agcaataatg gtggcaagca ggcgctggag 1680
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ccagcaggtg 1740
gtggccatcg ccagcaatgg cggtggcaag caggcgctgg agacggtcca gcggctgttg 1800
ccggtgctgt gccaggccca cggcttgacc ccggagcagg tggtggccat cgccagcaat 1860
attggtggca agcaggcgct ggagacggtg caggcgctgt tgccggtgct gtgccaggcc 1920
cacggcttga ccccggagca ggtggtggcc atcgccagcc acgatggcgg caagcaggcg 1980
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccctcag 2040
caggtggtgg ccatcgccag caatggcggc ggcaggccgg cgctggagag cattgttgcc 2100
cagttatctc gccctgatcc ggcgttggcc gcgttgacca acgaccacct cgtcgccttg 2160
gcctgcctcg gcgggcgtcc tgcgctggat gcagtgaaaa agggattggg ggatcctatc 2220
agccgttccc agctggtgaa gtccgagctg gaggagaaga aatccgagtt gaggcacaag 2280
ctgaagtacg tgccccacga gtacatcgag ctgatcgaga tcgcccggaa cagcacccag 2340
gaccgtatcc tggagatgaa ggtgatggag ttcttcatga aggtgtacgg ctacaggggc 2400
aagcacctgg gcggctccag gaagcccgac ggcgccatct acaccgtggg ctcccccatc 2460
gactacggcg tgatcgtgga caccaaggcc tactccggcg gctacaacct gcccatcggc 2520
caggccgacg aaatgcagag gtacgtggag gagaaccaga ccaggaacaa gcacatcaac 2580
cccaacgagt ggtggaaggt gtacccctcc agcgtgaccg agttcaagtt cctgttcgtg 2640
tccggccact tcaagggcaa ctacaaggcc cagctgacca ggctgaacca catcaccaac 2700
tgcaacggcg ccgtgctgtc cgtggaggag ctcctgatcg gcggcgagat gatcaaggcc 2760
ggcaccctga ccctggagga ggtgaggagg aagttcaaca acggcgagat caacttcgcg 2820
gccgactgat aa 2832

<210> 57

<211> 49
<212> DNA
<213> Artificial sequence

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

<220>
<223> TRAC_T02

<400> 57
tttagaaagt tcctgtgatg tcaagctggt cgagaaaagc tttgaaaca 49

<210> 58

<211> 49
<212> DNA
<213> Artificial sequence

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

<220>
<223> TRAC_T03

<400> 58
tccagtgaca agtctgtctg cctattcacc gattttgatt ctcaaacaa 49

<210> 59

<211> 49
<212> DNA
<213> Artificial sequence

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

<220>
<223> TRAC_T04

<400> 59
tatatcacag acaaaactgt gctagacatg aggtctatgg acttcaaga 49

<210> 60

<211> 49
<212> DNA
<213> Artificial sequence

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

<220>
<223> TRAC_T05

<400> 60
tgaggtctat ggacttcaag agcaacagtg ctgtggcctg gagcaacaa 49

<210> 61

<211> 47
<212> DNA
<213> Artificial sequence

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

<220>
<223> CD52_T01

<400> 61
ttcctcttcc tcctaccacc atcagcctcc tttacctgta ccataac 47

<210> 62

<211> 43
<212> DNA
<213> Artificial sequence

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

<220>
<223> CD52_T04

<400> 62
ttcctcctac tcaccacagc ctcctggtct tacctgtacc ata 43

<210> 63

<211> 43
<212> DNA
<213> Artificial sequence

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

<220>
<223> CD52_T05

<400> 63
tcctactcac catcagctcc tggttatttg ctcttacctg tac 43

<210> 64

<211> 47
<212> DNA
<213> Artificial sequence

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

<220>
<223> CD52_T06

<400> 64
ttatcccact tctcctctac agatacaaac tttttgtcct gagagtc 47

<210> 65

<211> 47
<212> DNA
<213> Artificial sequence

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

<220>
<223> CD52_T07

<400> 65
tggactctca ggacaaacga caccagccaa atgctgaggg gctgctg 47

<210> 66

<211> 60
<212> DNA
<213> Artificial sequence

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

<220>
<223> Forward composite primer for CD52, including SEQ ID NO: 128, 10N, and SEQ ID NO: 136

<220>
<221> modified_base
<222> (31)..(40)
<223> a or c or t or g

<400> 66
ccatctcatc cctgcgtgtc tccgactcag nnnnnnnnnn cagatctgca gaaaggaagc 60

<210> 67

<211> 61
<212> DNA
<213> Artificial sequence

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

<220>
<223> Forward composite primer for TRAC, including SEQ ID NO: 128, 10N, and SEQ ID NO: 137

<220>
<221> modified_base
<222> (31)..(40)
<223> a or c or t or g

<400> 67
ccatctcatc cctgcgtgtc tccgactcag nnnnnnnnnn atcactggca tctggactcc 60
a 61

<210> 68

<211> 62
<212> DNA
<213> Artificial sequence

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

<220>
<223> Forward composite primer for TRBC1, including
SEQ ID NO: 128, 10N, and SEQ ID NO: 138

<220>
<221> modified_base
<222> (31)..(40)
<223> a or c or t or g

<400> 68
ccatctcatc cctgcgtgtc tccgactcag nnnnnnnnnn agagccccta ccagaaccag 60
ac 62

<210> 69

<211> 62
<212> DNA
<213> Artificial sequence

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

<220>
<223> Forward composite primer for TRBC2, including
SEQ ID NO: 128, 10N, and SEQ ID NO: 139

<220>
<221> modified_base
<222> (31).. (40)
<223> a or c or t or g

<400> 69
ccatctcatc cctgcgtgtc tccgactcag nnnnnnnnnn ggacctagta acataattgt 60
gc 62

<210> 70

<211> 51
<212> DNA
<213> Artificial sequence

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

<220>
<223> Reverse composite primer for CD52, including
SEQ ID NO: 132 SEQ ID NO: 140

<400> 70
cctatcccct gtgtgccttg gcagtctcag cctgttggag tccatctgct g 51

<210> 71

<211> 50
<212> DNA
<213> Artificial sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Oligonucleotide

<220>
<223> Reverse composite primer for TRAC,
including SEQ ID NO: 132 and SEQ ID NO: 141

<400> 71
cctatcccct gtgtgccttg gcagtctcag cctcatgtct agcacagttt 50

<210> 72

<211> 51
<212> DNA
<213> Artificial sequence

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

<220>
<223> Reverse composite primer for TRBC1 and 2,
including SEQ ID NO: 132 and SEQ ID NO: 142

<400> 72
cctatcccct gtgtgccttg gcagtctcag accagctcag ctccacgtgg t 51

<210> 73

<211> 495
<212> PRT
<213> Artificial sequence

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

<220>
<223> anti-CD19 CAR

<400> 73
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Ile
20 25 30

Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr
35 40 45

Phe Thr Ser Tyr Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly
50 55 60

Leu Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys Tyr
65 70 75 80

Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser
85 90 95

```
Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala
            100                 105                 110

Val Tyr Tyr Cys Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Arg Val Phe
        115                 120                 125

Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly
    130                 135                 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met
145                 150                 155                 160

Thr Gln Ala Ala Pro Ser Ile Pro Val Thr Pro Gly Glu Ser Val Ser
                165                 170                 175

Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Asn Ser Asn Gly Asn Thr
            180                 185                 190

Tyr Leu Tyr Trp Phe Leu Gln Arg Pro Gly Gln Ser Pro Gln Leu Leu
        195                 200                 205

Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro Asp Arg Phe Ser
    210                 215                 220

Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu Arg Ile Ser Arg Val Glu
225                 230                 235                 240

Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His Leu Glu Tyr Pro
                245                 250                 255

Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ser Asp Pro
            260                 265                 270

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
        275                 280                 285

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
    290                 295                 300

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
305                 310                 315                 320

Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
                325                 330                 335

Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
            340                 345                 350

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
        355                 360                 365
```

Cys Ser Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu Leu Arg
370 375 380

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
385 390 395 400

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
405 410 415

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
420 425 430

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
435 440 445

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
450 455 460

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
465 470 475 480

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490 495

<210> 74

<211> 49
<212> DNA
<213> Artificial sequence

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

<220>
<223> CTLA4_T01

<400> 74
tggccctgca ctctcctgtt ttttcttctc ttcatccctg tcttctgca 49

<210> 75

<211> 49
<212> DNA
<213> Artificial sequence

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

<220>
<223> CTLA4_T03

<400> 75
ttttccatgc tagcaatgca cgtggcccag cctgctgtgg tactggcca 49

<210> 76

<211> 49
<212> DNA
<213> Artificial sequence

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

<220>
<223> CTLA4_T04

<400> 76
tccatgctag caatgcacgt ggcccagcct gctgtggtac tggccagca 49

<210> 77

<211> 49
<212> DNA
<213> Artificial sequence

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

<220>
<223> PDCD1_T01

<400> 77
ttctccccag ccctgctcgt ggtgaccgaa ggggacaacg ccaccttca 49

<210> 78

<211> 49
<212> DNA
<213> Artificial sequence

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

<220>
<223> PDCD1_T03

<400> 78
tacctctgtg gggccatctc cctggccccc aaggcgcaga tcaaagaga 49

<210> 79

<211> 530
<212> PRT
<213> Artificial sequence

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

<220>
<223> Repeat CTLA4_T01-L

<400> 79
Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
1 5 10 15

```
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
            20                  25                  30

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

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
    50                  55                  60

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

Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
                85                  90                  95

Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
            100                 105                 110

Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
        115                 120                 125

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

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

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val
                165                 170                 175

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

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln
        195                 200                 205

Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu
    210                 215                 220

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
225                 230                 235                 240

Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala
                245                 250                 255

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly
            260                 265                 270

Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys
        275                 280                 285
```

```
Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala
    290                 295                 300

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly
305                 310                 315                 320

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
                325                 330                 335

Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn
            340                 345                 350

Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
        355                 360                 365

Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
    370                 375                 380

Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
385                 390                 395                 400

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala
                405                 410                 415

Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
            420                 425                 430

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
        435                 440                 445

Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val
    450                 455                 460

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
465                 470                 475                 480

Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu
                485                 490                 495

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
            500                 505                 510

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala
        515                 520                 525

Leu Glu
    530
```

<210> 80

<211> 530

<212> PRT
<213> Artificial sequence

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

<220>
<223> Repeat CTLA4_T01-R

<400> 80

```
Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
1               5                  10                  15

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
            20                  25                  30

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

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
    50                  55                  60

Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn
65                  70                  75                  80

Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val
                85                  90                  95

Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
            100                 105                 110

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
        115                 120                 125

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

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

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
                165                 170                 175

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

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

Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu
    210                 215                 220

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
```

225 230 235 240

Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala
245 250 255

Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala His Gly
260 265 270

Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys
275 280 285

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
290 295 300

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

Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys
325 330 335

Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn
340 345 350

Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
355 360 365

Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
370 375 380

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
385 390 395 400

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala
405 410 415

Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
420 425 430

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
435 440 445

Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val
450 455 460

Gln Ala Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln
465 470 475 480

Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu
485 490 495

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr

500 505 510

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala
515 520 525

Leu Glu
530

<210> 81

<211> 530
<212> PRT
<213> Artificial sequence

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

<220>
<223> RepeatCTLA4_T03-L

<400> 81
Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys
1 5 10 15

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
20 25 30

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

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
50 55 60

Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn
65 70 75 80

Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
85 90 95

Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
100 105 110

Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
115 120 125

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

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

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
165 170 175

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

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

Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu
210 215 220

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
225 230 235 240

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala
245 250 255

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly
260 265 270

Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys
275 280 285

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
290 295 300

His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly
305 310 315 320

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
325 330 335

Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn
340 345 350

Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val
355 360 365

Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
370 375 380

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
385 390 395 400

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala
405 410 415

Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
420 425 430

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
435 440 445

Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val
450 455 460

Gln Ala Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
465 470 475 480

Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu
485 490 495

Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
500 505 510

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala
515 520 525

Leu Glu
530

<210> 82

<211> 530
<212> PRT
<213> Artificial sequence

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

<220>
<223> Repeat CTLA4_T03-R

<400> 82
Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
1 5 10 15

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
20 25 30

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

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
50 55 60

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

Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
85 90 95

Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
100 105 110

Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu

115 120 125

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

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

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val
165 170 175

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

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln
195 200 205

Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu
210 215 220

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
225 230 235 240

Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala
245 250 255

Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala His Gly
260 265 270

Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys
275 280 285

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
290 295 300

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly
305 310 315 320

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
325 330 335

Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn
340 345 350

Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val
355 360 365

Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
370 375 380

Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu

385 390 395 400

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala
405 410 415

Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala
420 425 430

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val
435 440 445

Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val
450 455 460

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
465 470 475 480

Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu
485 490 495

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
500 505 510

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala
515 520 525

Leu Glu
530

<210> 83

<211> 530
<212> PRT
<213> Artificial sequence

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

<220>
<223> Repeat CTLA4_T04-L

<400> 83
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys
1 5 10 15

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
20 25 30

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

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
50 55 60

```
Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn
65                  70                  75                  80

Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val
                85                  90                  95

Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
            100                 105                 110

Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
        115                 120                 125

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala
    130                 135                 140

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

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
                165                 170                 175

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

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln
        195                 200                 205

Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu
    210                 215                 220

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
225                 230                 235                 240

Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala
                245                 250                 255

Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala His Gly
            260                 265                 270

Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
        275                 280                 285

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
    290                 295                 300

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly
305                 310                 315                 320

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
                325                 330                 335
```

```
Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn
            340                 345                 350

Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val
        355                 360                 365

Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
    370                 375                 380

Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu
385                 390                 395                 400

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala
                405                 410                 415

Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
            420                 425                 430

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val
        435                 440                 445

Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val
    450                 455                 460

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
465                 470                 475                 480

Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu
                485                 490                 495

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
            500                 505                 510

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala
        515                 520                 525

Leu Glu
    530
```

<210> 84

<211> 530
<212> PRT
<213> Artificial sequence

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

<220>
<223> Repeat CTLA4_T04-R

<400> 84
Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys

1 5 10 15

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
20 25 30

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

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
50 55 60

Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn
65 70 75 80

Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
85 90 95

Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
100 105 110

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
115 120 125

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala
130 135 140

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

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
165 170 175

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

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
195 200 205

Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu
210 215 220

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
225 230 235 240

Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala
245 250 255

Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala His Gly
260 265 270

Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys

275 280 285

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
290 295 300

His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly
305 310 315 320

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
325 330 335

Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn
340 345 350

Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val
355 360 365

Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
370 375 380

Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
385 390 395 400

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala
405 410 415

Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
420 425 430

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
435 440 445

Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val
450 455 460

Gln Ala Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
465 470 475 480

Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu
485 490 495

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
500 505 510

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala
515 520 525

Leu Glu
530

<210> 85

<211> 530
<212> PRT
<213> Artificial sequence

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

<220>
<223> Repeat PDCD1_T01-L

<400> 85
Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys
1 5 10 15

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
20 25 30

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

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
50 55 60

Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn
65 70 75 80

Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
85 90 95

Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
100 105 110

Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
115 120 125

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

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

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
165 170 175

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

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
195 200 205

Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu
210 215 220

```
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
225                 230                 235                 240

Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala
                245                 250                 255

Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala His Gly
            260                 265                 270

Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
        275                 280                 285

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
    290                 295                 300

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly
305                 310                 315                 320

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
                325                 330                 335

Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His
            340                 345                 350

Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
        355                 360                 365

Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
    370                 375                 380

Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
385                 390                 395                 400

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala
                405                 410                 415

Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
            420                 425                 430

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val
        435                 440                 445

Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val
    450                 455                 460

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
465                 470                 475                 480

Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu
                485                 490                 495
```

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
500 505 510

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala
515 520 525

Leu Glu
530

<210> 86

<211> 529
<212> PRT
<213> Artificial sequence

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

<220>
<223> RepeatPDCD1_T01-R

<400> 86
Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
1 5 10 15

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
20 25 30

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly
35 40 45

Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys
50 55 60

Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn
65 70 75 80

Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val
85 90 95

Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
100 105 110

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
115 120 125

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala
130 135 140

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

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val

165 170 175

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

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln
195 200 205

Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu
210 215 220

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
225 230 235 240

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala
245 250 255

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly
260 265 270

Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Lys Gln
275 280 285

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His
290 295 300

Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly
305 310 315 320

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
325 330 335

Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly
340 345 350

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
355 360 365

Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser
370 375 380

Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
385 390 395 400

Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile
405 410 415

Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
420 425 430

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val

435 440 445

Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
450 455 460

Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln
465 470 475 480

Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr
485 490 495

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro
500 505 510

Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala Leu
515 520 525

Glu

<210> 87

<211> 530
<212> PRT
<213> Artificial sequence

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

<220>
<223> Repeat PDCD1_T03-L

<400> 87
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys
1 5 10 15

Gln Ala Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala
20 25 30

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

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
50 55 60

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

Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
85 90 95

Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
100 105 110

```
Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
        115                 120                 125

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

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

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val
                165                 170                 175

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

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln
        195                 200                 205

Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu
    210                 215                 220

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
225                 230                 235                 240

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala
                245                 250                 255

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly
            260                 265                 270

Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
        275                 280                 285

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
    290                 295                 300

His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly
305                 310                 315                 320

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
                325                 330                 335

Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn
            340                 345                 350

Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
        355                 360                 365

Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
    370                 375                 380
```

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
385 390 395 400

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala
405 410 415

Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
420 425 430

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
435 440 445

Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val
450 455 460

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
465 470 475 480

Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu
485 490 495

Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
500 505 510

Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala
515 520 525

Leu Glu
530

<210> 88

<211> 529
<212> PRT
<213> Artificial sequence

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

<220>
<223> Repeat PDCD1_T03-R

<400> 88
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys
1 5 10 15

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
20 25 30

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

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys

```
    50                  55                  60

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

Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
                85                  90                  95

Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
            100                 105                 110

Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
        115                 120                 125

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala
    130                 135                 140

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

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val
                165                 170                 175

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

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln
        195                 200                 205

Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu
    210                 215                 220

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
225                 230                 235                 240

Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala
                245                 250                 255

Leu Glu Thr Val Gln Ala Leu Leu Pro Val Leu Cys Gln Ala His Gly
            260                 265                 270

Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys
        275                 280                 285

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
    290                 295                 300

His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly
305                 310                 315                 320

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
```

325 330 335

Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn
340 345 350

Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
355 360 365

Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val Ala Ile Ala
370 375 380

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
385 390 395 400

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala
405 410 415

Ile Ala Ser Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
420 425 430

Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Gln Gln Val Val
435 440 445

Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
450 455 460

Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln
465 470 475 480

Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr
485 490 495

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro
500 505 510

Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala Leu
515 520 525

Glu

<210> 89

<211> 2814
<212> DNA
<213> Artificial sequence

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

<220>

<223> CTLA4_T01-L TALEN

<400> 89
atgggcgatc ctaaaaagaa acgtaaggtc atcgattacc catacgatgt tccagattac 60
gctatcgata tcgccgatct acgcacgctc ggctacagcc agcagcaaca ggagaagatc 120
aaaccgaagg ttcgttcgac agtggcgcag caccacgagg cactggtcgg ccacgggttt 180
acacacgcgc acatcgttgc gttaagccaa cacccggcag cgttagggac cgtcgctgtc 240
aagtatcagg acatgatcgc agcgttgcca gaggcgacac acgaagcgat cgttggcgtc 300
ggcaaacagt ggtccggcgc acgcgctctg gaggccttgc tcacggtggc gggagagttg 360
agaggtccac cgttacagtt ggacacaggc caacttctca agattgcaaa acgtggcggc 420
gtgaccgcag tggaggcagt gcatgcatgg cgcaatgcac tgacgggtgc cccgctcaac 480
ttgacccccc agcaggtggt ggccatcgcc agcaataatg gtggcaagca ggcgctggag 540
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ccagcaggtg 600
gtggccatcg ccagcaataa tggtggcaag caggcgctgg agacggtcca gcggctgttg 660
ccggtgctgt gccaggccca cggcttgacc ccggagcagg tggtggccat cgccagccac 720
gatggcggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 780
cacggcttga ccccggagca ggtggtggcc atcgccagcc acgatggcgg caagcaggcg 840
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccggag 900
caggtggtgg ccatcgccag ccacgatggc ggcaagcagg cgctggagac ggtccagcgg 960
ctgttgccgg tgctgtgcca ggcccacggc ttgacccccc agcaggtggt ggccatcgcc 1020
agcaatggcg gtggcaagca ggcgctggag acggtccagc ggctgttgcc ggtgctgtgc 1080
caggcccacg gcttgacccc ccagcaggtg gtggccatcg ccagcaataa tggtggcaag 1140
caggcgctgg agacggtcca gcggctgttg ccggtgctgt gccaggccca cggcttgacc 1200
ccggagcagg tggtggccat cgccagccac gatggcggca agcaggcgct ggagacggtc 1260
cagcggctgt tgccggtgct gtgccaggcc cacggcttga ccccggagca ggtggtggcc 1320
atcgccagca atattggtgg caagcaggcg ctggagacgg tgcaggcgct gttgccggtg 1380
ctgtgccagg cccacggctt gaccccggag caggtggtgg ccatcgccag ccacgatggc 1440
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 1500
ttgacccccc agcaggtggt ggccatcgcc agcaatggcg gtggcaagca ggcgctggag 1560
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ggagcaggtg 1620
gtggccatcg ccagccacga tggcggcaag caggcgctgg agacggtcca gcggctgttg 1680
ccggtgctgt gccaggccca cggcttgacc ccccagcagg tggtggccat cgccagcaat 1740
ggcggtggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 1800
cacggcttga ccccggagca ggtggtggcc atcgccagcc acgatggcgg caagcaggcg 1860
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccggag 1920
caggtggtgg ccatcgccag ccacgatggc ggcaagcagg cgctggagac ggtccagcgg 1980
ctgttgccgg tgctgtgcca ggcccacggc ttgaccctc agcaggtggt ggccatcgcc 2040
agcaatggcg gcggcaggcc ggcgctggag agcattgttg cccagttatc tcgccctgat 2100
ccggcgttgg ccgcgttgac caacgaccac ctcgtcgcct tggcctgcct cggcgggcgt 2160
cctgcgctgg atgcagtgaa aaagggattg ggggatccta tcagccgttc ccagctggtg 2220
aagtccgagc tggaggagaa gaaatccgag ttgaggcaca agctgaagta cgtgccccac 2280
gagtacatcg agctgatcga gatcgcccgg aacagcaccc aggaccgtat cctggagatg 2340
aaggtgatgg agttcttcat gaaggtgtac ggctacaggg gcaagcacct gggcggctcc 2400
aggaagcccg acggcgccat ctacaccgtg ggctccccca tcgactacgg cgtgatcgtg 2460
gacaccaagg cctactccgg cggctacaac ctgcccatcg gccaggccga cgaaatgcag 2520
aggtacgtgg aggagaacca gaccaggaac aagcacatca accccaacga gtggtggaag 2580
gtgtaccct ccagcgtgac cgagttcaag ttcctgttcg tgtccggcca cttcaagggc 2640
aactacaagg cccagctgac caggctgaac cacatcacca actgcaacgg cgccgtgctg 2700
tccgtggagg agctcctgat cggcggcgag atgatcaagg ccggcaccct gaccctggag 2760
gaggtgagga ggaagttcaa caacggcgag atcaacttcg cggccgactg ataa 2814

<210> 90

<211> 2832
<212> DNA
<213> Artificial sequence

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

<220>
<223> CTLA4_T01-R TALEN

<400> 90
atgggcgatc ctaaaaagaa acgtaaggtc atcgataagg agaccgccgc tgccaagttc 60
gagagacagc acatggacag catcgatatc gccgatctac gcacgctcgg ctacagccag 120

cagcaacagg agaagatcaa accgaaggtt cgttcgacag tggcgcagca ccacgaggca 180
ctggtcggcc acgggtttac acacgcgcac atcgttgcgt taagccaaca cccggcagcg 240
ttagggaccg tcgctgtcaa gtatcaggac atgatcgcag cgttgccaga ggcgacacac 300
gaagcgatcg ttggcgtcgg caaacagtgg tccggcgcac gcgctctgga ggccttgctc 360
acggtggcgg gagagttgag aggtccaccg ttacagttgg acacaggcca acttctcaag 420
attgcaaaac gtggcggcgt gaccgcagtg gaggcagtgc atgcatggcg caatgcactg 480
acgggtgccc cgctcaactt gaccccccag caggtggtgg ccatcgccag caataatggt 540
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 600
ttgaccccgg agcaggtggt ggccatcgcc agccacgatg gcggcaagca ggcgctggag 660
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ggagcaggtg 720
gtggccatcg ccagcaatat tggtggcaag caggcgctgg agacggtgca ggcgctgttg 780
ccggtgctgt gccaggccca cggcttgacc ccccagcagg tggtggccat cgccagcaat 840
aatggtggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 900
cacggcttga ccccggagca ggtggtggcc atcgccagca atattggtgg caagcaggcg 960
ctggagacgg tgcaggcgct gttgccggtg ctgtgccagg cccacggctt gaccccggag 1020
caggtggtgg ccatcgccag caatattggt ggcaagcagg cgctggagac ggtgcaggcg 1080
ctgttgccgg tgctgtgcca ggcccacggc ttgacccccc agcaggtggt ggccatcgcc 1140
agcaataatg gtggcaagca ggcgctggag acggtccagc ggctgttgcc ggtgctgtgc 1200
caggcccacg gcttgacccc ggagcaggtg gtggccatcg ccagcaatat tggtggcaag 1260
caggcgctgg agacggtgca ggcgctgttg ccggtgctgt gccaggccca cggcttgacc 1320
ccggagcagg tggtggccat cgccagccac gatggcggca agcaggcgct ggagacggtc 1380
cagcggctgt tgccggtgct gtgccaggcc cacggcttga ccccggagca ggtggtggcc 1440
atcgccagca atattggtgg caagcaggcg ctggagacgg tgcaggcgct gttgccggtg 1500
ctgtgccagg cccacggctt gacccccccag caggtggtgg ccatcgccag caataatggt 1560
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 1620
ttgacccccc agcaggtggt ggccatcgcc agcaataatg gtggcaagca ggcgctggag 1680
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ccagcaggtg 1740
gtggccatcg ccagcaataa tggtggcaag caggcgctgg agacggtcca gcggctgttg 1800
ccggtgctgt gccaggccca cggcttgacc ccggagcagg tggtggccat cgccagcaat 1860
attggtggca agcaggcgct ggagacggtg caggcgctgt tgccggtgct gtgccaggcc 1920
cacggcttga ccccccagca ggtggtggcc atcgccagca atggcggtgg caagcaggcg 1980
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gacccctcag 2040
caggtggtgg ccatcgccag caatggcggc ggcaggccgg cgctggagag cattgttgcc 2100
cagttatctc gccctgatcc ggcgttggcc gcgttgacca acgaccacct cgtcgccttg 2160
gcctgcctcg gcgggcgtcc tgcgctggat gcagtgaaaa agggattggg ggatcctatc 2220
agccgttccc agctggtgaa gtccgagctg gaggagaaga aatccgagtt gaggcacaag 2280
ctgaagtacg tgccccacga gtacatcgag ctgatcgaga tcgcccggaa cagcacccag 2340
gaccgtatcc tggagatgaa ggtgatggag ttcttcatga aggtgtacgg ctacaggggc 2400
aagcacctgg gcggctccag gaagcccgac ggcgccatct acaccgtggg ctcccccatc 2460
gactacggcg tgatcgtgga caccaaggcc tactccggcg gctacaacct gcccatcggc 2520
caggccgacg aaatgcagag gtacgtggag gagaaccaga ccaggaacaa gcacatcaac 2580
cccaacgagt ggtggaaggt gtacccctcc agcgtgaccg agttcaagtt cctgttcgtg 2640
tccggccact tcaagggcaa ctacaaggcc cagctgacca ggctgaacca catcaccaac 2700
tgcaacggcg ccgtgctgtc cgtggaggag ctcctgatcg gcggcgagat gatcaaggcc 2760
ggcaccctga ccctggagga ggtgaggagg aagttcaaca acggcgagat caacttcgcg 2820
gccgactgat aa 2832

<210> 91

<211> 2814
<212> DNA
<213> Artificial sequence

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

<220>
<223> CTLA4_T03-L TALEN

<400> 91
atgggcgatc ctaaaaagaa acgtaaggtc atcgattacc catacgatgt tccagattac 60
gctatcgata tcgccgatct acgcacgctc ggctacagcc agcagcaaca ggagaagatc 120
aaaccgaagg ttcgttcgac agtggcgcag caccacgagg cactggtcgg ccacgggttt 180
acacacgcgc acatcgttgc gttaagccaa cacccggcag cgttagggac cgtcgctgtc 240
aagtatcagg acatgatcgc agcgttgcca gaggcgacac acgaagcgat cgttggcgtc 300
ggcaaacagt ggtccggcgc acgcgctctg gaggccttgc tcacggtggc gggagagttg 360

agaggtccac cgttacagtt ggacacaggc caacttctca agattgcaaa acgtggcggc 420
gtgaccgcag tggaggcagt gcatgcatgg cgcaatgcac tgacgggtgc cccgctcaac 480
ttgacccccc agcaggtggt ggccatcgcc agcaatggcg gtggcaagca ggcgctggag 540
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ccagcaggtg 600
gtggccatcg ccagcaatgg cggtggcaag caggcgctgg agacggtcca gcggctgttg 660
ccggtgctgt gccaggccca cggcttgacc ccccagcagg tggtggccat cgccagcaat 720
ggcggtggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 780
cacggcttga ccccggagca ggtggtggcc atcgccagcc acgatggcgg caagcaggcg 840
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccggag 900
caggtggtgg ccatcgccag ccacgatggc ggcaagcagg cgctggagac ggtccagcgg 960
ctgttgccgg tgctgtgcca ggcccacggc ttgaccccgg agcaggtggt ggccatcgcc 1020
agcaatattg gtggcaagca ggcgctggag acggtgcagg cgctgttgcc ggtgctgtgc 1080
caggcccacg gcttgacccc ccagcaggtg gtggccatcg ccagcaatgg cggtggcaag 1140
caggcgctgg agacggtcca gcggctgttg ccggtgctgt gccaggccca cggcttgacc 1200
ccccagcagg tggtggccat cgccagcaat aatggtggca agcaggcgct ggagacggtc 1260
cagcggctgt tgccggtgct gtgccaggcc cacggcttga ccccggagca ggtggtggcc 1320
atcgccagcc acgatggcgg caagcaggcg ctggagacgg tccagcggct gttgccggtg 1380
ctgtgccagg cccacggctt gacccccag caggtggtgg ccatcgccag caatggcggt 1440
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 1500
ttgaccccgg agcaggtggt ggccatcgcc agcaatattg gtggcaagca ggcgctggag 1560
acggtgcagg cgctgttgcc ggtgctgtgc caggcccacg gcttgacccc ccagcaggtg 1620
gtggccatcg ccagcaataa tggtggcaag caggcgctgg agacggtcca gcggctgttg 1680
ccggtgctgt gccaggccca cggcttgacc ccggagcagg tggtggccat cgccagccac 1740
gatggcggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 1800
cacggcttga ccccggagca ggtggtggcc atcgccagca atattggtgg caagcaggcg 1860
ctggagacgg tgcaggcgct gttgccggtg ctgtgccagg cccacggctt gaccccggag 1920
caggtggtgg ccatcgccag caatattggt ggcaagcagg cgctggagac ggtgcaggcg 1980
ctgttgccgg tgctgtgcca ggcccacggc ttgacccctc agcaggtggt ggccatcgcc 2040
agcaatggcg gcggcaggcc ggcgctggag agcattgttg cccagttatc tcgccctgat 2100
ccggcgttgg ccgcgttgac caacgaccac ctcgtcgcct tggcctgcct cggcgggcgt 2160
cctgcgctgg atgcagtgaa aaagggattg ggggatccta tcagccgttc ccagctggtg 2220
aagtccgagc tggaggagaa gaaatccgag ttgaggcaca agctgaagta cgtgccccac 2280
gagtacatcg agctgatcga gatcgcccgg aacagcaccc aggaccgtat cctggagatg 2340
aaggtgatgg agttcttcat gaaggtgtac ggctacaggg gcaagcacct gggcggctcc 2400
aggaagcccg acggcgccat ctacaccgtg ggctccccca tcgactacgg cgtgatcgtg 2460
gacaccaagg cctactccgg cggctacaac ctgcccatcg gccaggccga cgaaatgcag 2520
aggtacgtgg aggagaacca gaccaggaac aagcacatca accccaacga gtggtggaag 2580
gtgtaccccct ccagcgtgac cgagttcaag ttcctgttcg tgtccggcca cttcaagggc 2640
aactacaagg cccagctgac caggctgaac cacatcacca actgcaacgg cgccgtgctg 2700
tccgtggagg agctcctgat cggcggcgag atgatcaagg ccggcaccct gaccctggag 2760
gaggtgagga ggaagttcaa caacggcgag atcaacttcg cggccgactg ataa 2814

<210> 92

<211> 2832
<212> DNA
<213> Artificial sequence

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

<220>
<223> CTLA4_T03-RTALEN

<400> 92
atgggcgatc ctaaaaagaa acgtaaggtc atcgataagg agaccgccgc tgccaagttc 60
gagagacagc acatggacag catcgatatc gccgatctac gcacgctcgg ctacagccag 120
cagcaacagg agaagatcaa accgaaggtt cgttcgacag tggcgcagca ccacgaggca 180
ctggtcggcc acgggtttac acacgcgcac atcgttgcgt taagccaaca cccggcagcg 240
ttagggaccg tcgctgtcaa gtatcaggac atgatcgcag cgttgccaga ggcgacacac 300
gaagcgatcg ttggcgtcgg caaacagtgg tccggcgcac gcgctctgga ggccttgctc 360
acggtggcgg gagagttgag aggtccaccg ttacagttgg acacaggcca acttctcaag 420
attgcaaaac gtggcggcgt gaccgcagtg gaggcagtgc atgcatggcg caatgcactg 480
acgggtgccc cgctcaactt gacccccag caggtggtgg ccatcgccag caataatggt 540
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 600
ttgacccccc agcaggtggt ggccatcgcc agcaataatg gtggcaagca ggcgctggag 660

acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ggagcaggtg 720
gtggccatcg ccagccacga tggcggcaag caggcgctgg agacggtcca gcggctgttg 780
ccggtgctgt gccaggccca cggcttgacc ccggagcagg tggtggccat cgccagccac 840
gatggcggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 900
cacggcttga ccccggagca ggtggtggcc atcgccagca atattggtgg caagcaggcg 960
ctggagacgg tgcaggcgct gttgccggtg ctgtgccagg cccacggctt gacccccag 1020
caggtggtgg ccatcgccag caataatggt ggcaagcagg cgctggagac ggtccagcgg 1080
ctgttgccgg tgctgtgcca ggcccacggc ttgacccccc agcaggtggt ggccatcgcc 1140
agcaatggcg gtggcaagca ggcgctggag acggtccagc ggctgttgcc ggtgctgtgc 1200
caggcccacg gcttgacccc ggagcaggtg gtggccatcg ccagcaatat tggtggcaag 1260
caggcgctgg agacggtgca ggcgctgttg ccggtgctgt gccaggccca cggcttgacc 1320
ccggagcagg tggtggccat cgccagccac gatggcggca agcaggcgct ggagacggtc 1380
cagcggctgt tgccggtgct gtgccaggcc cacggcttga ccccggagca ggtggtggcc 1440
atcgccagcc acgatggcgg caagcaggcg ctggagacgg tccagcggct gttgccggtg 1500
ctgtgccagg cccacggctt gaccccggag caggtggtgg ccatcgccag caatattggt 1560
ggcaagcagg cgctggagac ggtgcaggcg ctgttgccgg tgctgtgcca ggcccacggc 1620
ttgaccccgg agcaggtggt ggccatcgcc agccacgatg gcggcaagca ggcgctggag 1680
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ggagcaggtg 1740
gtggccatcg ccagcaatat tggtggcaag caggcgctgg agacggtgca ggcgctgttg 1800
ccggtgctgt gccaggccca cggcttgacc ccccagcagg tggtggccat cgccagcaat 1860
aatggtggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 1920
cacggcttga ccccggagca ggtggtggcc atcgccagcc acgatggcgg caagcaggcg 1980
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gacccctcag 2040
caggtggtgg ccatcgccag caatggcggc ggcaggccgg cgctggagag cattgttgcc 2100
cagttatctc gccctgatcc ggcgttggcc gcgttgacca acgaccacct cgtcgccttg 2160
gcctgcctcg gcgggcgtcc tgcgctggat gcagtgaaaa agggattggg ggatcctatc 2220
agccgttccc agctggtgaa gtccgagctg gaggagaaga aatccgagtt gaggcacaag 2280
ctgaagtacg tgccccacga gtacatcgag ctgatcgaga tcgcccggaa cagcacccag 2340
gaccgtatcc tggagatgaa ggtgatggag ttcttcatga aggtgtacgg ctacaggggc 2400
aagcacctgg gcggctccag gaagcccgac ggcgccatct acaccgtggg ctcccccatc 2460
gactacggcg tgatcgtgga caccaaggcc tactccggcg gctacaacct gcccatcggc 2520
caggccgacg aaatgcagag gtacgtggag gagaaccaga ccaggaacaa gcacatcaac 2580
cccaacgagt ggtggaaggt gtacccctcc agcgtgaccg agttcaagtt cctgttcgtg 2640
tccggccact tcaagggcaa ctacaaggcc cagctgacca ggctgaacca catcaccaac 2700
tgcaacggcg ccgtgctgtc cgtggaggag ctcctgatcg gcggcgagat gatcaaggcc 2760
ggcaccctga ccctggagga ggtgaggagg aagttcaaca acggcgagat caacttcgcg 2820
gccgactgat aa 2832

<210> 93

<211> 2814
<212> DNA
<213> Artificial sequence

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

<220>
<223> CTLA4_T04-L TALEN

<400> 93
atgggcgatc ctaaaaagaa acgtaaggtc atcgattacc catacgatgt tccagattac 60
gctatcgata tcgccgatct acgcacgctc ggctacagcc agcagcaaca ggagaagatc 120
aaaccgaagg ttcgttcgac agtggcgcag caccacgagg cactggtcgg ccacgggttt 180
acacacgcgc acatcgttgc gttaagccaa cacccggcag cgttagggac cgtcgctgtc 240
aagtatcagg acatgatcgc agcgttgcca gaggcgacac acgaagcgat cgttggcgtc 300
ggcaaacagt ggtccggcgc acgcgctctg gaggccttgc tcacggtggc gggagagttg 360
agaggtccac cgttacagtt ggacacaggc caacttctca agattgcaaa acgtggcggc 420
gtgaccgcag tggaggcagt gcatgcatgg cgcaatgcac tgacgggtgc cccgctcaac 480
ttgaccccgg agcaggtggt ggccatcgcc agccacgatg gcggcaagca ggcgctggag 540
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ggagcaggtg 600
gtggccatcg ccagccacga tggcggcaag caggcgctgg agacggtcca gcggctgttg 660
ccggtgctgt gccaggccca cggcttgacc ccggagcagg tggtggccat cgccagcaat 720
attggtggca agcaggcgct ggagacggtg caggcgctgt tgccggtgct gtgccaggcc 780
cacggcttga ccccccagca ggtggtggcc atcgccagca atggcggtgg caagcaggcg 840
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gacccccag 900

caggtggtgg ccatcgccag caataatggt ggcaagcagg cgctggagac ggtccagcgg 960
ctgttgccgg tgctgtgcca ggcccacggc ttgaccccgg agcaggtggt ggccatcgcc 1020
agccacgatg gcggcaagca ggcgctggag acggtccagc ggctgttgcc ggtgctgtgc 1080
caggcccacg gcttgacccc ccagcaggtg gtggccatcg ccagcaatgg cggtggcaag 1140
caggcgctgg agacggtcca gcggctgttg ccggtgctgt gccaggccca cggcttgacc 1200
ccggagcagg tggtggccat cgccagcaat attggtggca agcaggcgct ggagacggtg 1260
caggcgctgt tgccggtgct gtgccaggcc cacggcttga ccccccagca ggtggtggcc 1320
atcgccagca ataatggtgg caagcaggcg ctggagacgg tccagcggct gttgccggtg 1380
ctgtgccagg cccacggctt gaccccggag caggtggtgg ccatcgccag ccacgatggc 1440
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 1500
ttgaccccgg agcaggtggt ggccatcgcc agcaatattg gtggcaagca ggcgctggag 1560
acggtgcagg cgctgttgcc ggtgctgtgc caggcccacg gcttgacccc ggagcaggtg 1620
gtggccatcg ccagcaatat tggtggcaag caggcgctgg agacggtgca ggcgctgttg 1680
ccggtgctgt gccaggccca cggcttgacc ccccagcagg tggtggccat cgccagcaat 1740
ggcggtggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 1800
cacggcttga ccccccagca ggtggtggcc atcgccagca ataatggtgg caagcaggcg 1860
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccggag 1920
caggtggtgg ccatcgccag ccacgatggc ggcaagcagg cgctggagac ggtccagcgg 1980
ctgttgccgg tgctgtgcca ggcccacggc ttgaccctc agcaggtggt ggccatcgcc 2040
agcaatggcg gcggcaggcc ggcgctggag agcattgttg cccagttatc tcgccctgat 2100
ccggcgttgg ccgcgttgac caacgaccac ctcgtcgcct tggcctgcct cggcgggcgt 2160
cctgcgctgg atgcagtgaa aaagggattg ggggatccta tcagccgttc ccagctggtg 2220
aagtccgagc tggaggagaa gaaatccgag ttgaggcaca agctgaagta cgtgccccac 2280
gagtacatcg agctgatcga gatcgcccgg aacagcaccc aggaccgtat cctggagatg 2340
aaggtgatgg agttcttcat gaaggtgtac ggctacaggg gcaagcacct gggcggctcc 2400
aggaagcccg acggcgccat ctacaccgtg ggctccccca tcgactacgg cgtgatcgtg 2460
gacaccaagg cctactccgg cggctacaac ctgcccatcg gccaggccga cgaaatgcag 2520
aggtacgtgg aggagaacca gaccaggaac aagcacatca accccaacga gtggtggaag 2580
gtgtaccct ccagcgtgac cgagttcaag ttcctgttcg tgtccggcca cttcaagggc 2640
aactacaagg cccagctgac caggctgaac cacatcacca actgcaacgg cgccgtgctg 2700
tccgtggagg agctcctgat cggcggcgag atgatcaagg ccggcaccct gaccctggag 2760
gaggtgagga ggaagttcaa caacggcgag atcaacttcg cggccgactg ataa 2814

<210> 94

<211> 2832
<212> DNA
<213> Artificial sequence

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

<220>
<223> CTLA4_T04-R TALEN

<400> 94
atgggcgatc ctaaaaagaa acgtaaggtc atcgataagg agaccgccgc tgccaagttc 60
gagagacagc acatggacag catcgatatc gccgatctac gcacgctcgg ctacagccag 120
cagcaacagg agaagatcaa accgaaggtt cgttcgacag tggcgcagca ccacgaggca 180
ctggtcggcc acgggtttac acacgcgcac atcgttgcgt taagccaaca cccggcagcg 240
ttagggaccg tcgctgtcaa gtatcaggac atgatcgcag cgttgccaga ggcgacacac 300
gaagcgatcg ttggcgtcgg caaacagtgg tccggcgcac gcgctctgga ggccttgctc 360
acggtggcgg gagagttgag aggtccaccg ttacagttgg acacaggcca acttctcaag 420
attgcaaaac gtggcggcgt gaccgcagtg gaggcagtgc atgcatggcg caatgcactg 480
acgggtgccc cgctcaactt gacccccag caggtggtgg ccatcgccag caataatggt 540
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 600
ttgaccccgg agcaggtggt ggccatcgcc agccacgatg gcggcaagca ggcgctggag 660
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ccagcaggtg 720
gtggccatcg ccagcaatgg cggtggcaag caggcgctgg agacggtcca gcggctgttg 780
ccggtgctgt gccaggccca cggcttgacc ccccagcagg tggtggccat cgccagcaat 840
aatggtggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 900
cacggcttga ccccccagca ggtggtggcc atcgccagca ataatggtgg caagcaggcg 960
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccggag 1020
caggtggtgg ccatcgccag ccacgatggc ggcaagcagg cgctggagac ggtccagcgg 1080
ctgttgccgg tgctgtgcca ggcccacggc ttgaccccgg agcaggtggt ggccatcgcc 1140
agccacgatg gcggcaagca ggcgctggag acggtccagc ggctgttgcc ggtgctgtgc 1200

caggcccacg gcttgacccc ggagcaggtg gtggccatcg ccagcaatat tggtggcaag 1260
caggcgctgg agacggtgca ggcgctgttg ccggtgctgt gccaggccca cggcttgacc 1320
ccccagcagg tggtggccat cgccagcaat aatggtggca agcaggcgct ggagacggtc 1380
cagcggctgt tgccggtgct gtgccaggcc cacggcttga ccccccagca ggtggtggcc 1440
atcgccagca atggcggtgg caagcaggcg ctggagacgg tccagcggct gttgccggtg 1500
ctgtgccagg cccacggctt gaccccggag caggtggtgg ccatcgccag caatattggt 1560
ggcaagcagg cgctggagac ggtgcaggcg ctgttgccgg tgctgtgcca ggcccacggc 1620
ttgaccccgg agcaggtggt ggccatcgcc agccacgatg gcggcaagca ggcgctggag 1680
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ggagcaggtg 1740
gtggccatcg ccagccacga tggcggcaag caggcgctgg agacggtcca gcggctgttg 1800
ccggtgctgt gccaggccca cggcttgacc ccggagcagg tggtggccat cgccagcaat 1860
attggtggca agcaggcgct ggagacggtg caggcgctgt tgccggtgct gtgccaggcc 1920
cacggcttga ccccggagca ggtggtggcc atcgccagcc acgatggcgg caagcaggcg 1980
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccctcag 2040
caggtggtgg ccatcgccag caatggcggc ggcaggccgg cgctggagag cattgttgcc 2100
cagttatctc gccctgatcc ggcgttggcc gcgttgacca acgaccacct cgtcgccttg 2160
gcctgcctcg gcgggcgtcc tgcgctggat gcagtgaaaa agggattggg ggatcctatc 2220
agccgttccc agctggtgaa gtccgagctg gaggagaaga aatccgagtt gaggcacaag 2280
ctgaagtacg tgccccacga gtacatcgag ctgatcgaga tcgcccggaa cagcacccag 2340
gaccgtatcc tggagatgaa ggtgatggag ttcttcatga aggtgtacgg ctacaggggc 2400
aagcacctgg gcggctccag gaagcccgac ggcgccatct acaccgtggg ctcccccatc 2460
gactacggcg tgatcgtgga caccaaggcc tactccggcg gctacaacct gcccatcggc 2520
caggccgacg aaatgcagag gtacgtggag gagaaccaga ccaggaacaa gcacatcaac 2580
cccaacgagt ggtggaaggt gtacccctcc agcgtgaccg agttcaagtt cctgttcgtg 2640
tccggccact tcaagggcaa ctacaaggcc cagctgacca ggctgaacca catcaccaac 2700
tgcaacggcg ccgtgctgtc cgtggaggag ctcctgatcg gcggcgagat gatcaaggcc 2760
ggcaccctga ccctggagga ggtgaggagg aagttcaaca acggcgagat caacttcgcg 2820
gccgactgat aa 2832

<210> 95

<211> 2814
<212> DNA
<213> Artificial sequence

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

<220>
<223> PDCD1_T01-L TALEN

<400> 95
atgggcgatc ctaaaaagaa acgtaaggtc atcgattacc catacgatgt tccagattac 60
gctatcgata tcgccgatct acgcacgctc ggctacagcc agcagcaaca ggagaagatc 120
aaaccgaagg ttcgttcgac agtggcgcag caccacgagg cactggtcgg ccacgggttt 180
acacacgcgc acatcgttgc gttaagccaa cacccggcag cgttagggac cgtcgctgtc 240
aagtatcagg acatgatcgc agcgttgcca gaggcgacac acgaagcgat cgttggcgtc 300
ggcaaacagt ggtccggcgc acgcgctctg gaggccttgc tcacggtggc gggagagttg 360
agaggtccac cgttacagtt ggacacaggc caacttctca agattgcaaa acgtggcggc 420
gtgaccgcag tggaggcagt gcatgcatgg cgcaatgcac tgacgggtgc cccgctcaac 480
ttgaccccc agcaggtggt ggccatcgcc agcaatggcg gtggcaagca ggcgctggag 540
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ggagcaggtg 600
gtggccatcg ccagccacga tggcggcaag caggcgctgg agacggtcca gcggctgttg 660
ccggtgctgt gccaggccca cggcttgacc ccccagcagg tggtggccat cgccagcaat 720
ggcggtggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 780
cacggcttga ccccggagca ggtggtggcc atcgccagcc acgatggcgg caagcaggcg 840
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccggag 900
caggtggtgg ccatcgccag ccacgatggc ggcaagcagg cgctggagac ggtccagcgg 960
ctgttgccgg tgctgtgcca ggcccacggc ttgaccccgg agcaggtggt ggccatcgcc 1020
agccacgatg gcggcaagca ggcgctggag acggtccagc ggctgttgcc ggtgctgtgc 1080
caggcccacg gcttgacccc ggagcaggtg gtggccatcg ccagccacga tggcggcaag 1140
caggcgctgg agacggtcca gcggctgttg ccggtgctgt gccaggccca cggcttgacc 1200
ccggagcagg tggtggccat cgccagcaat attggtggca agcaggcgct ggagacggtg 1260
caggcgctgt tgccggtgct gtgccaggcc cacggcttga ccccccagca ggtggtggcc 1320
atcgccagca ataatggtgg caagcaggcg ctggagacgg tccagcggct gttgccggtg 1380
ctgtgccagg cccacggctt gaccccggag caggtggtgg ccatcgccag ccacgatggc 1440

ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 1500
ttgaccccgg agcaggtggt ggccatcgcc agccacgatg gcggcaagca ggcgctggag 1560
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ggagcaggtg 1620
gtggccatcg ccagccacga tggcggcaag caggcgctgg agacggtcca gcggctgttg 1680
ccggtgctgt gccaggccca cggcttgacc ccccagcagg tggtggccat cgccagcaat 1740
ggcggtggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 1800
cacggcttga ccccccagca ggtggtggcc atcgccagca ataatggtgg caagcaggcg 1860
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccggag 1920
caggtggtgg ccatcgccag ccacgatggc ggcaagcagg cgctggagac ggtccagcgg 1980
ctgttgccgg tgctgtgcca ggcccacggc ttgaccctc agcaggtggt ggccatcgcc 2040
agcaatggcg gcggcaggcc ggcgctggag agcattgttg cccagttatc tcgccctgat 2100
ccggcgttgg ccgcgttgac caacgaccac ctcgtcgcct tggcctgcct cggcgggcgt 2160
cctgcgctgg atgcagtgaa aaagggattg ggggatccta tcagccgttc ccagctggtg 2220
aagtccgagc tggaggagaa gaaatccgag ttgaggcaca agctgaagta cgtgccccac 2280
gagtacatcg agctgatcga gatcgcccgg aacagcaccc aggaccgtat cctggagatg 2340
aaggtgatgg agttcttcat gaaggtgtac ggctacaggg gcaagcacct gggcggctcc 2400
aggaagcccg acggcgccat ctacaccgtg ggctccccca tcgactacgg cgtgatcgtg 2460
gacaccaagg cctactccgg cggctacaac ctgcccatcg gccaggccga cgaaatgcag 2520
aggtacgtgg aggagaacca gaccaggaac aagcacatca accccaacga gtggtggaag 2580
gtgtaccct ccagcgtgac cgagttcaag ttcctgttcg tgtccggcca cttcaagggc 2640
aactacaagg cccagctgac caggctgaac cacatcacca actgcaacgg cgccgtgctg 2700
tccgtggagg agctcctgat cggcggcgag atgatcaagg ccggcaccct gaccctggag 2760
gaggtgagga ggaagttcaa caacggcgag atcaacttcg cggccgactg ataa 2814

<210> 96

<211> 2829
<212> DNA
<213> Artificial sequence

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

<220>
<223> PDCD1_T01-R TALEN

<400> 96
atgggcgatc ctaaaaagaa acgtaaggtc atcgataagg agaccgccgc tgccaagttc 60
gagagacagc acatggacag catcgatatc gccgatctac gcacgctcgg ctacagccag 120
cagcaacagg agaagatcaa accgaaggtt cgttcgacag tggcgcagca ccacgaggca 180
ctggtcggcc acgggtttac acacgcgcac atcgttgcgt taagccaaca cccggcagcg 240
ttagggaccg tcgctgtcaa gtatcaggac atgatcgcag cgttgccaga ggcgacacac 300
gaagcgatcg ttggcgtcgg caaacagtgg tccggcgcac gcgctctgga ggccttgctc 360
acggtggcgg gagagttgag aggtccaccg ttacagttgg acacaggcca acttctcaag 420
attgcaaaac gtggcggcgt gaccgcagtg gaggcagtgc atgcatggcg caatgcactg 480
acgggtgccc cgctcaactt gacccccag caagtcgtcg caatcgccag caataacgga 540
gggaagcaag ccctcgaaac cgtgcagcgg ttgcttcctg tgctctgcca ggcccacggc 600
cttacccctg agcaggtggt ggccatcgca agtaacattg gaggaaagca agccttggag 660
acagtgcagg ccctgttgcc cgtgctgtgc caggcacacg gcctcacacc agagcaggtc 720
gtggccattg cctccaacat cgggggggaaa caggctctgg agaccgtcca ggccctgctg 780
cccgtcctct gtcaagctca cggcctgact ccccaacaag tggtcgccat cgcctctaat 840
aacggcggga agcaggcact ggaaacagtg cagagactgc tccctgtgct ttgccaagct 900
catgggttga ccccccaaca ggtcgtcgct attgcctcaa acaacggggg caagcaggcc 960
cttgagactg tgcagaggct gttgccagtg ctgtgtcagg ctcacgggct cactccacaa 1020
caggtggtcg caattgccag caacggcggc ggaaagcaag ctcttgaaac cgtgcaacgc 1080
ctcctgcccg tgctctgtca ggctcatggc ctgacaccac aacaagtcgt ggccatcgcc 1140
agtaataatg gcgggaaaca ggctcttgag accgtccaga ggctgctccc agtgctctgc 1200
caggcacacg ggctgacccc ccagcaggtg gtggctatcg ccagcaataa tgggggcaag 1260
caggccctgg aaacagtcca gcgcctgctg ccagtgcttt gccaggctca cgggctcact 1320
cccgaacagg tcgtggcaat cgcctccaac ggagggaagc aggctctgga gaccgtgcag 1380
agactgctgc ccgtcttgtg ccaggcccac ggactcacac ctcagcaggt cgtcgccatt 1440
gcctctaaca acgggggcaa acaagccctg gagacagtgc agcggctgtt gcctgtgttg 1500
tgccaagccc acggcttgac tcctcaacaa gtggtcgcca tcgcctcaaa tggcggcgga 1560
aaacaagctc tggagacagt gcagaggttg ctgcccgtcc tctgccaagc ccacggcctg 1620
actccccaac aggtcgtcgc cattgccagc aacggcggag gaaagcaggc tctcgaaact 1680
gtgcagcggc tgcttcctgt gctgtgtcag gctcatgggc tgaccccca gcaagtggtg 1740

gctattgcct ctaacaatgg aggcaagcaa gcccttgaga cagtccagag gctgttgcca 1800
gtgctgtgcc aggcccacgg gctcacaccc cagcaggtgg tcgccatcgc cagtaacggc 1860
gggggcaaac aggcattgga aaccgtccag cgcctgcttc cagtgctctg ccaggcacac 1920
ggactgacac ccgaacaggt ggtggccatt gcatcccatg atgggggcaa gcaggccctg 1980
gagaccgtgc agagactcct gccagtgttg tgccaagctc acggcctcac ccctcagcaa 2040
gtcgtggcca tcgcctcaaa cggggggggc cggcctgcac tggagagcat tgttgcccag 2100
ttatctcgcc ctgatccggc gttggccgcg ttgaccaacg accacctcgt cgccttggcc 2160
tgcctcggcg ggcgtcctgc gctggatgca gtgaaaaagg gattgggggа tcctatcagc 2220
cgttcccagc tggtgaagtc cgagctggag gagaagaaat ccgagttgag gcacaagctg 2280
aagtacgtgc cccacgagta catcgagctg atcgagatcg cccggaacag cacccaggac 2340
cgtatcctgg agatgaaggt gatggagttc ttcatgaagg tgtacggcta caggggcaag 2400
cacctgggcg gctccaggaa gcccgacggc gccatctaca ccgtgggctc ccccatcgac 2460
tacggcgtga tcgtggacac caaggcctac tccggcggct acaacctgcc catcggccag 2520
gccgacgaaa tgcagaggta cgtggaggag aaccagacca ggaacaagca catcaacccc 2580
aacgagtggt ggaaggtgta cccctccagc gtgaccgagt tcaagttcct gttcgtgtcc 2640
ggccacttca agggcaacta caaggcccag ctgaccaggc tgaaccacat caccaactgc 2700
aacggcgccg tgctgtccgt ggaggagctc ctgatcggcg gcgagatgat caaggccggc 2760
accctgaccc tggaggaggt gaggaggaag ttcaacaacg gcgagatcaa cttcgcggcc 2820
gactgataa 2829

<210> 97

<211> 2814
<212> DNA
<213> Artificial sequence

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

<220>
<223> PDCD1_T03-L TALEN

<400> 97
atgggcgatc ctaaaaagaa acgtaaggtc atcgattacc catacgatgt tccagattac 60
gctatcgata tcgccgatct acgcacgctc ggctacagcc agcagcaaca ggagaagatc 120
aaaccgaagg ttcgttcgac agtggcgcag caccacgagg cactggtcgg ccacgggttt 180
acacacgcgc acatcgttgc gttaagccaa cacccggcag cgttagggac cgtcgctgtc 240
aagtatcagg acatgatcgc agcgttgcca gaggcgacac acgaagcgat cgttggcgtc 300
ggcaaacagt ggtccggcgc acgcgctctg gaggccttgc tcacggtggc gggagagttg 360
agaggtccac cgttacagtt ggacacaggc caacttctca agattgcaaa acgtggcggc 420
gtgaccgcag tggaggcagt gcatgcatgg cgcaatgcac tgacgggtgc cccgctcaac 480
ttgaccccgg agcaggtggt ggccatcgcc agcaatattg gtggcaagca ggcgctggag 540
acggtgcagg cgctgttgcc ggtgctgtgc caggcccacg gcttgacccc ggagcaggtg 600
gtggccatcg ccagccacga tggcggcaag caggcgctgg agacggtcca gcggctgttg 660
ccggtgctgt gccaggccca cggcttgacc ccggagcagg tggtggccat cgccagccac 720
gatggcggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 780
cacggcttga ccccccagca ggtggtggcc atcgccagca atggcggtgg caagcaggcg 840
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccggag 900
caggtggtgg ccatcgccag ccacgatggc ggcaagcagg cgctggagac ggtccagcgg 960
ctgttgccgg tgctgtgcca ggcccacggc ttgacccccc agcaggtggt ggccatcgcc 1020
agcaatggcg gtggcaagca ggcgctggag acggtccagc ggctgttgcc ggtgctgtgc 1080
caggcccacg gcttgacccc ccagcaggtg gtggccatcg ccagcaataa tggtggcaag 1140
caggcgctgg agacggtcca gcggctgttg ccggtgctgt gccaggccca cggcttgacc 1200
ccccagcagg tggtggccat cgccagcaat ggcggtggca agcaggcgct ggagacggtc 1260
cagcggctgt tgccggtgct gtgccaggcc cacggcttga ccccccagca ggtggtggcc 1320
atcgccagca ataatggtgg caagcaggcg ctggagacgg tccagcggct gttgccggtg 1380
ctgtgccagg cccacggctt gacccccag caggtggtgg ccatcgccag caataatggt 1440
ggcaagcagg cgctggagac ggtccagcgg ctgttgccgg tgctgtgcca ggcccacggc 1500
ttgacccccc agcaggtggt ggccatcgcc agcaataatg gtggcaagca ggcgctggag 1560
acggtccagc ggctgttgcc ggtgctgtgc caggcccacg gcttgacccc ccagcaggtg 1620
gtggccatcg ccagcaataa tggtggcaag caggcgctgg agacggtcca gcggctgttg 1680
ccggtgctgt gccaggccca cggcttgacc ccggagcagg tggtggccat cgccagccac 1740
gatggcggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 1800
cacggcttga ccccggagca ggtggtggcc atcgccagcc acgatggcgg caagcaggcg 1860
ctggagacgg tccagcggct gttgccggtg ctgtgccagg cccacggctt gaccccggag 1920
caggtggtgg ccatcgccag caatattggt ggcaagcagg cgctggagac ggtgcaggcg 1980

ctgttgccgg tgctgtgcca ggcccacggc ttgacccctc agcaggtggt ggccatcgcc 2040
agcaatggcg gcggcaggcc ggcgctggag agcattgttg cccagttatc tcgccctgat 2100
ccggcgttgg ccgcgttgac caacgaccac ctcgtcgcct tggcctgcct cggcgggcgt 2160
cctgcgctgg atgcagtgaa aaagggattg ggggatccta tcagccgttc ccagctggtg 2220
aagtccgagc tggaggagaa gaaatccgag ttgaggcaca agctgaagta cgtgccccac 2280
gagtacatcg agctgatcga gatcgcccgg aacagcaccc aggaccgtat cctggagatg 2340
aaggtgatgg agttcttcat gaaggtgtac ggctacaggg gcaagcacct gggcggctcc 2400
aggaagcccg acggcgccat ctacaccgtg ggctccccca tcgactacgg cgtgatcgtg 2460
gacaccaagg cctactccgg cggctacaac ctgcccatcg gccaggccga cgaaatgcag 2520
aggtacgtgg aggagaacca gaccaggaac aagcacatca accccaacga gtggtggaag 2580
gtgtaccccc ccagcgtgac cgagttcaag ttcctgttcg tgtccggcca cttcaagggc 2640
aactacaagg cccagctgac caggctgaac cacatcacca actgcaacgg cgccgtgctg 2700
tccgtggagg agctcctgat cggcggcgag atgatcaagg ccggcaccct gaccctggag 2760
gaggtgagga ggaagttcaa caacggcgag atcaacttcg cggccgactg ataa 2814

<210> 98

<211> 2829
<212> DNA
<213> Artificial sequence

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

<220>
<223> PDCD1_T03-R TALEN

<400> 98
atgggcgatc ctaaaaagaa acgtaaggtc atcgataagg agaccgccgc tgccaagttc 60
gagagacagc acatggacag catcgatatc gccgatctac gcacgctcgg ctacagccag 120
cagcaacagg agaagatcaa accgaaggtt cgttcgacag tggcgcagca ccacgaggca 180
ctggtcggcc acgggtttac acacgcgcac atcgttgcgt taagccaaca cccggcagcg 240
ttagggaccg tcgctgtcaa gtatcaggac atgatcgcag cgttgccaga ggcgacacac 300
gaagcgatcg ttggcgtcgg caaacagtgg tccggcgcac gcgctctgga ggccttgctc 360
acggtggcgg gagagttgag aggtccaccg ttacagttgg acacaggcca acttctcaag 420
attgcaaaac gtggcggcgt gaccgcagtg gaggcagtgc atgcatggcg caatgcactg 480
acgggtgccc cgctcaactt gacccccgag caagtcgtcg caatcgccag ccatgatgga 540
gggaagcaag ccctcgaaac cgtgcagcgg ttgcttcctg tgctctgcca ggcccacggc 600
cttacccctc agcaggtggt ggccatcgca agtaacggag gaggaaagca agccttggag 660
acagtgcagc gcctgttgcc cgtgctgtgc caggcacacg gcctcacacc agagcaggtc 720
gtggccattg cctcccatga cgggggggaaa caggctctgg agaccgtcca gaggctgctg 780
cccgtcctct gtcaagctca cggcctgact ccccaacaag tggtcgccat cgcctctaat 840
ggcggcggga agcaggcact ggaaacagtg cagagactgc tccctgtgct ttgccaagct 900
catgggttga ccccccaaca ggtcgtcgct attgcctcaa acgggggggg caagcaggcc 960
cttgagactg tgcagaggct gttgccagtg ctgtgtcagg ctcacgggct cactccacaa 1020
caggtggtcg caattgccag caacggcggc ggaaagcaag ctcttgaaac cgtgcaacgc 1080
ctcctgcccg tgctctgtca ggctcatggc ctgacaccac aacaagtcgt ggccatcgcc 1140
agtaataatg gcgggaaaca ggctcttgag accgtccaga ggctgctccc agtgctctgc 1200
caggcacacg ggctgacccc cgagcaggtg gtggctatcg ccagcaatat tgggggcaag 1260
caggccctgg aaacagtcca ggccctgctg ccagtgcttt gccaggctca cgggctcact 1320
ccccagcagg tcgtggcaat cgcctccaac ggcggaggga agcaggctct ggagaccgtg 1380
cagagactgc tgcccgtctt gtgccaggcc cacggactca cacctgaaca ggtcgtcgcc 1440
attgcctctc acgatggggg caaacaagcc ctggagacag tgcagcggct gttgcctgtg 1500
ttgtgccaag cccacggctt gactcctcaa caagtggtcg ccatcgcctc aaatggcggc 1560
ggaaaacaag ctctggagac agtgcagagg ttgctgcccg tcctctgcca agcccacggc 1620
ctgactcccc aacaggtcgt cgccattgcc agcaacaacg gaggaaagca ggctctcgaa 1680
actgtgcagc ggctgcttcc tgtgctgtgt caggctcatg ggctgacccc cgagcaagtg 1740
gtggctattg cctctaatgg aggcaagcaa gcccttgaga cagtccagag gctgttgcca 1800
gtgctgtgcc aggcccacgg gctcacaccc cagcaggtgg tcgccatcgc cagtaacaac 1860
gggggcaaac aggcattgga aaccgtccag cgcctgcttc cagtgctctg ccaggcacac 1920
ggactgacac ccgaacaggt ggtggccatt gcatcccatg atgggggcaa gcaggccctg 1980
gagaccgtgc agagactcct gccagtgttg tgccaagctc acggcctcac ccctcagcaa 2040
gtcgtggcca tcgcctcaaa cgggggggggc cggcctgcac tggagagcat tgttgcccag 2100
ttatctcgcc ctgatccggc gttggccgcg ttgaccaacg accacctcgt cgccttggcc 2160
tgcctcggcg ggcgtcctgc gctggatgca gtgaaaaagg gattgggggga tcctatcagc 2220
cgttcccagc tggtgaagtc cgagctggag gagaagaaat ccgagttgag gcacaagctg 2280

aagtacgtgc cccacgagta catcgagctg atcgagatcg cccggaacag cacccaggac 2340
cgtatcctgg agatgaaggt gatggagttc ttcatgaagg tgtacggcta caggggcaag 2400
cacctgggcg gctccaggaa gcccgacggc gccatctaca ccgtgggctc ccccatcgac 2460
tacggcgtga tcgtggacac caaggcctac tccggcggct acaacctgcc catcggccag 2520
gccgacgaaa tgcagaggta cgtggaggag aaccagacca ggaacaagca catcaacccc 2580
aacgagtggt ggaaggtgta cccctccagc gtgaccgagt tcaagttcct gttcgtgtcc 2640
ggccacttca agggcaacta caaggcccag ctgaccaggc tgaaccacat caccaactgc 2700
aacggcgccg tgctgtccgt ggaggagctc ctgatcggcg gcgagatgat caaggccggc 2760
accctgaccc tggaggaggt gaggaggaag ttcaacaacg gcgagatcaa cttcgcggcc 2820
gactgataa 2829

<210> 99

<211> 60
<212> DNA
<213> Artificial sequence

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

<220>
<223> Forward composite primer for CTLA4_T01,
including SEQ ID NO: 128, 10N, and SEQ ID NO: 143

<220>
<221> modified_base
<222> (31).. (40)
<223> a or c or t or g

<400> 99
ccatctcatc cctgcgtgtc tccgactcag nnnnnnnnnn ctctacttcc tgaagacctg 60

<210> 100

<211> 60
<212> DNA
<213> Artificial sequence

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

<220>
<223> Forward composite primer for CTLA4_T03/T04,
including SEQ ID NO: 128, 10N, and SEQ ID NO: 144

<220>
<221> modified_base
<222> (31)..(40)
<223> a or c or t or g

<400> 100
ccatctcatc cctgcgtgtc tccgactcag nnnnnnnnnn acagttgaga gatggagggg 60

<210> 101

<211> 59
<212> DNA
<213> Artificial sequence

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

<220>
<223> Forward composite primer for PDCD1_T01,
including SEQ ID NO: 128, 10N, and SEQ ID NO: 145

<220>
<221> modified_base
<222> (31)..(40)
<223> a or c or t or g

<400> 101
ccatctcatc cctgcgtgtc tccgactcag nnnnnnnnnn ccacagaggt aggtgccgc 59

<210> 102

<211> 60
<212> DNA
<213> Artificial sequence

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

<220>
<223> Forward composite primer for PDCD1_T03,
including SEQ ID NO: 128, 10N, and SEQ ID NO: 146

<220>
<221> modified_base
<222> (31)..(40)
<223> a or c or t or g

<400> 102
ccatctcatc cctgcgtgtc tccgactcag nnnnnnnnnn gacagagatg ccggtcacca 60

<210> 103

<211> 50
<212> DNA
<213> Artificial sequence

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

<220>
<223> Reverse composite primer for CTLA4_T01,
including SEQ ID NO: 132 and SEQ ID NO: 147

<400> 103
cctatcccct gtgtgccttg gcagtctcag tggaatacag agccagccaa 50

<210> 104

<211> 50
<212> DNA
<213> Artificial sequence

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

<220>
<223> Reverse composite primer for CTLA4_T03/04,
including SEQ ID NO: 132 and SEQ ID NO: 148

<400> 104
cctatcccct gtgtgccttg gcagtctcag ggtgcccgtg cagatggaat 50

<210> 105

<211> 50
<212> DNA
<213> Artificial sequence

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

<220>
<223> Reverse composite primer for PDCD1_T01, including SEQ ID NO: 132 and SEQ ID NO: 149

<400> 105
cctatcccct gtgtgccttg gcagtctcag ggctctgcag tggaggccag 50

<210> 106

<211> 50
<212> DNA
<213> Artificial sequence

<220>
<223> Reverse composite primer for PDCD1_T03, including SEQ ID NO: 132 and SEQ ID NO: 150

<400> 106
cctatcccct gtgtgccttg gcagtctcag ggacaacgcc accttcacct 50

<210> 107

<211> 281
<212> PRT
<213> Artificial sequence

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

<220>
<223> pTalpha-FL

<400> 107
Met Ala Gly Thr Trp Leu Leu Leu Leu Leu Ala Leu Gly Cys Pro Ala
1 5 10 15

Leu Pro Thr Gly Val Gly Gly Thr Pro Phe Pro Ser Leu Ala Pro Pro
20 25 30

Ile Met Leu Leu Val Asp Gly Lys Gln Gln Met Val Val Cys Leu
35 40 45

Val Leu Asp Val Ala Pro Pro Gly Leu Asp Ser Pro Ile Trp Phe Ser
50 55 60

Ala Gly Asn Gly Ser Ala Leu Asp Ala Phe Thr Tyr Gly Pro Ser Pro

65 70 75 80

Ala Thr Asp Gly Thr Trp Thr Asn Leu Ala His Leu Ser Leu Pro Ser
85 90 95

Glu Glu Leu Ala Ser Trp Glu Pro Leu Val Cys His Thr Gly Pro Gly
100 105 110

Ala Glu Gly His Ser Arg Ser Thr Gln Pro Met His Leu Ser Gly Glu
115 120 125

Ala Ser Thr Ala Arg Thr Cys Pro Gln Glu Pro Leu Arg Gly Thr Pro
130 135 140

Gly Gly Ala Leu Trp Leu Gly Val Leu Arg Leu Leu Leu Phe Lys Leu
145 150 155 160

Leu Leu Phe Asp Leu Leu Leu Thr Cys Ser Cys Leu Cys Asp Pro Ala
165 170 175

Gly Pro Leu Pro Ser Pro Ala Thr Thr Thr Arg Leu Arg Ala Leu Gly
180 185 190

Ser His Arg Leu His Pro Ala Thr Glu Thr Gly Gly Arg Glu Ala Thr
195 200 205

Ser Ser Pro Arg Pro Gln Pro Arg Asp Arg Arg Trp Gly Asp Thr Pro
210 215 220

Pro Gly Arg Lys Pro Gly Ser Pro Val Trp Gly Glu Gly Ser Tyr Leu
225 230 235 240

Ser Ser Tyr Pro Thr Cys Pro Ala Gln Ala Trp Cys Ser Arg Ser Arg
245 250 255

Leu Arg Ala Pro Ser Ser Ser Leu Gly Ala Phe Phe Arg Gly Asp Leu
260 265 270

Pro Pro Pro Leu Gln Ala Gly Ala Ala
275 280

<210> 108

<211> 263
<212> PRT
<213> Artificial sequence

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

<220>
<223> pTalpha-Delta18

<400> 108

```
Met Ala Gly Thr Trp Leu Leu Leu Leu Leu Ala Leu Gly Cys Pro Ala
1               5                  10                  15

Leu Pro Thr Gly Val Gly Gly Thr Pro Phe Pro Ser Leu Ala Pro Pro
            20                  25                  30

Ile Met Leu Leu Val Asp Gly Lys Gln Gln Met Val Val Val Cys Leu
        35                  40                  45

Val Leu Asp Val Ala Pro Pro Gly Leu Asp Ser Pro Ile Trp Phe Ser
    50                  55                  60

Ala Gly Asn Gly Ser Ala Leu Asp Ala Phe Thr Tyr Gly Pro Ser Pro
65                  70                  75                  80

Ala Thr Asp Gly Thr Trp Thr Asn Leu Ala His Leu Ser Leu Pro Ser
                85                  90                  95

Glu Glu Leu Ala Ser Trp Glu Pro Leu Val Cys His Thr Gly Pro Gly
            100                 105                 110

Ala Glu Gly His Ser Arg Ser Thr Gln Pro Met His Leu Ser Gly Glu
        115                 120                 125

Ala Ser Thr Ala Arg Thr Cys Pro Gln Glu Pro Leu Arg Gly Thr Pro
    130                 135                 140

Gly Gly Ala Leu Trp Leu Gly Val Leu Arg Leu Leu Leu Phe Lys Leu
145                 150                 155                 160

Leu Leu Phe Asp Leu Leu Leu Thr Cys Ser Cys Leu Cys Asp Pro Ala
                165                 170                 175

Gly Pro Leu Pro Ser Pro Ala Thr Thr Thr Arg Leu Arg Ala Leu Gly
            180                 185                 190

Ser His Arg Leu His Pro Ala Thr Glu Thr Gly Gly Arg Glu Ala Thr
        195                 200                 205

Ser Ser Pro Arg Pro Gln Pro Arg Asp Arg Arg Trp Gly Asp Thr Pro
    210                 215                 220

Pro Gly Arg Lys Pro Gly Ser Pro Val Trp Gly Glu Gly Ser Tyr Leu
225                 230                 235                 240

Ser Ser Tyr Pro Thr Cys Pro Ala Gln Ala Trp Cys Ser Arg Ser Arg
                245                 250                 255

Leu Arg Ala Pro Ser Ser Ser
            260
```

<210> 109

<211> 233
<212> PRT
<213> Artificial sequence

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

<220>
<223> pTalpha-Delta48

<400> 109

```
Met Ala Gly Thr Trp Leu Leu Leu Leu Leu Ala Leu Gly Cys Pro Ala
1               5                  10                  15

Leu Pro Thr Gly Val Gly Gly Thr Pro Phe Pro Ser Leu Ala Pro Pro
            20                  25                  30

Ile Met Leu Leu Val Asp Gly Lys Gln Gln Met Val Val Val Cys Leu
        35                  40                  45

Val Leu Asp Val Ala Pro Pro Gly Leu Asp Ser Pro Ile Trp Phe Ser
    50                  55                  60

Ala Gly Asn Gly Ser Ala Leu Asp Ala Phe Thr Tyr Gly Pro Ser Pro
65                  70                  75                  80

Ala Thr Asp Gly Thr Trp Thr Asn Leu Ala His Leu Ser Leu Pro Ser
                85                  90                  95

Glu Glu Leu Ala Ser Trp Glu Pro Leu Val Cys His Thr Gly Pro Gly
            100                 105                 110

Ala Glu Gly His Ser Arg Ser Thr Gln Pro Met His Leu Ser Gly Glu
        115                 120                 125

Ala Ser Thr Ala Arg Thr Cys Pro Gln Glu Pro Leu Arg Gly Thr Pro
    130                 135                 140

Gly Gly Ala Leu Trp Leu Gly Val Leu Arg Leu Leu Leu Phe Lys Leu
145                 150                 155                 160

Leu Leu Phe Asp Leu Leu Leu Thr Cys Ser Cys Leu Cys Asp Pro Ala
                165                 170                 175

Gly Pro Leu Pro Ser Pro Ala Thr Thr Thr Arg Leu Arg Ala Leu Gly
            180                 185                 190

Ser His Arg Leu His Pro Ala Thr Glu Thr Gly Gly Arg Glu Ala Thr
        195                 200                 205

Ser Ser Pro Arg Pro Gln Pro Arg Asp Arg Arg Trp Gly Asp Thr Pro
```

210 215 220

Pro Gly Arg Lys Pro Gly Ser Pro Val
225 230

<210> 110

<211> 219
<212> PRT
<213> Artificial sequence

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

<220>
<223> pTalpha-Delta62

<400> 110
Met Ala Gly Thr Trp Leu Leu Leu Leu Leu Ala Leu Gly Cys Pro Ala
1 5 10 15

Leu Pro Thr Gly Val Gly Gly Thr Pro Phe Pro Ser Leu Ala Pro Pro
20 25 30

Ile Met Leu Leu Val Asp Gly Lys Gln Gln Met Val Val Val Cys Leu
35 40 45

Val Leu Asp Val Ala Pro Pro Gly Leu Asp Ser Pro Ile Trp Phe Ser
50 55 60

Ala Gly Asn Gly Ser Ala Leu Asp Ala Phe Thr Tyr Gly Pro Ser Pro
65 70 75 80

Ala Thr Asp Gly Thr Trp Thr Asn Leu Ala His Leu Ser Leu Pro Ser
85 90 95

Glu Glu Leu Ala Ser Trp Glu Pro Leu Val Cys His Thr Gly Pro Gly
100 105 110

Ala Glu Gly His Ser Arg Ser Thr Gln Pro Met His Leu Ser Gly Glu
115 120 125

Ala Ser Thr Ala Arg Thr Cys Pro Gln Glu Pro Leu Arg Gly Thr Pro
130 135 140

Gly Gly Ala Leu Trp Leu Gly Val Leu Arg Leu Leu Leu Phe Lys Leu
145 150 155 160

Leu Leu Phe Asp Leu Leu Leu Thr Cys Ser Cys Leu Cys Asp Pro Ala
165 170 175

Gly Pro Leu Pro Ser Pro Ala Thr Thr Thr Arg Leu Arg Ala Leu Gly
180 185 190

Ser His Arg Leu His Pro Ala Thr Glu Thr Gly Gly Arg Glu Ala Thr
195 200 205

Ser Ser Pro Arg Pro Gln Pro Arg Asp Arg Arg
210 215

<210> 111

<211> 203
<212> PRT
<213> Artificial sequence

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

<220>
<223> pTalpha-Delta78

<400> 111
Met Ala Gly Thr Trp Leu Leu Leu Leu Ala Leu Gly Cys Pro Ala
1 5 10 15

Leu Pro Thr Gly Val Gly Gly Thr Pro Phe Pro Ser Leu Ala Pro Pro
20 25 30

Ile Met Leu Leu Val Asp Gly Lys Gln Gln Met Val Val Val Cys Leu
35 40 45

Val Leu Asp Val Ala Pro Pro Gly Leu Asp Ser Pro Ile Trp Phe Ser
50 55 60

Ala Gly Asn Gly Ser Ala Leu Asp Ala Phe Thr Tyr Gly Pro Ser Pro
65 70 75 80

Ala Thr Asp Gly Thr Trp Thr Asn Leu Ala His Leu Ser Leu Pro Ser
85 90 95

Glu Glu Leu Ala Ser Trp Glu Pro Leu Val Cys His Thr Gly Pro Gly
100 105 110

Ala Glu Gly His Ser Arg Ser Thr Gln Pro Met His Leu Ser Gly Glu
115 120 125

Ala Ser Thr Ala Arg Thr Cys Pro Gln Glu Pro Leu Arg Gly Thr Pro
130 135 140

Gly Gly Ala Leu Trp Leu Gly Val Leu Arg Leu Leu Leu Phe Lys Leu
145 150 155 160

Leu Leu Phe Asp Leu Leu Leu Thr Cys Ser Cys Leu Cys Asp Pro Ala
165 170 175

Gly Pro Leu Pro Ser Pro Ala Thr Thr Thr Arg Leu Arg Ala Leu Gly

180 185 190

Ser His Arg Leu His Pro Ala Thr Glu Thr Gly
195 200

<210> 112

<211> 189
<212> PRT
<213> Artificial sequence

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

<220>
<223> pTalpha-Delta92

<400> 112
Met Ala Gly Thr Trp Leu Leu Leu Leu Leu Ala Leu Gly Cys Pro Ala
1 5 10 15

Leu Pro Thr Gly Val Gly Gly Thr Pro Phe Pro Ser Leu Ala Pro Pro
20 25 30

Ile Met Leu Leu Val Asp Gly Lys Gln Gln Met Val Val Val Cys Leu
35 40 45

Val Leu Asp Val Ala Pro Pro Gly Leu Asp Ser Pro Ile Trp Phe Ser
50 55 60

Ala Gly Asn Gly Ser Ala Leu Asp Ala Phe Thr Tyr Gly Pro Ser Pro
65 70 75 80

Ala Thr Asp Gly Thr Trp Thr Asn Leu Ala His Leu Ser Leu Pro Ser
85 90 95

Glu Glu Leu Ala Ser Trp Glu Pro Leu Val Cys His Thr Gly Pro Gly
100 105 110

Ala Glu Gly His Ser Arg Ser Thr Gln Pro Met His Leu Ser Gly Glu
115 120 125

Ala Ser Thr Ala Arg Thr Cys Pro Gln Glu Pro Leu Arg Gly Thr Pro
130 135 140

Gly Gly Ala Leu Trp Leu Gly Val Leu Arg Leu Leu Leu Phe Lys Leu
145 150 155 160

Leu Leu Phe Asp Leu Leu Leu Thr Cys Ser Cys Leu Cys Asp Pro Ala
165 170 175

Gly Pro Leu Pro Ser Pro Ala Thr Thr Thr Arg Leu Arg
180 185

<210> 113

<211> 171
<212> PRT
<213> Artificial sequence

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

<220>
<223> pTalpha-Delta110

<400> 113
Met Ala Gly Thr Trp Leu Leu Leu Leu Leu Ala Leu Gly Cys Pro Ala
1 5 10 15

Leu Pro Thr Gly Val Gly Gly Thr Pro Phe Pro Ser Leu Ala Pro Pro
20 25 30

Ile Met Leu Leu Val Asp Gly Lys Gln Gln Met Val Val Val Cys Leu
35 40 45

Val Leu Asp Val Ala Pro Pro Gly Leu Asp Ser Pro Ile Trp Phe Ser
50 55 60

Ala Gly Asn Gly Ser Ala Leu Asp Ala Phe Thr Tyr Gly Pro Ser Pro
65 70 75 80

Ala Thr Asp Gly Thr Trp Thr Asn Leu Ala His Leu Ser Leu Pro Ser
85 90 95

Glu Glu Leu Ala Ser Trp Glu Pro Leu Val Cys His Thr Gly Pro Gly
100 105 110

Ala Glu Gly His Ser Arg Ser Thr Gln Pro Met His Leu Ser Gly Glu
115 120 125

Ala Ser Thr Ala Arg Thr Cys Pro Gln Glu Pro Leu Arg Gly Thr Pro
130 135 140

Gly Gly Ala Leu Trp Leu Gly Val Leu Arg Leu Leu Leu Phe Lys Leu
145 150 155 160

Leu Leu Phe Asp Leu Leu Leu Thr Cys Ser Cys
165 170

<210> 114

<211> 167
<212> PRT
<213> Artificial sequence

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

<220>
<223> pTalpha-Delta114

<400> 114
Met Ala Gly Thr Trp Leu Leu Leu Leu Leu Ala Leu Gly Cys Pro Ala
1 5 10 15

Leu Pro Thr Gly Val Gly Gly Thr Pro Phe Pro Ser Leu Ala Pro Pro
20 25 30

Ile Met Leu Leu Val Asp Gly Lys Gln Gln Met Val Val Val Cys Leu
35 40 45

Val Leu Asp Val Ala Pro Pro Gly Leu Asp Ser Pro Ile Trp Phe Ser
50 55 60

Ala Gly Asn Gly Ser Ala Leu Asp Ala Phe Thr Tyr Gly Pro Ser Pro
65 70 75 80

Ala Thr Asp Gly Thr Trp Thr Asn Leu Ala His Leu Ser Leu Pro Ser
85 90 95

Glu Glu Leu Ala Ser Trp Glu Pro Leu Val Cys His Thr Gly Pro Gly
100 105 110

Ala Glu Gly His Ser Arg Ser Thr Gln Pro Met His Leu Ser Gly Glu
115 120 125

Ala Ser Thr Ala Arg Thr Cys Pro Gln Glu Pro Leu Arg Gly Thr Pro
130 135 140

Gly Gly Ala Leu Trp Leu Gly Val Leu Arg Leu Leu Leu Phe Lys Leu
145 150 155 160

Leu Leu Phe Asp Leu Leu Leu
165

<210> 115

<211> 344
<212> PRT
<213> Artificial sequence

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

<220>
<223> pTalpha-FL-CD28

<400> 115
Met Ala Gly Thr Trp Leu Leu Leu Leu Leu Ala Leu Gly Cys Pro Ala
1 5 10 15

Leu Pro Thr Gly Val Gly Gly Thr Pro Phe Pro Ser Leu Ala Pro Pro

```
            20                  25                  30

Ile Met Leu Leu Val Asp Gly Lys Gln Gln Met Val Val Val Cys Leu
        35                  40                  45

Val Leu Asp Val Ala Pro Pro Gly Leu Asp Ser Pro Ile Trp Phe Ser
    50                  55                  60

Ala Gly Asn Gly Ser Ala Leu Asp Ala Phe Thr Tyr Gly Pro Ser Pro
65                  70                  75                  80

Ala Thr Asp Gly Thr Trp Thr Asn Leu Ala His Leu Ser Leu Pro Ser
                85                  90                  95

Glu Glu Leu Ala Ser Trp Glu Pro Leu Val Cys His Thr Gly Pro Gly
            100                 105                 110

Ala Glu Gly His Ser Arg Ser Thr Gln Pro Met His Leu Ser Gly Glu
        115                 120                 125

Ala Ser Thr Ala Arg Thr Cys Pro Gln Glu Pro Leu Arg Gly Thr Pro
    130                 135                 140

Gly Gly Ala Leu Trp Leu Gly Val Leu Arg Leu Leu Leu Phe Lys Leu
145                 150                 155                 160

Leu Leu Phe Asp Leu Leu Leu Thr Cys Ser Cys Leu Cys Asp Pro Ala
                165                 170                 175

Gly Pro Leu Pro Ser Pro Ala Thr Thr Thr Arg Leu Arg Ala Leu Gly
            180                 185                 190

Ser His Arg Leu His Pro Ala Thr Glu Thr Gly Gly Arg Glu Ala Thr
        195                 200                 205

Ser Ser Pro Arg Pro Gln Pro Arg Asp Arg Arg Trp Gly Asp Thr Pro
    210                 215                 220

Pro Gly Arg Lys Pro Gly Ser Pro Val Trp Gly Glu Gly Ser Tyr Leu
225                 230                 235                 240

Ser Ser Tyr Pro Thr Cys Pro Ala Gln Ala Trp Cys Ser Arg Ser Arg
                245                 250                 255

Leu Arg Ala Pro Ser Ser Ser Leu Gly Ala Phe Phe Arg Gly Asp Leu
            260                 265                 270

Pro Pro Pro Leu Gln Ala Gly Ala Ala Ala Ser Gly Gly Val Leu Ala
        275                 280                 285

Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg
```

290 295 300

Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr Pro
305 310 315 320

Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
325 330 335

Arg Asp Phe Ala Ala Tyr Arg Ser
340

<210> 116

<211> 311
<212> PRT
<213> Artificial sequence

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

<220>
<223> pTalpha-FL-CD8

<400> 116
Met Ala Gly Thr Trp Leu Leu Leu Leu Ala Leu Gly Cys Pro Ala
1 5 10 15

Leu Pro Thr Gly Val Gly Gly Thr Pro Phe Pro Ser Leu Ala Pro Pro
20 25 30

Ile Met Leu Leu Val Asp Gly Lys Gln Gln Met Val Val Val Cys Leu
35 40 45

Val Leu Asp Val Ala Pro Pro Gly Leu Asp Ser Pro Ile Trp Phe Ser
50 55 60

Ala Gly Asn Gly Ser Ala Leu Asp Ala Phe Thr Tyr Gly Pro Ser Pro
65 70 75 80

Ala Thr Asp Gly Thr Trp Thr Asn Leu Ala His Leu Ser Leu Pro Ser
85 90 95

Glu Glu Leu Ala Ser Trp Glu Pro Leu Val Cys His Thr Gly Pro Gly
100 105 110

Ala Glu Gly His Ser Arg Ser Thr Gln Pro Met His Leu Ser Gly Glu
115 120 125

Ala Ser Thr Ala Arg Thr Cys Pro Gln Glu Pro Leu Arg Gly Thr Pro
130 135 140

Gly Gly Ala Leu Trp Leu Gly Val Leu Arg Leu Leu Leu Phe Lys Leu
145 150 155 160

```
Leu Leu Phe Asp Leu Leu Leu Thr Cys Ser Cys Leu Cys Asp Pro Ala
                165                 170                 175

Gly Pro Leu Pro Ser Pro Ala Thr Thr Thr Arg Leu Arg Ala Leu Gly
            180                 185                 190

Ser His Arg Leu His Pro Ala Thr Glu Thr Gly Gly Arg Glu Ala Thr
        195                 200                 205

Ser Ser Pro Arg Pro Gln Pro Arg Asp Arg Arg Trp Gly Asp Thr Pro
    210                 215                 220

Pro Gly Arg Lys Pro Gly Ser Pro Val Trp Gly Glu Gly Ser Tyr Leu
225                 230                 235                 240

Ser Ser Tyr Pro Thr Cys Pro Ala Gln Ala Trp Cys Ser Arg Ser Arg
                245                 250                 255

Leu Arg Ala Pro Ser Ser Ser Leu Gly Ala Phe Phe Arg Gly Asp Leu
            260                 265                 270

Pro Pro Pro Leu Gln Ala Gly Ala Ala Ala Ser His Arg Asn Arg Arg
        275                 280                 285

Arg Val Cys Lys Cys Pro Arg Pro Val Val Lys Ser Gly Asp Lys Pro
    290                 295                 300

Ser Leu Ser Ala Arg Tyr Val
305                 310
```

<210> 117

<211> 325
<212> PRT
<213> Artificial sequence

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

<220>
<223> pTalpha-FL-41BB

<400> 117

```
Met Ala Gly Thr Trp Leu Leu Leu Leu Leu Ala Leu Gly Cys Pro Ala
1               5                   10                  15

Leu Pro Thr Gly Val Gly Gly Thr Pro Phe Pro Ser Leu Ala Pro Pro
            20                  25                  30

Ile Met Leu Leu Val Asp Gly Lys Gln Gln Met Val Val Val Cys Leu
        35                  40                  45

Val Leu Asp Val Ala Pro Pro Gly Leu Asp Ser Pro Ile Trp Phe Ser
```

50 55 60

Ala Gly Asn Gly Ser Ala Leu Asp Ala Phe Thr Tyr Gly Pro Ser Pro
65 70 75 80

Ala Thr Asp Gly Thr Trp Thr Asn Leu Ala His Leu Ser Leu Pro Ser
85 90 95

Glu Glu Leu Ala Ser Trp Glu Pro Leu Val Cys His Thr Gly Pro Gly
100 105 110

Ala Glu Gly His Ser Arg Ser Thr Gln Pro Met His Leu Ser Gly Glu
115 120 125

Ala Ser Thr Ala Arg Thr Cys Pro Gln Glu Pro Leu Arg Gly Thr Pro
130 135 140

Gly Gly Ala Leu Trp Leu Gly Val Leu Arg Leu Leu Leu Phe Lys Leu
145 150 155 160

Leu Leu Phe Asp Leu Leu Leu Thr Cys Ser Cys Leu Cys Asp Pro Ala
165 170 175

Gly Pro Leu Pro Ser Pro Ala Thr Thr Thr Arg Leu Arg Ala Leu Gly
180 185 190

Ser His Arg Leu His Pro Ala Thr Glu Thr Gly Gly Arg Glu Ala Thr
195 200 205

Ser Ser Pro Arg Pro Gln Pro Arg Asp Arg Arg Trp Gly Asp Thr Pro
210 215 220

Pro Gly Arg Lys Pro Gly Ser Pro Val Trp Gly Glu Gly Ser Tyr Leu
225 230 235 240

Ser Ser Tyr Pro Thr Cys Pro Ala Gln Ala Trp Cys Ser Arg Ser Arg
245 250 255

Leu Arg Ala Pro Ser Ser Ser Leu Gly Ala Phe Phe Arg Gly Asp Leu
260 265 270

Pro Pro Pro Leu Gln Ala Gly Ala Ala Gly Ser Lys Arg Gly Arg Lys
275 280 285

Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr
290 295 300

Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu
305 310 315 320

Gly Gly Cys Glu Leu

325

<210> 118

<211> 296
<212> PRT
<213> Artificial sequence

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

<220>
<223> pTalpha-Delta48-CD28

<400> 118

```
Met Ala Gly Thr Trp Leu Leu Leu Leu Leu Ala Leu Gly Cys Pro Ala
1               5                  10                  15

Leu Pro Thr Gly Val Gly Gly Thr Pro Phe Pro Ser Leu Ala Pro Pro
            20                  25                  30

Ile Met Leu Leu Val Asp Gly Lys Gln Gln Met Val Val Val Cys Leu
        35                  40                  45

Val Leu Asp Val Ala Pro Pro Gly Leu Asp Ser Pro Ile Trp Phe Ser
    50                  55                  60

Ala Gly Asn Gly Ser Ala Leu Asp Ala Phe Thr Tyr Gly Pro Ser Pro
65                  70                  75                  80

Ala Thr Asp Gly Thr Trp Thr Asn Leu Ala His Leu Ser Leu Pro Ser
                85                  90                  95

Glu Glu Leu Ala Ser Trp Glu Pro Leu Val Cys His Thr Gly Pro Gly
            100                 105                 110

Ala Glu Gly His Ser Arg Ser Thr Gln Pro Met His Leu Ser Gly Glu
        115                 120                 125

Ala Ser Thr Ala Arg Thr Cys Pro Gln Glu Pro Leu Arg Gly Thr Pro
    130                 135                 140

Gly Gly Ala Leu Trp Leu Gly Val Leu Arg Leu Leu Leu Phe Lys Leu
145                 150                 155                 160

Leu Leu Phe Asp Leu Leu Leu Thr Cys Ser Cys Leu Cys Asp Pro Ala
                165                 170                 175

Gly Pro Leu Pro Ser Pro Ala Thr Thr Thr Arg Leu Arg Ala Leu Gly
            180                 185                 190

Ser His Arg Leu His Pro Ala Thr Glu Thr Gly Gly Arg Glu Ala Thr
        195                 200                 205
```

Ser Ser Pro Arg Pro Gln Pro Arg Asp Arg Arg Trp Gly Asp Thr Pro
210 215 220

Pro Gly Arg Lys Pro Gly Ser Pro Val Ala Ser Gly Gly Val Leu Ala
225 230 235 240

Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg
245 250 255

Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr Pro
260 265 270

Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
275 280 285

Arg Asp Phe Ala Ala Tyr Arg Ser
290 295

<210> 119

<211> 263
<212> PRT
<213> Artificial sequence

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

<220>
<223> pTalpha-Delta48-CD8

<400> 119
Met Ala Gly Thr Trp Leu Leu Leu Leu Leu Ala Leu Gly Cys Pro Ala
1 5 10 15

Leu Pro Thr Gly Val Gly Gly Thr Pro Phe Pro Ser Leu Ala Pro Pro
20 25 30

Ile Met Leu Leu Val Asp Gly Lys Gln Gln Met Val Val Val Cys Leu
35 40 45

Val Leu Asp Val Ala Pro Pro Gly Leu Asp Ser Pro Ile Trp Phe Ser
50 55 60

Ala Gly Asn Gly Ser Ala Leu Asp Ala Phe Thr Tyr Gly Pro Ser Pro
65 70 75 80

Ala Thr Asp Gly Thr Trp Thr Asn Leu Ala His Leu Ser Leu Pro Ser
85 90 95

Glu Glu Leu Ala Ser Trp Glu Pro Leu Val Cys His Thr Gly Pro Gly
100 105 110

Ala Glu Gly His Ser Arg Ser Thr Gln Pro Met His Leu Ser Gly Glu

115 120 125

Ala Ser Thr Ala Arg Thr Cys Pro Gln Glu Pro Leu Arg Gly Thr Pro
130 135 140

Gly Gly Ala Leu Trp Leu Gly Val Leu Arg Leu Leu Leu Phe Lys Leu
145 150 155 160

Leu Leu Phe Asp Leu Leu Leu Thr Cys Ser Cys Leu Cys Asp Pro Ala
165 170 175

Gly Pro Leu Pro Ser Pro Ala Thr Thr Thr Arg Leu Arg Ala Leu Gly
180 185 190

Ser His Arg Leu His Pro Ala Thr Glu Thr Gly Gly Arg Glu Ala Thr
195 200 205

Ser Ser Pro Arg Pro Gln Pro Arg Asp Arg Arg Trp Gly Asp Thr Pro
210 215 220

Pro Gly Arg Lys Pro Gly Ser Pro Val Ala Ser His Arg Asn Arg Arg
225 230 235 240

Arg Val Cys Lys Cys Pro Arg Pro Val Val Lys Ser Gly Asp Lys Pro
245 250 255

Ser Leu Ser Ala Arg Tyr Val
260

<210> 120

<211> 277
<212> PRT
<213> Artificial sequence

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

<220>
<223> pTalpha-Delta48-41BB

<400> 120
Met Ala Gly Thr Trp Leu Leu Leu Leu Leu Ala Leu Gly Cys Pro Ala
1 5 10 15

Leu Pro Thr Gly Val Gly Gly Thr Pro Phe Pro Ser Leu Ala Pro Pro
20 25 30

Ile Met Leu Leu Val Asp Gly Lys Gln Gln Met Val Val Val Cys Leu
35 40 45

Val Leu Asp Val Ala Pro Pro Gly Leu Asp Ser Pro Ile Trp Phe Ser
50 55 60

```
Ala Gly Asn Gly Ser Ala Leu Asp Ala Phe Thr Tyr Gly Pro Ser Pro
65                  70                  75                  80

Ala Thr Asp Gly Thr Trp Thr Asn Leu Ala His Leu Ser Leu Pro Ser
                85                  90                  95

Glu Glu Leu Ala Ser Trp Glu Pro Leu Val Cys His Thr Gly Pro Gly
            100                 105                 110

Ala Glu Gly His Ser Arg Ser Thr Gln Pro Met His Leu Ser Gly Glu
        115                 120                 125

Ala Ser Thr Ala Arg Thr Cys Pro Gln Glu Pro Leu Arg Gly Thr Pro
    130                 135                 140

Gly Gly Ala Leu Trp Leu Gly Val Leu Arg Leu Leu Leu Phe Lys Leu
145                 150                 155                 160

Leu Leu Phe Asp Leu Leu Leu Thr Cys Ser Cys Leu Cys Asp Pro Ala
                165                 170                 175

Gly Pro Leu Pro Ser Pro Ala Thr Thr Thr Arg Leu Arg Ala Leu Gly
            180                 185                 190

Ser His Arg Leu His Pro Ala Thr Glu Thr Gly Gly Arg Glu Ala Thr
        195                 200                 205

Ser Ser Pro Arg Pro Gln Pro Arg Asp Arg Arg Trp Gly Asp Thr Pro
    210                 215                 220

Pro Gly Arg Lys Pro Gly Ser Pro Val Gly Ser Lys Arg Gly Arg Lys
225                 230                 235                 240

Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr
                245                 250                 255

Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu
            260                 265                 270

Gly Gly Cys Glu Leu
        275
```

<210> 121

<211> 172
<212> PRT
<213> Artificial sequence

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

<220>

<223> pTalpha-Delta114-TCRalpha.IC

<400> 121

```
Met Ala Gly Thr Trp Leu Leu Leu Leu Leu Ala Leu Gly Cys Pro Ala
1               5                  10                  15

Leu Pro Thr Gly Val Gly Gly Thr Pro Phe Pro Ser Leu Ala Pro Pro
            20                  25                  30

Ile Met Leu Leu Val Asp Gly Lys Gln Gln Met Val Val Val Cys Leu
        35                  40                  45

Val Leu Asp Val Ala Pro Pro Gly Leu Asp Ser Pro Ile Trp Phe Ser
    50                  55                  60

Ala Gly Asn Gly Ser Ala Leu Asp Ala Phe Thr Tyr Gly Pro Ser Pro
65                  70                  75                  80

Ala Thr Asp Gly Thr Trp Thr Asn Leu Ala His Leu Ser Leu Pro Ser
                85                  90                  95

Glu Glu Leu Ala Ser Trp Glu Pro Leu Val Cys His Thr Gly Pro Gly
            100                 105                 110

Ala Glu Gly His Ser Arg Ser Thr Gln Pro Met His Leu Ser Gly Glu
        115                 120                 125

Ala Ser Thr Ala Arg Thr Cys Pro Gln Glu Pro Leu Arg Gly Thr Pro
    130                 135                 140

Gly Gly Ala Leu Trp Leu Gly Val Leu Arg Leu Leu Leu Phe Lys Leu
145                 150                 155                 160

Leu Leu Phe Asp Leu Leu Leu Arg Leu Trp Ser Ser
                165                 170
```

<210> 122

<211> 173
<212> PRT
<213> Artificial sequence

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

<220>
<223> pTalpha.EC-TCRalpha. TM. IC

<400> 122

```
Met Ala Gly Thr Trp Leu Leu Leu Leu Leu Ala Leu Gly Cys Pro Ala
1               5                  10                  15

Leu Pro Thr Gly Val Gly Gly Thr Pro Phe Pro Ser Leu Ala Pro Pro
            20                  25                  30
```

Ile Met Leu Leu Val Asp Gly Lys Gln Gln Met Val Val Val Cys Leu
35 40 45

Val Leu Asp Val Ala Pro Pro Gly Leu Asp Ser Pro Ile Trp Phe Ser
50 55 60

Ala Gly Asn Gly Ser Ala Leu Asp Ala Phe Thr Tyr Gly Pro Ser Pro
65 70 75 80

Ala Thr Asp Gly Thr Trp Thr Asn Leu Ala His Leu Ser Leu Pro Ser
85 90 95

Glu Glu Leu Ala Ser Trp Glu Pro Leu Val Cys His Thr Gly Pro Gly
100 105 110

Ala Glu Gly His Ser Arg Ser Thr Gln Pro Met His Leu Ser Gly Glu
115 120 125

Ala Ser Thr Ala Arg Thr Cys Pro Gln Glu Pro Leu Arg Gly Thr Pro
130 135 140

Gly Gly Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala
145 150 155 160

Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
165 170

<210> 123

<211> 233
<212> PRT
<213> Artificial sequence

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

<220>
<223> pTalpha.EC-Delta48-1xMUT

<400> 123
Met Ala Gly Thr Trp Leu Leu Leu Leu Leu Ala Leu Gly Cys Pro Ala
1 5 10 15

Leu Pro Thr Gly Val Gly Gly Thr Pro Phe Pro Ser Leu Ala Pro Pro
20 25 30

Ile Met Leu Leu Val Asp Gly Lys Gln Gln Met Val Val Val Cys Leu
35 40 45

Val Leu Asp Val Ala Pro Pro Gly Leu Asp Ser Pro Ile Arg Phe Ser
50 55 60

Ala Gly Asn Gly Ser Ala Leu Asp Ala Phe Thr Tyr Gly Pro Ser Pro

65 70 75 80

Ala Thr Asp Gly Thr Trp Thr Asn Leu Ala His Leu Ser Leu Pro Ser
85 90 95

Glu Glu Leu Ala Ser Trp Glu Pro Leu Val Cys His Thr Gly Pro Gly
100 105 110

Ala Glu Gly His Ser Arg Ser Thr Gln Pro Met His Leu Ser Gly Glu
115 120 125

Ala Ser Thr Ala Arg Thr Cys Pro Gln Glu Pro Leu Arg Gly Thr Pro
130 135 140

Gly Gly Ala Leu Trp Leu Gly Val Leu Arg Leu Leu Leu Phe Lys Leu
145 150 155 160

Leu Leu Phe Asp Leu Leu Leu Thr Cys Ser Cys Leu Cys Asp Pro Ala
165 170 175

Gly Pro Leu Pro Ser Pro Ala Thr Thr Thr Arg Leu Arg Ala Leu Gly
180 185 190

Ser His Arg Leu His Pro Ala Thr Glu Thr Gly Gly Arg Glu Ala Thr
195 200 205

Ser Ser Pro Arg Pro Gln Pro Arg Asp Arg Arg Trp Gly Asp Thr Pro
210 215 220

Pro Gly Arg Lys Pro Gly Ser Pro Val
225 230

<210> 124

<211> 233
<212> PRT
<213> Artificial sequence

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

<220>
<223> pTalpha.EC-Delta48-4xMUT

<400> 124
Met Ala Gly Thr Trp Leu Leu Leu Leu Leu Ala Leu Gly Cys Pro Ala
1 5 10 15

Leu Pro Thr Gly Val Gly Gly Thr Pro Phe Pro Ser Leu Ala Pro Pro
20 25 30

Ile Met Leu Leu Val Ala Gly Ala Gln Gln Met Val Val Val Cys Leu
35 40 45

```
Val Leu Asp Val Ala Pro Pro Gly Leu Asp Ser Pro Ile Trp Phe Ser
    50                  55                  60

Ala Gly Asn Gly Ser Ala Leu Asp Ala Phe Thr Tyr Gly Pro Ser Pro
65                  70                  75                  80

Ala Thr Asp Gly Thr Trp Thr Asn Leu Ala His Leu Ser Leu Pro Ser
                85                  90                  95

Glu Glu Leu Ala Ser Trp Glu Pro Leu Val Cys His Thr Gly Pro Gly
            100                 105                 110

Ala Glu Gly His Ser Ala Ser Thr Gln Pro Met His Leu Ser Gly Glu
        115                 120                 125

Ala Ser Thr Ala Ala Thr Cys Pro Gln Glu Pro Leu Arg Gly Thr Pro
    130                 135                 140

Gly Gly Ala Leu Trp Leu Gly Val Leu Arg Leu Leu Leu Phe Lys Leu
145                 150                 155                 160

Leu Leu Phe Asp Leu Leu Leu Thr Cys Ser Cys Leu Cys Asp Pro Ala
                165                 170                 175

Gly Pro Leu Pro Ser Pro Ala Thr Thr Thr Arg Leu Arg Ala Leu Gly
            180                 185                 190

Ser His Arg Leu His Pro Ala Thr Glu Thr Gly Gly Arg Glu Ala Thr
        195                 200                 205

Ser Ser Pro Arg Pro Gln Pro Arg Asp Arg Arg Trp Gly Asp Thr Pro
    210                 215                 220

Pro Gly Arg Lys Pro Gly Ser Pro Val
225                 230
```

<210> 125

<211> 9
<212> PRT
<213> Unknown

<220>
<223> Description of unknown: "LAGLIDAG" family motif endonuclease sequence

<400> 125

```
Leu Ala Gly Leu Ile Asp Ala Asp Gly
1               5
```

<210> 126

<211> 30
<212> DNA

<213> Artificial sequence

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

<220>
<223> Forward adaptator sequence

<400> 126
ccatctcatc cctgcgtgtc tccgactcag 30

<210> 127

<211> 20
<212> DNA
<213> Artificial sequence

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

<220>
<223> locus specific forward sequence for GR exon 2

<400> 127
ggttcattta acaagctgcc 20

<210> 128

<211> 20
<212> DNA
<213> Artificial sequence

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

<220>
<223> locus specific forward sequence for GR exon 3

<400> 128
gcattctgac tatgccgtga 20

<210> 129

<211> 29
<212> DNA
<213> Artificial sequence

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

<220>
<223> locus specific forward sequence for GR exon 5

<400> 129
tcagcaggcc actacaggag tctcacaag 29

<210> 130

<211> 30
<212> DNA

<213> Artificial sequence

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

<220>
<223> Reverse adaptator sequence

<400> 130
cctatcccct gtgtgccttg gcagtctcag 30

<210> 131

<211> 20
<212> DNA
<213> Artificial sequence

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

<220>
<223> locus specific reverse sequence for GR exon 2

<400> 131
agccagtgag ggtgaagacg 20

<210> 132

<211> 21
<212> DNA
<213> Artificial sequence

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

<220>
<223> locus specific reverse sequence for GR exon 3

<400> 132
gggctttgca tataaatgga a 21

<210> 133

<211> 29
<212> DNA
<213> Artificial sequence

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

<220>
<223> locus specific reverse sequence for GR exon 5

<400> 133
ctgactctcc ccttcatagt ccccagaac 29

<210> 134

<211> 20
<212> DNA

<213> Artificial sequence

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

<220>
<223> locus specific forward sequence for CD52

<400> 134
cagatctgca gaaaggaagc 20

<210> 135

<211> 21
<212> DNA
<213> Artificial sequence

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

<220>
<223> locus specific forward sequence for TRAC

<400> 135
atcactggca tctggactcc a 21

<210> 136

<211> 22
<212> DNA
<213> Artificial sequence

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

<220>
<223> locus specific forward sequence for TRBC1

<400> 136
agagccccta ccagaaccag ac 22

<210> 137

<211> 22
<212> DNA
<213> Artificial sequence

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

<220>
<223> locus specific forward sequence for TRBC2

<400> 137
ggacctagta acataattgt gc 22

<210> 138

<211> 21
<212> DNA

<213> Artificial sequence

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

<220>
<223> endogenous locus specific reverse sequence for CD52

<400> 138
cctgttggag tccatctgct g 21

<210> 139

<211> 20
<212> DNA
<213> Artificial sequence

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

<220>
<223> endogenous locus specific reverse sequence for TRAC

<400> 139
cctcatgtct agcacagttt 20

<210> 140

<211> 21
<212> DNA
<213> Artificial sequence

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

<220>
<223> endogenous locus specific reverse sequence for TRBC1 and TRBC2

<400> 140
accagctcag ctccacgtgg t 21

<210> 141

<211> 20
<212> DNA
<213> Artificial sequence

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

<220>
<223> locus specific forward sequence for CTLA4_T01

<400> 141
ctctacttcc tgaagacctg 20

<210> 142

<211> 20
<212> DNA

<213> Artificial sequence

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

<220>
<223> locus specific forward sequence for CTLA4_T03/T04

<400> 142
acagttgaga gatggagggg 20

<210> 143

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

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

<220>
<223> locus specific forward sequence for PDCD1_T01

<400> 143
ccacagaggt aggtgccgc 19

<210> 144

<211> 20
<212> DNA
<213> Artificial sequence

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

<220>
<223> locus specific forward sequence for PDCD1_T03

<400> 144
gacagagatg ccggtcacca 20

<210> 145

<211> 20
<212> DNA
<213> Artificial sequence

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

<220>
<223> endogenous locus specific reverse sequence for CTLA4_T01

<400> 145
tggaatacag agccagccaa 20

<210> 146

<211> 20
<212> DNA

<213> Artificial sequence

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

<220>
<223> endogenous locus specific reverse sequence for CTLA4_T03/T04

<400> 146
ggtgcccgtg cagatggaat 20

<210> 147

<211> 20
<212> DNA
<213> Artificial sequence

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

<220>
<223> endogenous locus specific reverse sequence for PDCD1_T01

<400> 147
ggctctgcag tggaggccag 20

<210> 148

<211> 20
<212> DNA
<213> Artificial sequence

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

<220>
<223> endogenous locus specific reverse sequence for PDCD1_T03

<400> 148
ggacaacgcc accttcacct 20

<210> 149

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 149
ttgtcccaca gatatcc 17

<210> 150

<211> 17
<212> DNA
<213> Artificial sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 150
ttcctcctac tcaccat 17

<210> 151

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 151
ttgctctcac cagtata 17

<210> 152

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 152
tcactcttac ctggacc 17

<210> 153

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 153
tctcagatga tacaccc 17

<210> 154

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 154
tgatcccaca gaaatac 17

<210> 155

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 155
ttcctctaac ctgtatt 17

<210> 156

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 156
tagtccccca gatatga 17

<210> 157

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 157
ttgtcacaca tataccg 17

<210> 158

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 158
taactcttac ctgtagt 17

<210> 159

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 159
ttactccaac taactat 17

<210> 160

<211> 17

<212> DNA
<213> Artificial sequence

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

<400> 160
tggctcatac ctgtagt 17

<210> 161

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 161
ttgctcatac atgtgca 17

<210> 162

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 162
ttgtcccaca gacattc 17

<210> 163

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 163
tcacacctgg tacatag 17

<210> 164

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 164
ttgtcccaca gctaccc 17

<210> 165

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 165
tctcaactga aacaagg 17

<210> 166

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 166
ccgtgtacca gctgaga 17

<210> 167

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 167
ggtacaggta agagcaa 17

<210> 168

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 168
ttttcaggta agtgcaa 17

<210> 169

<211> 18
<212> DNA
<213> Artificial sequence

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

<400> 169
cctacaggtt aagggcca 18

<210> 170

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 170
agtacaggca tgagcca 17

<210> 171

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 171
gcatttctgt gggatca 17

<210> 172

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 172
gatccaggta aggtcaa 17

<210> 173

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 173
aaggtgtgga tgaggaa 17

<210> 174

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 174

tggtatttgt gtgacaa 17

<210> 175

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 175
agatttctct ggggcaa 17

<210> 176

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 176
ccgtttaccg gcttaga 17

<210> 177

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 177
aggatgaggt ggaggaa 17

<210> 178

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 178
atgctgtgta ggtggta 17

<210> 179

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 179
ccacgtagca gctggga 17

<210> 180

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 180
gtgtttagta gggggaa 17

<210> 181

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 181
gagtctttgt aggacaa 17

<210> 182

<211> 17
<212> DNA
<213> Artificial sequence

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

<400> 182
tgtaatgtca agagcaa 17

<210> 183

<211> 109
<212> DNA
<213> homo sapiens

<220>

<400> 183
catgtcctaa ccctgatcct cttgtcccac agatatccag aaccctgacc ctgccgtgta 60
ccagctgaga gactctaaat ccagtgacaa gtcctattca ccgattttg 109

<210> 184

<211> 92
<212> DNA
<213> homo sapiens

<220>

<400> 184
catgtcctaa ccctgatcct cttgtcccac agatatccgt gtaccagctg agagactcta 60
aatccagtga caagtcctat tcaccgattt tg 92

<210> 185

<211> 100
<212> DNA
<213> homo sapiens

<220>

<400> 185
catgtcctaa ccctgatcct cttgtcccac agatatccag atatccgtgt accagctgag 60
agactctaaa tccagtgaca agtcctattc accgattttg 100

<210> 186

<211> 78
<212> DNA
<213> homo sapiens

<220>

<400> 186
catgtcctaa ccctcgatcc tgccgtgtac agctgagag actctaaatc cagtgacaag 60
tcctattcac cgattttg 78

<210> 187

<211> 104
<212> DNA
<213> homo sapiens

<220>

<400> 187
catgtcctaa ccctgatcct cttgtcccac agatatccag aaccctgacc gtgtaccagc 60
tgagagactc taaatccagt gacaagtcct attcaccgat tttg 104

<210> 188

<211> 97
<212> DNA
<213> homo sapiens

<220>

<400> 188
catgtcctaa ccctgatcct cttgtcccac agatatccag aaccctgacc agctgagaga 60
ctctaaatcc agtgacaagt cctattcacc gattttg 97

<210> 189

<211> 45
<212> DNA
<213> homo sapiens

<220>

<400> 189
catgtcctaa ccctgatcct cttgtcccac agatatccag atttg 45

<210> 190

<211> 72
<212> DNA
<213> homo sapiens

<220>

<400> 190
catgtcctaa ccctgatcct cttgtcccac agagactcta aatccagtga caagtcctat 60
tcaccgattt tg 72

<210> 191

<211> 102
<212> DNA
<213> homo sapiens

<220>

<400> 191
catgtcctaa ccctgatcct cttgtcccac agatatccag aacctgccgt gtaccagctg 60
agagactcta aatccagtga caagtcctat tcaccgattt tg 102

<210> 192

<211> 82
<212> DNA
<213> homo sapiens

<220>

<400> 192
catgtcctaa ccctgatcct cttgtcccac agaccagctg agagactcta aatccagtga 60
caagtcctat tcaccgattt tg 82

<210> 193

<211> 121
<212> PRT
<213> Artificial sequence

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

<220>
<223> scFV-fragment 4G7 (antigen: human CD19)VH

<400> 193
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Ile Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe

50 55 60

Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Arg Val Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Leu Thr Val Ser Ser
115 120

<210> 194

<211> 115
<212> PRT
<213> Artificial sequence

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

<220>
<223> scFV 4G7 VL

<400> 194
Asp Ile Val Met Thr Gln Ala Ala Pro Ser Ile Pro Val Thr Pro Gly
1 5 10 15

Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Asn Ser
20 25 30

Asn Gly Asn Thr Tyr Leu Tyr Trp Phe Leu Gln Arg Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His
85 90 95

Leu Glu Tyr Pro Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105 110

Arg Ala Asp
115

<210> 195

<211> 251

<212> PRT
<213> Artificial sequence

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

<220>
<223> scFV 4G7

<400> 195

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Ile Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Arg Val Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ala Ala
130 135 140

Pro Ser Ile Pro Val Thr Pro Gly Glu Ser Val Ser Ile Ser Cys Arg
145 150 155 160

Ser Ser Lys Ser Leu Leu Asn Ser Asn Gly Asn Thr Tyr Leu Tyr Trp
165 170 175

Phe Leu Gln Arg Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Arg Met
180 185 190

Ser Asn Leu Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser
195 200 205

Gly Thr Ala Phe Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val
210 215 220

Gly Val Tyr Tyr Cys Met Gln His Leu Glu Tyr Pro Phe Thr Phe Gly

225 230 235 240

Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala Asp
245 250

<210> 196

<211> 45
<212> PRT
<213> homo sapiens

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

<220>
<223> fragment of T-cell surface glycoprotein CD8 alpha chain isoform 1 precursor

<400> 196
Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1 5 10 15

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
20 25 30

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
35 40 45

<210> 197

<211> 112
<212> PRT
<213> homo sapiens

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

<220>
<223> fragment of T-cell surface glycoprotein CD3 zeta chain

<400> 197
Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
20 25 30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
35 40 45

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
50 55 60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65 70 75 80

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
85 90 95

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
100 105 110

<210> 198

<211> 21
<212> PRT
<213> homo sapiens

<220>
<223> Immunoreceptor tyrosine-based activation motif of FcRI epsilon gamma chain (residues 62 to 82 of NP_004097.1)

<400> 198
Asp Gly Val Tyr Thr Gly Leu Ser Thr Arg Asn Gln Glu Thr Tyr Glu
1 5 10 15

Thr Leu Lys His Glu
20

<210> 199

<211> 17
<212> PRT
<213> homo sapiens

<220>
<223> Immunoreceptor tyrosine-based activation motif of FcRI epsilon beta chain

<400> 199
Asp Arg Val Tyr Glu Glu Leu Asn Ile Tyr Ser Ala Thr Tyr Ser Glu
1 5 10 15

Leu

<210> 200

<211> 42
<212> PRT
<213> homo sapiens

<220>
<223> fragment of 4-1BB ligand receptor

<400> 200
Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
1 5 10 15

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
20 25 30

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
35 40

<210> 201

<211> 41
<212> PRT
<213> homo sapiens

<220>
<223> Fragment of T-cell-specific surface glycoprotein CD28

<400> 201
Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr
1 5 10 15

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
20 25 30

Pro Arg Asp Phe Ala Ala Tyr Arg Ser
35 40

<210> 202

<211> 257
<212> PRT
<213> homo sapiens

<220>
<223> high affinity immunoglobulin epsilon receptor subunit alpha precursor

<400> 202
Met Ala Pro Ala Met Glu Ser Pro Thr Leu Leu Cys Val Ala Leu Leu
1 5 10 15

Phe Phe Ala Pro Asp Gly Val Leu Ala Val Pro Gln Lys Pro Lys Val
20 25 30

Ser Leu Asn Pro Pro Trp Asn Arg Ile Phe Lys Gly Glu Asn Val Thr
35 40 45

Leu Thr Cys Asn Gly Asn Asn Phe Phe Glu Val Ser Ser Thr Lys Trp
50 55 60

Phe His Asn Gly Ser Leu Ser Glu Glu Thr Asn Ser Ser Leu Asn Ile
65 70 75 80

Val Asn Ala Lys Phe Glu Asp Ser Gly Glu Tyr Lys Cys Gln His Gln
85 90 95

Gln Val Asn Glu Ser Glu Pro Val Tyr Leu Glu Val Phe Ser Asp Trp
100 105 110

Leu Leu Leu Gln Ala Ser Ala Glu Val Val Met Glu Gly Gln Pro Leu
115 120 125

Phe Leu Arg Cys His Gly Trp Arg Asn Trp Asp Val Tyr Lys Val Ile
130 135 140

Tyr Tyr Lys Asp Gly Glu Ala Leu Lys Tyr Trp Tyr Glu Asn His Asn
145 150 155 160

Ile Ser Ile Thr Asn Ala Thr Val Glu Asp Ser Gly Thr Tyr Tyr Cys
165 170 175

Thr Gly Lys Val Trp Gln Leu Asp Tyr Glu Ser Glu Pro Leu Asn Ile
180 185 190

Thr Val Ile Lys Ala Pro Arg Glu Lys Tyr Trp Leu Gln Phe Phe Ile
195 200 205

Pro Leu Leu Val Val Ile Leu Phe Ala Val Asp Thr Gly Leu Phe Ile
210 215 220

Ser Thr Gln Gln Gln Val Thr Phe Leu Leu Lys Ile Lys Arg Thr Arg
225 230 235 240

Lys Gly Phe Arg Leu Leu Asn Pro His Pro Lys Pro Asn Pro Lys Asn
245 250 255

Asn

<210> 203

<211> 244
<212> PRT
<213> homo sapiens

<220>
<223> high affinity immunoglobulin epsilon receptor subunit beta isoform 1

<400> 203
Met Asp Thr Glu Ser Asn Arg Arg Ala Asn Leu Ala Leu Pro Gln Glu
1 5 10 15

Pro Ser Ser Val Pro Ala Phe Glu Val Leu Glu Ile Ser Pro Gln Glu
20 25 30

Val Ser Ser Gly Arg Leu Leu Lys Ser Ala Ser Ser Pro Pro Leu His
35 40 45

Thr Trp Leu Thr Val Leu Lys Lys Glu Gln Glu Phe Leu Gly Val Thr
50 55 60

Gln Ile Leu Thr Ala Met Ile Cys Leu Cys Phe Gly Thr Val Val Cys
65 70 75 80

Ser Val Leu Asp Ile Ser His Ile Glu Gly Asp Ile Phe Ser Ser Phe
85 90 95

```
Lys Ala Gly Tyr Pro Phe Trp Gly Ala Ile Phe Phe Ser Ile Ser Gly
            100                 105                 110

Met Leu Ser Ile Ile Ser Glu Arg Arg Asn Ala Thr Tyr Leu Val Arg
        115                 120                 125

Gly Ser Leu Gly Ala Asn Thr Ala Ser Ser Ile Ala Gly Gly Thr Gly
    130                 135                 140

Ile Thr Ile Leu Ile Ile Asn Leu Lys Lys Ser Leu Ala Tyr Ile His
145                 150                 155                 160

Ile His Ser Cys Gln Lys Phe Phe Glu Thr Lys Cys Phe Met Ala Ser
                165                 170                 175

Phe Ser Thr Glu Ile Val Val Met Met Leu Phe Leu Thr Ile Leu Gly
            180                 185                 190

Leu Gly Ser Ala Val Ser Leu Thr Ile Cys Gly Ala Gly Glu Glu Leu
        195                 200                 205

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

Tyr Ser Ala Thr Tyr Ser Glu Leu Glu Asp Pro Gly Glu Met Ser Pro
225                 230                 235                 240

Pro Ile Asp Leu
```

<210> 204

<211> 86
<212> PRT
<213> homo sapiens

<220>
<223> high affinity immunoglobulin epsilon receptor subunit gamma precursor

<400> 204

```
Met Ile Pro Ala Val Val Leu Leu Leu Leu Leu Leu Val Glu Gln Ala
1               5                   10                  15

Ala Ala Leu Gly Glu Pro Gln Leu Cys Tyr Ile Leu Asp Ala Ile Leu
            20                  25                  30

Phe Leu Tyr Gly Ile Val Leu Thr Leu Leu Tyr Cys Arg Leu Lys Ile
        35                  40                  45

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

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

His Glu Lys Pro Pro Gln
85

<210> 205

<211> 25
<212> PRT
<213> homo sapiens

<220>
<223> signal peptide of Fc epsilon RI alpha chain

<400> 205
Met Ala Pro Ala Met Glu Ser Pro Thr Leu Leu Cys Val Ala Leu Leu
1 5 10 15

Phe Phe Ala Pro Asp Gly Val Leu Ala
20 25

<210> 206

<211> 373
<212> PRT
<213> Artificial sequence

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

<220>
<223> FcRI alpha 4g7scFV-CD8 chain of multichain CAR

<400> 206
Met Ala Pro Ala Met Glu Ser Pro Thr Leu Leu Cys Val Ala Leu Leu
1 5 10 15

Phe Phe Ala Pro Asp Gly Val Leu Ala Glu Val Gln Leu Gln Gln Ser
20 25 30

Gly Pro Glu Leu Ile Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys
35 40 45

Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Val Met His Trp Val Lys Gln
50 55 60

Lys Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn
65 70 75 80

Asp Gly Thr Lys Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr
85 90 95

Ser Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr
100 105 110

```
Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Thr Tyr Tyr Tyr
        115                 120                 125

Gly Ser Arg Val Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
    130                 135                 140

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
145                 150                 155                 160

Ser Asp Ile Val Met Thr Gln Ala Ala Pro Ser Ile Pro Val Thr Pro
                165                 170                 175

Gly Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Asn
            180                 185                 190

Ser Asn Gly Asn Thr Tyr Leu Tyr Trp Phe Leu Gln Arg Pro Gly Gln
        195                 200                 205

Ser Pro Gln Leu Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val
    210                 215                 220

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu Arg
225                 230                 235                 240

Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln
                245                 250                 255

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

Lys Arg Ala Asp Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
        275                 280                 285

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
    290                 295                 300

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
305                 310                 315                 320

Asp Phe Phe Ile Pro Leu Leu Val Val Ile Leu Phe Ala Val Asp Thr
                325                 330                 335

Gly Leu Phe Ile Ser Thr Gln Gln Gln Val Thr Phe Leu Leu Lys Ile
            340                 345                 350

Lys Arg Thr Arg Lys Gly Phe Arg Leu Leu Asn Pro His Pro Lys Pro
        355                 360                 365

Asn Pro Lys Asn Asn
    370
```

<210> 207

<211> 415
<212> PRT
<213> Artificial sequence

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

<220>
<223> FcRI alpha-4g7scFV-CD8-4-1BB chain of multichain CAR

<400> 207

```
Met Ala Pro Ala Met Glu Ser Pro Thr Leu Leu Cys Val Ala Leu Leu
1               5                  10                  15

Phe Phe Ala Pro Asp Gly Val Leu Ala Glu Val Gln Leu Gln Gln Ser
            20                  25                  30

Gly Pro Glu Leu Ile Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys
        35                  40                  45

Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Val Met His Trp Val Lys Gln
    50                  55                  60

Lys Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn
65                  70                  75                  80

Asp Gly Thr Lys Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr
                85                  90                  95

Ser Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr
            100                 105                 110

Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Thr Tyr Tyr Tyr
        115                 120                 125

Gly Ser Arg Val Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
    130                 135                 140

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
145                 150                 155                 160

Ser Asp Ile Val Met Thr Gln Ala Ala Pro Ser Ile Pro Val Thr Pro
                165                 170                 175

Gly Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Asn
            180                 185                 190

Ser Asn Gly Asn Thr Tyr Leu Tyr Trp Phe Leu Gln Arg Pro Gly Gln
        195                 200                 205

Ser Pro Gln Leu Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val
```

210 215 220

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu Arg
225 230 235 240

Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln
245 250 255

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

Lys Arg Ala Asp Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
275 280 285

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
290 295 300

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
305 310 315 320

Asp Phe Phe Ile Pro Leu Leu Val Val Ile Leu Phe Ala Val Asp Thr
325 330 335

Gly Leu Phe Ile Ser Thr Gln Gln Gln Val Thr Phe Leu Leu Lys Ile
340 345 350

Lys Arg Thr Arg Lys Gly Phe Arg Leu Leu Asn Pro His Pro Lys Pro
355 360 365

Asn Pro Lys Asn Asn Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
370 375 380

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
385 390 395 400

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
405 410 415

<210> 208

<211> 257
<212> PRT
<213> Artificial sequence

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

<220>
<223> FcRI beta-deltaITAM-41BB chain of multichain CAR

<400> 208
Met Asp Thr Glu Ser Asn Arg Arg Ala Asn Leu Ala Leu Pro Gln Glu
1 5 10 15

```
Pro Ser Ser Val Pro Ala Phe Glu Val Leu Glu Ile Ser Pro Gln Glu
            20                  25                  30

Val Ser Ser Gly Arg Leu Leu Lys Ser Ala Ser Ser Pro Pro Leu His
        35                  40                  45

Thr Trp Leu Thr Val Leu Lys Lys Glu Gln Glu Phe Leu Gly Val Thr
    50                  55                  60

Gln Ile Leu Thr Ala Met Ile Cys Leu Cys Phe Gly Thr Val Val Cys
65                  70                  75                  80

Ser Val Leu Asp Ile Ser His Ile Glu Gly Asp Ile Phe Ser Ser Phe
                85                  90                  95

Lys Ala Gly Tyr Pro Phe Trp Gly Ala Ile Phe Phe Ser Ile Ser Gly
            100                 105                 110

Met Leu Ser Ile Ile Ser Glu Arg Arg Asn Ala Thr Tyr Leu Val Arg
        115                 120                 125

Gly Ser Leu Gly Ala Asn Thr Ala Ser Ser Ile Ala Gly Gly Thr Gly
    130                 135                 140

Ile Thr Ile Leu Ile Ile Asn Leu Lys Lys Ser Leu Ala Tyr Ile His
145                 150                 155                 160

Ile His Ser Cys Gln Lys Phe Phe Glu Thr Lys Cys Phe Met Ala Ser
                165                 170                 175

Phe Ser Thr Glu Ile Val Val Met Met Leu Phe Leu Thr Ile Leu Gly
            180                 185                 190

Leu Gly Ser Ala Val Ser Leu Thr Ile Cys Gly Ala Gly Glu Glu Leu
        195                 200                 205

Lys Gly Asn Lys Val Pro Glu Lys Arg Gly Arg Lys Lys Leu Leu Tyr
    210                 215                 220

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
225                 230                 235                 240

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
                245                 250                 255

Leu
```

<210> 209

<211> 369
<212> PRT
<213> Artificial sequence

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

<220>
<223> FcRbeta-deltaITAM-41BB-CD3zeta chain of multichain CAR

<400> 209

```
Met Asp Thr Glu Ser Asn Arg Arg Ala Asn Leu Ala Leu Pro Gln Glu
1               5                  10                  15

Pro Ser Ser Val Pro Ala Phe Glu Val Leu Glu Ile Ser Pro Gln Glu
            20                  25                  30

Val Ser Ser Gly Arg Leu Leu Lys Ser Ala Ser Ser Pro Pro Leu His
        35                  40                  45

Thr Trp Leu Thr Val Leu Lys Lys Glu Gln Glu Phe Leu Gly Val Thr
    50                  55                  60

Gln Ile Leu Thr Ala Met Ile Cys Leu Cys Phe Gly Thr Val Val Cys
65                  70                  75                  80

Ser Val Leu Asp Ile Ser His Ile Glu Gly Asp Ile Phe Ser Ser Phe
                85                  90                  95

Lys Ala Gly Tyr Pro Phe Trp Gly Ala Ile Phe Phe Ser Ile Ser Gly
            100                 105                 110

Met Leu Ser Ile Ile Ser Glu Arg Arg Asn Ala Thr Tyr Leu Val Arg
        115                 120                 125

Gly Ser Leu Gly Ala Asn Thr Ala Ser Ser Ile Ala Gly Gly Thr Gly
    130                 135                 140

Ile Thr Ile Leu Ile Ile Asn Leu Lys Lys Ser Leu Ala Tyr Ile His
145                 150                 155                 160

Ile His Ser Cys Gln Lys Phe Phe Glu Thr Lys Cys Phe Met Ala Ser
                165                 170                 175

Phe Ser Thr Glu Ile Val Val Met Met Leu Phe Leu Thr Ile Leu Gly
            180                 185                 190

Leu Gly Ser Ala Val Ser Leu Thr Ile Cys Gly Ala Gly Glu Glu Leu
        195                 200                 205

Lys Gly Asn Lys Val Pro Glu Lys Arg Gly Arg Lys Lys Leu Leu Tyr
    210                 215                 220
```

```
Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
225                 230                 235                 240

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
                245                 250                 255

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
            260                 265                 270

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
        275                 280                 285

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
    290                 295                 300

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
305                 310                 315                 320

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
                325                 330                 335

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
            340                 345                 350

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
        355                 360                 365

Arg
```

<210> 210

<211> 286
<212> PRT
<213> Artificial sequence

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

<220>
<223> FcRbeta-41BB chain of the multi-chain CAR

<400> 210

```
Met Asp Thr Glu Ser Asn Arg Arg Ala Asn Leu Ala Leu Pro Gln Glu
1               5                   10                  15

Pro Ser Ser Val Pro Ala Phe Glu Val Leu Glu Ile Ser Pro Gln Glu
            20                  25                  30

Val Ser Ser Gly Arg Leu Leu Lys Ser Ala Ser Ser Pro Pro Leu His
        35                  40                  45

Thr Trp Leu Thr Val Leu Lys Lys Glu Gln Glu Phe Leu Gly Val Thr
    50                  55                  60
```

Gln Ile Leu Thr Ala Met Ile Cys Leu Cys Phe Gly Thr Val Val Cys
65 70 75 80

Ser Val Leu Asp Ile Ser His Ile Glu Gly Asp Ile Phe Ser Ser Phe
85 90 95

Lys Ala Gly Tyr Pro Phe Trp Gly Ala Ile Phe Phe Ser Ile Ser Gly
100 105 110

Met Leu Ser Ile Ile Ser Glu Arg Arg Asn Ala Thr Tyr Leu Val Arg
115 120 125

Gly Ser Leu Gly Ala Asn Thr Ala Ser Ser Ile Ala Gly Gly Thr Gly
130 135 140

Ile Thr Ile Leu Ile Ile Asn Leu Lys Lys Ser Leu Ala Tyr Ile His
145 150 155 160

Ile His Ser Cys Gln Lys Phe Phe Glu Thr Lys Cys Phe Met Ala Ser
165 170 175

Phe Ser Thr Glu Ile Val Val Met Met Leu Phe Leu Thr Ile Leu Gly
180 185 190

Leu Gly Ser Ala Val Ser Leu Thr Ile Cys Gly Ala Gly Glu Glu Leu
195 200 205

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

Tyr Ser Ala Thr Tyr Ser Glu Leu Glu Asp Pro Gly Glu Met Ser Pro
225 230 235 240

Pro Ile Asp Leu Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys
245 250 255

Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys
260 265 270

Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
275 280 285

<210> 211

<211> 327
<212> PRT
<213> Artificial sequence

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

<220>
<223> FcRbeta-deltaITAM-CD3zeta chain of the multi-chain CAR

<400> 211

```
Met Asp Thr Glu Ser Asn Arg Arg Ala Asn Leu Ala Leu Pro Gln Glu
1               5                  10                  15

Pro Ser Ser Val Pro Ala Phe Glu Val Leu Glu Ile Ser Pro Gln Glu
            20                  25                  30

Val Ser Ser Gly Arg Leu Leu Lys Ser Ala Ser Ser Pro Pro Leu His
        35                  40                  45

Thr Trp Leu Thr Val Leu Lys Lys Glu Gln Glu Phe Leu Gly Val Thr
    50                  55                  60

Gln Ile Leu Thr Ala Met Ile Cys Leu Cys Phe Gly Thr Val Val Cys
65                  70                  75                  80

Ser Val Leu Asp Ile Ser His Ile Glu Gly Asp Ile Phe Ser Ser Phe
                85                  90                  95

Lys Ala Gly Tyr Pro Phe Trp Gly Ala Ile Phe Phe Ser Ile Ser Gly
            100                 105                 110

Met Leu Ser Ile Ile Ser Glu Arg Arg Asn Ala Thr Tyr Leu Val Arg
        115                 120                 125

Gly Ser Leu Gly Ala Asn Thr Ala Ser Ser Ile Ala Gly Gly Thr Gly
    130                 135                 140

Ile Thr Ile Leu Ile Ile Asn Leu Lys Lys Ser Leu Ala Tyr Ile His
145                 150                 155                 160

Ile His Ser Cys Gln Lys Phe Phe Glu Thr Lys Cys Phe Met Ala Ser
                165                 170                 175

Phe Ser Thr Glu Ile Val Val Met Met Leu Phe Leu Thr Ile Leu Gly
            180                 185                 190

Leu Gly Ser Ala Val Ser Leu Thr Ile Cys Gly Ala Gly Glu Glu Leu
        195                 200                 205

Lys Gly Asn Lys Val Pro Glu Arg Val Lys Phe Ser Arg Ser Ala Asp
    210                 215                 220

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
225                 230                 235                 240

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
                245                 250                 255
```

```
Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
            260                 265                 270

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
        275                 280                 285

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
    290                 295                 300

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

Met Gln Ala Leu Pro Pro Arg
                325
```

<210> 212

<211> 215
<212> PRT
<213> Artificial sequence

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

<220>
<223> FcRgamma-delta ITAM-41BB-CD3zeta chain of the multi-chain CAR

<400> 212

```
Met Ile Pro Ala Val Val Leu Leu Leu Leu Leu Val Glu Gln Ala
1               5                   10                  15

Ala Ala Leu Gly Glu Pro Gln Leu Cys Tyr Ile Leu Asp Ala Ile Leu
            20                  25                  30

Phe Leu Tyr Gly Ile Val Leu Thr Leu Leu Tyr Cys Arg Leu Lys Ile
        35                  40                  45

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

Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val
65                  70                  75                  80

Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu
                85                  90                  95

Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp
            100                 105                 110

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
        115                 120                 125

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
    130                 135                 140
```

```
Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
145                 150                 155                 160

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
                165                 170                 175

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

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
        195                 200                 205

Met Gln Ala Leu Pro Pro Arg
    210                 215

<210>  213

<211>  173
<212>  PRT
<213>  Artificial sequence

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

<220>
<223>  FcRgamma-deltaITAM-CD3zeta chain of multi-chain CAR

<400>  213
Met Ile Pro Ala Val Val Leu Leu Leu Leu Leu Leu Val Glu Gln Ala
1               5                   10                  15

Ala Ala Leu Gly Glu Pro Gln Leu Cys Tyr Ile Leu Asp Ala Ile Leu
            20                  25                  30

Phe Leu Tyr Gly Ile Val Leu Thr Leu Leu Tyr Cys Arg Leu Lys Ile
        35                  40                  45

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

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
65                  70                  75                  80

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
                85                  90                  95

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
            100                 105                 110

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
        115                 120                 125
```

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
130 135 140

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
145 150 155 160

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
165 170

<210> 214

<211> 1119
<212> DNA
<213> Artificial sequence

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

<220>
<223> FcRgamma-CD3zeta chain of multi-chain CAR

<400> 214
atggctcctg ccatggaatc ccctactcta ctgtgtgtag ccttactgtt cttcgctcca 60
gatggcgtgt tagcagaggt gcagttgcag cagtcagggc cagagttgat taagcccgga 120
gcctccgtca agatgtcctg caaggccagc gggtacactt tcaccagcta cgtcatgcat 180
tgggtgaagc agaagccagg ccaggggctt gagtggattg ggtacatcaa cccctacaac 240
gacgggacca aatacaacga gaaattcaag ggcaaagcca cactcacctc cgataagtcc 300
tcctctaccg cctacatgga gctcagctcc ctgacctccg aggatagcgc tgtgtattac 360
tgcgcaaggg gcacatacta ctatggctct agggtgttcg actactgggg gcagggcact 420
actctcacag tgagctcagg cggaggaggc agtggcggag ggggaagtgg gggcggcggc 480
agcgatattg tcatgaccca ggcagccctt agtatccctg tgactccagg cgagagcgtg 540
agcatcagct gccggtccag caagagcctg ctgaacagta acggaaacac atacctctac 600
tggtttctgc agaggcccgg ccagagccct cagctgctga tttaccgcat gtcaaatctt 660
gcctctgggg tgcccgatag atttagtggg agcggatccg gcacagcttt tacattgcgg 720
atctccagag tcgaggccga agacgtgggg gtctattact gtatgcaaca cctggaatac 780
ccctttacct tcggagccgg cacaaagctg gagctgaagc gggctgacac cacaaccccc 840
gctccaaggc cccctacccc cgcaccaact attgcctccc agccactctc actgcggcct 900
gaggcctgtc ggcccgctgc tggaggcgca gtgcatacaa ggggcctcga tttcgcctgc 960
gatttttta tcccattgtt ggtggtgatt ctgtttgctg tggacacagg attatttatc 1020
tcaactcagc agcaggtcac atttctcttg aagattaaga gaaccaggaa aggcttcaga 1080
cttctgaacc cacatcctaa gccaaacccc aaaaacaac 1119

<210> 215

<211> 1119
<212> DNA
<213> Artificial sequence

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

<220>
<223> FcRalpha-4g7scFV-CD8 chain of multichain CAR

<400> 215
atggctcctg ccatggaatc ccctactcta ctgtgtgtag ccttactgtt cttcgctcca 60
gatggcgtgt tagcagaggt gcagttgcag cagtcagggc cagagttgat taagcccgga 120
gcctccgtca agatgtcctg caaggccagc gggtacactt tcaccagcta cgtcatgcat 180
tgggtgaagc agaagccagg ccaggggctt gagtggattg ggtacatcaa cccctacaac 240
gacgggacca aatacaacga gaaattcaag ggcaaagcca cactcacctc cgataagtcc 300
tcctctaccg cctacatgga gctcagctcc ctgacctccg aggatagcgc tgtgtattac 360

tgcgcaaggg gcacatacta ctatggctct agggtgttcg actactgggg gcagggcact 420
actctcacag tgagctcagg cggaggaggc agtggcggag ggggaagtgg gggcggcggc 480
agcgatattg tcatgaccca ggcagcccct agtatccctg tgactccagg cgagagcgtg 540
agcatcagct gccggtccag caagagcctg ctgaacagta acggaaacac atacctctac 600
tggtttctgc agaggcccgg ccagagccct cagctgctga tttaccgcat gtcaaatctt 660
gcctctgggg tgcccgatag atttagtggg agcggatccg gcacagcttt tacattgcgg 720
atctccagag tcgaggccga agacgtgggg gtctattact gtatgcaaca cctggaatac 780
ccctttacct tcggagccgg cacaaagctg gagctgaagc gggctgacac cacaaccccc 840
gctccaaggc cccctacccc cgcaccaact attgcctccc agccactctc actgcggcct 900
gaggcctgtc ggcccgctgc tggaggcgca gtgcatacaa ggggcctcga tttcgcctgc 960
gatttttta tcccattgtt ggtggtgatt ctgtttgctg tggacacagg attatttatc 1020
tcaactcagc agcaggtcac atttctcttg aagattaaga gaaccaggaa aggcttcaga 1080
cttctgaacc cacatcctaa gccaaacccc aaaaacaac 1119

<210> 216

<211> 1245
<212> DNA
<213> Artificial sequence

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

<220>
<223> FcRalpha-4g7scFV-CD8-4-1BB chain of multichain CAR

<400> 216
atggctcctg ccatggaatc ccctactcta ctgtgtgtag ccttactgtt cttcgctcca 60
gatggcgtgt tagcagaggt gcagttgcag cagtcagggc cagagttgat taagcccgga 120
gcctccgtca agatgtcctg caaggccagc gggtacactt tcaccagcta cgtcatgcat 180
tgggtgaagc agaagccagg ccaggggctt gagtggattg ggtacatcaa cccctacaac 240
gacgggacca aatacaacga gaaattcaag ggcaaagcca cactcacctc cgataagtcc 300
tcctctaccg cctacatgga gctcagctcc ctgacctccg aggatagcgc tgtgtattac 360
tgcgcaaggg gcacatacta ctatggctct agggtgttcg actactgggg gcagggcact 420
actctcacag tgagctcagg cggaggaggc agtggcggag ggggaagtgg gggcggcggc 480
agcgatattg tcatgaccca ggcagcccct agtatccctg tgactccagg cgagagcgtg 540
agcatcagct gccggtccag caagagcctg ctgaacagta acggaaacac atacctctac 600
tggtttctgc agaggcccgg ccagagccct cagctgctga tttaccgcat gtcaaatctt 660
gcctctgggg tgcccgatag atttagtggg agcggatccg gcacagcttt tacattgcgg 720
atctccagag tcgaggccga agacgtgggg gtctattact gtatgcaaca cctggaatac 780
ccctttacct tcggagccgg cacaaagctg gagctgaagc gggctgacac cacaaccccc 840
gctccaaggc cccctacccc cgcaccaact attgcctccc agccactctc actgcggcct 900
gaggcctgtc ggcccgctgc tggaggcgca gtgcatacaa ggggcctcga tttcgcctgc 960
gatttttta tcccattgtt ggtggtgatt ctgtttgctg tggacacagg attatttatc 1020
tcaactcagc agcaggtcac atttctcttg aagattaaga gaaccaggaa aggcttcaga 1080
cttctgaacc cacatcctaa gccaaacccc aaaaacaaca aacggggccg gaagaagctc 1140
ctctacattt ttaagcagcc tttcatgcgg ccagtgcaga caacccaaga ggaggatggg 1200
tgttcctgca gattccctga ggaagaggaa ggcgggtgcg agctg 1245

<210> 217

<211> 771
<212> DNA
<213> Artificial sequence

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

<220>
<223> FcRbeta-deltaITAM-41BB chain of multichain CAR

<400> 217
atggacacag aaagtaatag gagagcaaat cttgctctcc cacaggagcc ttccagtgtg 60
cctgcatttg aagtcttgga aatatctccc caggaagtat cttcaggcag actattgaag 120

tcggcctcat ccccaccact gcatacatgg ctgacagttt tgaaaaaaga gcaggagttc 180
ctgggggtaa cacaaattct gactgctatg atatgccttt gttttggaac agttgtctgc 240
tctgtacttg atatttcaca cattgaggga gacatttttt catcatttaa agcaggttat 300
ccattctggg gagccatatt tttttctatt tctggaatgt tgtcaattat atctgaaagg 360
agaaatgcaa catatctggt gagaggaagc ctgggagcaa acactgccag cagcatagct 420
gggggaacgg gaattaccat cctgatcatc aacctgaaga agagcttggc ctatatccac 480
atccacagtt gccagaaatt ttttgagacc aagtgcttta tggcttcctt ttccactgaa 540
attgtagtga tgatgctgtt tctcaccatt ctgggacttg gtagtgctgt gtcactcaca 600
atctgtggag ctggggaaga actcaaagga aacaaggttc cagagaaacg gggccggaag 660
aagctcctct acatttttaa gcagcctttc atgcggccag tgcagacaac ccaagaggag 720
gatgggtgtt cctgcagatt ccctgaggaa gaggaaggcg ggtgcgagct g 771

<210> 218

<211> 1107
<212> DNA
<213> Artificial sequence

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

<220>
<223> FcRbeta-deltaITAM-41BB-CD3zeta chain of multichain CAR

<400> 218
atggacacag aaagtaatag gagagcaaat cttgctctcc cacaggagcc ttccagtgtg 60
cctgcatttg aagtcttgga aatatctccc caggaagtat cttcaggcag actattgaag 120
tcggcctcat ccccaccact gcatacatgg ctgacagttt tgaaaaaaga gcaggagttc 180
ctgggggtaa cacaaattct gactgctatg atatgccttt gttttggaac agttgtctgc 240
tctgtacttg atatttcaca cattgaggga gacatttttt catcatttaa agcaggttat 300
ccattctggg gagccatatt tttttctatt tctggaatgt tgtcaattat atctgaaagg 360
agaaatgcaa catatctggt gagaggaagc ctgggagcaa acactgccag cagcatagct 420
gggggaacgg gaattaccat cctgatcatc aacctgaaga agagcttggc ctatatccac 480
atccacagtt gccagaaatt ttttgagacc aagtgcttta tggcttcctt ttccactgaa 540
attgtagtga tgatgctgtt tctcaccatt ctgggacttg gtagtgctgt gtcactcaca 600
atctgtggag ctggggaaga actcaaagga aacaaggttc cagagaaacg gggccggaag 660
aagctcctct acatttttaa gcagcctttc atgcggccag tgcagacaac ccaagaggag 720
gatgggtgtt cctgcagatt ccctgaggaa gaggaaggcg ggtgcgagct gagagtgaag 780
ttctccagga gcgcagatgc ccccgcctat caacagggcc agaaccagct ctacaacgag 840
cttaacctcg ggaggcgcga agaatacgac gtgttggata agagaagggg gcgggacccc 900
gagatgggag gaaagccccg gaggaagaac cctcaggagg gcctgtacaa cgagctgcag 960
aaggataaga tggccgaggc ctactcagag atcgggatga aggggagcg gcgccgcggg 1020
aaggggcacg atgggctcta ccaggggctg agcacagcca caaaggacac atacgacgcc 1080
ttgcacatgc aggcccttcc accccgg 1107

<210> 219

<211> 858
<212> DNA
<213> Artificial sequence

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

<220>
<223> FcRbeta-41BB chain of the multi-chain CAR

<400> 219
atggacacag aaagtaatag gagagcaaat cttgctctcc cacaggagcc ttccagtgtg 60
cctgcatttg aagtcttgga aatatctccc caggaagtat cttcaggcag actattgaag 120
tcggcctcat ccccaccact gcatacatgg ctgacagttt tgaaaaaaga gcaggagttc 180
ctgggggtaa cacaaattct gactgctatg atatgccttt gttttggaac agttgtctgc 240
tctgtacttg atatttcaca cattgaggga gacatttttt catcatttaa agcaggttat 300
ccattctggg gagccatatt tttttctatt tctggaatgt tgtcaattat atctgaaagg 360

agaaatgcaa catatctggt gagaggaagc ctgggagcaa acactgccag cagcatagct 420
gggggaacgg gaattaccat cctgatcatc aacctgaaga agagcttggc ctatatccac 480
atccacagtt gccagaaatt ttttgagacc aagtgcttta tggcttcctt ttccactgaa 540
attgtagtga tgatgctgtt tctcaccatt ctgggacttg gtagtgctgt gtcactcaca 600
atctgtggag ctggggaaga actcaaagga aacaaggttc cagaggatcg tgtttatgaa 660
gaattaaaca tatattcagc tacttacagt gagttggaag acccagggga aatgtctcct 720
cccattgatt taaaacgggg ccggaagaag ctcctctaca tttttaagca gcctttcatg 780
cggccagtgc agacaaccca agaggaggat gggtgttcct gcagattccc tgaggaagag 840
gaaggcgggt gcgagctg 858

<210> 220

<211> 981
<212> DNA
<213> Artificial sequence

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

<220>
<223> FcRbeta-deltaITAM-CD3zeta chain of the multi-chain CAR

<400> 220
atggacacag aaagtaatag gagagcaaat cttgctctcc cacaggagcc ttccagtgtg 60
cctgcatttg aagtcttgga aatatctccc caggaagtat cttcaggcag actattgaag 120
tcggcctcat ccccaccact gcatacatgg ctgacagttt tgaaaaaaga gcaggagttc 180
ctgggggtaa cacaaattct gactgctatg atatgccttt gttttggaac agttgtctgc 240
tctgtacttg atatttcaca cattgaggga gacatttttt catcatttaa agcaggttat 300
ccattctggg gagccatatt tttttctatt tctggaatgt tgtcaattat atctgaaagg 360
agaaatgcaa catatctggt gagaggaagc ctgggagcaa acactgccag cagcatagct 420
gggggaacgg gaattaccat cctgatcatc aacctgaaga agagcttggc ctatatccac 480
atccacagtt gccagaaatt ttttgagacc aagtgcttta tggcttcctt ttccactgaa 540
attgtagtga tgatgctgtt tctcaccatt ctgggacttg gtagtgctgt gtcactcaca 600
atctgtggag ctggggaaga actcaaagga aacaaggttc cagagagagt gaagttctcc 660
aggagcgcag atgcccccgc ctatcaacag ggccagaacc agctctacaa cgagcttaac 720
ctcgggaggc gcgaagaata cgacgtgttg gataagagaa gggggcggga ccccgagatg 780
ggaggaaagc cccggaggaa gaaccctcag gagggcctgt acaacgagct gcagaaggat 840
aagatggccg aggcctactc agagatcggg atgaaggggg agcggcgccg cgggaagggg 900
cacgatgggc tctaccaggg gctgagcaca gccacaaagg acacatacga cgccttgcac 960
atgcaggccc ttccaccccg g 981

<210> 221

<211> 648
<212> DNA
<213> Artificial sequence

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

<220>
<223> FcRgamma-delta ITAM-41BB-CD3zeta chain of the multi-chain CAR

<400> 221
atgattccag cagtggtctt gctcttactc cttttggttg aacaagcagc ggccctggga 60
gagcctcagc tctgctatat cctggatgcc atcctgtttc tgtatggaat tgtcctcacc 120
ctcctctact gtcgactgaa gatccaagtg cgaaaggcag ctataaccag ctatgagaaa 180
tcaaaacggg gccggaagaa gctcctctac atttttaagc agcctttcat gcggccagtg 240
cagacaaccc aagaggagga tgggtgttcc tgcagattcc ctgaggaaga ggaaggcggg 300
tgcgagctga gagtgaagtt ctccaggagc gcagatgccc ccgcctatca acagggccag 360
aaccagctct acaacgagct taacctcggg aggcgcgaag aatacgacgt gttggataag 420
agaaggggc gggaccccga gatgggagga aagccccgga ggaagaaccc tcaggagggc 480
ctgtacaacg agctgcagaa ggataagatg gccgaggcct actcagagat cgggatgaag 540
ggggagcggc gccgcgggaa ggggcacgat gggctctacc aggggctgag cacagccaca 600

aaggacacat acgacgcctt gcacatgcag gcccttccac cccggtga 648

<210> 222

<211> 522
<212> DNA
<213> Artificial sequence

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

<220>
<223> FcRgamma-deltaITAM-CD3zeta chain of multi-chain CAR

<400> 222
atgattccag cagtggtctt gctcttactc cttttggttg aacaagcagc ggccctggga 60
gagcctcagc tctgctatat cctggatgcc atcctgtttc tgtatggaat tgtcctcacc 120
ctcctctact gtcgactgaa gatccaagtg cgaaaggcag ctataaccag ctatgagaaa 180
tcaagagtga agttctccag gagcgcagat gcccccgcct atcaacaggg ccagaaccag 240
ctctacaacg agcttaacct cgggaggcgc gaagaatacg acgtgttgga taagagaagg 300
gggcgggacc ccgagatggg aggaaagccc cggaggaaga accctcagga gggcctgtac 360
aacgagctgc agaaggataa gatggccgag gcctactcag agatcgggat gaaggggag 420
cggcgccgcg ggaaggggca cgatgggctc taccaggggc tgagcacagc cacaaaggac 480
acatacgacg ccttgcacat gcaggccctt ccaccccggt ga 522

<210> 223

<211> 597
<212> DNA
<213> Artificial sequence

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

<220>
<223> FcRgamma-CD3zeta chain of multi-chain CAR

<400> 223
atgattccag cagtggtctt gctcttactc cttttggttg aacaagcagc ggccctggga 60
gagcctcagc tctgctatat cctggatgcc atcctgtttc tgtatggaat tgtcctcacc 120
ctcctctact gtcgactgaa gatccaagtg cgaaaggcag ctataaccag ctatgagaaa 180
tcagatggtg tttacacggg cctgagcacc aggaaccagg agacttacga gactctgaag 240
catgagaaac caccacagag agtgaagttc tccaggagcg cagatgcccc cgcctatcaa 300
cagggccaga accagctcta caacgagctt aacctcggga ggcgcgaaga atacgacgtg 360
ttggataaga gaaggggcg ggaccccgag atgggaggaa agccccggag gaagaaccct 420
caggagggcc tgtacaacga gctgcagaag gataagatgg ccgaggccta ctcagagatc 480
gggatgaagg gggagcggcg ccgcgggaag gggcacgatg ggctctacca ggggctgagc 540
acagccacaa aggacacata cgacgccttg cacatgcagg cccttccacc ccggtga 597

<210> 224

<211> 2247
<212> DNA
<213> Artificial sequence

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

<220>
<223> csm1

<400> 224

atggctcctg ccatggaatc ccctactcta ctgtgtgtag ccttactgtt cttcgctcca 60
gatggcgtgt tagcagaggt gcagttgcag cagtcagggc cagagttgat taagcccgga 120
gcctccgtca agatgtcctg caaggccagc gggtacactt tcaccagcta cgtcatgcat 180
tgggtgaagc agaagccagg ccaggggctt gagtggattg ggtacatcaa cccctacaac 240
gacgggacca aatacaacga gaaattcaag ggcaaagcca cactcacctc cgataagtcc 300
tcctctaccg cctacatgga gctcagctcc ctgacctccg aggatagcgc tgtgtattac 360
tgcgcaaggg gcacatacta ctatggctct agggtgttcg actactgggg gcagggcact 420
actctcacag tgagctcagg cggaggaggc agtggcggag ggggaagtgg gggcggcggc 480
agcgatattg tcatgaccca ggcagccccc agtatccctg tgactccagg cgagagcgtg 540
agcatcagct gccggtccag caagagcctg ctgaacagta acggaaacac atacctctac 600
tggtttctgc agaggcccgg ccagagccct cagctgctga tttaccgcat gtcaaatctt 660
gcctctgggg tgcccgatag atttagtggg agcggatccg gcacagcttt tacattgcgg 720
atctccagag tcgaggccga agacgtgggg gtctattact gtatgcaaca cctggaatac 780
ccctttacct tcggagccgg cacaaagctg gagctgaagc gggctgacac cacaaccccc 840
gctccaaggc cccctacccc cgcaccaact attgcctccc agccactctc actgcggcct 900
gaggcctgtc ggcccgctgc tggaggcgca gtgcatacaa ggggcctcga tttcgcctgc 960
gatttttta tcccattgtt ggtggtgatt ctgtttgctg tggacacagg attatttatc 1020
tcaactcagc agcaggtcac atttctcttg aagattaaga gaaccaggaa aggcttcaga 1080
cttctgaacc cacatcctaa gccaaacccc aaaaacaaca gagccgaggg cagaggcagc 1140
ctgctgacct gcggcgacgt ggaggagaac ccaggcccca tggacacaga aagtaatagg 1200
agagcaaatc ttgctctccc acaggagcct tccagtgtgc ctgcatttga agtcttggaa 1260
atatctcccc aggaagtatc ttcaggcaga ctattgaagt cggcctcatc cccaccactg 1320
catacatggc tgacagtttt gaaaaaagag caggagttcc tgggggtaac acaaattctg 1380
actgctatga tatgcctttg ttttggaaca gttgtctgct ctgtacttga tatttcacac 1440
attgagggag acatttttc atcatttaaa gcaggttatc cattctgggg agccatattt 1500
ttttctattt ctggaatgtt gtcaattata tctgaaagga gaaatgcaac atatctggtg 1560
agaggaagcc tgggagcaaa cactgccagc agcatagctg ggggaacggg aattaccatc 1620
ctgatcatca acctgaagaa gagcttggcc tatatccaca tccacagttg ccagaaattt 1680
tttgagacca agtgctttat ggcttccttt tccactgaaa ttgtagtgat gatgctgttt 1740
ctcaccattc tgggacttgg tagtgctgtg tcactcacaa tctgtggagc tggggaagaa 1800
ctcaaaggaa acaaggttcc agaggatcgt gtttatgaag aattaaacat atattcagct 1860
acttacagtg agttggaaga cccaggggaa atgtctcctc ccattgattt aggttctggc 1920
gtgaaacaga ctttgaattt tgaccttctc aagttggcgg gagacgtgga gtccaaccca 1980
gggcccatga ttccagcagt ggtcttgctc ttactccttt tggttgaaca agcagcggcc 2040
ctgggagagc ctcagctctg ctatatcctg gatgccatcc tgtttctgta tggaattgtc 2100
ctcaccctcc tctactgtcg actgaagatc caagtgcgaa aggcagctat aaccagctat 2160
gagaaatcag atggtgttta cacgggcctg agcaccagga accaggagac ttacgagact 2220
ctgaagcatg agaaaccacc acagtga 2247

<210> 225

<211> 2634
<212> DNA
<213> Artificial sequence

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

<220>
<223> csm2

<400> 225
atggctcctg ccatggaatc ccctactcta ctgtgtgtag ccttactgtt cttcgctcca 60
gatggcgtgt tagcagaggt gcagttgcag cagtcagggc cagagttgat taagcccgga 120
gcctccgtca agatgtcctg caaggccagc gggtacactt tcaccagcta cgtcatgcat 180
tgggtgaagc agaagccagg ccaggggctt gagtggattg ggtacatcaa cccctacaac 240
gacgggacca aatacaacga gaaattcaag ggcaaagcca cactcacctc cgataagtcc 300
tcctctaccg cctacatgga gctcagctcc ctgacctccg aggatagcgc tgtgtattac 360
tgcgcaaggg gcacatacta ctatggctct agggtgttcg actactgggg gcagggcact 420
actctcacag tgagctcagg cggaggaggc agtggcggag ggggaagtgg gggcggcggc 480
agcgatattg tcatgaccca ggcagccccc agtatccctg tgactccagg cgagagcgtg 540
agcatcagct gccggtccag caagagcctg ctgaacagta acggaaacac atacctctac 600
tggtttctgc agaggcccgg ccagagccct cagctgctga tttaccgcat gtcaaatctt 660
gcctctgggg tgcccgatag atttagtggg agcggatccg gcacagcttt tacattgcgg 720
atctccagag tcgaggccga agacgtgggg gtctattact gtatgcaaca cctggaatac 780
ccctttacct tcggagccgg cacaaagctg gagctgaagc gggctgacac cacaaccccc 840

gctccaaggc cccctacccc cgcaccaact attgcctccc agccactctc actgcggcct 900
gaggcctgtc ggcccgctgc tggaggcgca gtgcatacaa ggggcctcga tttcgcctgc 960
gatttttta tcccattgtt ggtggtgatt ctgtttgctg tggacacagg attatttatc 1020
tcaactcagc agcaggtcac atttctcttg aagattaaga gaaccaggaa aggcttcaga 1080
cttctgaacc cacatcctaa gccaaacccc aaaaacaaca gagccgaggg cagaggcagc 1140
ctgctgacct gcggcgacgt ggaggagaac ccaggcccca tggacacaga aagtaatagg 1200
agagcaaatc ttgctctccc acaggagcct tccagtgtgc ctgcatttga agtcttggaa 1260
atatctcccc aggaagtatc ttcaggcaga ctattgaagt cggcctcatc cccaccactg 1320
catacatggc tgacagtttt gaaaaaagag caggagttcc tgggggtaac acaaattctg 1380
actgctatga tatgcctttg ttttggaaca gttgtctgct ctgtacttga tatttcacac 1440
attgagggag acatttttc atcatttaaa gcaggttatc cattctgggg agccatattt 1500
ttttctattt ctggaatgtt gtcaattata tctgaaagga gaaatgcaac atatctggtg 1560
agaggaagcc tgggagcaaa cactgccagc agcatagctg ggggaacggg aattaccatc 1620
ctgatcatca acctgaagaa gagcttggcc tatatccaca tccacagttg ccagaaattt 1680
tttgagacca agtgctttat ggcttccttt tccactgaaa ttgtagtgat gatgctgttt 1740
ctcaccattc tgggacttgg tagtgctgtg tcactcacaa tctgtggagc tggggaagaa 1800
ctcaaaggaa acaaggttcc agaggatcgt gtttatgaag aattaaacat atattcagct 1860
acttacagtg agttggaaga cccaggggaa atgtctcctc ccattgattt aggttctggc 1920
gtgaaacaga ctttgaattt tgaccttctc aagttggcgg gagacgtgga gtccaaccca 1980
gggcccatga ttccagcagt ggtcttgctc ttactccttt tggttgaaca agcagcggcc 2040
ctgggagagc ctcagctctg ctatatcctg gatgccatcc tgtttctgta tggaattgtc 2100
ctcaccctcc tctactgtcg actgaagatc caagtgcgaa aggcagctat aaccagctat 2160
gagaaatcaa aacggggccg gaagaagctc ctctacattt ttaagcagcc tttcatgcgg 2220
ccagtgcaga caacccaaga ggaggatggg tgttcctgca gattccctga ggaagaggaa 2280
ggcgggtgcg agctgagagt gaagttctcc aggagcgcag atgcccccgc ctatcaacag 2340
ggccagaacc agctctacaa cgagcttaac ctcgggaggc gcgaagaata cgacgtgttg 2400
gataagagaa gggggcggga ccccgagatg ggaggaaagc cccggaggaa gaaccctcag 2460
gagggcctgt acaacgagct gcagaaggat aagatggccg aggcctactc agagatcggg 2520
atgaaggggg agcggcgccg cgggaagggg cacgatgggc tctaccaggg gctgagcaca 2580
gccacaaagg acacatacga cgccttgcac atgcaggccc ttccaccccg gtga 2634

<210> 226

<211> 2547
<212> DNA
<213> Artificial sequence

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

<220>
<223> csm4

<400> 226
atggctcctg ccatggaatc ccctactcta ctgtgtgtag ccttactgtt cttcgctcca 60
gatggcgtgt tagcagaggt gcagttgcag cagtcagggc cagagttgat taagcccgga 120
gcctccgtca agatgtcctg caaggccagc gggtacactt tcaccagcta cgtcatgcat 180
tgggtgaagc agaagccagg ccaggggctt gagtggattg ggtacatcaa cccctacaac 240
gacgggacca aatacaacga gaaattcaag ggcaaagcca cactcacctc cgataagtcc 300
tcctctaccg cctacatgga gctcagctcc ctgacctccg aggatagcgc tgtgtattac 360
tgcgcaaggg gcacatacta ctatggctct agggtgttcg actactgggg gcagggcact 420
actctcacag tgagctcagg cggaggaggc agtggcggag ggggaagtgg gggcggcggc 480
agcgatattg tcatgaccca ggcagccct agtatccctg tgactccagg cgagagcgtg 540
agcatcagct gccggtccag caagagcctg ctgaacagta acggaaacac atacctctac 600
tggtttctgc agaggcccgg ccagagccct cagctgctga tttaccgcat gtcaaatctt 660
gcctctgggg tgcccgatag atttagtggg agcggatccg gcacagcttt tacattgcgg 720
atctccagag tcgaggccga agacgtgggg gtctattact gtatgcaaca cctggaatac 780
ccctttacct tcggagccgg cacaaagctg gagctgaagc gggctgacac cacaaccccc 840
gctccaaggc cccctacccc cgcaccaact attgcctccc agccactctc actgcggcct 900
gaggcctgtc ggcccgctgc tggaggcgca gtgcatacaa ggggcctcga tttcgcctgc 960
gatttttta tcccattgtt ggtggtgatt ctgtttgctg tggacacagg attatttatc 1020
tcaactcagc agcaggtcac atttctcttg aagattaaga gaaccaggaa aggcttcaga 1080
cttctgaacc cacatcctaa gccaaacccc aaaaacaaca gagccgaggg cagaggcagc 1140
ctgctgacct gcggcgacgt ggaggagaac ccaggcccca tggacacaga aagtaatagg 1200
agagcaaatc ttgctctccc acaggagcct tccagtgtgc ctgcatttga agtcttggaa 1260
atatctcccc aggaagtatc ttcaggcaga ctattgaagt cggcctcatc cccaccactg 1320

catacatggc tgacagtttt gaaaaaagag caggagttcc tgggggtaac acaaattctg 1380
actgctatga tatgcctttg ttttggaaca gttgtctgct ctgtacttga tatttcacac 1440
attgagggag acatttttc atcatttaaa gcaggttatc cattctgggg agccatattt 1500
ttttctattt ctggaatgtt gtcaattata tctgaaagga gaaatgcaac atatctggtg 1560
agaggaagcc tgggagcaaa cactgccagc agcatagctg ggggaacggg aattaccatc 1620
ctgatcatca acctgaagaa gagcttggcc tatatccaca tccacagttg ccagaaattt 1680
tttgagacca agtgctttat ggcttccttt tccactgaaa ttgtagtgat gatgctgttt 1740
ctcaccattc tgggacttgg tagtgctgtg tcactcacaa tctgtggagc tggggaagaa 1800
ctcaaaggaa acaaggttcc agagaaacgg ggccggaaga agctcctcta catttttaag 1860
cagcctttca tgcggccagt gcagacaacc caagaggagg atgggtgttc ctgcagattc 1920
cctgaggaag aggaaggcgg gtgcgagctg ggttctggcg tgaaacagac tttgaatttt 1980
gaccttctca agttggcggg agacgtggag tccaacccag ggcccatgat tccagcagtg 2040
gtcttgctct tactcctttt ggttgaacaa gcagcggccc tgggagagcc tcagctctgc 2100
tatatcctgg atgccatcct gtttctgtat ggaattgtcc tcaccctcct ctactgtcga 2160
ctgaagatcc aagtgcgaaa ggcagctata accagctatg agaaatcaag agtgaagttc 2220
tccaggagcg cagatgcccc cgcctatcaa cagggccaga accagctcta caacgagctt 2280
aacctcggga ggcgcgaaga atacgacgtg ttggataaga gaaggggcg ggaccccgag 2340
atgggaggaa agccccggag gaagaaccct caggagggcc tgtacaacga gctgcagaag 2400
gataagatgg ccgaggccta ctcagagatc gggatgaagg gggagcggcg ccgcgggaag 2460
gggcacgatg ggctctacca ggggctgagc acagccacaa aggacacata cgacgccttg 2520
cacatgcagg cccttccacc ccggtga 2547

<210> 227

<211> 2622
<212> DNA
<213> Artificial sequence

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

<220>
<223> csm5

<400> 227
atggctcctg ccatggaatc ccctactcta ctgtgtgtag ccttactgtt cttcgctcca 60
gatggcgtgt tagcagaggt gcagttgcag cagtcagggc cagagttgat taagcccgga 120
gcctccgtca agatgtcctg caaggccagc gggtacactt tcaccagcta cgtcatgcat 180
tgggtgaagc agaagccagg ccaggggctt gagtggattg ggtacatcaa cccctacaac 240
gacgggacca aatacaacga gaaattcaag ggcaaagcca cactcacctc cgataagtcc 300
tcctctaccg cctacatgga gctcagctcc ctgacctccg aggatagcgc tgtgtattac 360
tgcgcaaggg gcacatacta ctatggctct agggtgttcg actactgggg gcagggcact 420
actctcacag tgagctcagg cggaggaggc agtggcggag ggggaagtgg gggcggcggc 480
agcgatattg tcatgaccca ggcagccct agtatccctg tgactccagg cgagagcgtg 540
agcatcagct gccggtccag caagagcctg ctgaacagta acggaaacac atacctctac 600
tggtttctgc agaggcccgg ccagagccct cagctgctga tttaccgcat gtcaaatctt 660
gcctctgggg tgcccgatag atttagtggg agcggatccg gcacagcttt tacattgcgg 720
atctccagag tcgaggccga agacgtgggg gtctattact gtatgcaaca cctggaatac 780
ccctttacct tcggagccgg cacaaagctg gagctgaagc gggctgacac cacaaccccc 840
gctccaaggc cccctacccc cgcaccaact attgcctccc agccactctc actgcggcct 900
gaggcctgtc ggcccgctgc tggaggcgca gtgcatacaa ggggcctcga tttcgcctgc 960
gatttttta tcccattgtt ggtggtgatt ctgtttgctg tggacacagg attatttatc 1020
tcaactcagc agcaggtcac atttctcttg aagattaaga gaaccaggaa aggcttcaga 1080
cttctgaacc cacatcctaa gccaaacccc aaaaacaaca gagccgaggg cagaggcagc 1140
ctgctgacct gcggcgacgt ggaggagaac ccaggcccca tggacacaga aagtaatagg 1200
agagcaaatc ttgctctccc acaggagcct tccagtgtgc ctgcatttga agtcttggaa 1260
atatctcccc aggaagtatc ttcaggcaga ctattgaagt cggcctcatc cccaccactg 1320
catacatggc tgacagtttt gaaaaaagag caggagttcc tgggggtaac acaaattctg 1380
actgctatga tatgcctttg ttttggaaca gttgtctgct ctgtacttga tatttcacac 1440
attgagggag acatttttc atcatttaaa gcaggttatc cattctgggg agccatattt 1500
ttttctattt ctggaatgtt gtcaattata tctgaaagga gaaatgcaac atatctggtg 1560
agaggaagcc tgggagcaaa cactgccagc agcatagctg ggggaacggg aattaccatc 1620
ctgatcatca acctgaagaa gagcttggcc tatatccaca tccacagttg ccagaaattt 1680
tttgagacca agtgctttat ggcttccttt tccactgaaa ttgtagtgat gatgctgttt 1740
ctcaccattc tgggacttgg tagtgctgtg tcactcacaa tctgtggagc tggggaagaa 1800
ctcaaaggaa acaaggttcc agagaaacgg ggccggaaga agctcctcta catttttaag 1860

cagcctttca tgcggccagt gcagacaacc caagaggagg atgggtgttc ctgcagattc 1920
cctgaggaag aggaaggcgg gtgcgagctg agagtgaagt tctccaggag cgcagatgcc 1980
cccgcctatc aacagggcca gaaccagctc tacaacgagc ttaacctcgg gaggcgcgaa 2040
gaatacgacg tgttggataa gagaaggggg cgggaccccg agatgggagg aaagccccgg 2100
aggaagaacc ctcaggaggg cctgtacaac gagctgcaga aggataagat ggccgaggcc 2160
tactcagaga tcgggatgaa gggggagcgg cgccgcggga aggggcacga tgggctctac 2220
caggggctga gcacagccac aaaggacaca tacgacgcct tgcacatgca ggcccttcca 2280
ccccggggtt ctggcgtgaa acagactttg aattttgacc ttctcaagtt ggcgggagac 2340
gtggagtcca acccagggcc catgattcca gcagtggtct tgctcttact ccttttggtt 2400
gaacaagcag cggccctggg agagcctcag ctctgctata tcctggatgc catcctgttt 2460
ctgtatggaa ttgtcctcac cctcctctac tgtcgactga agatccaagt gcgaaaggca 2520
gctataacca gctatgagaa atcagatggt gtttacacgg gcctgagcac caggaaccag 2580
gagacttacg agactctgaa gcatgagaaa ccaccacagt ga 2622

<210> 228

<211> 2709
<212> DNA
<213> Artificial sequence

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

<220>
<223> csm6

<400> 228
atggctcctg ccatggaatc ccctactcta ctgtgtgtag ccttactgtt cttcgctcca 60
gatggcgtgt tagcagaggt gcagttgcag cagtcagggc cagagttgat taagcccgga 120
gcctccgtca agatgtcctg caaggccagc gggtacactt tcaccagcta cgtcatgcat 180
tgggtgaagc agaagccagg ccaggggctt gagtggattg ggtacatcaa cccctacaac 240
gacgggacca aatacaacga gaaattcaag ggcaaagcca cactcacctc cgataagtcc 300
tcctctaccg cctacatgga gctcagctcc ctgacctccg aggatagcgc tgtgtattac 360
tgcgcaaggg gcacatacta ctatggctct agggtgttcg actactgggg gcagggcact 420
actctcacag tgagctcagg cggaggaggc agtggcggag ggggaagtgg gggcggcggc 480
agcgatattg tcatgaccca ggcagccccc agtatccctg tgactccagg cgagagcgtg 540
agcatcagct gccggtccag caagagcctg ctgaacagta acggaaacac atacctctac 600
tggtttctgc agaggcccgg ccagagccct cagctgctga tttaccgcat gtcaaatctt 660
gcctctgggg tgcccgatag atttagtggg agcggatccg gcacagcttt tacattgcgg 720
atctccagag tcgaggccga agacgtgggg gtctattact gtatgcaaca cctggaatac 780
ccctttacct tcggagccgg cacaaagctg gagctgaagc gggctgacac cacaaccccc 840
gctccaaggc cccctacccc cgcaccaact attgcctccc agccactctc actgcggcct 900
gaggcctgtc ggcccgctgc tggaggcgca gtgcatacaa ggggcctcga tttcgcctgc 960
gatttttta tcccattgtt ggtggtgatt ctgtttgctg tggacacagg attatttatc 1020
tcaactcagc agcaggtcac atttctcttg aagattaaga gaaccaggaa aggcttcaga 1080
cttctgaacc cacatcctaa gccaaacccc aaaaacaaca gagccgaggg cagaggcagc 1140
ctgctgacct gcggcgacgt ggaggagaac ccaggcccca tggacacaga aagtaatagg 1200
agagcaaatc ttgctctccc acaggagcct tccagtgtgc ctgcatttga agtcttggaa 1260
atatctcccc aggaagtatc ttcaggcaga ctattgaagt cggcctcatc cccaccactg 1320
catacatggc tgacagtttt gaaaaaagag caggagttcc tgggggtaac acaaattctg 1380
actgctatga tatgcctttg ttttggaaca gttgtctgct ctgtacttga tatttcacac 1440
attgagggag acatttttc atcatttaaa gcaggttatc cattctgggg agccatattt 1500
ttttctattt ctggaatgtt gtcaattata tctgaaagga gaaatgcaac atatctggtg 1560
agaggaagcc tgggagcaaa cactgccagc agcatagctg ggggaacggg aattaccatc 1620
ctgatcatca acctgaagaa gagcttggcc tatatccaca tccacagttg ccagaaattt 1680
tttgagacca agtgctttat ggcttccttt tccactgaaa ttgtagtgat gatgctgttt 1740
ctcaccattc tgggacttgg tagtgctgtg tcactcacaa tctgtggagc tggggaagaa 1800
ctcaaaggaa acaaggttcc agaggatcgt gtttatgaag aattaaacat atattcagct 1860
acttacagtg agttggaaga cccaggggaa atgtctcctc ccattgattt aaaacggggc 1920
cggaagaagc tcctctacat ttttaagcag cctttcatgc ggccagtgca gacaacccaa 1980
gaggaggatg ggtgttcctg cagattccct gaggaagagg aaggcgggtg cgagctgggt 2040
tctggcgtga aacagacttt gaattttgac cttctcaagt tggcgggaga cgtggagtcc 2100
aacccagggc ccatgattcc agcagtggtc ttgctcttac tccttttggt tgaacaagca 2160
gcggccctgg gagagcctca gctctgctat atcctggatg ccatcctgtt tctgtatgga 2220
attgtcctca ccctcctcta ctgtcgactg aagatccaag tgcgaaaggc agctataacc 2280
agctatgaga aatcagatgg tgtttacacg ggcctgagca ccaggaacca ggagacttac 2340

gagactctga agcatgagaa accaccacag agagtgaagt tctccaggag cgcagatgcc 2400
cccgcctatc aacagggcca gaaccagctc tacaacgagc ttaacctcgg gaggcgcgaa 2460
gaatacgacg tgttggataa gagaaggggg cgggaccccg agatgggagg aaagccccgg 2520
aggaagaacc ctcaggaggg cctgtacaac gagctgcaga aggataagat ggccgaggcc 2580
tactcagaga tcgggatgaa gggggagcgg cgccgcggga aggggcacga tgggctctac 2640
caggggctga gcacagccac aaaggacaca tacgacgcct tgcacatgca ggcccttcca 2700
ccccggtga 2709

<210> 229

<211> 2373
<212> DNA
<213> Artificial sequence

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

<220>
<223> csm7

<400> 229
atggctcctg ccatggaatc ccctactcta ctgtgtgtag ccttactgtt cttcgctcca 60
gatggcgtgt tagcagaggt gcagttgcag cagtcagggc cagagttgat taagcccgga 120
gcctccgtca agatgtcctg caaggccagc gggtacactt tcaccagcta cgtcatgcat 180
tgggtgaagc agaagccagg ccaggggctt gagtggattg ggtacatcaa cccctacaac 240
gacgggacca aatacaacga gaaattcaag ggcaaagcca cactcacctc cgataagtcc 300
tcctctaccg cctacatgga gctcagctcc ctgacctccg aggatagcgc tgtgtattac 360
tgcgcaaggg gcacatacta ctatggctct agggtgttcg actactgggg gcagggcact 420
actctcacag tgagctcagg cggaggaggc agtggcggag ggggaagtgg gggcggcggc 480
agcgatattg tcatgaccca ggcagccccc agtatccctg tgactccagg cgagagcgtg 540
agcatcagct gccggtccag caagagcctg ctgaacagta acggaaacac atacctctac 600
tggtttctgc agaggcccgg ccagagccct cagctgctga tttaccgcat gtcaaatctt 660
gcctctgggg tgcccgatag atttagtggg agcggatccg gcacagcttt tacattgcgg 720
atctccagag tcgaggccga agacgtgggg gtctattact gtatgcaaca cctggaatac 780
ccctttacct tcggagccgg cacaaagctg gagctgaagc gggctgacac cacaaccccc 840
gctccaaggc cccctacccc cgcaccaact attgcctccc agccactctc actgcggcct 900
gaggcctgtc ggcccgctgc tggaggcgca gtgcatacaa ggggcctcga tttcgcctgc 960
gatttttta tcccattgtt ggtggtgatt ctgtttgctg tggacacagg attatttatc 1020
tcaactcagc agcaggtcac atttctcttg aagattaaga gaaccaggaa aggcttcaga 1080
cttctgaacc cacatcctaa gccaaacccc aaaaacaaca aacggggccg gaagaagctc 1140
ctctacattt ttaagcagcc tttcatgcgg ccagtgcaga caacccaaga ggaggatggg 1200
tgttcctgca gattccctga ggaagaggaa ggcgggtgcg agctgagagc cgagggcaga 1260
ggcagcctgc tgacctgcgg cgacgtggag gagaacccag gccccatgga cacagaaagt 1320
aataggagag caaatcttgc tctcccacag gagccttcca gtgtgcctgc atttgaagtc 1380
ttggaaatat ctccccagga agtatcttca ggcagactat tgaagtcggc ctcatcccca 1440
ccactgcata catggctgac agttttgaaa aaagagcagg agttcctggg ggtaacacaa 1500
attctgactg ctatgatatg cctttgtttt ggaacagttg tctgctctgt acttgatatt 1560
tcacacattg agggagacat tttttcatca tttaaagcag gttatccatt ctggggagcc 1620
atatttttt ctatttctgg aatgttgtca attatatctg aaaggagaaa tgcaacatat 1680
ctggtgagag gaagcctggg agcaaacact gccagcagca tagctggggg aacgggaatt 1740
accatcctga tcatcaacct gaagaagagc ttggcctata tccacatcca cagttgccag 1800
aaatttttg agaccaagtg ctttatggct tccttttcca ctgaaattgt agtgatgatg 1860
ctgtttctca ccattctggg acttggtagt gctgtgtcac tcacaatctg tggagctggg 1920
gaagaactca aaggaaacaa ggttccagag gatcgtgttt atgaagaatt aaacatatat 1980
tcagctactt acagtgagtt ggaagaccca ggggaaatgt ctcctcccat tgatttaggt 2040
tctggcgtga aacagacttt gaattttgac cttctcaagt tggcgggaga cgtggagtcc 2100
aacccagggc ccatgattcc agcagtggtc ttgctcttac tccttttggt tgaacaagca 2160
gcggccctgg gagagcctca gctctgctat atcctggatg ccatcctgtt tctgtatgga 2220
attgtcctca ccctcctcta ctgtcgactg aagatccaag tgcgaaaggc agctataacc 2280
agctatgaga aatcagatgg tgtttacacg ggcctgagca ccaggaacca ggagacttac 2340
gagactctga agcatgagaa accaccacag tga 2373

<210> 230

<211> 2622

<212> DNA
<213> Artificial sequence

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

<220>
<223> csm8

<400> 230
atggctcctg ccatggaatc ccctactcta ctgtgtgtag ccttactgtt cttcgctcca 60
gatggcgtgt tagcagaggt gcagttgcag cagtcagggc cagagttgat taagcccgga 120
gcctccgtca agatgtcctg caaggccagc gggtacactt tcaccagcta cgtcatgcat 180
tgggtgaagc agaagccagg ccaggggctt gagtggattg ggtacatcaa cccctacaac 240
gacgggacca aatacaacga gaaattcaag ggcaaagcca cactcacctc cgataagtcc 300
tcctctaccg cctacatgga gctcagctcc ctgacctccg aggatagcgc tgtgtattac 360
tgcgcaaggg gcacatacta ctatggctct agggtgttcg actactgggg gcagggcact 420
actctcacag tgagctcagg cggaggaggc agtggcggag ggggaagtgg gggcggcggc 480
agcgatattg tcatgaccca ggcagcccct agtatccctg tgactccagg cgagagcgtg 540
agcatcagct gccggtccag caagagcctg ctgaacagta acggaaacac atacctctac 600
tggtttctgc agaggcccgg ccagagccct cagctgctga tttaccgcat gtcaaatctt 660
gcctctgggg tgcccgatag atttagtggg agcggatccg gcacagcttt tacattgcgg 720
atctccagag tcgaggccga agacgtgggg gtctattact gtatgcaaca cctggaatac 780
ccctttacct tcggagccgg cacaaagctg gagctgaagc gggctgacac cacaccccc 840
gctccaaggc cccctacccc cgcaccaact attgcctccc agccactctc actgcggcct 900
gaggcctgtc ggcccgctgc tggaggcgca gtgcatacaa ggggcctcga tttcgcctgc 960
gatttttta tcccattgtt ggtggtgatt ctgtttgctg tggacacagg attatttatc 1020
tcaactcagc agcaggtcac atttctcttg aagattaaga gaaccaggaa aggcttcaga 1080
cttctgaacc cacatcctaa gccaaacccc aaaaacaaca aacggggccg gaagaagctc 1140
ctctacattt ttaagcagcc tttcatgcgg ccagtgcaga caacccaaga ggaggatggg 1200
tgttcctgca gattccctga ggaagaggaa ggcgggtgcg agctgagagc cgagggcaga 1260
ggcagcctgc tgacctgcgg cgacgtggag gagaacccag gccccatgga cacagaaagt 1320
aataggagag caaatcttgc tctcccacag gagccttcca gtgtgcctgc atttgaagtc 1380
ttggaaatat ctccccagga agtatcttca ggcagactat tgaagtcggc ctcatcccca 1440
ccactgcata catggctgac agttttgaaa aaagagcagg agttcctggg ggtaacacaa 1500
attctgactg ctatgatatg cctttgtttt ggaacagttg tctgctctgt acttgatatt 1560
tcacacattg agggagacat tttttcatca tttaaagcag gttatccatt ctggggagcc 1620
atatttttt ctatttctgg aatgttgtca attatatctg aaaggagaaa tgcaacatat 1680
ctggtgagag gaagcctggg agcaaacact gccagcagca tagctggggg aacgggaatt 1740
accatcctga tcatcaacct gaagaagagc ttggcctata tccacatcca cagttgccag 1800
aaatttttg agaccaagtg ctttatggct tccttttcca ctgaaattgt agtgatgatg 1860
ctgtttctca ccattctggg acttggtagt gctgtgtcac tcacaatctg tggagctggg 1920
gaagaactca aaggaaacaa ggttccagag agagtgaagt tctccaggag cgcagatgcc 1980
cccgcctatc aacagggcca gaaccagctc tacaacgagc ttaacctcgg gaggcgcgaa 2040
gaatacgacg tgttggataa gagaaggggg cgggaccccg agatgggagg aaagccccgg 2100
aggaagaacc ctcaggaggg cctgtacaac gagctgcaga aggataagat ggccgaggcc 2160
tactcagaga tcgggatgaa gggggagcgg cgccgcggga aggggcacga tgggctctac 2220
caggggctga gcacagccac aaaggacaca tacgacgcct tgcacatgca ggcccttcca 2280
ccccggggtt ctggcgtgaa acagactttg aattttgacc ttctcaagtt ggcgggagac 2340
gtggagtcca acccagggcc catgattcca gcagtggtct tgctcttact ccttttggtt 2400
gaacaagcag cggccctggg agagcctcag ctctgctata tcctggatgc catcctgttt 2460
ctgtatggaa ttgtcctcac cctcctctac tgtcgactga agatccaagt gcgaaaggca 2520
gctataacca gctatgagaa atcagatggt gtttacacgg gcctgagcac caggaaccag 2580
gagacttacg agactctgaa gcatgagaaa ccaccacagt ga 2622

<210> 231

<211> 2709
<212> DNA
<213> Artificial sequence

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

<220>

<223> csm9

<400> 231
atggctcctg ccatggaatc ccctactcta ctgtgtgtag ccttactgtt cttcgctcca 60
gatggcgtgt tagcagaggt gcagttgcag cagtcagggc cagagttgat taagcccgga 120
gcctccgtca agatgtcctg caaggccagc gggtacactt tcaccagcta cgtcatgcat 180
tgggtgaagc agaagccagg ccaggggctt gagtggattg ggtacatcaa cccctacaac 240
gacgggacca aatacaacga gaaattcaag ggcaaagcca cactcacctc cgataagtcc 300
tcctctaccg cctacatgga gctcagctcc ctgacctccg aggatagcgc tgtgtattac 360
tgcgcaaggg gcacatacta ctatggctct agggtgttcg actactgggg gcagggcact 420
actctcacag tgagctcagg cggaggaggc agtggcggag ggggaagtgg gggcggcggc 480
agcgatattg tcatgaccca ggcagccccc agtatccctg tgactccagg cgagagcgtg 540
agcatcagct gccggtccag caagagcctg ctgaacagta acggaaacac atacctctac 600
tggtttctgc agaggcccgg ccagagccct cagctgctga tttaccgcat gtcaaatctt 660
gcctctgggg tgcccgatag atttagtggg agcggatccg gcacagcttt tacattgcgg 720
atctccagag tcgaggccga agacgtgggg gtctattact gtatgcaaca cctggaatac 780
ccctttacct tcggagccgg cacaaagctg gagctgaagc gggctgacac cacaaccccc 840
gctccaaggc cccctacccc cgcaccaact attgcctccc agccactctc actgcggcct 900
gaggcctgtc ggcccgctgc tggaggcgca gtgcatacaa ggggcctcga tttcgcctgc 960
gatttttta tcccattgtt ggtggtgatt ctgtttgctg tggacacagg attatttatc 1020
tcaactcagc agcaggtcac atttctcttg aagattaaga gaaccaggaa aggcttcaga 1080
cttctgaacc cacatcctaa gccaaacccc aaaaacaaca aacggggccg gaagaagctc 1140
ctctacattt ttaagcagcc tttcatgcgg ccagtgcaga caacccaaga ggaggatggg 1200
tgttcctgca gattccctga ggaagaggaa ggcgggtgcg agctgagagc cgagggcaga 1260
ggcagcctgc tgacctgcgg cgacgtggag gagaacccag gccccatgga cacagaaagt 1320
aataggagag caaatcttgc tctcccacag gagccttcca gtgtgcctgc atttgaagtc 1380
ttggaaatat ctccccagga agtatcttca ggcagactat tgaagtcggc ctcatcccca 1440
ccactgcata catggctgac agttttgaaa aaagagcagg agttcctggg ggtaacacaa 1500
attctgactg ctatgatatg cctttgtttt ggaacagttg tctgctctgt acttgatatt 1560
tcacacattg agggagacat tttttcatca tttaaagcag gttatccatt ctggggagcc 1620
atatttttt ctatttctgg aatgttgtca attatatctg aaaggagaaa tgcaacatat 1680
ctggtgagag gaagcctggg agcaaacact gccagcagca tagctggggg aacgggaatt 1740
accatcctga tcatcaacct gaagaagagc ttggcctata tccacatcca cagttgccag 1800
aaatttttg agaccaagtg ctttatggct tccttttcca ctgaaattgt agtgatgatg 1860
ctgtttctca ccattctggg acttggtagt gctgtgtcac tcacaatctg tggagctggg 1920
gaagaactca aaggaaacaa ggttccagag gatcgtgttt atgaagaatt aaacatatat 1980
tcagctactt acagtgagtt ggaagaccca ggggaaatgt ctcctcccat tgatttaggt 2040
tctggcgtga aacagacttt gaattttgac cttctcaagt tggcgggaga cgtggagtcc 2100
aacccagggc ccatgattcc agcagtggtc ttgctcttac tccttttggt tgaacaagca 2160
gcggccctgg gagagcctca gctctgctat atcctggatg ccatcctgtt tctgtatgga 2220
attgtcctca ccctcctcta ctgtcgactg aagatccaag tgcgaaaggc agctataacc 2280
agctatgaga aatcagatgg tgtttacacg ggcctgagca ccaggaacca ggagacttac 2340
gagactctga agcatgagaa accaccacag agagtgaagt tctccaggag cgcagatgcc 2400
cccgcctatc aacagggcca gaaccagctc tacaacgagc ttaacctcgg gaggcgcgaa 2460
gaatacgacg tgttggataa gagaaggggg cgggaccccg agatgggagg aaagccccgg 2520
aggaagaacc ctcaggaggg cctgtacaac gagctgcaga aggataagat ggccgaggcc 2580
tactcagaga tcgggatgaa gggggagcgg cgccgcggga aggggcacga tgggctctac 2640
caggggctga gcacagccac aaaggacaca tacgacgcct tgcacatgca ggcccttcca 2700
ccccggtga 2709

<210> 232

<211> 2670
<212> DNA
<213> Artificial sequence

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

<220>
<223> csm10

<400> 232
atggctcctg ccatggaatc ccctactcta ctgtgtgtag ccttactgtt cttcgctcca 60
gatggcgtgt tagcagaggt gcagttgcag cagtcagggc cagagttgat taagcccgga 120
gcctccgtca agatgtcctg caaggccagc gggtacactt tcaccagcta cgtcatgcat 180

```
tgggtgaagc agaagccagg ccaggggctt gagtggattg ggtacatcaa cccctacaac    240
gacgggacca aatacaacga gaaattcaag ggcaaagcca cactcacctc cgataagtcc    300
tcctctaccg cctacatgga gctcagctcc ctgacctccg aggatagcgc tgtgtattac    360
tgcgcaaggg gcacatacta ctatggctct agggtgttcg actactgggg gcagggcact    420
actctcacag tgagctcagg cggaggaggc agtggcggag ggggaagtgg gggcggcggc    480
agcgatattg tcatgaccca ggcagccccc agtatccctg tgactccagg cgagagcgtg    540
agcatcagct gccggtccag caagagcctg ctgaacagta acggaaacac atacctctac    600
tggtttctgc agaggcccgg ccagagcccc cagctgctga tttaccgcat gtcaaatctt    660
gcctctgggg tgcccgatag atttagtggg agcggatccg gcacagcttt tacattgcgg    720
atctccagag tcgaggccga agacgtgggg gtctattact gtatgcaaca cctggaatac    780
ccctttacct tcggagccgg cacaaagctg gagctgaagc gggctgacac cacaaccccc    840
gctccaaggc cccctacccc cgcaccaact attgcctccc agccactctc actgcggcct    900
gaggcctgtc ggcccgctgc tggaggcgca gtgcatacaa ggggcctcga tttcgcctgc    960
gatttttta tcccattgtt ggtggtgatt ctgtttgctg tggacacagg attatttatc   1020
tcaactcagc agcaggtcac atttctcttg aagattaaga gaaccaggaa aggcttcaga   1080
cttctgaacc cacatcctaa gccaaacccc aaaaacaacc ggagcaagcg gagcagaggc   1140
ggccacagcg actacatgaa catgaccccc agacggcctg gccccacccg gaagcactac   1200
cagccctacg ccccacccag ggactttgcc gcctaccggt ccagagccga gggcagaggc   1260
agcctgctga cctgcggcga cgtggaggag aacccaggcc ccatggacac agaaagtaat   1320
aggagagcaa atcttgctct cccacaggag ccttccagtg tgcctgcatt tgaagtcttg   1380
gaaatatctc cccaggaagt atcttcaggc agactattga agtcggcctc atccccacca   1440
ctgcatacat ggctgacagt tttgaaaaaa gagcaggagt tcctgggggt aacacaaatt   1500
ctgactgcta tgatatgcct ttgttttgga acagttgtct gctctgtact tgatatttca   1560
cacattgagg gagacatttt ttcatcattt aaagcaggtt atccattctg gggagccata   1620
ttttttttcta tttctggaat gttgtcaatt atatctgaaa ggagaaatgc aacatatctg   1680
gtgagaggaa gcctgggagc aaacactgcc agcagcatag ctgggggaac gggaattacc   1740
atcctgatca tcaacctgaa gaagagcttg gcctatatcc acatccacag ttgccagaaa   1800
ttttttgaga ccaagtgctt tatggcttcc ttttccactg aaattgtagt gatgatgctg   1860
tttctcacca ttctgggact tggtagtgct gtgtcactca caatctgtgg agctggggaa   1920
gaactcaaag gaaacaaggt tccagagaaa cggggccgga agaagctcct ctacattttt   1980
aagcagcctt tcatgcggcc agtgcagaca acccaagagg aggatgggtg ttcctgcaga   2040
ttccctgagg aagaggaagg cgggtgcgag ctgggttctg gcgtgaaaca gactttgaat   2100
tttgaccttc tcaagttggc gggagacgtg gagtccaacc cagggcccat gattccagca   2160
gtggtcttgc tcttactcct tttggttgaa caagcagcgg ccctgggaga gcctcagctc   2220
tgctatatcc tggatgccat cctgtttctg tatggaattg tcctcaccct cctctactgt   2280
cgactgaaga tccaagtgcg aaaggcagct ataaccagct atgagaaatc aagagtgaag   2340
ttctccagga gcgcagatgc ccccgcctat caacagggcc agaaccagct ctacaacgag   2400
cttaacctcg ggaggcgcga agaatacgac gtgttggata agagaagggg gcgggacccc   2460
gagatgggag gaaagccccg gaggaagaac cctcaggagg gcctgtacaa cgagctgcag   2520
aaggataaga tggccgaggc ctactcagag atcgggatga agggggagcg gcgccgcggg   2580
aaggggcacg atgggctcta ccaggggctg agcacagcca caaaggacac atacgacgcc   2640
ttgcacatgc aggcccttcc accccggtga                                    2670
```