SEQUENCE LISTING

<110> GALETTO ROMAN
GROSSE STEPHANIE
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MANNIOUI CECILE
POIROT LAURENT
SMITH JULIANNE
SCHARENBERG ANDREW

<120> Methods for engineering allogeneic and immunosuppressive resistant T cell for immunotherapy

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<170> PatentIn version 3.5

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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
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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
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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
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Leu Glu
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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
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```
            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
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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
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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

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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
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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
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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
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Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala
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Leu Glu
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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

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            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
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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

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Leu Glu
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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

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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
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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
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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

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            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
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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

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<213> Artificialsequence

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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
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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> Artificialsequence

<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
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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> Artificialsequence

<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

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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
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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> Artificialsequence

<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
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<210> 17

<211> 530
<212> PRT
<213> Artificialsequence

<220>
<223> Repeat-GRex5T3-L1

<400> 17

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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
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```
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>  Artificialsequence

<220>
<223>  Repeat-GRex5T3-R1

<400>  18
Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
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```
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
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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> Artificialsequence

<220>
<223> GRex2-L TALEN

<400> 19
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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
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gtggccatcg ccagcaatgg cggtggcaag caggcgctgg agacggtcca gcggctgttg 660
ccggtgctgt gccaggccca cggcttgacc ccccagcagg tggtggccat cgccagcaat 720
ggcggtggca agcaggcgct ggagacggtc cagcggctgt tgccggtgct gtgccaggcc 780
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caggtggtgg ccatcgccag caatattggt ggcaagcagg cgctggagac ggtgcaggcg 960
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atcgccagca atattggtgg caagcaggcg ctggagacgg tgcaggcgct gttgccggtg 1380
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cacggcttga ccccggagca ggtggtggcc atcgccagcc acgatggcgg caagcaggcg 1860
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aggtacgtgg aggagaacca gaccaggaac aagcacatca accccaacga gtggtggaag 2580
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tccgtggagg agctcctgat cggcggcgag atgatcaagg ccggcaccct gaccctggag 2760
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<211> 2832
<212> DNA
<213> Artificialsequence

<220>
<223> GRex2-R TALEN

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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
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cacggcttga ccccccagca ggtggtggcc atcgccagca atggcggtgg caagcaggcg 960
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agcaatggcg gcggcaggcc ggcgctggag agcattgttg cccagttatc tcgccctgat 2100
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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
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<211> 2832
<212> DNA
<213> Artificialsequence

<220>
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cagcaacagg agaagatcaa accgaaggtt cgttcgacag tggcgcagca ccacgaggca 180
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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
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cacggcttga ccccggagca ggtggtggcc atcgccagcc acgatggcgg caagcaggcg 960
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ctgttgccgg tgctgtgcca ggcccacggc ttgaccccgg agcaggtggt ggccatcgcc 1140
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tgcaacggcg ccgtgctgtc cgtggaggag ctcctgatcg gcggcgagat gatcaaggcc 2760
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<210> 31

<211> 60
<212> DNA
<213> Artificialsequence

<220>
<223> Forward primer GR exon 2

<220>
<221> misc_feature
<222> (31); (32); (33); (34); (35); (36); (37); (38); (39); (40)
<223> n is a or c or t or g

<400> 31
ccatctcatc cctgcgtgtc tccgactcag nnnnnnnnnn ggttcattta acaagctgcc 60

<210> 32

<211> 60
<212> DNA
<213> Artificialsequence

<220>
<223> Forward primer GR exon 3

<220>
<221> misc_feature
<222> (31); (32); (33); (34); (35); (36); (37); (38); (39); (40)
<223> n is a or c or t or g

<400> 32
ccatctcatc cctgcgtgtc tccgactcag nnnnnnnnnn gcattctgac tatgaagtga 60

<210> 33

<211> 69
<212> DNA
<213> Artificialsequence

<220>
<223> Forward primer GR exon 5

<220>
<221> misc_feature
<222> (31); (32); (33); (34); (35); (36); (37); (38); (39); (40)
<223> n is 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> Artificialsequence

<220>
<223> Reverse primer GR exon 2

<400> 34
cctatcccct gtgtgccttg gcagtctcag agccagtgag ggtgaagacg 50

<210> 35

<211> 50
<212> DNA
<213> Artificialsequence

<220>
<223> Reverse primer GR exon 3

<400> 35
cctatcccct gtgtgccttg gcagtctcag gggctttgca tataatggaa 50

<210> 36

<211> 59
<212> DNA
<213> Artificialsequence

<220>
<223> Reverse primer GR exon 5

<400> 36
cctatcccct gtgtgccttg gcagtctcag ctgactctcc ccttcatagt ccccagaac 59

<210> 37

<211> 49
<212> DNA
<213> Artificialsequence

<220>
<223> TRAC_T01

<400> 37
ttgtcccaca gatatccaga accctgaccc tgccgtgtac cagctgaga 49

<210> 38

<211> 49
<212> DNA
<213> Artificialsequence

<220>
<223> TRBC_T01

<400> 38
tgtgtttgag ccatcagaag cagagatctc ccacacccaa aaggccaca 49

<210> 39

<211> 50
<212> DNA
<213> Artificialsequence

<220>
<223> TRBC_T02

<400> 39
ttcccacccg aggtcgctgt gtttgagcca tcagaagcag agatctccca 50

<210> 40

<211> 49
<212> DNA

<213> Artificialsequence

<220>
<223> CD52_T02

<400> 40
ttcctcctac tcaccatcag cctcctggtt atggtacagg taagagcaa 49

<210> 41

<211> 530
<212> PRT
<213> Artificialsequence

<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> Artificialsequence

<220>
<223> Repeat TRAC_T01-R

<400> 42

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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> Artificialsequence

<220>
<223> Repeat TRBC_T01-L

<400> 43

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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> Artificialsequence

<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>  Artificialsequence

<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
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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
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Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
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Pro Gln Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Arg Pro Ala
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Leu Glu
530

<210> 46

<211> 530
<212> PRT
<213> Artificialsequence

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<223> Repeat TRBC_T02-R

<400> 46
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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

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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
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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
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<211> 530
<212> PRT
<213> Artificialsequence

<220>
<223> Repeat CD52_T02-L

<400> 47
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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

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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
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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
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<211> 530
<212> PRT
<213> Artificialsequence

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<223> Repeat CD52_T02-R

<400> 48

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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
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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
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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

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<211> 2814
<212> DNA
<213> Artificialsequence

<220>
<223> TRAC_T01-L TALEN

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<211> 2832
<212> DNA
<213> Artificialsequence

<220>
<223> TRAC_T01-R TALEN

<400> 50

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<211> 2814
<212> DNA
<213> Artificialsequence

<220>
<223> TRBC_T01-L TALEN

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<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
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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
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caggcccacg gcttgacccc ggagcaggtg gtggccatcg ccagcaatat tggtggcaag 1260
caggcgctgg agacggtgca ggcgctgttg ccggtgctgt gccaggccca cggcttgacc 1320
ccggagcagg tggtggccat cgccagccac gatggcggca agcaggcgct ggagacggtc 1380
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ctgtgccagg cccacggctt gacccccag caggtggtgg ccatcgccag caatggcggt 1560
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ccggtgctgt gccaggccca cggcttgacc ccggagcagg tggtggccat cgccagcaat 1860
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agccgttccc agctggtgaa gtccgagctg gaggagaaga aatccgagtt gaggcacaag 2280
ctgaagtacg tgccccacga gtacatcgag ctgatcgaga tcgcccggaa cagcacccag 2340
gaccgtatcc tggagatgaa ggtgatggag ttcttcatga aggtgtacgg ctacaggggc 2400
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tgcaacggcg ccgtgctgtc cgtggaggag ctcctgatcg gcggcgagat gatcaaggcc 2760
ggcaccctga ccctggagga ggtgaggagg aagttcaaca acggcgagat caacttcgcg 2820
gccgactgat aa 2832

<210> 57

<211> 49
<212> DNA
<213> Artificialsequence

<220>
<223> TRAC_T02

<400> 57
tttagaaagt tcctgtgatg tcaagctggt cgagaaaagc tttgaaaca 49

<210> 58

<211> 49
<212> DNA
<213> Artificialsequence

<220>
<223> TRAC_T03

<400> 58
tccagtgaca agtctgtctg cctattcacc gattttgatt ctcaaacaa 49

<210> 59

<211> 49
<212> DNA
<213> Artificialsequence

<220>
<223> TRAC_T04

<400> 59
tatatcacag acaaaactgt gctagacatg aggtctatgg acttcaaga 49

<210> 60

<211> 49
<212> DNA
<213> Artificialsequence

<220>
<223> TRAC_T05

<400> 60
tgaggtctat ggacttcaag agcaacagtg ctgtggcctg gagcaacaa 49

<210> 61

<211> 47
<212> DNA
<213> Artificial sequence

<220>
<223> CD52_T01

<400> 61
ttcctcttcc tcctaccacc atcagcctcc tttacctgta ccataac 47

<210> 62

<211> 43
<212> DNA
<213> Artificial sequence

<220>
<223> CD52_T04

<400> 62
ttcctcctac tcaccacagc ctcctggtct tacctgtacc ata 43

<210> 63

<211> 43
<212> DNA
<213> Artificial sequence

<220>
<223> CD52_T05

<400> 63
tcctactcac catcagctcc tggttatttg ctcttacctg tac 43

<210> 64

<211> 47
<212> DNA
<213> Artificial sequence

<220>
<223> CD52_T06

<400> 64
ttatcccact tctcctctac agatacaaac tttttgtcct gagagtc 47

<210> 65

<211> 47
<212> DNA
<213> Artificial sequence

<220>
<223> CD52_T07

<400> 65
tggactctca ggacaaacga caccagccaa atgctgaggg gctgctg 47

<210> 66

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

<220>
<223> Forward primer CD52

<220>
<221> misc_feature
<222> (31); (32); (33); (34); (35); (36); (37); (38); (39); (40)
<223> n is 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> Forward primer TRAC

<220>
<221> misc_feature
<222> (31); (32); (33); (34); (35); (36); (37); (38); (39); (40)
<223> n is 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> Forward primer TRBC1

<220>
<221> misc_feature

<222> (31); (32); (33); (34); (35); (36); (37); (38); (39); (40)
<223> n is 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> Forward primer TRBC2

<220>
<221> misc_feature
<222> (31); (32); (33); (34); (35); (36); (37); (38); (39); (40)
<223> n is 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> Reverse primer GR CD52

<400> 70
cctatcccct gtgtgccttg gcagtctcag cctgttggag tccatctgct g 51

<210> 71

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

<220>
<223> Reverse primer GR TRAC

<400> 71
cctatcccct gtgtgccttg gcagtctcag cctcatgtct agcacagttt 50

<210> 72

<211> 51
<212> DNA
<213> Artificial sequence

<220>
<223> Reverse primer GR TRBC1-2

<400> 72
cctatcccct gtgtgccttg gcagtctcag accagctcag ctccacgtgg t 51

<210> 73

<211> 495
<212> PRT
<213> Artificial sequence

<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 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
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<210> 74

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

<220>
<223> CTLA4_T01

<400> 74
tggccctgca ctctcctgtt ttttcttctc ttcatccctg tcttctgca 49

<210> 75

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

<220>
<223> CTLA4_T03

<400> 75
ttttccatgc tagcaatgca cgtggcccag cctgctgtgg tactggcca 49

<210> 76

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

<220>
<223> CTLA4_T04

<400> 76
tccatgctag caatgcacgt ggcccagcct gctgtggtac tggccagca 49

<210> 77

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

<220>
<223> PDCD1_T01

<400> 77
ttctccccag ccctgctcgt ggtgaccgaa ggggacaacg ccaccttca 49

<210> 78

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

<220>
<223> PDCD1_T03

<400> 78
tacctctgtg gggccatctc cctggccccc aaggcgcaga tcaaagaga 49

<210> 79

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

<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> Repeat CTLA4_T01-R

<400> 80

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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>  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> 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> 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
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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> 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> 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> RepeatPDCD1_T01-R

<400> 86

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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> 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> 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> CTLA4_T01-L TALEN

<400> 89
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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
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gggggcaaac aggcattgga aaccgtccag cgcctgcttc cagtgctctg ccaggcacac 1920
ggactgacac ccgaacaggt ggtggccatt gcatcccatg atgggggcaa gcaggccctg 1980
gagaccgtgc agagactcct gccagtgttg tgccaagctc acggcctcac ccctcagcaa 2040
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ttatctcgcc ctgatccggc gttggccgcg ttgaccaacg accacctcgt cgccttggcc 2160
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ggccacttca agggcaacta caaggcccag ctgaccaggc tgaaccacat caccaactgc 2700
aacggcgccg tgctgtccgt ggaggagctc ctgatcggcg gcgagatgat caaggccggc 2760
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gactgataa 2829

<210> 99

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

<220>
<223> Forward primer CTLA4_T01

<220>
<221> misc_feature
<222> (31); (32); (33); (34); (35); (36); (37); (38); (39); (40)
<223> n is 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> Forward primer CTLA4_T03/T04

<220>
<221> misc_feature
<222> (31); (32); (33); (34); (35); (36); (37); (38); (39); (40)
<223> n is 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> Forward primer PDCD1_T01

<220>
<221> misc_feature
<222> (31); (32); (33); (34); (35); (36); (37); (38); (39); (40)
<223> n is 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> Forward primer PDCD1_T03

<220>
<221> misc_feature
<222> (31); (32); (33); (34); (35); (36); (37); (38); (39); (40)
<223> n is 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> Reverse primer CTLA4_T01

<400> 103
cctatcccct gtgtgccttg gcagtctcag tggaatacag agccagccaa 50

<210> 104

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

<220>
<223> Reverse primer CTLA4_T03/04

<400> 104
cctatcccct gtgtgccttg gcagtctcag ggtgcccgtg cagatggaat 50

<210> 105

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

<220>
<223> Reverse primer PDCD1_T01

<400> 105
cctatcccct gtgtgccttg gcagtctcag ggctctgcag tggaggccag 50

<210> 106

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

<220>
<223> Reverse primer PDCD1_T03

<400> 106
cctatcccct gtgtgccttg gcagtctcag ggacaacgcc accttcacct 50

<210> 107

<211> 281
<212> PRT
<213> Artificialsequence

<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 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> Artificialsequence

<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

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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
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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> Artificialsequence

<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> Artificialsequence

<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>  Artificialsequence

<220>
<223>  pTalpha-Delta78

<400>  111
Met Ala Gly Thr Trp Leu Leu Leu Leu Leu Ala Leu Gly Cys Pro Ala
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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> Artificialsequence

<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> Artificialsequence

<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> Artificialsequence

<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> Artificialsequence

<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
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340

<210> 116

<211> 311
<212> PRT
<213> Artificialsequence

<220>
<223> pTalpha-FL-CD8

<400> 116

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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 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
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<210> 117

<211> 325
<212> PRT
<213> Artificialsequence

<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
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<210> 118

<211> 296
<212> PRT
<213> Artificialsequence

<220>
<223> pTalpha-Delta48-CD28

<400> 118

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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
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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
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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> Artificialsequence

<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> Artificialsequence

<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

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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
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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> Artificialsequence

<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> Artificialsequence

<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> Artificialsequence

<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> Artificialsequence

<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

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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
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Pro Gly Arg Lys Pro Gly Ser Pro Val
225 230

<210> 125

<211> 848
<212> PRT
<213> Artificialsequence

<220>
<223> Multi-chain CAR

<400> 125
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 Arg Ala Glu Gly Arg Gly Ser Leu Leu Thr Cys
    370                 375                 380

Gly Asp Val Glu Glu Asn Pro Gly Pro Met Asp Thr Glu Ser Asn Arg
385                 390                 395                 400

Arg Ala Asn Leu Ala Leu Pro Gln Glu Pro Ser Ser Val Pro Ala Phe
                405                 410                 415

Glu Val Leu Glu Ile Ser Pro Gln Glu Val Ser Ser Gly Arg Leu Leu
            420                 425                 430

Lys Ser Ala Ser Ser Pro Pro Leu His Thr Trp Leu Thr Val Leu Lys
        435                 440                 445

Lys Glu Gln Glu Phe Leu Gly Val Thr Gln Ile Leu Thr Ala Met Ile
    450                 455                 460

Cys Leu Cys Phe Gly Thr Val Val Cys Ser Val Leu Asp Ile Ser His
465                 470                 475                 480

Ile Glu Gly Asp Ile Phe Ser Ser Phe Lys Ala Gly Tyr Pro Phe Trp
                485                 490                 495

Gly Ala Ile Phe Phe Ser Ile Ser Gly Met Leu Ser Ile Ile Ser Glu
            500                 505                 510

Arg Arg Asn Ala Thr Tyr Leu Val Arg Gly Ser Leu Gly Ala Asn Thr
        515                 520                 525

Ala Ser Ser Ile Ala Gly Gly Thr Gly Ile Thr Ile Leu Ile Ile Asn
    530                 535                 540

Leu Lys Lys Ser Leu Ala Tyr Ile His Ile His Ser Cys Gln Lys Phe
545                 550                 555                 560

Phe Glu Thr Lys Cys Phe Met Ala Ser Phe Ser Thr Glu Ile Val Val
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565 570 575

Met Met Leu Phe Leu Thr Ile Leu Gly Leu Gly Ser Ala Val Ser Leu
580 585 590

Thr Ile Cys Gly Ala Gly Glu Glu Leu Lys Gly Asn Lys Val Pro Glu
595 600 605

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
610 615 620

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
625 630 635 640

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Gly Ser Gly Val Lys Gln
645 650 655

Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn
660 665 670

Pro Gly Pro Met Ile Pro Ala Val Val Leu Leu Leu Leu Leu Leu Val
675 680 685

Glu Gln Ala Ala Ala Leu Gly Glu Pro Gln Leu Cys Tyr Ile Leu Asp
690 695 700

Ala Ile Leu Phe Leu Tyr Gly Ile Val Leu Thr Leu Leu Tyr Cys Arg
705 710 715 720

Leu Lys Ile Gln Val Arg Lys Ala Ala Ile Thr Ser Tyr Glu Lys Ser
725 730 735

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
740 745 750

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
755 760 765

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys

```
    770                 775                 780

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
785                 790                 795                 800

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
                805                 810                 815

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
            820                 825                 830

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
        835                 840                 845
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<210> 126

<211> 2547
<212> DNA
<213> Artificialsequence

<220>
<223> Multi-chain CAR

<400> 126

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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
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atctccagag tcgaggccga agacgtgggg gtctattact gtatgcaaca cctggaatac    780
ccctttacct tcggagccgg cacaaagctg gagctgaagc gggctgacac cacaaccccc    840
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gaggcctgtc ggcccgctgc tggaggcgca gtgcatacaa ggggcctcga tttcgcctgc    960
gatttttta tcccattgtt ggtggtgatt ctgtttgctg tggacacagg attatttatc   1020
tcaactcagc agcaggtcac atttctcttg aagattaaga gaaccaggaa aggcttcaga   1080
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agagcaaatc ttgctctccc acaggagcct tccagtgtgc ctgcatttga agtcttggaa   1260
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agaggaagcc tgggagcaaa cactgccagc agcatagctg ggggaacggg aattaccatc   1620
ctgatcatca acctgaagaa gagcttggcc tatatccaca tccacagttg ccagaaattt   1680
tttgagacca agtgctttat ggcttccttt tccactgaaa ttgtagtgat gatgctgttt   1740
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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
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gataagatgg ccgaggccta ctcagagatc gggatgaagg gggagcggcg ccgcgggaag   2460
gggcacgatg ggctctacca ggggctgagc acagccacaa aggacacata cgacgccttg   2520
cacatgcagg cccttccacc ccggtga                                       2547
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