SEQUENCE LISTING

<110> UCL Business PLC

<120> T Cell

<130> P103294PCT2

<150> GB 1410934.2
<151> 2014-06-19

<160> 53

<170> PatentIn version 3.5

<210> 1
<211> 1129
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric antigen receptor (CAR)

<400> 1

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Met Ser Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15

His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu
            20                  25                  30

Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln
        35                  40                  45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
    50                  55                  60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65                  70                  75                  80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
                85                  90                  95

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

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

Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser Gly Pro Gly
145                 150                 155                 160

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

```
Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg
            180                 185                 190

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr
        195                 200                 205

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

Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr
225                 230                 235                 240

Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala
                245                 250                 255

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser 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 Phe Trp
305                 310                 315                 320

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
                325                 330                 335

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Arg Val Lys Phe Ser Arg
            340                 345                 350

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
        355                 360                 365

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
    370                 375                 380

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
385                 390                 395                 400

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
                405                 410                 415

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
            420                 425                 430

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
        435                 440                 445
```

```
Ala Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Glu Gly Arg Gly
    450                 455                 460

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala
465                 470                 475                 480

Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr Asp Ala
                485                 490                 495

Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
            500                 505                 510

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp Ile Tyr
        515                 520                 525

Phe Asn Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
    530                 535                 540

Leu Ile Tyr Asp Thr Asn Arg Leu Ala Asp Gly Val Pro Ser Arg Phe
545                 550                 555                 560

Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser Ser Leu
                565                 570                 575

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Lys Asn Tyr
            580                 585                 590

Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ser Gly
        595                 600                 605

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    610                 615                 620

Gly Gly Ser Arg Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
625                 630                 635                 640

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
                645                 650                 655

Thr Leu Ser Asn Tyr Gly Met His Trp Ile Arg Gln Ala Pro Gly Lys
            660                 665                 670

Gly Leu Glu Trp Val Ser Ser Ile Ser Leu Asn Gly Gly Ser Thr Tyr
        675                 680                 685

Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
    690                 695                 700

Lys Ser Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
705                 710                 715                 720
```

```
Ala Val Tyr Tyr Cys Ala Ala Gln Asp Ala Tyr Thr Gly Gly Tyr Phe
                725                 730                 735

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Met Asp Pro
            740                 745                 750

Ala Glu Pro Lys Ser Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro
        755                 760                 765

Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
    770                 775                 780

Lys Asp Thr Leu Met Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val
785                 790                 795                 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
                805                 810                 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
            820                 825                 830

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
        835                 840                 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
    850                 855                 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
865                 870                 875                 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
                885                 890                 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
            900                 905                 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
        915                 920                 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
    930                 935                 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
945                 950                 955                 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
                965                 970                 975

Ser Leu Ser Leu Ser Pro Gly Lys Lys Asp Pro Lys Phe Trp Val Leu
            980                 985                 990
```

```
Val Val Val Gly Gly Val Leu Ala  Cys Tyr Ser Leu Leu  Val Thr Val
        995                 1000                1005


Ala Phe  Ile Ile Phe Trp Val  Arg Ser Arg Val Lys  Phe Ser Arg
    1010                1015                1020


Ser Ala  Asp Ala Pro Ala Tyr  Gln Gln Gly Gln Asn  Gln Leu Tyr
    1025                1030                1035


Asn Glu  Leu Asn Leu Gly Arg  Arg Glu Glu Tyr Asp  Val Leu Asp
    1040                1045                1050


Lys Arg  Arg Gly Arg Asp Pro  Glu Met Gly Gly Lys  Pro Arg Arg
    1055                1060                1065


Lys Asn  Pro Gln Glu Gly Leu  Tyr Asn Glu Leu Gln  Lys Asp Lys
    1070                1075                1080


Met Ala  Glu Ala Tyr Ser Glu  Ile Gly Met Lys Gly  Glu Arg Arg
    1085                1090                1095


Arg Gly  Lys Gly His Asp Gly  Leu Tyr Gln Gly Leu  Ser Thr Ala
    1100                1105                1110


Thr Lys  Asp Thr Tyr Asp Ala  Leu His Met Gln Ala  Leu Pro Pro
    1115                1120                1125


Arg
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<210> 2
<211> 1350
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric antigen receptor (CAR)

<400> 2

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Met Ser Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15


His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu
            20                  25                  30


Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln
        35                  40                  45


Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
    50                  55                  60


Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
```

65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
85 90 95

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

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

Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser Gly Pro Gly
145 150 155 160

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

Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg
180 185 190

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr
195 200 205

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

Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr
225 230 235 240

Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala
245 250 255

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser 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 Phe Trp
305 310 315 320

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
325 330 335

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Arg Val Lys Phe Ser Arg

```
            340                 345                 350

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
        355                 360                 365

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
    370                 375                 380

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
385                 390                 395                 400

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
                405                 410                 415

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
            420                 425                 430

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
        435                 440                 445

Ala Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Glu Gly Arg Gly
    450                 455                 460

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala
465                 470                 475                 480

Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr Asp Ala
                485                 490                 495

Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
            500                 505                 510

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp Ile Tyr
        515                 520                 525

Phe Asn Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
    530                 535                 540

Leu Ile Tyr Asp Thr Asn Arg Leu Ala Asp Gly Val Pro Ser Arg Phe
545                 550                 555                 560

Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser Ser Leu
                565                 570                 575

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Lys Asn Tyr
            580                 585                 590

Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ser Gly
        595                 600                 605

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
```

610 615 620

Gly Gly Ser Arg Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
625 630 635 640

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
645 650 655

Thr Leu Ser Asn Tyr Gly Met His Trp Ile Arg Gln Ala Pro Gly Lys
660 665 670

Gly Leu Glu Trp Val Ser Ser Ile Ser Leu Asn Gly Gly Ser Thr Tyr
675 680 685

Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
690 695 700

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

Ala Val Tyr Tyr Cys Ala Ala Gln Asp Ala Tyr Thr Gly Gly Tyr Phe
725 730 735

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Met Asp Pro
740 745 750

Ala Glu Pro Lys Ser Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro
755 760 765

Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
770 775 780

Lys Asp Thr Leu Met Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val
785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
820 825 830

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys Lys Asp Pro Lys Ala Val Phe Gly
980 985 990

Cys Ile Phe Gly Ala Leu Val Ile Val Thr Val Gly Gly Phe Ile Phe
995 1000 1005

Trp Arg Lys Lys Arg Lys Asp Ala Lys Asn Asn Glu Val Ser Phe
1010 1015 1020

Ser Gln Ile Lys Pro Lys Lys Ser Lys Leu Ile Arg Val Glu Asn
1025 1030 1035

Phe Glu Ala Tyr Phe Lys Lys Gln Gln Ala Asp Ser Asn Cys Gly
1040 1045 1050

Phe Ala Glu Glu Tyr Glu Asp Leu Lys Leu Val Gly Ile Ser Gln
1055 1060 1065

Pro Lys Tyr Ala Ala Glu Leu Ala Glu Asn Arg Gly Lys Asn Arg
1070 1075 1080

Tyr Asn Asn Val Leu Pro Tyr Asp Ile Ser Arg Val Lys Leu Ser
1085 1090 1095

Val Gln Thr His Ser Thr Asp Asp Tyr Ile Asn Ala Asn Tyr Met
1100 1105 1110

Pro Gly Tyr His Ser Lys Lys Asp Phe Ile Ala Thr Gln Gly Pro
1115 1120 1125

Leu Pro Asn Thr Leu Lys Asp Phe Trp Arg Met Val Trp Glu Lys
1130 1135 1140

Asn Val Tyr Ala Ile Ile Met Leu Thr Lys Cys Val Glu Gln Gly

1145 1150 1155

Arg Thr Lys Cys Glu Glu Tyr Trp Pro Ser Lys Gln Ala Gln Asp
1160 1165 1170

Tyr Gly Asp Ile Thr Val Ala Met Thr Ser Glu Ile Val Leu Pro
1175 1180 1185

Glu Trp Thr Ile Arg Asp Phe Thr Val Lys Asn Ile Gln Thr Ser
1190 1195 1200

Glu Ser His Pro Leu Arg Gln Phe His Phe Thr Ser Trp Pro Asp
1205 1210 1215

His Gly Val Pro Asp Thr Thr Asp Leu Leu Ile Asn Phe Arg Tyr
1220 1225 1230

Leu Val Arg Asp Tyr Met Lys Gln Ser Pro Pro Glu Ser Pro Ile
1235 1240 1245

Leu Val His Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Phe Ile
1250 1255 1260

Ala Ile Asp Arg Leu Ile Tyr Gln Ile Glu Asn Glu Asn Thr Val
1265 1270 1275

Asp Val Tyr Gly Ile Val Tyr Asp Leu Arg Met His Arg Pro Leu
1280 1285 1290

Met Val Gln Thr Glu Asp Gln Tyr Val Phe Leu Asn Gln Cys Val
1295 1300 1305

Leu Asp Ile Val Arg Ser Gln Lys Asp Ser Lys Val Asp Leu Ile
1310 1315 1320

Tyr Gln Asn Thr Thr Ala Met Thr Ile Tyr Glu Asn Leu Ala Pro
1325 1330 1335

Val Thr Thr Phe Gly Lys Thr Asn Gly Tyr Ile Ala
1340 1345 1350

<210> 3
<211> 1717
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric antigen receptor (CAR)

<400> 3

Met Ser Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu
            20                  25                  30

Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln
        35                  40                  45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
    50                  55                  60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65                  70                  75                  80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
                85                  90                  95

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

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

Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser Gly Pro Gly
145                 150                 155                 160

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

Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg
            180                 185                 190

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr
        195                 200                 205

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

Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr
225                 230                 235                 240

Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala
                245                 250                 255

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser 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 Phe Trp
305                 310                 315                 320

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
                325                 330                 335

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Arg Val Lys Phe Ser Arg
            340                 345                 350

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
        355                 360                 365

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
    370                 375                 380

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
385                 390                 395                 400

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
                405                 410                 415

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
            420                 425                 430

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
        435                 440                 445

Ala Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Glu Gly Arg Gly
    450                 455                 460

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala
465                 470                 475                 480

Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr Asp Ala
                485                 490                 495

Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
            500                 505                 510

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp Ile Tyr
        515                 520                 525

Phe Asn Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
    530                 535                 540

Leu Ile Tyr Asp Thr Asn Arg Leu Ala Asp Gly Val Pro Ser Arg Phe
545                 550                 555                 560
```

```
Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser Ser Leu
                565                 570                 575

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Lys Asn Tyr
            580                 585                 590

Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ser Gly
        595                 600                 605

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    610                 615                 620

Gly Gly Ser Arg Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
625                 630                 635                 640

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
                645                 650                 655

Thr Leu Ser Asn Tyr Gly Met His Trp Ile Arg Gln Ala Pro Gly Lys
            660                 665                 670

Gly Leu Glu Trp Val Ser Ser Ile Ser Leu Asn Gly Gly Ser Thr Tyr
        675                 680                 685

Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
    690                 695                 700

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

Ala Val Tyr Tyr Cys Ala Ala Gln Asp Ala Tyr Thr Gly Gly Tyr Phe
                725                 730                 735

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Met Asp Pro
            740                 745                 750

Ala Glu Pro Lys Ser Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro
        755                 760                 765

Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
    770                 775                 780

Lys Asp Thr Leu Met Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val
785                 790                 795                 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
                805                 810                 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
            820                 825                 830
```

```
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
        835                 840                 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
    850                 855                 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
865                 870                 875                 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
                885                 890                 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
            900                 905                 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
        915                 920                 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
    930                 935                 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
945                 950                 955                 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
                965                 970                 975

Ser Leu Ser Leu Ser Pro Gly Lys Lys Asp Pro Lys Ala Leu Ile Ala
            980                 985                 990

Phe Leu Ala Phe Leu Ile Ile Val  Thr Ser Ile Ala Leu  Leu Val Val
        995                 1000                1005

Leu Tyr  Lys Ile Tyr Asp Leu  His Lys Lys Arg Ser  Cys Asn Leu
    1010                1015                1020

Asp Glu  Gln Gln Glu Leu Val  Glu Arg Asp Asp Glu  Lys Gln Leu
    1025                1030                1035

Met Asn  Val Glu Pro Ile His  Ala Asp Ile Leu Leu  Glu Thr Tyr
    1040                1045                1050

Lys Arg  Lys Ile Ala Asp Glu  Gly Arg Leu Phe Leu  Ala Glu Phe
    1055                1060                1065

Gln Ser  Ile Pro Arg Val Phe  Ser Lys Phe Pro Ile  Lys Glu Ala
    1070                1075                1080

Arg Lys  Pro Phe Asn Gln Asn  Lys Asn Arg Tyr Val  Asp Ile Leu
    1085                1090                1095
```

```
Pro Tyr  Asp Tyr Asn Arg Val  Glu Leu Ser Glu Ile  Asn Gly Asp
    1100                1105                1110

Ala Gly  Ser Asn Tyr Ile Asn  Ala Ser Tyr Ile Asp  Gly Phe Lys
    1115                1120                1125

Glu Pro  Arg Lys Tyr Ile Ala  Ala Gln Gly Pro Arg  Asp Glu Thr
    1130                1135                1140

Val Asp  Asp Phe Trp Arg Met  Ile Trp Glu Gln Lys  Ala Thr Val
    1145                1150                1155

Ile Val  Met Val Thr Arg Cys  Glu Glu Gly Asn Arg  Asn Lys Cys
    1160                1165                1170

Ala Glu  Tyr Trp Pro Ser Met  Glu Glu Gly Thr Arg  Ala Phe Gly
    1175                1180                1185

Asp Val  Val Val Lys Ile Asn  Gln His Lys Arg Cys  Pro Asp Tyr
    1190                1195                1200

Ile Ile  Gln Lys Leu Asn Ile  Val Asn Lys Lys Glu  Lys Ala Thr
    1205                1210                1215

Gly Arg  Glu Val Thr His Ile  Gln Phe Thr Ser Trp  Pro Asp His
    1220                1225                1230

Gly Val  Pro Glu Asp Pro His  Leu Leu Leu Lys Leu  Arg Arg Arg
    1235                1240                1245

Val Asn  Ala Phe Ser Asn Phe  Phe Ser Gly Pro Ile  Val Val His
    1250                1255                1260

Cys Ser  Ala Gly Val Gly Arg  Thr Gly Thr Tyr Ile  Gly Ile Asp
    1265                1270                1275

Ala Met  Leu Glu Gly Leu Glu  Ala Glu Asn Lys Val  Asp Val Tyr
    1280                1285                1290

Gly Tyr  Val Val Lys Leu Arg  Arg Gln Arg Cys Leu  Met Val Gln
    1295                1300                1305

Val Glu  Ala Gln Tyr Ile Leu  Ile His Gln Ala Leu  Val Glu Tyr
    1310                1315                1320

Asn Gln  Phe Gly Glu Thr Glu  Val Asn Leu Ser Glu  Leu His Pro
    1325                1330                1335

Tyr Leu  His Asn Met Lys Lys  Arg Asp Pro Pro Ser  Glu Pro Ser
    1340                1345                1350
```

```
Pro Leu  Glu Ala Glu Phe Gln  Arg Leu Pro Ser Tyr  Arg Ser Trp
    1355                 1360                 1365

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

Arg Asn  Ser Asn Val Ile Pro  Tyr Asp Tyr Asn Arg  Val Pro Leu
    1385                 1390                 1395

Lys His  Glu Leu Glu Met Ser  Lys Glu Ser Glu His  Asp Ser Asp
    1400                 1405                 1410

Glu Ser  Ser Asp Asp Asp Ser  Asp Ser Glu Glu Pro  Ser Lys Tyr
    1415                 1420                 1425

Ile Asn  Ala Ser Phe Ile Met  Ser Tyr Trp Lys Pro  Glu Val Met
    1430                 1435                 1440

Ile Ala  Ala Gln Gly Pro Leu  Lys Glu Thr Ile Gly  Asp Phe Trp
    1445                 1450                 1455

Gln Met  Ile Phe Gln Arg Lys  Val Lys Val Ile Val  Met Leu Thr
    1460                 1465                 1470

Glu Leu  Lys His Gly Asp Gln  Glu Ile Cys Ala Gln  Tyr Trp Gly
    1475                 1480                 1485

Glu Gly  Lys Gln Thr Tyr Gly  Asp Ile Glu Val Asp  Leu Lys Asp
    1490                 1495                 1500

Thr Asp  Lys Ser Ser Thr Tyr  Thr Leu Arg Val Phe  Glu Leu Arg
    1505                 1510                 1515

His Ser  Lys Arg Lys Asp Ser  Arg Thr Val Tyr Gln  Tyr Gln Tyr
    1520                 1525                 1530

Thr Asn  Trp Ser Val Glu Gln  Leu Pro Ala Glu Pro  Lys Glu Leu
    1535                 1540                 1545

Ile Ser  Met Ile Gln Val Val  Lys Gln Lys Leu Pro  Gln Lys Asn
    1550                 1555                 1560

Ser Ser  Glu Gly Asn Lys His  His Lys Ser Thr Pro  Leu Leu Ile
    1565                 1570                 1575

His Cys  Arg Asp Gly Ser Gln  Gln Thr Gly Ile Phe  Cys Ala Leu
    1580                 1585                 1590

Leu Asn  Leu Leu Glu Ser Ala  Glu Thr Glu Glu Val  Val Asp Ile
    1595                 1600                 1605
```

```
Phe Gln  Val Val Lys Ala Leu  Arg Lys Ala Arg Pro  Gly Met Val
    1610                 1615                 1620

Ser Thr  Phe Glu Gln Tyr Gln  Phe Leu Tyr Asp Val  Ile Ala Ser
    1625                 1630                 1635

Thr Tyr  Pro Ala Gln Asn Gly  Gln Val Lys Lys Asn  Asn His Gln
    1640                 1645                 1650

Glu Asp  Lys Ile Glu Phe Asp  Asn Glu Val Asp Lys  Val Lys Gln
    1655                 1660                 1665

Asp Ala  Asn Cys Val Asn Pro  Leu Gly Ala Pro Glu  Lys Leu Pro
    1670                 1675                 1680

Glu Ala  Lys Glu Gln Ala Glu  Gly Ser Glu Pro Thr  Ser Gly Thr
    1685                 1690                 1695

Glu Gly  Pro Glu His Ser Val  Asn Gly Pro Ala Ser  Pro Ala Leu
    1700                 1705                 1710

Asn Gln  Gly Ser
    1715
```

<210> 4
<211> 1114
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric antigen receptor (CAR)

<400> 4

```
Met Ser Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15

His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu
            20                  25                  30

Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln
        35                  40                  45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
    50                  55                  60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65                  70                  75                  80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
                85                  90                  95

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
```

100 105 110

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

Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser Gly Pro Gly
145 150 155 160

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

Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg
180 185 190

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr
195 200 205

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

Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr
225 230 235 240

Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala
245 250 255

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser 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 Phe Trp
305 310 315 320

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
325 330 335

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Arg Val Lys Phe Ser Arg
340 345 350

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
355 360 365

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg

370 375 380

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
385 390 395 400

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
405 410 415

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
420 425 430

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
435 440 445

Ala Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Glu Gly Arg Gly
450 455 460

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala
465 470 475 480

Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr Asp Ala
485 490 495

Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
500 505 510

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp Ile Tyr
515 520 525

Phe Asn Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
530 535 540

Leu Ile Tyr Asp Thr Asn Arg Leu Ala Asp Gly Val Pro Ser Arg Phe
545 550 555 560

Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser Ser Leu
565 570 575

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Lys Asn Tyr
580 585 590

Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ser Gly
595 600 605

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
610 615 620

Gly Gly Ser Arg Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
625 630 635 640

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe

645 650 655

Thr Leu Ser Asn Tyr Gly Met His Trp Ile Arg Gln Ala Pro Gly Lys
660 665 670

Gly Leu Glu Trp Val Ser Ser Ile Ser Leu Asn Gly Gly Ser Thr Tyr
675 680 685

Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
690 695 700

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

Ala Val Tyr Tyr Cys Ala Ala Gln Asp Ala Tyr Thr Gly Gly Tyr Phe
725 730 735

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Met Asp Pro
740 745 750

Ala Thr Thr Thr Lys Pro Val Leu Arg Thr Pro Ser Pro Val His Pro
755 760 765

Thr Gly Thr Ser Gln Pro Gln Arg Pro Glu Asp Cys Arg Pro Arg Gly
770 775 780

Ser Val Lys Gly Thr Gly Leu Asp Phe Ala Cys Asp Ile Tyr Trp Ala
785 790 795 800

Pro Leu Ala Gly Ile Cys Val Ala Leu Leu Leu Ser Leu Ile Ile Thr
805 810 815

Leu Ile Cys Tyr His Arg Ser Arg Lys Arg Val Cys Lys Ser Gly Gly
820 825 830

Gly Ser Phe Trp Glu Glu Phe Glu Ser Leu Gln Lys Gln Glu Val Lys
835 840 845

Asn Leu His Gln Arg Leu Glu Gly Gln Arg Pro Glu Asn Lys Gly Lys
850 855 860

Asn Arg Tyr Lys Asn Ile Leu Pro Phe Asp His Ser Arg Val Ile Leu
865 870 875 880

Gln Gly Arg Asp Ser Asn Ile Pro Gly Ser Asp Tyr Ile Asn Ala Asn
885 890 895

Tyr Ile Lys Asn Gln Leu Leu Gly Pro Asp Glu Asn Ala Lys Thr Tyr
900 905 910

Ile Ala Ser Gln Gly Cys Leu Glu Ala Thr Val Asn Asp Phe Trp Gln

915 920 925

Met Ala Trp Gln Glu Asn Ser Arg Val Ile Val Met Thr Thr Arg Glu
930 935 940

Val Glu Lys Gly Arg Asn Lys Cys Val Pro Tyr Trp Pro Glu Val Gly
945 950 955 960

Met Gln Arg Ala Tyr Gly Pro Tyr Ser Val Thr Asn Cys Gly Glu His
965 970 975

Asp Thr Thr Glu Tyr Lys Leu Arg Thr Leu Gln Val Ser Pro Leu Asp
980 985 990

Asn Gly Asp Leu Ile Arg Glu Ile Trp His Tyr Gln Tyr Leu Ser Trp
995 1000 1005

Pro Asp His Gly Val Pro Ser Glu Pro Gly Gly Val Leu Ser Phe
1010 1015 1020

Leu Asp Gln Ile Asn Gln Arg Gln Glu Ser Leu Pro His Ala Gly
1025 1030 1035

Pro Ile Ile Val His Cys Ser Ala Gly Ile Gly Arg Thr Gly Thr
1040 1045 1050

Ile Ile Val Ile Asp Met Leu Met Glu Asn Ile Ser Thr Lys Gly
1055 1060 1065

Leu Asp Cys Asp Ile Asp Ile Gln Lys Thr Ile Gln Met Val Arg
1070 1075 1080

Ala Gln Arg Ser Gly Met Val Gln Thr Glu Ala Gln Tyr Lys Phe
1085 1090 1095

Ile Tyr Val Ala Ile Ala Gln Phe Ile Glu Thr Thr Lys Lys Lys
1100 1105 1110

Leu

<210> 5
<211> 918
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric antigen receptor (CAR)

<400> 5

Met Ser Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

```
His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu
            20                  25                  30

Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln
        35                  40                  45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
    50                  55                  60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65                  70                  75                  80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
                85                  90                  95

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

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

Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser Gly Pro Gly
145                 150                 155                 160

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

Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg
            180                 185                 190

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr
        195                 200                 205

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

Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr
225                 230                 235                 240

Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala
                245                 250                 255

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser 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 Phe Trp
305                 310                 315                 320

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
                325                 330                 335

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Arg Val Lys Phe Ser Arg
            340                 345                 350

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
        355                 360                 365

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
    370                 375                 380

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
385                 390                 395                 400

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
                405                 410                 415

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
            420                 425                 430

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
        435                 440                 445

Ala Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Glu Gly Arg Gly
    450                 455                 460

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala
465                 470                 475                 480

Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr Asp Ala
                485                 490                 495

Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
            500                 505                 510

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp Ile Tyr
        515                 520                 525

Phe Asn Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
    530                 535                 540

Leu Ile Tyr Asp Thr Asn Arg Leu Ala Asp Gly Val Pro Ser Arg Phe
545                 550                 555                 560
```

```
Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser Ser Leu
                565                 570                 575

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Lys Asn Tyr
            580                 585                 590

Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ser Gly
        595                 600                 605

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    610                 615                 620

Gly Gly Ser Arg Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
625                 630                 635                 640

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
                645                 650                 655

Thr Leu Ser Asn Tyr Gly Met His Trp Ile Arg Gln Ala Pro Gly Lys
            660                 665                 670

Gly Leu Glu Trp Val Ser Ser Ile Ser Leu Asn Gly Gly Ser Thr Tyr
        675                 680                 685

Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
    690                 695                 700

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

Ala Val Tyr Tyr Cys Ala Ala Gln Asp Ala Tyr Thr Gly Gly Tyr Phe
                725                 730                 735

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Met Asp Pro
            740                 745                 750

Ala Thr Thr Thr Lys Pro Val Leu Arg Thr Pro Ser Pro Val His Pro
        755                 760                 765

Thr Gly Thr Ser Gln Pro Gln Arg Pro Glu Asp Cys Arg Pro Arg Gly
    770                 775                 780

Ser Val Lys Gly Thr Gly Leu Asp Phe Ala Cys Asp Ile Leu Ile Gly
785                 790                 795                 800

Val Ser Val Val Phe Leu Phe Cys Leu Leu Leu Leu Val Leu Phe Cys
                805                 810                 815

Leu His Arg Gln Asn Gln Ile Lys Gln Gly Pro Pro Arg Ser Lys Asp
            820                 825                 830
```

```
Glu Glu Gln Lys Pro Gln Gln Arg Pro Asp Leu Ala Val Asp Val Leu
        835                 840                 845

Glu Arg Thr Ala Asp Lys Ala Thr Val Asn Gly Leu Pro Glu Lys Asp
    850                 855                 860

Arg Glu Thr Asp Thr Ser Ala Leu Ala Ala Gly Ser Ser Gln Glu Val
865                 870                 875                 880

Thr Tyr Ala Gln Leu Asp His Trp Ala Leu Thr Gln Arg Thr Ala Arg
                885                 890                 895

Ala Val Ser Pro Gln Ser Thr Lys Pro Met Ala Glu Ser Ile Thr Tyr
            900                 905                 910

Ala Ala Val Ala Arg His
        915
```

<210> 6
<211> 1363
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric antigen receptor (CAR)

<400> 6

```
Met Ser Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15

His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu
            20                  25                  30

Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln
        35                  40                  45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
    50                  55                  60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65                  70                  75                  80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
                85                  90                  95

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

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

Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
```

130 135 140

Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser Gly Pro Gly
145 150 155 160

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

Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg
180 185 190

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr
195 200 205

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

Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr
225 230 235 240

Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala
245 250 255

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser 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 Phe Trp
305 310 315 320

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
325 330 335

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Arg Val Lys Phe Ser Arg
340 345 350

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
355 360 365

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
370 375 380

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
385 390 395 400

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala

405 410 415

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
420 425 430

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
435 440 445

Ala Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Glu Gly Arg Gly
450 455 460

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala
465 470 475 480

Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr Asp Ala
485 490 495

Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
500 505 510

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp Ile Tyr
515 520 525

Phe Asn Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
530 535 540

Leu Ile Tyr Asp Thr Asn Arg Leu Ala Asp Gly Val Pro Ser Arg Phe
545 550 555 560

Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser Ser Leu
565 570 575

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Lys Asn Tyr
580 585 590

Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ser Gly
595 600 605

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
610 615 620

Gly Gly Ser Arg Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
625 630 635 640

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
645 650 655

Thr Leu Ser Asn Tyr Gly Met His Trp Ile Arg Gln Ala Pro Gly Lys
660 665 670

Gly Leu Glu Trp Val Ser Ser Ile Ser Leu Asn Gly Gly Ser Thr Tyr

675 680 685

Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
690 695 700

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

Ala Val Tyr Tyr Cys Ala Ala Gln Asp Ala Tyr Thr Gly Gly Tyr Phe
725 730 735

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Met Asp Pro
740 745 750

Ala Thr Thr Thr Lys Pro Val Leu Arg Thr Pro Ser Pro Val His Pro
755 760 765

Thr Gly Thr Ser Gln Pro Gln Arg Pro Glu Asp Cys Arg Pro Arg Gly
770 775 780

Ser Val Lys Gly Thr Gly Leu Asp Phe Ala Cys Asp Ile Leu Ile Gly
785 790 795 800

Val Ser Val Val Phe Leu Phe Cys Leu Leu Leu Leu Val Leu Phe Cys
805 810 815

Leu His Arg Gln Asn Gln Ile Lys Gln Gly Pro Pro Arg Ser Lys Asp
820 825 830

Glu Glu Gln Lys Pro Gln Gln Arg Pro Asp Leu Ala Val Asp Val Leu
835 840 845

Glu Arg Thr Ala Asp Lys Ala Thr Val Asn Gly Leu Pro Glu Lys Asp
850 855 860

Arg Glu Thr Asp Thr Ser Ala Leu Ala Ala Gly Ser Ser Gln Glu Val
865 870 875 880

Thr Tyr Ala Gln Leu Asp His Trp Ala Leu Thr Gln Arg Thr Ala Arg
885 890 895

Ala Val Ser Pro Gln Ser Thr Lys Pro Met Ala Glu Ser Ile Thr Tyr
900 905 910

Ala Ala Val Ala Arg His Arg Ala Glu Gly Arg Gly Ser Leu Leu Thr
915 920 925

Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Trp Tyr His Gly His Met
930 935 940

Ser Gly Gly Gln Ala Glu Thr Leu Leu Gln Ala Lys Gly Glu Pro Trp

945 950 955 960

Thr Phe Leu Val Arg Glu Ser Leu Ser Gln Pro Gly Asp Phe Val Leu
965 970 975

Ser Val Leu Ser Asp Gln Pro Lys Ala Gly Pro Gly Ser Pro Leu Arg
980 985 990

Val Thr His Ile Lys Val Met Cys Glu Gly Gly Arg Tyr Thr Val Gly
995 1000 1005

Gly Leu Glu Thr Phe Asp Ser Leu Thr Asp Leu Val Glu His Phe
1010 1015 1020

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

Arg Gln Pro Tyr Ser Gly Gly Gly Gly Ser Phe Glu Ala Tyr Phe
1040 1045 1050

Lys Lys Gln Gln Ala Asp Ser Asn Cys Gly Phe Ala Glu Glu Tyr
1055 1060 1065

Glu Asp Leu Lys Leu Val Gly Ile Ser Gln Pro Lys Tyr Ala Ala
1070 1075 1080

Glu Leu Ala Glu Asn Arg Gly Lys Asn Arg Tyr Asn Asn Val Leu
1085 1090 1095

Pro Tyr Asp Ile Ser Arg Val Lys Leu Ser Val Gln Thr His Ser
1100 1105 1110

Thr Asp Asp Tyr Ile Asn Ala Asn Tyr Met Pro Gly Tyr His Ser
1115 1120 1125

Lys Lys Asp Phe Ile Ala Thr Gln Gly Pro Leu Pro Asn Thr Leu
1130 1135 1140

Lys Asp Phe Trp Arg Met Val Trp Glu Lys Asn Val Tyr Ala Ile
1145 1150 1155

Ile Met Leu Thr Lys Cys Val Glu Gln Gly Arg Thr Lys Cys Glu
1160 1165 1170

Glu Tyr Trp Pro Ser Lys Gln Ala Gln Asp Tyr Gly Asp Ile Thr
1175 1180 1185

Val Ala Met Thr Ser Glu Ile Val Leu Pro Glu Trp Thr Ile Arg
1190 1195 1200

Asp Phe Thr Val Lys Asn Ile Gln Thr Ser Glu Ser His Pro Leu

1205 1210 1215

Arg Gln Phe His Phe Thr Ser Trp Pro Asp His Gly Val Pro Asp
1220 1225 1230

Thr Thr Asp Leu Leu Ile Asn Phe Arg Tyr Leu Val Arg Asp Tyr
1235 1240 1245

Met Lys Gln Ser Pro Pro Glu Ser Pro Ile Leu Val His Cys Ser
1250 1255 1260

Ala Gly Val Gly Arg Thr Gly Thr Phe Ile Ala Ile Asp Arg Leu
1265 1270 1275

Ile Tyr Gln Ile Glu Asn Glu Asn Thr Val Asp Val Tyr Gly Ile
1280 1285 1290

Val Tyr Asp Leu Arg Met His Arg Pro Leu Met Val Gln Thr Glu
1295 1300 1305

Asp Gln Tyr Val Phe Leu Asn Gln Cys Val Leu Asp Ile Val Arg
1310 1315 1320

Ser Gln Lys Asp Ser Lys Val Asp Leu Ile Tyr Gln Asn Thr Thr
1325 1330 1335

Ala Met Thr Ile Tyr Glu Asn Leu Ala Pro Val Thr Thr Phe Gly
1340 1345 1350

Lys Thr Asn Gly Tyr Ile Ala Ser Gly Ser
1355 1360

<210> 7
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Signal peptide

<400> 7

Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
1 5 10 15

Asp His Ala Asp Gly
20

<210> 8
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Signal peptide

<400> 8

Met Ser Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro
20

<210> 9
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Signal peptide

<400> 9

Met Ala Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr
1 5 10 15

Asp Ala Arg Cys
20

<210> 10
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer (hinge-CH2CH3 of human IgG1)

<400> 10

Ala Glu Pro Lys Ser Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys Lys Asp
225 230

<210> 11
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer (human CD8 stalk)

<400> 11

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1 5 10 15

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
20 25 30

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
35 40 45

<210> 12
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer (human IgG1 hinge)

<400> 12

Ala Glu Pro Lys Ser Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

Lys Asp Pro Lys

20

<210> 13
<211> 185
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer (CD2 ectodomain)

<400> 13

Lys Glu Ile Thr Asn Ala Leu Glu Thr Trp Gly Ala Leu Gly Gln Asp
1 5 10 15

Ile Asn Leu Asp Ile Pro Ser Phe Gln Met Ser Asp Asp Ile Asp Asp
20 25 30

Ile Lys Trp Glu Lys Thr Ser Asp Lys Lys Lys Ile Ala Gln Phe Arg
35 40 45

Lys Glu Lys Glu Thr Phe Lys Glu Lys Asp Thr Tyr Lys Leu Phe Lys
50 55 60

Asn Gly Thr Leu Lys Ile Lys His Leu Lys Thr Asp Asp Gln Asp Ile
65 70 75 80

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

Ile Phe Asp Leu Lys Ile Gln Glu Arg Val Ser Lys Pro Lys Ile Ser
100 105 110

Trp Thr Cys Ile Asn Thr Thr Leu Thr Cys Glu Val Met Asn Gly Thr
115 120 125

Asp Pro Glu Leu Asn Leu Tyr Gln Asp Gly Lys His Leu Lys Leu Ser
130 135 140

Gln Arg Val Ile Thr His Lys Trp Thr Thr Ser Leu Ser Ala Lys Phe
145 150 155 160

Lys Cys Thr Ala Gly Asn Lys Val Ser Lys Glu Ser Ser Val Glu Pro
165 170 175

Val Ser Cys Pro Glu Lys Gly Leu Asp
180 185

<210> 14
<211> 259
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer (CD34 ectodomain)

<400> 14

```
Ser Leu Asp Asn Asn Gly Thr Ala Thr Pro Glu Leu Pro Thr Gln Gly
1               5                  10                  15

Thr Phe Ser Asn Val Ser Thr Asn Val Ser Tyr Gln Glu Thr Thr Thr
            20                  25                  30

Pro Ser Thr Leu Gly Ser Thr Ser Leu His Pro Val Ser Gln His Gly
        35                  40                  45

Asn Glu Ala Thr Thr Asn Ile Thr Glu Thr Thr Val Lys Phe Thr Ser
    50                  55                  60

Thr Ser Val Ile Thr Ser Val Tyr Gly Asn Thr Asn Ser Ser Val Gln
65                  70                  75                  80

Ser Gln Thr Ser Val Ile Ser Thr Val Phe Thr Thr Pro Ala Asn Val
                85                  90                  95

Ser Thr Pro Glu Thr Thr Leu Lys Pro Ser Leu Ser Pro Gly Asn Val
            100                 105                 110

Ser Asp Leu Ser Thr Thr Ser Thr Ser Leu Ala Thr Ser Pro Thr Lys
        115                 120                 125

Pro Tyr Thr Ser Ser Ser Pro Ile Leu Ser Asp Ile Lys Ala Glu Ile
    130                 135                 140

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

Glu Gln Asn Lys Thr Ser Ser Cys Ala Glu Phe Lys Lys Asp Arg Gly
                165                 170                 175

Glu Gly Leu Ala Arg Val Leu Cys Gly Glu Glu Gln Ala Asp Ala Asp
            180                 185                 190

Ala Gly Ala Gln Val Cys Ser Leu Leu Leu Ala Gln Ser Glu Val Arg
        195                 200                 205

Pro Gln Cys Leu Leu Leu Val Leu Ala Asn Arg Thr Glu Ile Ser Ser
    210                 215                 220

Lys Leu Gln Leu Met Lys Lys His Gln Ser Asp Leu Lys Lys Leu Gly
225                 230                 235                 240

Ile Leu Asp Phe Thr Glu Gln Asp Val Ala Ser His Gln Ser Tyr Ser
                245                 250                 255

Gln Lys Thr
```

<210> 15
<211> 140
<212> PRT
<213> Artificial Sequence

<220>
<223> CD28 transmembrane domain and CD3 Z endodomains

<400> 15

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
1 5 10 15

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Arg Val Lys Phe
20 25 30

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
35 40 45

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
50 55 60

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
65 70 75 80

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
85 90 95

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
100 105 110

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
115 120 125

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
130 135 140

<210> 16
<211> 180
<212> PRT
<213> Artificial Sequence

<220>
<223> CD28 transmembrane domain and CD28 and CD3 Zeta endodomains

<400> 16

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
1 5 10 15

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
20 25 30

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly

35 40 45

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
50 55 60

Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
65 70 75 80

Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
85 90 95

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
100 105 110

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
115 120 125

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

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
145 150 155 160

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
165 170 175

Leu Pro Pro Arg
180

<210> 17
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> CD28 transmembrane domain and CD28, OX40 and CD3 Zeta endodomains

<400> 17

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
1 5 10 15

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
20 25 30

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
35 40 45

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
50 55 60

Ala Tyr Arg Ser Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro
65 70 75 80

Pro Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp
85 90 95

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

Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
115 120 125

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
130 135 140

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
145 150 155 160

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
165 170 175

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
180 185 190

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
195 200 205

His Met Gln Ala Leu Pro Pro Arg
210 215

<210> 18
<211> 729
<212> PRT
<213> Artificial Sequence

<220>
<223> CD45 transmembrane and endodomain

<400> 18

Ala Leu Ile Ala Phe Leu Ala Phe Leu Ile Ile Val Thr Ser Ile Ala
1 5 10 15

Leu Leu Val Val Leu Tyr Lys Ile Tyr Asp Leu His Lys Lys Arg Ser
20 25 30

Cys Asn Leu Asp Glu Gln Gln Glu Leu Val Glu Arg Asp Asp Glu Lys
35 40 45

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

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

Gln Ser Ile Pro Arg Val Phe Ser Lys Phe Pro Ile Lys Glu Ala Arg

85 90 95

Lys Pro Phe Asn Gln Asn Lys Asn Arg Tyr Val Asp Ile Leu Pro Tyr
100 105 110

Asp Tyr Asn Arg Val Glu Leu Ser Glu Ile Asn Gly Asp Ala Gly Ser
115 120 125

Asn Tyr Ile Asn Ala Ser Tyr Ile Asp Gly Phe Lys Glu Pro Arg Lys
130 135 140

Tyr Ile Ala Ala Gln Gly Pro Arg Asp Glu Thr Val Asp Asp Phe Trp
145 150 155 160

Arg Met Ile Trp Glu Gln Lys Ala Thr Val Ile Val Met Val Thr Arg
165 170 175

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

Glu Glu Gly Thr Arg Ala Phe Gly Asp Val Val Val Lys Ile Asn Gln
195 200 205

His Lys Arg Cys Pro Asp Tyr Ile Ile Gln Lys Leu Asn Ile Val Asn
210 215 220

Lys Lys Glu Lys Ala Thr Gly Arg Glu Val Thr His Ile Gln Phe Thr
225 230 235 240

Ser Trp Pro Asp His Gly Val Pro Glu Asp Pro His Leu Leu Leu Lys
245 250 255

Leu Arg Arg Arg Val Asn Ala Phe Ser Asn Phe Phe Ser Gly Pro Ile
260 265 270

Val Val His Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Tyr Ile Gly
275 280 285

Ile Asp Ala Met Leu Glu Gly Leu Glu Ala Glu Asn Lys Val Asp Val
290 295 300

Tyr Gly Tyr Val Val Lys Leu Arg Arg Gln Arg Cys Leu Met Val Gln
305 310 315 320

Val Glu Ala Gln Tyr Ile Leu Ile His Gln Ala Leu Val Glu Tyr Asn
325 330 335

Gln Phe Gly Glu Thr Glu Val Asn Leu Ser Glu Leu His Pro Tyr Leu
340 345 350

His Asn Met Lys Lys Arg Asp Pro Pro Ser Glu Pro Ser Pro Leu Glu

355 360 365

Ala Glu Phe Gln Arg Leu Pro Ser Tyr Arg Ser Trp Arg Thr Gln His
370 375 380

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

Ile Pro Tyr Asp Tyr Asn Arg Val Pro Leu Lys His Glu Leu Glu Met
405 410 415

Ser Lys Glu Ser Glu His Asp Ser Asp Glu Ser Ser Asp Asp Asp Ser
420 425 430

Asp Ser Glu Glu Pro Ser Lys Tyr Ile Asn Ala Ser Phe Ile Met Ser
435 440 445

Tyr Trp Lys Pro Glu Val Met Ile Ala Ala Gln Gly Pro Leu Lys Glu
450 455 460

Thr Ile Gly Asp Phe Trp Gln Met Ile Phe Gln Arg Lys Val Lys Val
465 470 475 480

Ile Val Met Leu Thr Glu Leu Lys His Gly Asp Gln Glu Ile Cys Ala
485 490 495

Gln Tyr Trp Gly Glu Gly Lys Gln Thr Tyr Gly Asp Ile Glu Val Asp
500 505 510

Leu Lys Asp Thr Asp Lys Ser Ser Thr Tyr Thr Leu Arg Val Phe Glu
515 520 525

Leu Arg His Ser Lys Arg Lys Asp Ser Arg Thr Val Tyr Gln Tyr Gln
530 535 540

Tyr Thr Asn Trp Ser Val Glu Gln Leu Pro Ala Glu Pro Lys Glu Leu
545 550 555 560

Ile Ser Met Ile Gln Val Val Lys Gln Lys Leu Pro Gln Lys Asn Ser
565 570 575

Ser Glu Gly Asn Lys His His Lys Ser Thr Pro Leu Leu Ile His Cys
580 585 590

Arg Asp Gly Ser Gln Gln Thr Gly Ile Phe Cys Ala Leu Leu Asn Leu
595 600 605

Leu Glu Ser Ala Glu Thr Glu Glu Val Val Asp Ile Phe Gln Val Val
610 615 620

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

625 630 635 640

Tyr Gln Phe Leu Tyr Asp Val Ile Ala Ser Thr Tyr Pro Ala Gln Asn
645 650 655

Gly Gln Val Lys Lys Asn Asn His Gln Glu Asp Lys Ile Glu Phe Asp
660 665 670

Asn Glu Val Asp Lys Val Lys Gln Asp Ala Asn Cys Val Asn Pro Leu
675 680 685

Gly Ala Pro Glu Lys Leu Pro Glu Ala Lys Glu Gln Ala Glu Gly Ser
690 695 700

Glu Pro Thr Ser Gly Thr Glu Gly Pro Glu His Ser Val Asn Gly Pro
705 710 715 720

Ala Ser Pro Ala Leu Asn Gln Gly Ser
725

<210> 19
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<223> CD148 transmembrane and endodomain

<400> 19

Ala Val Phe Gly Cys Ile Phe Gly Ala Leu Val Ile Val Thr Val Gly
1 5 10 15

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

Val Ser Phe Ser Gln Ile Lys Pro Lys Lys Ser Lys Leu Ile Arg Val
35 40 45

Glu Asn Phe Glu Ala Tyr Phe Lys Lys Gln Gln Ala Asp Ser Asn Cys
50 55 60

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

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

Asn Asn Val Leu Pro Tyr Asp Ile Ser Arg Val Lys Leu Ser Val Gln
100 105 110

Thr His Ser Thr Asp Asp Tyr Ile Asn Ala Asn Tyr Met Pro Gly Tyr
115 120 125

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

Leu Lys Asp Phe Trp Arg Met Val Trp Glu Lys Asn Val Tyr Ala Ile
145                 150                 155                 160

Ile Met Leu Thr Lys Cys Val Glu Gln Gly Arg Thr Lys Cys Glu Glu
                165                 170                 175

Tyr Trp Pro Ser Lys Gln Ala Gln Asp Tyr Gly Asp Ile Thr Val Ala
            180                 185                 190

Met Thr Ser Glu Ile Val Leu Pro Glu Trp Thr Ile Arg Asp Phe Thr
        195                 200                 205

Val Lys Asn Ile Gln Thr Ser Glu Ser His Pro Leu Arg Gln Phe His
    210                 215                 220

Phe Thr Ser Trp Pro Asp His Gly Val Pro Asp Thr Thr Asp Leu Leu
225                 230                 235                 240

Ile Asn Phe Arg Tyr Leu Val Arg Asp Tyr Met Lys Gln Ser Pro Pro
                245                 250                 255

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

Thr Phe Ile Ala Ile Asp Arg Leu Ile Tyr Gln Ile Glu Asn Glu Asn
        275                 280                 285

Thr Val Asp Val Tyr Gly Ile Val Tyr Asp Leu Arg Met His Arg Pro
    290                 295                 300

Leu Met Val Gln Thr Glu Asp Gln Tyr Val Phe Leu Asn Gln Cys Val
305                 310                 315                 320

Leu Asp Ile Val Arg Ser Gln Lys Asp Ser Lys Val Asp Leu Ile Tyr
                325                 330                 335

Gln Asn Thr Thr Ala Met Thr Ile Tyr Glu Asn Leu Ala Pro Val Thr
            340                 345                 350

Thr Phe Gly Lys Thr Asn Gly Tyr Ile Ala
        355                 360
```

<210> 20
<211> 595
<212> PRT
<213> Artificial Sequence

<220>
<223> sequence of PTPN6

<400> 20

```
Met Val Arg Trp Phe His Arg Asp Leu Ser Gly Leu Asp Ala Glu Thr
1               5                  10                  15

Leu Leu Lys Gly Arg Gly Val His Gly Ser Phe Leu Ala Arg Pro Ser
            20                  25                  30

Arg Lys Asn Gln Gly Asp Phe Ser Leu Ser Val Arg Val Gly Asp Gln
        35                  40                  45

Val Thr His Ile Arg Ile Gln Asn Ser Gly Asp Phe Tyr Asp Leu Tyr
    50                  55                  60

Gly Gly Glu Lys Phe Ala Thr Leu Thr Glu Leu Val Glu Tyr Tyr Thr
65                  70                  75                  80

Gln Gln Gln Gly Val Leu Gln Asp Arg Asp Gly Thr Ile Ile His Leu
                85                  90                  95

Lys Tyr Pro Leu Asn Cys Ser Asp Pro Thr Ser Glu Arg Trp Tyr His
            100                 105                 110

Gly His Met Ser Gly Gly Gln Ala Glu Thr Leu Leu Gln Ala Lys Gly
        115                 120                 125

Glu Pro Trp Thr Phe Leu Val Arg Glu Ser Leu Ser Gln Pro Gly Asp
    130                 135                 140

Phe Val Leu Ser Val Leu Ser Asp Gln Pro Lys Ala Gly Pro Gly Ser
145                 150                 155                 160

Pro Leu Arg Val Thr His Ile Lys Val Met Cys Glu Gly Gly Arg Tyr
                165                 170                 175

Thr Val Gly Gly Leu Glu Thr Phe Asp Ser Leu Thr Asp Leu Val Glu
            180                 185                 190

His Phe Lys Lys Thr Gly Ile Glu Glu Ala Ser Gly Ala Phe Val Tyr
        195                 200                 205

Leu Arg Gln Pro Tyr Tyr Ala Thr Arg Val Asn Ala Ala Asp Ile Glu
    210                 215                 220

Asn Arg Val Leu Glu Leu Asn Lys Lys Gln Glu Ser Glu Asp Thr Ala
225                 230                 235                 240

Lys Ala Gly Phe Trp Glu Glu Phe Glu Ser Leu Gln Lys Gln Glu Val
                245                 250                 255

Lys Asn Leu His Gln Arg Leu Glu Gly Gln Arg Pro Glu Asn Lys Gly
```

260 265 270

Lys Asn Arg Tyr Lys Asn Ile Leu Pro Phe Asp His Ser Arg Val Ile
275 280 285

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

Asn Tyr Ile Lys Asn Gln Leu Leu Gly Pro Asp Glu Asn Ala Lys Thr
305 310 315 320

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

Gln Met Ala Trp Gln Glu Asn Ser Arg Val Ile Val Met Thr Thr Arg
340 345 350

Glu Val Glu Lys Gly Arg Asn Lys Cys Val Pro Tyr Trp Pro Glu Val
355 360 365

Gly Met Gln Arg Ala Tyr Gly Pro Tyr Ser Val Thr Asn Cys Gly Glu
370 375 380

His Asp Thr Thr Glu Tyr Lys Leu Arg Thr Leu Gln Val Ser Pro Leu
385 390 395 400

Asp Asn Gly Asp Leu Ile Arg Glu Ile Trp His Tyr Gln Tyr Leu Ser
405 410 415

Trp Pro Asp His Gly Val Pro Ser Glu Pro Gly Gly Val Leu Ser Phe
420 425 430

Leu Asp Gln Ile Asn Gln Arg Gln Glu Ser Leu Pro His Ala Gly Pro
435 440 445

Ile Ile Val His Cys Ser Ala Gly Ile Gly Arg Thr Gly Thr Ile Ile
450 455 460

Val Ile Asp Met Leu Met Glu Asn Ile Ser Thr Lys Gly Leu Asp Cys
465 470 475 480

Asp Ile Asp Ile Gln Lys Thr Ile Gln Met Val Arg Ala Gln Arg Ser
485 490 495

Gly Met Val Gln Thr Glu Ala Gln Tyr Lys Phe Ile Tyr Val Ala Ile
500 505 510

Ala Gln Phe Ile Glu Thr Thr Lys Lys Lys Leu Glu Val Leu Gln Ser
515 520 525

Gln Lys Gly Gln Glu Ser Glu Tyr Gly Asn Ile Thr Tyr Pro Pro Ala

530 535 540

Met Lys Asn Ala His Ala Lys Ala Ser Arg Thr Ser Ser Lys His Lys
545 550 555 560

Glu Asp Val Tyr Glu Asn Leu His Thr Lys Asn Lys Arg Glu Glu Lys
565 570 575

Val Lys Lys Gln Arg Ser Ala Asp Lys Glu Lys Ser Lys Gly Ser Leu
580 585 590

Lys Arg Lys
595

<210> 21
<211> 272
<212> PRT
<213> Artificial Sequence

<220>
<223> sequence of phosphatase domain of PTPN6

<400> 21

Phe Trp Glu Glu Phe Glu Ser Leu Gln Lys Gln Glu Val Lys Asn Leu
1 5 10 15

His Gln Arg Leu Glu Gly Gln Arg Pro Glu Asn Lys Gly Lys Asn Arg
20 25 30

Tyr Lys Asn Ile Leu Pro Phe Asp His Ser Arg Val Ile Leu Gln Gly
35 40 45

Arg Asp Ser Asn Ile Pro Gly Ser Asp Tyr Ile Asn Ala Asn Tyr Ile
50 55 60

Lys Asn Gln Leu Leu Gly Pro Asp Glu Asn Ala Lys Thr Tyr Ile Ala
65 70 75 80

Ser Gln Gly Cys Leu Glu Ala Thr Val Asn Asp Phe Trp Gln Met Ala
85 90 95

Trp Gln Glu Asn Ser Arg Val Ile Val Met Thr Thr Arg Glu Val Glu
100 105 110

Lys Gly Arg Asn Lys Cys Val Pro Tyr Trp Pro Glu Val Gly Met Gln
115 120 125

Arg Ala Tyr Gly Pro Tyr Ser Val Thr Asn Cys Gly Glu His Asp Thr
130 135 140

Thr Glu Tyr Lys Leu Arg Thr Leu Gln Val Ser Pro Leu Asp Asn Gly
145 150 155 160

Asp Leu Ile Arg Glu Ile Trp His Tyr Gln Tyr Leu Ser Trp Pro Asp
165 170 175

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

Ile Asn Gln Arg Gln Glu Ser Leu Pro His Ala Gly Pro Ile Ile Val
195 200 205

His Cys Ser Ala Gly Ile Gly Arg Thr Gly Thr Ile Ile Val Ile Asp
210 215 220

Met Leu Met Glu Asn Ile Ser Thr Lys Gly Leu Asp Cys Asp Ile Asp
225 230 235 240

Ile Gln Lys Thr Ile Gln Met Val Arg Ala Gln Arg Ser Gly Met Val
245 250 255

Gln Thr Glu Ala Gln Tyr Lys Phe Ile Tyr Val Ala Ile Ala Gln Phe
260 265 270

<210> 22
<211> 97
<212> PRT
<213> Artificial Sequence

<220>
<223> PDCD1 endodomain

<400> 22

Cys Ser Arg Ala Ala Arg Gly Thr Ile Gly Ala Arg Arg Thr Gly Gln
1 5 10 15

Pro Leu Lys Glu Asp Pro Ser Ala Val Pro Val Phe Ser Val Asp Tyr
20 25 30

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

Pro Cys Val Pro Glu Gln Thr Glu Tyr Ala Thr Ile Val Phe Pro Ser
50 55 60

Gly Met Gly Thr Ser Ser Pro Ala Arg Arg Gly Ser Ala Asp Gly Pro
65 70 75 80

Arg Ser Ala Gln Pro Leu Arg Pro Glu Asp Gly His Cys Ser Trp Pro
85 90 95

Leu

<210> 23

<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> BTLA4 endodomain

<400> 23

Lys Leu Gln Arg Arg Trp Lys Arg Thr Gln Ser Gln Gln Gly Leu Gln
1 5 10 15

Glu Asn Ser Ser Gly Gln Ser Phe Phe Val Arg Asn Lys Lys Val Arg
20 25 30

Arg Ala Pro Leu Ser Glu Gly Pro His Ser Leu Gly Cys Tyr Asn Pro
35 40 45

Met Met Glu Asp Gly Ile Ser Tyr Thr Thr Leu Arg Phe Pro Glu Met
50 55 60

Asn Ile Pro Arg Thr Gly Asp Ala Glu Ser Ser Glu Met Gln Arg Pro
65 70 75 80

Pro Pro Asp Cys Asp Asp Thr Val Thr Tyr Ser Ala Leu His Lys Arg
85 90 95

Gln Val Gly Asp Tyr Glu Asn Val Ile Pro Asp Phe Pro Glu Asp Glu
100 105 110

Gly Ile His Tyr Ser Glu Leu Ile Gln Phe Gly Val Gly Glu Arg Pro
115 120 125

Gln Ala Gln Glu Asn Val Asp Tyr Val Ile Leu Lys His
130 135 140

<210> 24
<211> 168
<212> PRT
<213> Artificial Sequence

<220>
<223> LILRB1 endodomain

<400> 24

Leu Arg His Arg Arg Gln Gly Lys His Trp Thr Ser Thr Gln Arg Lys
1 5 10 15

Ala Asp Phe Gln His Pro Ala Gly Ala Val Gly Pro Glu Pro Thr Asp
20 25 30

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

Asn Leu Tyr Ala Ala Val Lys His Thr Gln Pro Glu Asp Gly Val Glu

50 55 60

Met Asp Thr Arg Ser Pro His Asp Glu Asp Pro Gln Ala Val Thr Tyr
65 70 75 80

Ala Glu Val Lys His Ser Arg Pro Arg Arg Glu Met Ala Ser Pro Pro
85 90 95

Ser Pro Leu Ser Gly Glu Phe Leu Asp Thr Lys Asp Arg Gln Ala Glu
100 105 110

Glu Asp Arg Gln Met Asp Thr Glu Ala Ala Ala Ser Glu Ala Pro Gln
115 120 125

Asp Val Thr Tyr Ala Gln Leu His Ser Leu Thr Leu Arg Arg Glu Ala
130 135 140

Thr Glu Pro Pro Pro Ser Gln Glu Gly Pro Ser Pro Ala Val Pro Ser
145 150 155 160

Ile Tyr Ala Thr Leu Ala Ile His
165

<210> 25
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> LAIR1 endodomain

<400> 25

His Arg Gln Asn Gln Ile Lys Gln Gly Pro Pro Arg Ser Lys Asp Glu
1 5 10 15

Glu Gln Lys Pro Gln Gln Arg Pro Asp Leu Ala Val Asp Val Leu Glu
20 25 30

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

Glu Thr Asp Thr Ser Ala Leu Ala Ala Gly Ser Ser Gln Glu Val Thr
50 55 60

Tyr Ala Gln Leu Asp His Trp Ala Leu Thr Gln Arg Thr Ala Arg Ala
65 70 75 80

Val Ser Pro Gln Ser Thr Lys Pro Met Ala Glu Ser Ile Thr Tyr Ala
85 90 95

Ala Val Ala Arg His
100

<210> 26
<211> 62
<212> PRT
<213> Artificial Sequence

<220>
<223> CTLA4 endodomain

<400> 26

Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe Tyr
1 5 10 15

Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys Arg
20 25 30

Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu Pro
35 40 45

Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
50 55 60

<210> 27
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> KIR2DL1 endodomain

<400> 27

Gly Asn Ser Arg His Leu His Val Leu Ile Gly Thr Ser Val Val Ile
1 5 10 15

Ile Pro Phe Ala Ile Leu Leu Phe Phe Leu Leu His Arg Trp Cys Ala
20 25 30

Asn Lys Lys Asn Ala Val Val Met Asp Gln Glu Pro Ala Gly Asn Arg
35 40 45

Thr Val Asn Arg Glu Asp Ser Asp Glu Gln Asp Pro Gln Glu Val Thr
50 55 60

Tyr Thr Gln Leu Asn His Cys Val Phe Thr Gln Arg Lys Ile Thr Arg
65 70 75 80

Pro Ser Gln Arg Pro Lys Thr Pro Pro Thr Asp Ile Ile Val Tyr Thr
85 90 95

Glu Leu Pro Asn Ala Glu Ser Arg Ser Lys Val Val Ser Cys Pro
100 105 110

<210> 28
<211> 143
<212> PRT

<213> Artificial Sequence

<220>
<223> KIR2DL4 endodomain

<400> 28

Gly Ile Ala Arg His Leu His Ala Val Ile Arg Tyr Ser Val Ala Ile
1 5 10 15

Ile Leu Phe Thr Ile Leu Pro Phe Phe Leu Leu His Arg Trp Cys Ser
20 25 30

Lys Lys Lys Glu Asn Ala Ala Val Met Asn Gln Glu Pro Ala Gly His
35 40 45

Arg Thr Val Asn Arg Glu Asp Ser Asp Glu Gln Asp Pro Gln Glu Val
50 55 60

Thr Tyr Ala Gln Leu Asp His Cys Ile Phe Thr Gln Arg Lys Ile Thr
65 70 75 80

Gly Pro Ser Gln Arg Ser Lys Arg Pro Ser Thr Asp Thr Ser Val Cys
85 90 95

Ile Glu Leu Pro Asn Ala Glu Pro Arg Ala Leu Ser Pro Ala His Glu
100 105 110

His His Ser Gln Ala Leu Met Gly Ser Ser Arg Glu Thr Thr Ala Leu
115 120 125

Ser Gln Thr Gln Leu Ala Ser Ser Asn Val Pro Ala Ala Gly Ile
130 135 140

<210> 29
<211> 143
<212> PRT
<213> Artificial Sequence

<220>
<223> KIR2DL5 endodomain

<400> 29

Thr Gly Ile Arg Arg His Leu His Ile Leu Ile Gly Thr Ser Val Ala
1 5 10 15

Ile Ile Leu Phe Ile Ile Leu Phe Phe Phe Leu Leu His Cys Cys Cys
20 25 30

Ser Asn Lys Lys Asn Ala Ala Val Met Asp Gln Glu Pro Ala Gly Asp
35 40 45

Arg Thr Val Asn Arg Glu Asp Ser Asp Asp Gln Asp Pro Gln Glu Val
50 55 60

Thr Tyr Ala Gln Leu Asp His Cys Val Phe Thr Gln Thr Lys Ile Thr
65 70 75 80

Ser Pro Ser Gln Arg Pro Lys Thr Pro Pro Thr Asp Thr Thr Met Tyr
85 90 95

Met Glu Leu Pro Asn Ala Lys Pro Arg Ser Leu Ser Pro Ala His Lys
100 105 110

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

Ser Gln Asn Arg Val Ala Ser Ser His Val Pro Ala Ala Gly Ile
130 135 140

<210> 30
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> KIR3DL1 endodomain

<400> 30

Lys Asp Pro Arg His Leu His Ile Leu Ile Gly Thr Ser Val Val Ile
1 5 10 15

Ile Leu Phe Ile Leu Leu Leu Phe Phe Leu Leu His Leu Trp Cys Ser
20 25 30

Asn Lys Lys Asn Ala Ala Val Met Asp Gln Glu Pro Ala Gly Asn Arg
35 40 45

Thr Ala Asn Ser Glu Asp Ser Asp Glu Gln Asp Pro Glu Glu Val Thr
50 55 60

Tyr Ala Gln Leu Asp His Cys Val Phe Thr Gln Arg Lys Ile Thr Arg
65 70 75 80

Pro Ser Gln Arg Pro Lys Thr Pro Pro Thr Asp Thr Ile Leu Tyr Thr
85 90 95

Glu Leu Pro Asn Ala Lys Pro Arg Ser Lys Val Val Ser Cys Pro
100 105 110

<210> 31
<211> 97
<212> PRT
<213> Artificial Sequence

<220>
<223> KIR3DL3 endodomain

<400> 31

```
Lys Asp Pro Gly Asn Ser Arg His Leu His Val Leu Ile Gly Thr Ser
1               5                   10                  15

Val Val Ile Ile Pro Phe Ala Ile Leu Leu Phe Phe Leu Leu His Arg
            20                  25                  30

Trp Cys Ala Asn Lys Lys Asn Ala Val Val Met Asp Gln Glu Pro Ala
        35                  40                  45

Gly Asn Arg Thr Val Asn Arg Glu Asp Ser Asp Glu Gln Asp Pro Gln
    50                  55                  60

Glu Val Thr Tyr Ala Gln Leu Asn His Cys Val Phe Thr Gln Arg Lys
65                  70                  75                  80

Ile Thr Arg Pro Ser Gln Arg Pro Lys Thr Pro Pro Thr Asp Thr Ser
                85                  90                  95

Val
```

<210> 32
<211> 807
<212> PRT
<213> Artificial Sequence

<220>
<223> PTPN6-CD45 fusion protein

<400> 32

```
Trp Tyr His Gly His Met Ser Gly Gly Gln Ala Glu Thr Leu Leu Gln
1               5                   10                  15

Ala Lys Gly Glu Pro Trp Thr Phe Leu Val Arg Glu Ser Leu Ser Gln
            20                  25                  30

Pro Gly Asp Phe Val Leu Ser Val Leu Ser Asp Gln Pro Lys Ala Gly
        35                  40                  45

Pro Gly Ser Pro Leu Arg Val Thr His Ile Lys Val Met Cys Glu Gly
    50                  55                  60

Gly Arg Tyr Thr Val Gly Gly Leu Glu Thr Phe Asp Ser Leu Thr Asp
65                  70                  75                  80

Leu Val Glu His Phe Lys Lys Thr Gly Ile Glu Glu Ala Ser Gly Ala
                85                  90                  95

Phe Val Tyr Leu Arg Gln Pro Tyr Lys Ile Tyr Asp Leu His Lys Lys
            100                 105                 110

Arg Ser Cys Asn Leu Asp Glu Gln Gln Glu Leu Val Glu Arg Asp Asp
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115 120 125

Glu Lys Gln Leu Met Asn Val Glu Pro Ile His Ala Asp Ile Leu Leu
130 135 140

Glu Thr Tyr Lys Arg Lys Ile Ala Asp Glu Gly Arg Leu Phe Leu Ala
145 150 155 160

Glu Phe Gln Ser Ile Pro Arg Val Phe Ser Lys Phe Pro Ile Lys Glu
165 170 175

Ala Arg Lys Pro Phe Asn Gln Asn Lys Asn Arg Tyr Val Asp Ile Leu
180 185 190

Pro Tyr Asp Tyr Asn Arg Val Glu Leu Ser Glu Ile Asn Gly Asp Ala
195 200 205

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

Arg Lys Tyr Ile Ala Ala Gln Gly Pro Arg Asp Glu Thr Val Asp Asp
225 230 235 240

Phe Trp Arg Met Ile Trp Glu Gln Lys Ala Thr Val Ile Val Met Val
245 250 255

Thr Arg Cys Glu Glu Gly Asn Arg Asn Lys Cys Ala Glu Tyr Trp Pro
260 265 270

Ser Met Glu Glu Gly Thr Arg Ala Phe Gly Asp Val Val Val Lys Ile
275 280 285

Asn Gln His Lys Arg Cys Pro Asp Tyr Ile Ile Gln Lys Leu Asn Ile
290 295 300

Val Asn Lys Lys Glu Lys Ala Thr Gly Arg Glu Val Thr His Ile Gln
305 310 315 320

Phe Thr Ser Trp Pro Asp His Gly Val Pro Glu Asp Pro His Leu Leu
325 330 335

Leu Lys Leu Arg Arg Arg Val Asn Ala Phe Ser Asn Phe Phe Ser Gly
340 345 350

Pro Ile Val Val His Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Tyr
355 360 365

Ile Gly Ile Asp Ala Met Leu Glu Gly Leu Glu Ala Glu Asn Lys Val
370 375 380

Asp Val Tyr Gly Tyr Val Val Lys Leu Arg Arg Gln Arg Cys Leu Met

385 390 395 400

Val Gln Val Glu Ala Gln Tyr Ile Leu Ile His Gln Ala Leu Val Glu
405 410 415

Tyr Asn Gln Phe Gly Glu Thr Glu Val Asn Leu Ser Glu Leu His Pro
420 425 430

Tyr Leu His Asn Met Lys Lys Arg Asp Pro Pro Ser Glu Pro Ser Pro
435 440 445

Leu Glu Ala Glu Phe Gln Arg Leu Pro Ser Tyr Arg Ser Trp Arg Thr
450 455 460

Gln His Ile Gly Asn Gln Glu Glu Asn Lys Ser Lys Asn Arg Asn Ser
465 470 475 480

Asn Val Ile Pro Tyr Asp Tyr Asn Arg Val Leu Lys His Glu Leu Glu
485 490 495

Met Ser Lys Glu Ser Glu His Asp Ser Asp Glu Ser Ser Asp Asp Asp
500 505 510

Ser Asp Ser Glu Glu Pro Ser Lys Tyr Ile Asn Ala Ser Phe Ile Met
515 520 525

Ser Tyr Trp Lys Pro Glu Val Met Ile Ala Ala Gln Gly Pro Leu Lys
530 535 540

Glu Thr Ile Gly Asp Phe Met Ile Gln Arg Lys Val Lys Val Ile Val
545 550 555 560

Met Leu Thr Glu Leu Lys His Gly Asp Gln Glu Ile Cys Ala Gln Tyr
565 570 575

Trp Gly Glu Gly Lys Gln Thr Tyr Gly Asp Ile Glu Val Asp Leu Lys
580 585 590

Asp Thr Asp Lys Ser Ser Thr Tyr Thr Leu Arg Val Phe Glu Leu Arg
595 600 605

His Ser Lys Arg Lys Asp Ser Arg Thr Val Tyr Gln Tyr Gln Tyr Thr
610 615 620

Asn Trp Ser Val Glu Gln Leu Pro Ala Glu Pro Lys Glu Leu Ile Ser
625 630 635 640

Met Ile Gln Val Val Lys Gln Lys Leu Pro Gln Lys Asn Ser Ser Glu
645 650 655

Gly Asn Lys His His Lys Ser Thr Pro Leu Leu Ile His Cys Arg Asp

660 665 670

Gly Ser Gln Gln Thr Gly Ile Phe Cys Ala Leu Leu Asn Leu Leu Glu
675 680 685

Ser Ala Glu Thr Glu Glu Val Val Asp Ile Phe Gln Val Val Lys Ala
690 695 700

Leu Arg Lys Ala Arg Pro Gly Met Val Ser Thr Phe Glu Gln Tyr Gln
705 710 715 720

Phe Leu Tyr Asp Val Ile Ala Ser Thr Tyr Pro Ala Gln Asn Gly Gln
725 730 735

Val Lys Lys Asn Asn His Gln Glu Asp Lys Ile Glu Phe Asp Asn Glu
740 745 750

Val Asp Lys Val Lys Gln Asp Ala Asn Cys Val Asn Pro Leu Gly Ala
755 760 765

Pro Glu Lys Leu Pro Glu Ala Lys Glu Gln Ala Glu Gly Ser Glu Pro
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Glu Ser Leu Ser Gln Pro Gly Asp Phe Val Leu Ser Val Leu Ser Asp
20 25 30

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

Val Met Cys Glu Gly Gly Arg Tyr Thr Val Gly Gly Leu Glu Thr Phe
50 55 60

Asp Ser Leu Thr Asp Leu Val Glu His Phe Lys Lys Thr Gly Ile Glu
65 70 75 80

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Glu Ala Ser Gly Ala Phe Val Tyr Leu Arg Gln Pro Tyr Arg Lys Lys
                85                  90                  95

Arg Lys Asp Ala Lys Asn Asn Glu Val Ser Phe Ser Gln Ile Lys Pro
            100                 105                 110

Lys Lys Ser Lys Leu Ile Arg Val Glu Asn Phe Glu Ala Tyr Phe Lys
        115                 120                 125

Lys Gln Gln Ala Asp Ser Asn Cys Gly Phe Ala Glu Glu Tyr Glu Asp
    130                 135                 140

Leu Lys Leu Val Gly Ile Ser Gln Pro Lys Tyr Ala Ala Glu Leu Ala
145                 150                 155                 160

Glu Asn Arg Gly Lys Asn Arg Tyr Asn Asn Val Leu Pro Tyr Asp Ile
                165                 170                 175

Ser Arg Val Lys Leu Ser Val Gln Thr His Ser Thr Asp Asp Tyr Ile
            180                 185                 190

Asn Ala Asn Tyr Met Pro Gly Tyr His Ser Lys Lys Asp Phe Ile Ala
        195                 200                 205

Thr Gln Gly Pro Leu Pro Asn Thr Leu Lys Asp Phe Trp Arg Met Val
    210                 215                 220

Trp Glu Lys Asn Val Tyr Ala Ile Ile Met Leu Thr Lys Cys Val Glu
225                 230                 235                 240

Gln Gly Arg Thr Lys Cys Glu Glu Tyr Trp Pro Ser Lys Gln Ala Gln
                245                 250                 255

Asp Tyr Gly Asp Ile Thr Val Ala Met Thr Ser Glu Ile Val Leu Pro
            260                 265                 270

Glu Trp Thr Ile Arg Asp Phe Thr Val Lys Asn Ile Gln Thr Ser Glu
        275                 280                 285

Ser His Pro Leu Arg Gln Phe His Phe Thr Ser Trp Pro Asp His Gly
    290                 295                 300

Val Pro Asp Thr Thr Asp Leu Leu Ile Asn Phe Arg Tyr Leu Val Arg
305                 310                 315                 320

Asp Tyr Met Lys Gln Ser Pro Pro Glu Ser Pro Ile Leu Val His Cys
                325                 330                 335

Ser Ala Gly Val Gly Arg Thr Gly Thr Phe Ile Ala Ile Asp Arg Leu
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Ile Tyr Gln Ile Glu Asn Glu Asn Thr Val Asp Val Tyr Gly Ile Val
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Tyr Asp Leu Arg Met His Arg Pro Leu Met Val Gln Thr Glu Asp Gln
370 375 380

Tyr Val Phe Leu Asn Gln Cys Val Leu Asp Ile Val Arg Ser Gln Lys
385 390 395 400

Asp Ser Lys Val Asp Leu Ile Tyr Gln Asn Thr Thr Ala Met Thr Ile
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Tyr Glu Asn Leu Ala Pro Val Thr Thr Phe Gly Lys Thr Asn Gly Tyr
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Ile Ala

<210> 34
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accatcagag atttcacagt gaaaaatatc cagacaagtg agagtcaccc tctgagacag 3660

ttccatttca cctcctggcc agaccacggt gttcccgaca ccactgacct gctcatcaac 3720

ttccggtacc tcgttcgtga ctacatgaag cagagtcctc ccgaatcgcc gattctggtg 3780

cattgcagtg ctggggtcgg aaggacgggc actttcattg ccattgatcg tctcatctac 3840

cagatagaga atgagaacac cgtggatgtg tatgggattg tgtatgacct tcgaatgcat 3900

aggcctttaa tggtgcagac agaggaccag tatgttttcc tcaatcagtg tgttttggat 3960

attgtcagat cccagaaaga ctcaaaagta gatcttatct accagaacac aactgcaatg 4020

acaatctatg aaaaccttgc gcccgtgacc acatttggaa agaccaatgg ttacatcgcc 4080

agcggtagct aa 4092

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<400> 41

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Met Ser Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15

His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu
            20                  25                  30

Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln
        35                  40                  45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
    50                  55                  60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65                  70                  75                  80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
                85                  90                  95

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

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

Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser Gly Pro Gly
145                 150                 155                 160

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

Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg
            180                 185                 190

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr
        195                 200                 205

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

Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr
225                 230                 235                 240

Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala
                245                 250                 255

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp Pro
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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 Phe Trp
305 310 315 320

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
325 330 335

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Arg Val Lys Phe Ser Arg
340 345 350

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
355 360 365

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
370 375 380

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
385 390 395 400

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
405 410 415

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
420 425 430

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
435 440 445

Ala Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Glu Gly Arg Gly
450 455 460

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Glu
465 470 475 480

Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro Gly Ser
485 490 495

Thr Gly Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro
500 505 510

Ser Gln Thr Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Ala
515 520 525

Ser Tyr Asn Ile His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu

530 535 540

Trp Leu Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala
545 550 555 560

Leu Met Ser Arg Leu Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln Val
565 570 575

Phe Leu Lys Met Ser Ser Leu Thr Ala Ala Asp Thr Ala Val Tyr Tyr
580 585 590

Cys Ala Lys Arg Ser Asp Asp Tyr Ser Trp Phe Ala Tyr Trp Gly Gln
595 600 605

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
610 615 620

Gly Ser Gly Gly Gly Gly Ser Glu Asn Gln Met Thr Gln Ser Pro Ser
625 630 635 640

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Arg Ala
645 650 655

Ser Ser Ser Val Ser Ser Ser Tyr Leu His Trp Tyr Gln Gln Lys Ser
660 665 670

Gly Lys Ala Pro Lys Val Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser
675 680 685

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr
690 695 700

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
705 710 715 720

Gln Gln Tyr Ser Gly Tyr Pro Ile Thr Phe Gly Gln Gly Thr Lys Val
725 730 735

Glu Ile Lys Arg Ser Asp Pro Ala Glu Pro Lys Ser Pro Asp Lys Thr
740 745 750

His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
755 760 765

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ala Arg Thr
770 775 780

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
785 790 795 800

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys

805 810 815

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
820 825 830

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
835 840 845

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
850 855 860

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
865 870 875 880

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
885 890 895

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
900 905 910

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
915 920 925

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
930 935 940

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
945 950 955 960

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Lys
965 970 975

Asp Pro Lys Ala Val Phe Gly Cys Ile Phe Gly Ala Leu Val Ile Val
980 985 990

Thr Val Gly Gly Phe Ile Phe Trp Arg Lys Lys Arg Lys Asp Ala Lys
995 1000 1005

Asn Asn Glu Val Ser Phe Ser Gln Ile Lys Pro Lys Lys Ser Lys
1010 1015 1020

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

Ala Asp Ser Asn Cys Gly Phe Ala Glu Glu Tyr Glu Asp Leu Lys
1040 1045 1050

Leu Val Gly Ile Ser Gln Pro Lys Tyr Ala Ala Glu Leu Ala Glu
1055 1060 1065

Asn Arg Gly Lys Asn Arg Tyr Asn Asn Val Leu Pro Tyr Asp Ile

1070 1075 1080

Ser Arg Val Lys Leu Ser Val Gln Thr His Ser Thr Asp Asp Tyr
1085 1090 1095

Ile Asn Ala Asn Tyr Met Pro Gly Tyr His Ser Lys Lys Asp Phe
1100 1105 1110

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

Arg Met Val Trp Glu Lys Asn Val Tyr Ala Ile Ile Met Leu Thr
1130 1135 1140

Lys Cys Val Glu Gln Gly Arg Thr Lys Cys Glu Glu Tyr Trp Pro
1145 1150 1155

Ser Lys Gln Ala Gln Asp Tyr Gly Asp Ile Thr Val Ala Met Thr
1160 1165 1170

Ser Glu Ile Val Leu Pro Glu Trp Thr Ile Arg Asp Phe Thr Val
1175 1180 1185

Lys Asn Ile Gln Thr Ser Glu Ser His Pro Leu Arg Gln Phe His
1190 1195 1200

Phe Thr Ser Trp Pro Asp His Gly Val Pro Asp Thr Thr Asp Leu
1205 1210 1215

Leu Ile Asn Phe Arg Tyr Leu Val Arg Asp Tyr Met Lys Gln Ser
1220 1225 1230

Pro Pro Glu Ser Pro Ile Leu Val His Cys Ser Ala Gly Val Gly
1235 1240 1245

Arg Thr Gly Thr Phe Ile Ala Ile Asp Arg Leu Ile Tyr Gln Ile
1250 1255 1260

Glu Asn Glu Asn Thr Val Asp Val Tyr Gly Ile Val Tyr Asp Leu
1265 1270 1275

Arg Met His Arg Pro Leu Met Val Gln Thr Glu Asp Gln Tyr Val
1280 1285 1290

Phe Leu Asn Gln Cys Val Leu Asp Ile Val Arg Ser Gln Lys Asp
1295 1300 1305

Ser Lys Val Asp Leu Ile Tyr Gln Asn Thr Thr Ala Met Thr Ile
1310 1315 1320

Tyr Glu Asn Leu Ala Pro Val Thr Thr Phe Gly Lys Thr Asn Gly

1325 1330 1335

Tyr Ile Ala
1340

<210> 42
<211> 4026
<212> DNA
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<220>
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accatcagct gcagagccag ccaggacatc agcaagtacc tgaactggta ccagcagaag 180

cccgacggca ccgtgaagct gctgatctac cacaccagcc ggctgcacag cggcgtgccc 240

agccggttca gcggcagcgg cagcggcacc gactacagcc tgaccatcag caacctggag 300

caggaggaca tcgccaccta cttctgccag cagggcaaca ccctgcccta caccttcgga 360

ggcggcacca agctggagat caccaaggcc ggaggcggag gctctggcgg aggcggctct 420

ggcggaggcg gctctggcgg aggcggcagc gaggtgaagc tgcaggagtc tggcccaggc 480

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gactacggcg tgagctggat caggcagccc ccacggaagg gcctggagtg gctgggcgtg 600

atctggggca gcgagaccac ctactacaac agcgccctga agagccggct gaccatcatc 660

aaggacaaca gcaagagcca ggtgttcctg aagatgaaca gcctgcagac cgacgacacc 720

gccatctact actgcgccaa gcactactac tatggcggca gctacgctat ggactactgg 780

ggccagggca ccagcgtgac cgtgagctca gatcccacca cgacgccagc gccgcgacca 840

ccaacaccgg cgcccaccat cgcgtcgcag cccctgtccc tgcgcccaga ggcgtgccgg 900

ccagcggcgg ggggcgcagt gcacacgagg gggctggact tcgcctgtga tatcttttgg 960

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attattttct gggtgaggag agtgaagttc agcaggagcg cagacgcccc cgcgtaccag 1080

cagggccaga accagctcta taacgagctc aatctaggac gaagagagga gtacgatgtt 1140

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caggaaggcc tgtacaatga actgcagaaa gataagatgg cggaggccta cagtgagatt 1260

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acagccacca aggacaccta cgacgccctt cacatgcagg ccctgcctcc tcgcagagcc 1380

gagggcaggg gaagtcttct aacatgcggg gacgtggagg aaaatcccgg gcccatggag 1440

accgacaccc tgctgctgtg ggtgctgctg ctgtgggtgc caggcagcac cggccaggtg 1500

cagctgcagg agtctggccc aggcctggtg aagcccagcc agaccctgag catcacctgc 1560

accgtgagcg gcttcagcct ggccagctac aacatccact gggtgcggca gcccccaggc 1620

aagggcctgg agtggctggg cgtgatctgg gctggcggca gcaccaacta caacagcgcc 1680

ctgatgagcc ggctgaccat cagcaaggac aacagcaaga accaggtgtt cctgaagatg 1740

agcagcctga cagccgccga caccgccgtg tactactgcg ccaagcggag cgacgactac 1800

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accgactaca ccctgaccat cagcagcctg cagcccgagg acttcgccac ctactactgc 2160

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caggctcagg actatggaga cataactgtg gcaatgacat cagaaattgt tcttccggaa 3540

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cagttccatt tcacctcctg gccagaccac ggtgttcccg acaccactga cctgctcatc 3660

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gtgcattgca gtgctggggt cggaaggacg ggcactttca ttgccattga tcgtctcatc 3780

taccagatag agaatgagaa caccgtggat gtgtatggga ttgtgtatga ccttcgaatg 3840

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gatattgtca gatcccagaa agactcaaaa gtagatctta tctaccagaa cacaactgca 3960

atgacaatct atgaaaacct tgcgcccgtg accacatttg gaaagaccaa tggttacatc 4020

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<212> PRT
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<220>
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SFG.aCD19-CD8STK-CD28tmZ-2A-aCD5-HCH2CH3pvaa-dCD148

<400> 43

Met Ser Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu
20 25 30

Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln
35 40 45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
50 55 60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
85 90 95

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

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

Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser Gly Pro Gly
145 150 155 160

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

Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg
            180                 185                 190

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr
        195                 200                 205

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

Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr
225                 230                 235                 240

Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala
                245                 250                 255

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser 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 Phe Trp
305                 310                 315                 320

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
                325                 330                 335

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Arg Val Lys Phe Ser Arg
            340                 345                 350

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
        355                 360                 365

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
    370                 375                 380

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
385                 390                 395                 400

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
                405                 410                 415

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
            420                 425                 430
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Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
        435                 440                 445

Ala Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Glu Gly Arg Gly
    450                 455                 460

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Glu
465                 470                 475                 480

Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro Gly Ser
                485                 490                 495

Thr Gly Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Lys Pro
            500                 505                 510

Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser
        515                 520                 525

Thr Ser Gly Met Gly Val Gly Trp Ile Arg Gln Pro Ser Gly Lys Gly
    530                 535                 540

Leu Glu Trp Leu Ala His Ile Trp Trp Asp Asp Asp Val Tyr Tyr Asn
545                 550                 555                 560

Pro Ser Leu Lys Asn Gln Leu Thr Ile Ser Lys Asp Ala Ser Arg Asp
                565                 570                 575

Gln Val Phe Leu Lys Ile Thr Asn Leu Asp Thr Ala Asp Thr Ala Thr
            580                 585                 590

Tyr Tyr Cys Val Arg Arg Arg Ala Thr Gly Thr Gly Phe Asp Tyr Trp
        595                 600                 605

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
    610                 615                 620

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asn Ile Val Met Thr Gln Ser
625                 630                 635                 640

His Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Ala Cys
                645                 650                 655

Lys Ala Ser Gln Asp Val Gly Thr Ala Val Ala Trp Tyr Gln Gln Lys
            660                 665                 670

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg His
        675                 680                 685

Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
    690                 695                 700
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Thr Leu Thr Ile Thr Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe
705                 710                 715                 720

Cys His Gln Tyr Asn Ser Tyr Asn Thr Phe Gly Ser Gly Thr Arg Leu
                725                 730                 735

Glu Leu Lys Arg Ser Asp Pro Ala Glu Pro Lys Ser Pro Asp Lys Thr
            740                 745                 750

His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
        755                 760                 765

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ala Arg Thr
    770                 775                 780

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
785                 790                 795                 800

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
                805                 810                 815

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
            820                 825                 830

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
        835                 840                 845

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
    850                 855                 860

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
865                 870                 875                 880

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
                885                 890                 895

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
            900                 905                 910

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
        915                 920                 925

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
    930                 935                 940

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
945                 950                 955                 960

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Lys
                965                 970                 975
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Asp Pro Lys Ala Val Phe Gly Cys Ile Phe Gly Ala Leu Val Ile Val
            980                 985                 990

Thr Val Gly Gly Phe Ile Phe Trp  Arg Lys Lys Arg Lys  Asp Ala Lys
        995                 1000                1005

Asn Asn  Glu Val Ser Phe Ser  Gln Ile Lys Pro Lys  Lys Ser Lys
    1010                1015                1020

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

Ala Asp  Ser Asn Cys Gly Phe  Ala Glu Glu Tyr Glu  Asp Leu Lys
    1040                1045                1050

Leu Val  Gly Ile Ser Gln Pro  Lys Tyr Ala Ala Glu  Leu Ala Glu
    1055                1060                1065

Asn Arg  Gly Lys Asn Arg Tyr  Asn Asn Val Leu Pro  Tyr Asp Ile
    1070                1075                1080

Ser Arg  Val Lys Leu Ser Val  Gln Thr His Ser Thr  Asp Asp Tyr
    1085                1090                1095

Ile Asn  Ala Asn Tyr Met Pro  Gly Tyr His Ser Lys  Lys Asp Phe
    1100                1105                1110

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

Arg Met  Val Trp Glu Lys Asn  Val Tyr Ala Ile Ile  Met Leu Thr
    1130                1135                1140

Lys Cys  Val Glu Gln Gly Arg  Thr Lys Cys Glu Glu  Tyr Trp Pro
    1145                1150                1155

Ser Lys  Gln Ala Gln Asp Tyr  Gly Asp Ile Thr Val  Ala Met Thr
    1160                1165                1170

Ser Glu  Ile Val Leu Pro Glu  Trp Thr Ile Arg Asp  Phe Thr Val
    1175                1180                1185

Lys Asn  Ile Gln Thr Ser Glu  Ser His Pro Leu Arg  Gln Phe His
    1190                1195                1200

Phe Thr  Ser Trp Pro Asp His  Gly Val Pro Asp Thr  Thr Asp Leu
    1205                1210                1215

Leu Ile  Asn Phe Arg Tyr Leu  Val Arg Asp Tyr Met  Lys Gln Ser
    1220                1225                1230
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Pro Pro Glu Ser Pro Ile Leu Val His Cys Ser Ala Gly Val Gly
1235 1240 1245

Arg Thr Gly Thr Phe Ile Ala Ile Asp Arg Leu Ile Tyr Gln Ile
1250 1255 1260

Glu Asn Glu Asn Thr Val Asp Val Tyr Gly Ile Val Tyr Asp Leu
1265 1270 1275

Arg Met His Arg Pro Leu Met Val Gln Thr Glu Asp Gln Tyr Val
1280 1285 1290

Phe Leu Asn Gln Cys Val Leu Asp Ile Val Arg Ser Gln Lys Asp
1295 1300 1305

Ser Lys Val Asp Leu Ile Tyr Gln Asn Thr Thr Ala Met Thr Ile
1310 1315 1320

Tyr Glu Asn Leu Ala Pro Val Thr Thr Phe Gly Lys Thr Asn Gly
1325 1330 1335

Tyr Ile Ala
1340

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ccagacatcc agatgaccca gaccaccagc agcctgagcg ccagcctggg cgaccgggtg 120

accatcagct gcagagccag ccaggacatc agcaagtacc tgaactggta ccagcagaag 180

cccgacggca ccgtgaagct gctgatctac cacaccagcc ggctgcacag cggcgtgccc 240

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ggcggcacca agctggagat caccaaggcc ggaggcggag gctctggcgg aggcggctct 420

ggcggaggcg gctctggcgg aggcggcagc gaggtgaagc tgcaggagtc tggcccaggc 480

ctggtggccc caagccagag cctgagcgtg acctgcaccg tgagcggcgt gagcctgccc 540

gactacggcg tgagctggat caggcagccc ccacggaagg gcctggagtg gctgggcgtg 600

atctggggca gcgagaccac ctactacaac agcgccctga agagccggct gaccatcatc 660

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gccatctact actgcgccaa gcactactac tatggcggca gctacgctat ggactactgg 780

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gacgtgggca ccgccgtggc ctggtaccag cagaagcctg gccagagccc caagctgctg 2040

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gccaactaca tgcctggcta ccactccaag aaagatttta ttgccacaca aggaccttta 3360

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gtgcattgca gtgctggggt cggaaggacg ggcactttca ttgccattga tcgtctcatc 3780

taccagatag agaatgagaa caccgtggat gtgtatggga ttgtgtatga ccttcgaatg 3840

cataggcctt taatggtgca gacagaggac cagtatgttt tcctcaatca gtgtgttttg 3900

gatattgtca gatcccagaa agactcaaaa gtagatctta tctaccagaa cacaactgca 3960

atgacaatct atgaaaacct tgcgcccgtg accacatttg gaaagaccaa tggttacatc 4020

gcctaa 4026

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<211> 1342
<212> PRT
<213> Artificial Sequence

<220>
<223> Single-chain variable fragment (scFv)
SFG.aCD19-CD8STK-CD28tmZ-2A-aEGFRvIII-HCH2CH3pvaa-dCD148

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His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu
20 25 30

Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln
35 40 45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr

50 55 60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
85 90 95

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

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

Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser Gly Pro Gly
145 150 155 160

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

Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg
180 185 190

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr
195 200 205

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

Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr
225 230 235 240

Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala
245 250 255

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser 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 Phe Trp
305 310 315 320

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val

325 330 335

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Arg Val Lys Phe Ser Arg
340 345 350

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
355 360 365

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
370 375 380

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
385 390 395 400

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
405 410 415

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
420 425 430

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
435 440 445

Ala Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Glu Gly Arg Gly
450 455 460

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Glu
465 470 475 480

Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro Gly Ser
485 490 495

Thr Gly Gln Val Lys Leu Gln Gln Ser Gly Gly Gly Leu Val Lys Pro
500 505 510

Gly Ala Ser Leu Lys Leu Ser Cys Val Thr Ser Gly Phe Thr Phe Arg
515 520 525

Lys Phe Gly Met Ser Trp Val Arg Gln Thr Ser Asp Lys Arg Leu Glu
530 535 540

Trp Val Ala Ser Ile Ser Thr Gly Gly Tyr Asn Thr Tyr Tyr Ser Asp
545 550 555 560

Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn Thr
565 570 575

Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu Tyr
580 585 590

Tyr Cys Thr Arg Gly Tyr Ser Ser Thr Ser Tyr Ala Met Asp Tyr Trp

595 600 605

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
610 615 620

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser
625 630 635 640

Pro Ala Ser Leu Ser Val Ala Thr Gly Glu Lys Val Thr Ile Arg Cys
645 650 655

Met Thr Ser Thr Asp Ile Asp Asp Asp Met Asn Trp Tyr Gln Gln Lys
660 665 670

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

Pro Gly Val Pro Ser Arg Phe Ser Ser Ser Gly Thr Gly Thr Asp Phe
690 695 700

Val Phe Thr Ile Glu Asn Thr Leu Ser Glu Asp Val Gly Asp Tyr Tyr
705 710 715 720

Cys Leu Gln Ser Phe Asn Val Pro Leu Thr Phe Gly Asp Gly Thr Lys
725 730 735

Leu Glu Ile Lys Arg Ser Asp Pro Ala Glu Pro Lys Ser Pro Asp Lys
740 745 750

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser
755 760 765

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ala Arg
770 775 780

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
785 790 795 800

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
805 810 815

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
820 825 830

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
835 840 845

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
850 855 860

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu

865 870 875 880

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
885 890 895

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
900 905 910

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
915 920 925

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
930 935 940

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
945 950 955 960

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
965 970 975

Lys Asp Pro Lys Ala Val Phe Gly Cys Ile Phe Gly Ala Leu Val Ile
980 985 990

Val Thr Val Gly Gly Phe Ile Phe Trp Arg Lys Lys Arg Lys Asp Ala
995 1000 1005

Lys Asn Asn Glu Val Ser Phe Ser Gln Ile Lys Pro Lys Lys Ser
1010 1015 1020

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

Gln Ala Asp Ser Asn Cys Gly Phe Ala Glu Glu Tyr Glu Asp Leu
1040 1045 1050

Lys Leu Val Gly Ile Ser Gln Pro Lys Tyr Ala Ala Glu Leu Ala
1055 1060 1065

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

Ile Ser Arg Val Lys Leu Ser Val Gln Thr His Ser Thr Asp Asp
1085 1090 1095

Tyr Ile Asn Ala Asn Tyr Met Pro Gly Tyr His Ser Lys Lys Asp
1100 1105 1110

Phe Ile Ala Thr Gln Gly Pro Leu Pro Asn Thr Leu Lys Asp Phe
1115 1120 1125

Trp Arg Met Val Trp Glu Lys Asn Val Tyr Ala Ile Ile Met Leu

1130 1135 1140

Thr Lys Cys Val Glu Gln Gly Arg Thr Lys Cys Glu Glu Tyr Trp
1145 1150 1155

Pro Ser Lys Gln Ala Gln Asp Tyr Gly Asp Ile Thr Val Ala Met
1160 1165 1170

Thr Ser Glu Ile Val Leu Pro Glu Trp Thr Ile Arg Asp Phe Thr
1175 1180 1185

Val Lys Asn Ile Gln Thr Ser Glu Ser His Pro Leu Arg Gln Phe
1190 1195 1200

His Phe Thr Ser Trp Pro Asp His Gly Val Pro Asp Thr Thr Asp
1205 1210 1215

Leu Leu Ile Asn Phe Arg Tyr Leu Val Arg Asp Tyr Met Lys Gln
1220 1225 1230

Ser Pro Pro Glu Ser Pro Ile Leu Val His Cys Ser Ala Gly Val
1235 1240 1245

Gly Arg Thr Gly Thr Phe Ile Ala Ile Asp Arg Leu Ile Tyr Gln
1250 1255 1260

Ile Glu Asn Glu Asn Thr Val Asp Val Tyr Gly Ile Val Tyr Asp
1265 1270 1275

Leu Arg Met His Arg Pro Leu Met Val Gln Thr Glu Asp Gln Tyr
1280 1285 1290

Val Phe Leu Asn Gln Cys Val Leu Asp Ile Val Arg Ser Gln Lys
1295 1300 1305

Asp Ser Lys Val Asp Leu Ile Tyr Gln Asn Thr Thr Ala Met Thr
1310 1315 1320

Ile Tyr Glu Asn Leu Ala Pro Val Thr Thr Phe Gly Lys Thr Asn
1325 1330 1335

Gly Tyr Ile Ala
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<210> 46
<211> 4029
<212> DNA
<213> Artificial Sequence

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<223> Single-chain variable fragment (scFv)
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aatgccaact acatgcctgg ctaccactcc aagaaagatt ttattgccac acaaggacct 3360

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atcgcctaa 4029

<210> 47
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<220>
<223> Immunoreceptor tyrosine-based inhibition motif (ITIM)

<220>
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<223> Xaa may be Ser, Ile, Val or Leu

<220>
<221> misc_feature
<222> (2)..(2)
<223> Xaa can be any naturally occurring amino acid

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<221> misc_feature
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<223> Xaa can be any naturally occurring amino acid

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<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa may be Ile, Val or Leu

<400> 47

Xaa Xaa Tyr Xaa Xaa Xaa
1 5

<210> 48
<211> 1114
<212> PRT
<213> Artificial Sequence

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<223> Amino acid sequence of a AND NOT gate
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N6)

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20 25 30

Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln
35 40 45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
50 55 60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65 70 75 80

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Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
                85                  90                  95

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

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

Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser Gly Pro Gly
145                 150                 155                 160

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

Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg
            180                 185                 190

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr
        195                 200                 205

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

Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr
225                 230                 235                 240

Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala
                245                 250                 255

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser 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 Phe Trp
305                 310                 315                 320

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
                325                 330                 335

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Arg Val Lys Phe Ser Arg
            340                 345                 350
```

```
Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
        355                 360                 365

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
    370                 375                 380

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
385                 390                 395                 400

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
                405                 410                 415

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
            420                 425                 430

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
        435                 440                 445

Ala Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Glu Gly Arg Gly
    450                 455                 460

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala
465                 470                 475                 480

Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr Asp Ala
                485                 490                 495

Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
            500                 505                 510

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp Ile Tyr
        515                 520                 525

Phe Asn Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
    530                 535                 540

Leu Ile Tyr Asp Thr Asn Arg Leu Ala Asp Gly Val Pro Ser Arg Phe
545                 550                 555                 560

Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser Ser Leu
                565                 570                 575

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Lys Asn Tyr
            580                 585                 590

Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ser Gly
        595                 600                 605

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    610                 615                 620
```

```
Gly Gly Ser Arg Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
625                 630                 635                 640

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
                645                 650                 655

Thr Leu Ser Asn Tyr Gly Met His Trp Ile Arg Gln Ala Pro Gly Lys
            660                 665                 670

Gly Leu Glu Trp Val Ser Ser Ile Ser Leu Asn Gly Gly Ser Thr Tyr
        675                 680                 685

Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
    690                 695                 700

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

Ala Val Tyr Tyr Cys Ala Ala Gln Asp Ala Tyr Thr Gly Gly Tyr Phe
                725                 730                 735

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Met Asp Pro
            740                 745                 750

Ala Thr Thr Thr Lys Pro Val Leu Arg Thr Pro Ser Pro Val His Pro
        755                 760                 765

Thr Gly Thr Ser Gln Pro Gln Arg Pro Glu Asp Cys Arg Pro Arg Gly
    770                 775                 780

Ser Val Lys Gly Thr Gly Leu Asp Phe Ala Cys Asp Ile Tyr Trp Ala
785                 790                 795                 800

Pro Leu Ala Gly Ile Cys Val Ala Leu Leu Leu Ser Leu Ile Ile Thr
                805                 810                 815

Leu Ile Cys Tyr His Arg Ser Arg Lys Arg Val Cys Lys Ser Gly Gly
            820                 825                 830

Gly Ser Phe Trp Glu Glu Phe Glu Ser Leu Gln Lys Gln Glu Val Lys
        835                 840                 845

Asn Leu His Gln Arg Leu Glu Gly Gln Arg Pro Glu Asn Lys Gly Lys
    850                 855                 860

Asn Arg Tyr Lys Asn Ile Leu Pro Phe Asp His Ser Arg Val Ile Leu
865                 870                 875                 880

Gln Gly Arg Asp Ser Asn Ile Pro Gly Ser Asp Tyr Ile Asn Ala Asn
                885                 890                 895
```

Tyr Ile Lys Asn Gln Leu Leu Gly Pro Asp Glu Asn Ala Lys Thr Tyr
900 905 910

Ile Ala Ser Gln Gly Cys Leu Glu Ala Thr Val Asn Asp Phe Trp Gln
915 920 925

Met Ala Trp Gln Glu Asn Ser Arg Val Ile Val Met Thr Thr Arg Glu
930 935 940

Val Glu Lys Gly Arg Asn Lys Cys Val Pro Tyr Trp Pro Glu Val Gly
945 950 955 960

Met Gln Arg Ala Tyr Gly Pro Tyr Ser Val Thr Asn Cys Gly Glu His
965 970 975

Asp Thr Thr Glu Tyr Lys Leu Arg Thr Leu Gln Val Ser Pro Leu Asp
980 985 990

Asn Gly Asp Leu Ile Arg Glu Ile Trp His Tyr Gln Tyr Leu Ser Trp
995 1000 1005

Pro Asp His Gly Val Pro Ser Glu Pro Gly Gly Val Leu Ser Phe
1010 1015 1020

Leu Asp Gln Ile Asn Gln Arg Gln Glu Ser Leu Pro His Ala Gly
1025 1030 1035

Pro Ile Ile Val His Cys Ser Ala Gly Ile Gly Arg Thr Gly Thr
1040 1045 1050

Ile Ile Val Ile Asp Met Leu Met Glu Asn Ile Ser Thr Lys Gly
1055 1060 1065

Leu Asp Cys Asp Ile Asp Ile Gln Lys Thr Ile Gln Met Val Arg
1070 1075 1080

Ala Gln Arg Ser Gly Met Val Gln Thr Glu Ala Gln Tyr Lys Phe
1085 1090 1095

Ile Tyr Val Ala Ile Ala Gln Phe Ile Glu Thr Thr Lys Lys Lys
1100 1105 1110

Leu

<210> 49
<211> 918
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of a AND NOT gate

<400> 49

```
Met Ser Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15

His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu
            20                  25                  30

Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln
        35                  40                  45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
    50                  55                  60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65                  70                  75                  80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
                85                  90                  95

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

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

Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser Gly Pro Gly
145                 150                 155                 160

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

Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg
            180                 185                 190

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr
        195                 200                 205

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

Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr
225                 230                 235                 240

Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala
                245                 250                 255
```

```
Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser 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 Phe Trp
305                 310                 315                 320

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
                325                 330                 335

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Arg Val Lys Phe Ser Arg
            340                 345                 350

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
        355                 360                 365

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
    370                 375                 380

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
385                 390                 395                 400

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
                405                 410                 415

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
            420                 425                 430

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
        435                 440                 445

Ala Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Glu Gly Arg Gly
    450                 455                 460

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala
465                 470                 475                 480

Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr Asp Ala
                485                 490                 495

Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
            500                 505                 510

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp Ile Tyr
        515                 520                 525
```

```
Phe Asn Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
    530                 535                 540

Leu Ile Tyr Asp Thr Asn Arg Leu Ala Asp Gly Val Pro Ser Arg Phe
545                 550                 555                 560

Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser Ser Leu
                565                 570                 575

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Lys Asn Tyr
            580                 585                 590

Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ser Gly
        595                 600                 605

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    610                 615                 620

Gly Gly Ser Arg Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
625                 630                 635                 640

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
                645                 650                 655

Thr Leu Ser Asn Tyr Gly Met His Trp Ile Arg Gln Ala Pro Gly Lys
            660                 665                 670

Gly Leu Glu Trp Val Ser Ser Ile Ser Leu Asn Gly Gly Ser Thr Tyr
        675                 680                 685

Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
    690                 695                 700

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

Ala Val Tyr Tyr Cys Ala Ala Gln Asp Ala Tyr Thr Gly Gly Tyr Phe
                725                 730                 735

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Met Asp Pro
            740                 745                 750

Ala Thr Thr Thr Lys Pro Val Leu Arg Thr Pro Ser Pro Val His Pro
        755                 760                 765

Thr Gly Thr Ser Gln Pro Gln Arg Pro Glu Asp Cys Arg Pro Arg Gly
    770                 775                 780

Ser Val Lys Gly Thr Gly Leu Asp Phe Ala Cys Asp Ile Leu Ile Gly
785                 790                 795                 800
```

```
Val Ser Val Val Phe Leu Phe Cys Leu Leu Leu Val Leu Phe Cys
                805                 810                 815

Leu His Arg Gln Asn Gln Ile Lys Gln Gly Pro Pro Arg Ser Lys Asp
            820                 825                 830

Glu Glu Gln Lys Pro Gln Gln Arg Pro Asp Leu Ala Val Asp Val Leu
        835                 840                 845

Glu Arg Thr Ala Asp Lys Ala Thr Val Asn Gly Leu Pro Glu Lys Asp
    850                 855                 860

Arg Glu Thr Asp Thr Ser Ala Leu Ala Ala Gly Ser Ser Gln Glu Val
865                 870                 875                 880

Thr Tyr Ala Gln Leu Asp His Trp Ala Leu Thr Gln Arg Thr Ala Arg
                885                 890                 895

Ala Val Ser Pro Gln Ser Thr Lys Pro Met Ala Glu Ser Ile Thr Tyr
            900                 905                 910

Ala Ala Val Ala Arg His
        915


<210>  50
<211>  1362
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Amino acid sequence of a AND NOT gate
       (MP16092.SFG.aCD19fmc63-CD8STK-CD28tmZ-2A-aCD33glx-muCD8STK-LAIR1
       tm-endo-2A-PTPN6_SH2-dCD148)

<400>  50

Met Ser Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15

His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu
            20                  25                  30

Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln
        35                  40                  45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
    50                  55                  60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65                  70                  75                  80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
                85                  90                  95
```

```
Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
            100                 105                 110

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

Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser Gly Pro Gly
145                 150                 155                 160

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

Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg
            180                 185                 190

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr
        195                 200                 205

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

Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr
225                 230                 235                 240

Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala
                245                 250                 255

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser 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 Phe Trp
305                 310                 315                 320

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
                325                 330                 335

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Arg Val Lys Phe Ser Arg
            340                 345                 350

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
        355                 360                 365
```

```
Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
    370                 375                 380

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
385                 390                 395                 400

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
                405                 410                 415

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
            420                 425                 430

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
        435                 440                 445

Ala Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Glu Gly Arg Gly
    450                 455                 460

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala
465                 470                 475                 480

Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr Asp Ala
                485                 490                 495

Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
            500                 505                 510

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp Ile Tyr
        515                 520                 525

Phe Asn Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
    530                 535                 540

Leu Ile Tyr Asp Thr Asn Arg Leu Ala Asp Gly Val Pro Ser Arg Phe
545                 550                 555                 560

Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser Ser Leu
                565                 570                 575

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Lys Asn Tyr
            580                 585                 590

Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ser Gly
        595                 600                 605

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    610                 615                 620

Gly Gly Ser Arg Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
625                 630                 635                 640
```

```
Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
                645                 650                 655

Thr Leu Ser Asn Tyr Gly Met His Trp Ile Arg Gln Ala Pro Gly Lys
            660                 665                 670

Gly Leu Glu Trp Val Ser Ser Ile Ser Leu Asn Gly Gly Ser Thr Tyr
        675                 680                 685

Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
    690                 695                 700

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

Ala Val Tyr Tyr Cys Ala Ala Gln Asp Ala Tyr Thr Gly Gly Tyr Phe
                725                 730                 735

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Met Asp Pro
            740                 745                 750

Thr Thr Thr Lys Pro Val Leu Arg Thr Pro Ser Pro Val His Pro Thr
        755                 760                 765

Gly Thr Ser Gln Pro Gln Arg Pro Glu Asp Cys Arg Pro Arg Gly Ser
    770                 775                 780

Val Lys Gly Thr Gly Leu Asp Phe Ala Cys Asp Ile Leu Ile Gly Val
785                 790                 795                 800

Ser Val Val Phe Leu Phe Cys Leu Leu Leu Leu Val Leu Phe Cys Leu
                805                 810                 815

His Arg Gln Asn Gln Ile Lys Gln Gly Pro Pro Arg Ser Lys Asp Glu
            820                 825                 830

Glu Gln Lys Pro Gln Gln Arg Pro Asp Leu Ala Val Asp Val Leu Glu
        835                 840                 845

Arg Thr Ala Asp Lys Ala Thr Val Asn Gly Leu Pro Glu Lys Asp Arg
    850                 855                 860

Glu Thr Asp Thr Ser Ala Leu Ala Ala Gly Ser Ser Gln Glu Val Thr
865                 870                 875                 880

Tyr Ala Gln Leu Asp His Trp Ala Leu Thr Gln Arg Thr Ala Arg Ala
                885                 890                 895

Val Ser Pro Gln Ser Thr Lys Pro Met Ala Glu Ser Ile Thr Tyr Ala
            900                 905                 910
```

```
Ala Val Ala Arg His Arg Ala Glu Gly Arg Gly Ser Leu Leu Thr Cys
        915                 920                 925

Gly Asp Val Glu Glu Asn Pro Gly Pro Trp Tyr His Gly His Met Ser
    930                 935                 940

Gly Gly Gln Ala Glu Thr Leu Leu Gln Ala Lys Gly Glu Pro Trp Thr
945                 950                 955                 960

Phe Leu Val Arg Glu Ser Leu Ser Gln Pro Gly Asp Phe Val Leu Ser
                965                 970                 975

Val Leu Ser Asp Gln Pro Lys Ala Gly Pro Gly Ser Pro Leu Arg Val
            980                 985                 990

Thr His Ile Lys Val Met Cys Glu  Gly Gly Arg Tyr Thr  Val Gly Gly
        995                 1000                1005

Leu Glu  Thr Phe Asp Ser Leu  Thr Asp Leu Val Glu  His Phe Lys
    1010                1015                1020

Lys Thr  Gly Ile Glu Glu Ala  Ser Gly Ala Phe Val  Tyr Leu Arg
    1025                1030                1035

Gln Pro  Tyr Ser Gly Gly Gly  Gly Ser Phe Glu Ala  Tyr Phe Lys
    1040                1045                1050

Lys Gln  Gln Ala Asp Ser Asn  Cys Gly Phe Ala Glu  Glu Tyr Glu
    1055                1060                1065

Asp Leu  Lys Leu Val Gly Ile  Ser Gln Pro Lys Tyr  Ala Ala Glu
    1070                1075                1080

Leu Ala  Glu Asn Arg Gly Lys  Asn Arg Tyr Asn Asn  Val Leu Pro
    1085                1090                1095

Tyr Asp  Ile Ser Arg Val Lys  Leu Ser Val Gln Thr  His Ser Thr
    1100                1105                1110

Asp Asp  Tyr Ile Asn Ala Asn  Tyr Met Pro Gly Tyr  His Ser Lys
    1115                1120                1125

Lys Asp  Phe Ile Ala Thr Gln  Gly Pro Leu Pro Asn  Thr Leu Lys
    1130                1135                1140

Asp Phe  Trp Arg Met Val Trp  Glu Lys Asn Val Tyr  Ala Ile Ile
    1145                1150                1155

Met Leu  Thr Lys Cys Val Glu  Gln Gly Arg Thr Lys  Cys Glu Glu
    1160                1165                1170
```

```
Tyr Trp  Pro Ser Lys Gln Ala  Gln Asp Tyr Gly Asp  Ile Thr Val
    1175                1180                1185

Ala Met  Thr Ser Glu Ile Val  Leu Pro Glu Trp Thr  Ile Arg Asp
    1190                1195                1200

Phe Thr  Val Lys Asn Ile Gln  Thr Ser Glu Ser His  Pro Leu Arg
    1205                1210                1215

Gln Phe  His Phe Thr Ser Trp  Pro Asp His Gly Val  Pro Asp Thr
    1220                1225                1230

Thr Asp  Leu Leu Ile Asn Phe  Arg Tyr Leu Val Arg  Asp Tyr Met
    1235                1240                1245

Lys Gln  Ser Pro Pro Glu Ser  Pro Ile Leu Val His  Cys Ser Ala
    1250                1255                1260

Gly Val  Gly Arg Thr Gly Thr  Phe Ile Ala Ile Asp  Arg Leu Ile
    1265                1270                1275

Tyr Gln  Ile Glu Asn Glu Asn  Thr Val Asp Val Tyr  Gly Ile Val
    1280                1285                1290

Tyr Asp  Leu Arg Met His Arg  Pro Leu Met Val Gln  Thr Glu Asp
    1295                1300                1305

Gln Tyr  Val Phe Leu Asn Gln  Cys Val Leu Asp Ile  Val Arg Ser
    1310                1315                1320

Gln Lys  Asp Ser Lys Val Asp  Leu Ile Tyr Gln Asn  Thr Thr Ala
    1325                1330                1335

Met Thr  Ile Tyr Glu Asn Leu  Ala Pro Val Thr Thr  Phe Gly Lys
    1340                1345                1350

Thr Asn  Gly Tyr Ile Ala Ser  Gly Ser
    1355                1360
```

<210> 51
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> APRIL-based (A proliferation-inducing ligand-based) CAR, CD8 stalk APRIL CAR

<400> 51

```
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1               5                  10                  15
```

```
Gly Ser Thr Gly Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser
            20                  25                  30

Lys Asp Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg
        35                  40                  45

Arg Gly Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp
    50                  55                  60

Ala Gly Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr
65                  70                  75                  80

Phe Thr Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu
                85                  90                  95

Thr Leu Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala
            100                 105                 110

Tyr Asn Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp
        115                 120                 125

Ile Leu Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser
    130                 135                 140

Pro His Gly Thr Phe Leu Gly Phe Val Lys Leu Ser Gly Gly Gly Ser
145                 150                 155                 160

Asp Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
                165                 170                 175

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
            180                 185                 190

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
        195                 200                 205

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
    210                 215                 220

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

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
                245                 250                 255

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
            260                 265                 270

Ala Tyr Arg Ser Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro
        275                 280                 285
```

Pro Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp
290 295 300

Ala His Ser Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala
305 310 315 320

Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
325 330 335

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
340 345 350

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
355 360 365

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
370 375 380

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
385 390 395 400

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
405 410 415

His Met Gln Ala Leu Pro Pro Arg
420

<210> 52
<211> 398
<212> PRT
<213> Artificial Sequence

<220>
<223> APRIL-based (A proliferation-inducing ligand-based) CAR, APRIL IgG1 hinge based CAR

<400> 52

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser
20 25 30

Lys Asp Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg
35 40 45

Arg Gly Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp
50 55 60

Ala Gly Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr
65 70 75 80

Phe Thr Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu

85 90 95

Thr Leu Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala
100 105 110

Tyr Asn Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp
115 120 125

Ile Leu Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser
130 135 140

Pro His Gly Thr Phe Leu Gly Phe Val Lys Leu Ser Gly Gly Gly Ser
145 150 155 160

Asp Pro Ala Glu Pro Lys Ser Pro Asp Lys Thr His Thr Cys Pro Pro
165 170 175

Cys Pro Lys Asp Pro Lys Phe Trp Val Leu Val Val Val Gly Gly Val
180 185 190

Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp
195 200 205

Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
210 215 220

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
225 230 235 240

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

Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro Ile
260 265 270

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

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

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
305 310 315 320

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
325 330 335

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
340 345 350

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg

355 360 365

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
370 375 380

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
385 390 395

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Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser
20 25 30

Lys Asp Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg
35 40 45

Arg Gly Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp
50 55 60

Ala Gly Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr
65 70 75 80

Phe Thr Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu
85 90 95

Thr Leu Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala
100 105 110

Tyr Asn Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp
115 120 125

Ile Leu Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser
130 135 140

Pro His Gly Thr Phe Leu Gly Phe Val Lys Leu Ser Gly Gly Gly Ser
145 150 155 160

Asp Pro Ala Glu Pro Lys Ser Pro Asp Lys Thr His Thr Cys Pro Pro
165 170 175

Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro
180 185 190

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Lys Pro Lys Asp Thr Leu Met Ile Ala Arg Thr Pro Glu Val Thr Cys
        195                 200                 205

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
    210                 215                 220

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
225                 230                 235                 240

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
                245                 250                 255

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
            260                 265                 270

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

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
    290                 295                 300

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
305                 310                 315                 320

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
                325                 330                 335

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
            340                 345                 350

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
        355                 360                 365

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
    370                 375                 380

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Lys Asp Pro Lys Phe Trp
385                 390                 395                 400

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
                405                 410                 415

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

Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr
        435                 440                 445

Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr
    450                 455                 460
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Arg Ser Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly
465                 470                 475                 480

Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His
                485                 490                 495

Ser Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
            500                 505                 510

Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
        515                 520                 525

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
    530                 535                 540

Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu
545                 550                 555                 560

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
                565                 570                 575

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
            580                 585                 590

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
        595                 600                 605

Gln Ala Leu Pro Pro Arg
    610
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