SEQUENCE LISTING

<110> A2 BIOTHERAPEUTICS, INC.

<120> COMPOSITIONS AND METHODS FOR TREATING MESOTHELIN POSITIVE CANCERS

<130> A2BI-019/03WO 331656-2068

<150> US 63/085,971
<151> 2020-09-30

<150> US 63/068,245
<151> 2020-08-20

<160> 1255

<170> PatentIn version 3.5

<210> 1
<211> 622
<212> PRT
<213> Homo sapiens

<400> 1

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Met Ala Leu Pro Thr Ala Arg Pro Leu Leu Gly Ser Cys Gly Thr Pro
1               5                   10                  15


Ala Leu Gly Ser Leu Leu Phe Leu Leu Phe Ser Leu Gly Trp Val Gln
            20                  25                  30


Pro Ser Arg Thr Leu Ala Gly Glu Thr Gly Gln Glu Ala Ala Pro Leu
        35                  40                  45


Asp Gly Val Leu Ala Asn Pro Pro Asn Ile Ser Ser Leu Ser Pro Arg
    50                  55                  60


Gln Leu Leu Gly Phe Pro Cys Ala Glu Val Ser Gly Leu Ser Thr Glu
65                  70                  75                  80


Arg Val Arg Glu Leu Ala Val Ala Leu Ala Gln Lys Asn Val Lys Leu
                85                  90                  95


Ser Thr Glu Gln Leu Arg Cys Leu Ala His Arg Leu Ser Glu Pro Pro
            100                 105                 110


Glu Asp Leu Asp Ala Leu Pro Leu Asp Leu Leu Leu Phe Leu Asn Pro
```

```
        115                 120                 125

Asp Ala Phe Ser Gly Pro Gln Ala Cys Thr Arg Phe Phe Ser Arg Ile
    130                 135                 140

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

Arg Leu Leu Pro Ala Ala Leu Ala Cys Trp Gly Val Arg Gly Ser Leu
                165                 170                 175

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

Pro Gly Arg Phe Val Ala Glu Ser Ala Glu Val Leu Leu Pro Arg Leu
        195                 200                 205

Val Ser Cys Pro Gly Pro Leu Asp Gln Asp Gln Gln Glu Ala Ala Arg
    210                 215                 220

Ala Ala Leu Gln Gly Gly Gly Pro Pro Tyr Gly Pro Pro Ser Thr Trp
225                 230                 235                 240

Ser Val Ser Thr Met Asp Ala Leu Arg Gly Leu Leu Pro Val Leu Gly
                245                 250                 255

Gln Pro Ile Ile Arg Ser Ile Pro Gln Gly Ile Val Ala Ala Trp Arg
            260                 265                 270

Gln Arg Ser Ser Arg Asp Pro Ser Trp Arg Gln Pro Glu Arg Thr Ile
        275                 280                 285

Leu Arg Pro Arg Phe Arg Arg Glu Val Glu Lys Thr Ala Cys Pro Ser
    290                 295                 300

Gly Lys Lys Ala Arg Glu Ile Asp Glu Ser Leu Ile Phe Tyr Lys Lys
305                 310                 315                 320

Trp Glu Leu Glu Ala Cys Val Asp Ala Ala Leu Leu Ala Thr Gln Met
                325                 330                 335
```

```
Asp Arg Val Asn Ala Ile Pro Phe Thr Tyr Glu Gln Leu Asp Val Leu
            340                 345                 350

Lys His Lys Leu Asp Glu Leu Tyr Pro Gln Gly Tyr Pro Glu Ser Val
        355                 360                 365

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

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

Val Asn Lys Gly His Glu Met Ser Pro Gln Val Ala Thr Leu Ile Asp
                405                 410                 415

Arg Phe Val Lys Gly Arg Gly Gln Leu Asp Lys Asp Thr Leu Asp Thr
            420                 425                 430

Leu Thr Ala Phe Tyr Pro Gly Tyr Leu Cys Ser Leu Ser Pro Glu Glu
        435                 440                 445

Leu Ser Ser Val Pro Pro Ser Ser Ile Trp Ala Val Arg Pro Gln Asp
    450                 455                 460

Leu Asp Thr Cys Asp Pro Arg Gln Leu Asp Val Leu Tyr Pro Lys Ala
465                 470                 475                 480

Arg Leu Ala Phe Gln Asn Met Asn Gly Ser Glu Tyr Phe Val Lys Ile
                485                 490                 495

Gln Ser Phe Leu Gly Gly Ala Pro Thr Glu Asp Leu Lys Ala Leu Ser
            500                 505                 510

Gln Gln Asn Val Ser Met Asp Leu Ala Thr Phe Met Lys Leu Arg Thr
        515                 520                 525

Asp Ala Val Leu Pro Leu Thr Val Ala Glu Val Gln Lys Leu Leu Gly
    530                 535                 540

Pro His Val Glu Gly Leu Lys Ala Glu Glu Arg His Arg Pro Val Arg
```

545 550 555 560

Asp Trp Ile Leu Arg Gln Arg Gln Asp Asp Leu Asp Thr Leu Gly Leu
565 570 575

Gly Leu Gln Gly Gly Ile Pro Asn Gly Tyr Leu Val Leu Asp Leu Ser
580 585 590

Met Gln Glu Ala Leu Ser Gly Thr Pro Cys Leu Leu Gly Pro Gly Pro
595 600 605

Val Leu Thr Val Leu Ala Leu Leu Leu Ala Ser Thr Leu Ala
610 615 620

<210> 2
<211> 630
<212> PRT
<213> Homo sapiens

<400> 2

Met Ala Leu Pro Thr Ala Arg Pro Leu Leu Gly Ser Cys Gly Thr Pro
1 5 10 15

Ala Leu Gly Ser Leu Leu Phe Leu Leu Phe Ser Leu Gly Trp Val Gln
20 25 30

Pro Ser Arg Thr Leu Ala Gly Glu Thr Gly Gln Glu Ala Ala Pro Leu
35 40 45

Asp Gly Val Leu Ala Asn Pro Pro Asn Ile Ser Ser Leu Ser Pro Arg
50 55 60

Gln Leu Leu Gly Phe Pro Cys Ala Glu Val Ser Gly Leu Ser Thr Glu
65 70 75 80

Arg Val Arg Glu Leu Ala Val Ala Leu Ala Gln Lys Asn Val Lys Leu
85 90 95

Ser Thr Glu Gln Leu Arg Cys Leu Ala His Arg Leu Ser Glu Pro Pro
100 105 110

```
Glu Asp Leu Asp Ala Leu Pro Leu Asp Leu Leu Leu Phe Leu Asn Pro
        115                 120                 125

Asp Ala Phe Ser Gly Pro Gln Ala Cys Thr Arg Phe Phe Ser Arg Ile
    130                 135                 140

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

Arg Leu Leu Pro Ala Ala Leu Ala Cys Trp Gly Val Arg Gly Ser Leu
                165                 170                 175

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

Pro Gly Arg Phe Val Ala Glu Ser Ala Glu Val Leu Leu Pro Arg Leu
        195                 200                 205

Val Ser Cys Pro Gly Pro Leu Asp Gln Asp Gln Gln Glu Ala Ala Arg
    210                 215                 220

Ala Ala Leu Gln Gly Gly Gly Pro Pro Tyr Gly Pro Pro Ser Thr Trp
225                 230                 235                 240

Ser Val Ser Thr Met Asp Ala Leu Arg Gly Leu Leu Pro Val Leu Gly
                245                 250                 255

Gln Pro Ile Ile Arg Ser Ile Pro Gln Gly Ile Val Ala Ala Trp Arg
            260                 265                 270

Gln Arg Ser Ser Arg Asp Pro Ser Trp Arg Gln Pro Glu Arg Thr Ile
        275                 280                 285

Leu Arg Pro Arg Phe Arg Arg Glu Val Glu Lys Thr Ala Cys Pro Ser
    290                 295                 300

Gly Lys Lys Ala Arg Glu Ile Asp Glu Ser Leu Ile Phe Tyr Lys Lys
305                 310                 315                 320

Trp Glu Leu Glu Ala Cys Val Asp Ala Ala Leu Leu Ala Thr Gln Met
                325                 330                 335
```

```
Asp Arg Val Asn Ala Ile Pro Phe Thr Tyr Glu Gln Leu Asp Val Leu
            340                 345                 350

Lys His Lys Leu Asp Glu Leu Tyr Pro Gln Gly Tyr Pro Glu Ser Val
        355                 360                 365

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

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

Val Asn Lys Gly His Glu Met Ser Pro Gln Ala Pro Arg Arg Pro Leu
                405                 410                 415

Pro Gln Val Ala Thr Leu Ile Asp Arg Phe Val Lys Gly Arg Gly Gln
            420                 425                 430

Leu Asp Lys Asp Thr Leu Asp Thr Leu Thr Ala Phe Tyr Pro Gly Tyr
        435                 440                 445

Leu Cys Ser Leu Ser Pro Glu Glu Leu Ser Ser Val Pro Pro Ser Ser
    450                 455                 460

Ile Trp Ala Val Arg Pro Gln Asp Leu Asp Thr Cys Asp Pro Arg Gln
465                 470                 475                 480

Leu Asp Val Leu Tyr Pro Lys Ala Arg Leu Ala Phe Gln Asn Met Asn
                485                 490                 495

Gly Ser Glu Tyr Phe Val Lys Ile Gln Ser Phe Leu Gly Gly Ala Pro
            500                 505                 510

Thr Glu Asp Leu Lys Ala Leu Ser Gln Gln Asn Val Ser Met Asp Leu
        515                 520                 525

Ala Thr Phe Met Lys Leu Arg Thr Asp Ala Val Leu Pro Leu Thr Val
    530                 535                 540
```

```
Ala Glu Val Gln Lys Leu Leu Gly Pro His Val Glu Gly Leu Lys Ala
545                 550                 555                 560


Glu Glu Arg His Arg Pro Val Arg Asp Trp Ile Leu Arg Gln Arg Gln
                565                 570                 575


Asp Asp Leu Asp Thr Leu Gly Leu Gly Leu Gln Gly Gly Ile Pro Asn
            580                 585                 590


Gly Tyr Leu Val Leu Asp Leu Ser Met Gln Glu Ala Leu Ser Gly Thr
        595                 600                 605


Pro Cys Leu Leu Gly Pro Gly Pro Val Leu Thr Val Leu Ala Leu Leu
    610                 615                 620


Leu Ala Ser Thr Leu Ala
625                 630


<210>  3
<211>  237
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  MSLN scFv domain

<400>  3

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Glu Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80
```

```
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Ser Gly Trp Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110

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

Gly Ser Gly Gly Asp Ile Val Met Thr Gln Ser Ser Ser Leu Ser Ala
    130                 135                 140

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile
145                 150                 155                 160

Arg Tyr Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
                165                 170                 175

Leu Leu Ile Tyr Thr Ala Ser Ile Leu Gln Asn Gly Val Pro Ser Arg
            180                 185                 190

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
        195                 200                 205

Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Thr Tyr Thr
    210                 215                 220

Thr Pro Asp Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
225                 230                 235
```

<210> 4
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 4

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Arg Ala Pro Gly Ala
1               5                   10                  15
```

```
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Thr Phe Arg Gly Tyr
            20                  25                  30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Arg Ala Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95

Ala Arg Thr Ala Ser Cys Gly Gly Asp Cys Tyr Tyr Leu Asp Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr
    130                 135                 140

Gln Ser Pro Pro Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160

Thr Cys Arg Ala Ser Glu Asn Val Asn Ile Trp Leu Ala Trp Tyr Gln
                165                 170                 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ser Ser Ser
            180                 185                 190

Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Ala
        195                 200                 205

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr
    210                 215                 220

Tyr Tyr Cys Gln Gln Tyr Gln Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225                 230                 235                 240
```

Thr Lys Val Glu Ile Lys
245

<210> 5
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 5

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
20 25 30

Thr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Leu Ile Thr Pro Tyr Asn Gly Ala Ser Ser Tyr Asn Gln Lys Phe
50 55 60

Arg Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Tyr Asp Gly Arg Gly Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro
130 135 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser
145 150 155 160

Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly
165 170 175

Lys Ala Pro Lys Arg Leu Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly
180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu
195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
210 215 220

Gln Trp Ser Gly Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu
225 230 235 240

Ile Lys

<210> 6
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 6

Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Glu Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
20 25 30

Thr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Leu Ile Thr Pro Tyr Asn Gly Ala Ser Ser Tyr Asn Gln Lys Phe
50 55 60

Arg Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

```
Met Asp Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85                  90                  95

Ala Arg Gly Gly Tyr Asp Gly Arg Gly Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Glu Leu Thr Gln Ser Pro
    130                 135                 140

Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser
145                 150                 155                 160

Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Ser Gly
                165                 170                 175

Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly
            180                 185                 190

Val Pro Gly Arg Phe Ser Gly Ser Gly Ser Gly Asn Ser Tyr Ser Leu
        195                 200                 205

Thr Ile Ser Ser Val Glu Ala Glu Asp Asp Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Trp Ser Gly Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu
225                 230                 235                 240

Ile Lys
```

<210> 7
<211> 45
<212> PRT
<213> Unknown

<220>
<223> CD8alpha hinge

<400> 7

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

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

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

<210> 8
<211> 135
<212> DNA
<213> Unknown

<220>
<223> encodes CD8alpha hinge

<400> 8
accacgacgc cagcgccgcg accaccaaca ccggcgccca ccatcgcgtc gcagcccctg 60

tccctgcgcc cagaggcgtg ccggccagcg gcgggggggcg cagtgcacac gagggggctg 120

gacttcgcct gtgat 135

<210> 9
<211> 41
<212> PRT
<213> Unknown

<220>
<223> CD28 hinge

<400> 9

Cys Thr Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys
1 5 10 15

Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser
20 25 30

Pro Leu Phe Pro Gly Pro Ser Lys Pro
35 40

<210> 10
<211> 123

<212> DNA
<213> Unknown

<220>
<223> encodes CD28 hinge

<400> 10
tgtaccattg aagttatgta tcctcctcct tacctagaca atgagaagag caatggaacc 60

attatccatg tgaaagggaa acacctttgt ccaagtcccc tatttcccgg accttctaag 120

ccc 123

<210> 11
<211> 27
<212> PRT
<213> Unknown

<220>
<223> CD28 transmembrane domain

<400> 11

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
20 25

<210> 12
<211> 81
<212> DNA
<213> Unknown

<220>
<223> encodes CD28 transmembrane domain

<400> 12
ttctgggtgc tggtcgttgt gggcggcgtg ctggcctgct acagcctgct ggtgacagtg 60

gccttcatca tcttttgggt g 81

<210> 13
<211> 25
<212> PRT
<213> Unknown

<220>
<223> IL-2Rbeta transmembrane domain

<400> 13

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

Phe Ile Ile Leu Val Tyr Leu Leu Ile
20 25

<210> 14
<211> 75
<212> DNA
<213> Unknown

<220>
<223> encodes IL-2Rbeta transmembrane domain

<400> 14
attccgtggc tcggccacct cctcgtgggc ctcagcgggg cttttggctt catcatctta 60

gtgtacttgc tgatc 75

<210> 15
<211> 112
<212> PRT
<213> Unknown

<220>
<223> CD3zeta activation domain

<400> 15

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly
1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
20 25 30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
35 40 45

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
50 55 60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65 70 75 80

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
85 90 95

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
100 105 110

<210> 16
<211> 336
<212> DNA
<213> Unknown

<220>
<223> encodes CD3zeta activation domain

<400> 16
agagtgaagt tcagcaggag cgcagacgcc cccgcgtaca agcagggcca gaaccagctc 60

tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gcgtagaggc 120

cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 180

gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc 240

cggaggggca aggggcacga tggcctttac cagggactca gtacagccac caaggacacc 300

tacgacgccc ttcacatgca ggccctgccc cctcgc 336

<210> 17
<211> 43
<212> PRT
<213> Unknown

<220>
<223> CD3zeta activation domain

<400> 17

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
20 25 30

Asp Val Leu His Met Gln Ala Leu Pro Pro Arg
35 40

<210> 18
<211> 129

<212> DNA
<213> Unknown

<220>
<223> encodes CD3zeta activation domain

<400> 18
agagtgaagt tcagcaggag cgcagacgcc cccgcgtacc agcagggcca gaaccagctc 60

tataacgagc tcaatctagg acgaagagag gagtacgatg ttttgcacat gcaggccctg 120

ccccctcgc 129

<210> 19
<211> 41
<212> PRT
<213> Unknown

<220>
<223> CD28 co-stimulatory domain

<400> 19

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
1 5 10 15

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
20 25 30

Pro Arg Asp Phe Ala Ala Tyr Arg Ser
35 40

<210> 20
<211> 123
<212> DNA
<213> Unknown

<220>
<223> encodes CD28 co-stimulatory domain

<400> 20
aggagcaagc ggagcagact gctgcacagc gactacatga acatgacccc ccggaggcct 60

ggccccaccc ggaagcacta ccagccctac gcccctccca gggatttcgc cgcctaccgg 120

agc 123

<210> 21
<211> 23

<212> PRT
<213> Unknown

<220>
<223> TCR alpha transmembrane domain

<400> 21

Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu
1   5   10   15

Leu Met Thr Leu Arg Leu Trp
            20

<210> 22
<211> 69
<212> DNA
<213> Unknown

<220>
<223> encodes TCR alpha transmembrane domain

<400> 22
gtgattgggt tccgaatcct cctcctgaaa gtggccgggt ttaatctgct catgacgctg   60

cggctgtgg   69

<210> 23
<211> 23
<212> PRT
<213> Unknown

<220>
<223> TCR beta transmembrane domain

<400> 23

Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val
1   5   10   15

Leu Val Ser Ala Leu Val Leu
            20

<210> 24
<211> 69
<212> DNA
<213> Unknown

<220>

<223> encodes TCR beta transmembrane domain

<400> 24
accatcctct atgagatctt gctagggaag gccaccttgt atgccgtgct ggtcagtgcc 60

ctcgtgctg 69

<210> 25
<211> 10
<212> PRT
<213> Unknown

<220>
<223> TCR beta intracellular domain

<400> 25

Met Ala Met Val Lys Arg Lys Asp Ser Arg
1 5 10

<210> 26
<211> 30
<212> DNA
<213> Unknown

<220>
<223> encodes TCR beta intracellular domain

<400> 26
atggccatgg tcaagagaaa ggattccaga 30

<210> 27
<211> 532
<212> PRT
<213> Homo sapiens

<400> 27

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

Leu Gly Ala Leu Phe Pro Gly Pro Gly Asn Ala Gln Thr Ser Val Ser
            20 25 30

Pro Ser Lys Val Ile Leu Pro Arg Gly Gly Ser Val Leu Val Thr Cys
        35 40 45

Ser Thr Ser Cys Asp Gln Pro Lys Leu Leu Gly Ile Glu Thr Pro Leu

```
    50                  55                  60

Pro Lys Lys Glu Leu Leu Leu Pro Gly Asn Asn Arg Lys Val Tyr Glu
65                  70                  75                  80

Leu Ser Asn Val Gln Glu Asp Ser Gln Pro Met Cys Tyr Ser Asn Cys
                85                  90                  95

Pro Asp Gly Gln Ser Thr Ala Lys Thr Phe Leu Thr Val Tyr Trp Thr
            100                 105                 110

Pro Glu Arg Val Glu Leu Ala Pro Leu Pro Ser Trp Gln Pro Val Gly
        115                 120                 125

Lys Asn Leu Thr Leu Arg Cys Gln Val Glu Gly Gly Ala Pro Arg Ala
    130                 135                 140

Asn Leu Thr Val Val Leu Leu Arg Gly Glu Lys Glu Leu Lys Arg Glu
145                 150                 155                 160

Pro Ala Val Gly Glu Pro Ala Glu Val Thr Thr Thr Val Leu Val Arg
                165                 170                 175

Arg Asp His His Gly Ala Asn Phe Ser Cys Arg Thr Glu Leu Asp Leu
            180                 185                 190

Arg Pro Gln Gly Leu Glu Leu Phe Glu Asn Thr Ser Ala Pro Tyr Gln
        195                 200                 205

Leu Gln Thr Phe Val Leu Pro Ala Thr Pro Pro Gln Leu Val Ser Pro
    210                 215                 220

Arg Val Leu Glu Val Asp Thr Gln Gly Thr Val Val Cys Ser Leu Asp
225                 230                 235                 240

Gly Leu Phe Pro Val Ser Glu Ala Gln Val His Leu Ala Leu Gly Asp
                245                 250                 255

Gln Arg Leu Asn Pro Thr Val Thr Tyr Gly Asn Asp Ser Phe Ser Ala
            260                 265                 270
```

```
Lys Ala Ser Val Ser Val Thr Ala Glu Asp Glu Gly Thr Gln Arg Leu
        275                 280                 285

Thr Cys Ala Val Ile Leu Gly Asn Gln Ser Gln Glu Thr Leu Gln Thr
    290                 295                 300

Val Thr Ile Tyr Ser Phe Pro Ala Pro Asn Val Ile Leu Thr Lys Pro
305                 310                 315                 320

Glu Val Ser Glu Gly Thr Glu Val Thr Val Lys Cys Glu Ala His Pro
                325                 330                 335

Arg Ala Lys Val Thr Leu Asn Gly Val Pro Ala Gln Pro Leu Gly Pro
            340                 345                 350

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

Phe Ser Cys Ser Ala Thr Leu Glu Val Ala Gly Gln Leu Ile His Lys
    370                 375                 380

Asn Gln Thr Arg Glu Leu Arg Val Leu Tyr Gly Pro Arg Leu Asp Glu
385                 390                 395                 400

Arg Asp Cys Pro Gly Asn Trp Thr Trp Pro Glu Asn Ser Gln Gln Thr
                405                 410                 415

Pro Met Cys Gln Ala Trp Gly Asn Pro Leu Pro Glu Leu Lys Cys Leu
            420                 425                 430

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

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

Glu Val Thr Arg Lys Val Thr Val Asn Val Leu Ser Pro Arg Tyr Glu
465                 470                 475                 480

Ile Val Ile Ile Thr Val Val Ala Ala Ala Val Ile Met Gly Thr Ala
```

```
                485                 490                 495

Gly Leu Ser Thr Tyr Leu Tyr Asn Arg Gln Arg Lys Ile Lys Lys Tyr
            500                 505                 510

Arg Leu Gln Gln Ala Gln Lys Gly Thr Pro Met Lys Pro Asn Thr Gln
        515                 520                 525

Ala Thr Pro Pro
    530
```

<210> 28
<211> 271
<212> PRT
<213> Homo sapiens

<400> 28

```
Met Pro Glu Ala Pro Pro Leu Leu Leu Ala Ala Val Leu Leu Gly Leu
1               5                   10                  15

Val Leu Leu Val Val Leu Leu Leu Leu Leu Arg His Trp Gly Trp Gly
            20                  25                  30

Leu Cys Leu Ile Gly Trp Asn Glu Phe Ile Leu Gln Pro Ile His Asn
        35                  40                  45

Leu Leu Met Gly Asp Thr Lys Glu Gln Arg Ile Leu Asn His Val Leu
    50                  55                  60

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

Thr Tyr Cys Glu Gln Lys Glu Trp Ala Met Asn Val Gly Asp Lys Lys
                85                  90                  95

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

Leu Glu Leu Gly Ala Tyr Cys Gly Tyr Ser Ala Val Arg Met Ala Arg
        115                 120                 125
```

```
Leu Leu Ser Pro Gly Ala Arg Leu Ile Thr Ile Glu Ile Asn Pro Asp
    130                 135                 140

Cys Ala Ala Ile Thr Gln Arg Met Val Asp Phe Ala Gly Val Lys Asp
145                 150                 155                 160

Lys Val Thr Leu Val Val Gly Ala Ser Gln Asp Ile Ile Pro Gln Leu
                165                 170                 175

Lys Lys Lys Tyr Asp Val Asp Thr Leu Asp Met Val Phe Leu Asp His
            180                 185                 190

Trp Lys Asp Arg Tyr Leu Pro Asp Thr Leu Leu Leu Glu Glu Cys Gly
        195                 200                 205

Leu Leu Arg Lys Gly Thr Val Leu Leu Ala Asp Asn Val Ile Cys Pro
    210                 215                 220

Gly Ala Pro Asp Phe Leu Ala His Val Arg Gly Ser Ser Cys Phe Glu
225                 230                 235                 240

Cys Thr His Tyr Gln Ser Phe Leu Glu Tyr Arg Glu Val Val Asp Gly
                245                 250                 255

Leu Glu Lys Ala Ile Tyr Lys Gly Pro Gly Ser Glu Ala Gly Pro
            260                 265                 270
```

<210> 29
<211> 273
<212> PRT
<213> Homo sapiens

<400> 29

```
Met Ser Gly Ser Gln Ser Glu Val Ala Pro Ser Pro Gln Ser Pro Arg
1               5                   10                  15

Ser Pro Glu Met Gly Arg Asp Leu Arg Pro Gly Ser Arg Val Leu Leu
            20                  25                  30

Leu Leu Leu Leu Leu Leu Leu Val Tyr Leu Thr Gln Pro Gly Asn Gly
        35                  40                  45
```

```
Asn Glu Gly Ser Val Thr Gly Ser Cys Tyr Cys Gly Lys Arg Ile Ser
    50                  55                  60

Ser Asp Ser Pro Pro Ser Val Gln Phe Met Asn Arg Leu Arg Lys His
65                  70                  75                  80

Leu Arg Ala Tyr His Arg Cys Leu Tyr Tyr Thr Arg Phe Gln Leu Leu
                85                  90                  95

Ser Trp Ser Val Cys Gly Gly Asn Lys Asp Pro Trp Val Gln Glu Leu
            100                 105                 110

Met Ser Cys Leu Asp Leu Lys Glu Cys Gly His Ala Tyr Ser Gly Ile
        115                 120                 125

Val Ala His Gln Lys His Leu Leu Pro Thr Ser Pro Pro Ile Ser Gln
    130                 135                 140

Ala Ser Glu Gly Ala Ser Ser Asp Ile His Thr Pro Ala Gln Met Leu
145                 150                 155                 160

Leu Ser Thr Leu Gln Ser Thr Gln Arg Pro Thr Leu Pro Val Gly Ser
                165                 170                 175

Leu Ser Ser Asp Lys Glu Leu Thr Arg Pro Asn Glu Thr Thr Ile His
            180                 185                 190

Thr Ala Gly His Ser Leu Ala Ala Gly Pro Glu Ala Gly Glu Asn Gln
        195                 200                 205

Lys Gln Pro Glu Lys Asn Ala Gly Pro Thr Ala Arg Thr Ser Ala Thr
    210                 215                 220

Val Pro Val Leu Cys Leu Leu Ala Ile Ile Phe Ile Leu Thr Ala Ala
225                 230                 235                 240

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

Ser Pro Asp Leu Pro Val His Tyr Ile Pro Val Ala Pro Asp Ser Asn
```

260 265 270

Thr

<210> 30
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA scFv binding domain

<400> 30

Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly
85 90 95

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

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

Gly Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly
130 135 140

Ala Ser Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser

145 150 155 160

Tyr His Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp
165 170 175

Ile Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Glu Tyr Asn Glu Lys
180 185 190

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
195 200 205

Tyr Met His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
210 215 220

Cys Ala Arg Glu Glu Ile Thr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
225 230 235 240

Thr Ser Val Thr Val Ser Ser
245

<210> 31
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA scFv binding domain

<400> 31

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

His Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Glu Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr

65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Glu Ile Thr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ser
145 150 155 160

Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Lys Val Ser
180 185 190

Asn Arg Phe Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala
210 215 220

Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Arg Thr Phe Gly Gly
225 230 235 240

Gly Thr Lys Val Glu Ile Lys
245

<210> 32
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA scFv binding domain

<400> 32

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


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30


His Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Glu Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Gly Lys Ala Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Glu Glu Ile Thr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125


Gly Gly Gly Gly Ser Gly Gly Asp Ile Val Met Thr Gln Thr Pro Leu
    130                 135                 140


Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser
145                 150                 155                 160


Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr
                165                 170                 175


Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Lys Val Ser
            180                 185                 190


Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205
```

Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly
210 215 220

Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Arg Thr Phe Gly Gly
225 230 235 240

Gly Thr Lys Val Glu Ile Lys
245

<210> 33
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA scFv binding domain

<400> 33

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

His Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Glu Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Glu Ile Thr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

```
Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser
    130                 135                 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ser
145                 150                 155                 160

Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr
                165                 170                 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Val Ser
            180                 185                 190

Asn Arg Phe Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
    210                 215                 220

Thr Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Arg Thr Phe Gly Gly
225                 230                 235                 240

Gly Thr Lys Val Glu Ile Lys
                245
```

<210> 34
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA scFv binding domain

<400> 34

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30

His Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
```

```
Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Glu Tyr Asn Glu Lys Phe
    50                  55                  60

Lys Gly Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Glu Ile Thr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser
    130                 135                 140

Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ser
145                 150                 155                 160

Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr
                165                 170                 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Val Ser
            180                 185                 190

Asn Arg Phe Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205

Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala
    210                 215                 220

Thr Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Arg Thr Phe Gly Gln
225                 230                 235                 240

Gly Thr Lys Val Glu Val Lys
                245
```

<210> 35

<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA scFv binding domain

<400> 35

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

His Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Tyr Pro Gly Asn Val Asn Thr Glu Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Thr Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg Glu Glu Ile Thr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Asp Val Gln Met Thr Gln Ser Pro Ser
130 135 140

Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ser
145 150 155 160

Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Met Glu Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Val Ser

```
            180                 185                 190

Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205

Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala
    210                 215                 220

Thr Tyr Tyr Cys His Gln Gly Ser His Val Pro Arg Thr Phe Gly Gln
225                 230                 235                 240

Gly Thr Lys Val Glu Val Lys
                245
```

<210> 36
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA scFv binding domain

<400> 36

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30

His Ile Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45

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

Lys Gly Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

Met Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Phe Cys
                85                  90                  95

Ala Arg Glu Gly Thr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
```

```
            100                 105                 110

Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Gly Gly Asp Val Leu Met Thr Gln Thr Pro Leu
    130                 135                 140

Ser Leu Pro Val Ser Leu Gly Asp Gln Val Ser Ile Ser Cys Arg Ser
145                 150                 155                 160

Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr
                165                 170                 175

Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser
            180                 185                 190

Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205

Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly
    210                 215                 220

Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Arg Thr Phe Gly Gly
225                 230                 235                 240

Gly Thr Lys Leu Glu Ile Lys
                245
```

<210> 37
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA scFv binding domain

<400> 37

```
Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Thr Phe Thr Ser Tyr
```

```
            20                  25                  30

His Ile Gln Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45

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

Lys Gly Arg Ala Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

Leu Asn Leu Asp Ser Val Ser Ala Ala Asp Thr Ala Ile Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Gly Thr Tyr Tyr Ala Met Asp Tyr Trp Gly Lys Gly Ser
            100                 105                 110

Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser
    130                 135                 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ser
145                 150                 155                 160

Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr
                165                 170                 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Val Ser
            180                 185                 190

Asn Arg Phe Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205

Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala
    210                 215                 220

Thr Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Arg Thr Phe Gly Pro
225                 230                 235                 240
```

Gly Thr Lys Val Asp Ile Lys
245

<210> 38
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA scFv binding domain

<400> 38

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Leu Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

His Ile Gln Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

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

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Thr Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Thr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser
130 135 140

Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ser
145 150 155 160

```
Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr
                165                 170                 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Val Ser
            180                 185                 190

Asn Arg Phe Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala
    210                 215                 220

Thr Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Arg Thr Phe Gly Gln
225                 230                 235                 240

Gly Thr Lys Val Glu Val Lys
                245
```

<210> 39
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA scFv binding domain

<400> 39

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30

His Ile Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

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

Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80
```

```
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Gly Thr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Gly Gly Glu Ile Val Leu Thr Gln Ser Pro Gly
    130                 135                 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ser
145                 150                 155                 160

Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr
                165                 170                 175

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Lys Val Ser
            180                 185                 190

Asn Arg Phe Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205

Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala
    210                 215                 220

Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Arg Thr Phe Gly Gly
225                 230                 235                 240

Gly Thr Lys Val Glu Ile Lys
                245
```

<210> 40
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA scFv binding domain

<400> 40

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

Ser Val Lys Val Ser Cys Thr Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30

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

Gly Arg Ile Tyr Pro Gly Asp Gly Ser Thr Gln Tyr Asn Glu Lys Phe
    50                  55                  60

Lys Gly Lys Val Thr Ile Thr Ala Asp Lys Ser Met Asp Thr Ser Phe
65                  70                  75                  80

Met Glu Leu Thr Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Gly Thr Tyr Tyr Ala Met Asp Leu Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Gly Gly Glu Ile Val Leu Thr Gln Ser Pro Gly
    130                 135                 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ser
145                 150                 155                 160

Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Ala Trp Tyr
                165                 170                 175

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Ser Lys Val Ser
            180                 185                 190

Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205

Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala
```

```
    210                 215                 220

Val Tyr Tyr Cys Gln Gln Gly Ser His Val Pro Arg Thr Phe Gly Gly
225                 230                 235                 240

Gly Thr Lys Val Glu Ile Lys
                245
```

<210> 41
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA scFv binding domain

<400> 41

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30

His Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35                  40                  45

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

Lys Gly Lys Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Gly Thr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Gly Gly Asp Ile Val Met Thr Gln Thr Pro Leu
```

```
    130                 135                 140

Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser
145                 150                 155                 160

Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Asp Trp Tyr
                165                 170                 175

Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Lys Val Ser
            180                 185                 190

Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205

Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly
    210                 215                 220

Val Tyr Tyr Cys Met Gln Gly Ser His Val Pro Arg Thr Phe Gly Gly
225                 230                 235                 240

Gly Thr Lys Val Glu Ile Lys
                245
```

<210> 42
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA antigen binding domain CDR-L1

<400> 42

```
Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
1               5                   10                  15
```

<210> 43
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA antigen binding domain CDR-L2

<400> 43

Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg
1 5 10

<210> 44
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA antigen binding domain CDR-L3

<400> 44

Phe Gln Gly Ser His Val Pro Arg Thr
1 5

<210> 45
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA antigen binding domain CDR-H1

<400> 45

Ala Ser Gly Tyr Thr Phe Thr Ser Tyr His Ile His
1 5 10

<210> 46
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA antigen binding domain CDR-H2

<400> 46

Trp Ile Tyr Pro Gly Asn Val Asn Thr Glu Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly Lys

<210> 47
<211> 9
<212> PRT

<213> Artificial Sequence

<220>
<223> HLA antigen binding domain CDR-H3

<400> 47

Glu Glu Ile Thr Tyr Ala Met Asp Tyr
1 5

<210> 48
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA antigen binding domain CDR-L1

<400> 48

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

<210> 49
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA antigen binding domain CDR-L2

<400> 49

Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg
1 5 10

<210> 50
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA antigen binding domain CDR-L3

<400> 50

Met Gln Gly Ser His Val Pro Arg Thr
1 5

<210> 51

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

<220>
<223> HLA antigen binding domain CDR-H1

<400> 51

Ser Gly Tyr Thr Phe Thr Ser Tyr His Met His
1 5 10

<210> 52
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA antigen binding domain CDR-H2

<400> 52

Trp Ile Tyr Pro Gly Asp Gly Ser Thr Gln Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 53
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA antigen binding domain CDR-H3

<400> 53

Glu Gly Thr Tyr Tyr Ala Met Asp Tyr
1 5

<210> 54
<211> 670
<212> PRT
<213> Unknown

<220>
<223> LILRB1

<400> 54

```
Met Thr Pro Ile Leu Thr Val Leu Ile Cys Leu Gly Leu Ser Leu Gly
1               5                  10                  15

Pro Arg Thr His Val Gln Ala Gly His Leu Pro Lys Pro Thr Leu Trp
            20                  25                  30

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

Cys Gln Gly Gly Gln Glu Thr Gln Glu Tyr Arg Leu Tyr Arg Glu Lys
    50                  55                  60

Lys Thr Ala Leu Trp Ile Thr Arg Ile Pro Gln Glu Leu Val Lys Lys
65                  70                  75                  80

Gly Gln Phe Pro Ile Pro Ser Ile Thr Trp Glu His Ala Gly Arg Tyr
                85                  90                  95

Arg Cys Tyr Tyr Gly Ser Asp Thr Ala Gly Arg Ser Glu Ser Ser Asp
            100                 105                 110

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

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

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

Glu Asp Glu His Pro Gln Cys Leu Asn Ser Gln Pro His Ala Arg Gly
                165                 170                 175

Ser Ser Arg Ala Ile Phe Ser Val Gly Pro Val Ser Pro Ser Arg Arg
            180                 185                 190

Trp Trp Tyr Arg Cys Tyr Ala Tyr Asp Ser Asn Ser Pro Tyr Glu Trp
        195                 200                 205

Ser Leu Pro Ser Asp Leu Leu Glu Leu Leu Val Leu Gly Val Ser Lys
```

```
    210                 215                 220

Lys Pro Ser Leu Ser Val Gln Pro Gly Pro Ile Val Ala Pro Glu Glu
225                 230                 235                 240

Thr Leu Thr Leu Gln Cys Gly Ser Asp Ala Gly Tyr Asn Arg Phe Val
                245                 250                 255

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

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

Arg Ser Tyr Gly Gly Gln Tyr Arg Cys Tyr Gly Ala His Asn Leu Ser
    290                 295                 300

Ser Glu Trp Ser Ala Pro Ser Asp Pro Leu Asp Ile Leu Ile Ala Gly
305                 310                 315                 320

Gln Phe Tyr Asp Arg Val Ser Leu Ser Val Gln Pro Gly Pro Thr Val
                325                 330                 335

Ala Ser Gly Glu Asn Val Thr Leu Leu Cys Gln Ser Gln Gly Trp Met
            340                 345                 350

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

Leu Arg Ser Thr Tyr Gln Ser Gln Lys Tyr Gln Ala Glu Phe Pro Met
    370                 375                 380

Gly Pro Val Thr Ser Ala His Ala Gly Thr Tyr Arg Cys Tyr Gly Ser
385                 390                 395                 400

Gln Ser Ser Lys Pro Tyr Leu Leu Thr His Pro Ser Asp Pro Leu Glu
                405                 410                 415

Leu Val Val Ser Gly Pro Ser Gly Gly Pro Ser Ser Pro Thr Thr Gly
            420                 425                 430
```

```
Pro Thr Ser Thr Ser Gly Pro Glu Asp Gln Pro Leu Thr Pro Thr Gly
        435                 440                 445

Ser Asp Pro Gln Ser Gly Leu Gly Arg His Leu Gly Val Val Ile Gly
    450                 455                 460

Ile Leu Val Ala Val Ile Leu Leu Leu Leu Leu Leu Leu Leu Leu Phe
465                 470                 475                 480

Leu Ile Leu Arg His Arg Arg Gln Gly Lys His Trp Thr Ser Thr Gln
                485                 490                 495

Arg Lys Ala Asp Phe Gln His Pro Ala Gly Ala Val Gly Pro Glu Pro
            500                 505                 510

Thr Asp Arg Gly Leu Gln Trp Arg Ser Ser Pro Ala Ala Asp Ala Gln
        515                 520                 525

Glu Glu Asn Leu Tyr Ala Ala Val Lys His Thr Gln Pro Glu Asp Gly
    530                 535                 540

Val Glu Met Asp Thr Arg Ser Pro His Asp Glu Asp Pro Gln Ala Val
545                 550                 555                 560

Thr Tyr Ala Glu Val Lys His Ser Arg Pro Arg Arg Glu Met Ala Ser
                565                 570                 575

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

Ala Glu Glu Asp Arg Gln Met Asp Thr Glu Ala Ala Ala Ser Glu Ala
        595                 600                 605

Pro Gln Asp Val Thr Tyr Ala Gln Leu His Ser Leu Thr Leu Arg Arg
    610                 615                 620

Glu Ala Thr Glu Pro Pro Pro Ser Gln Glu Gly Pro Ser Pro Ala Val
625                 630                 635                 640

Pro Ser Ile Tyr Ala Thr Leu Ala Ile His Pro Ser Gln Glu Gly Pro
```

645 650 655

Ser Pro Ala Val Pro Ser Ile Tyr Ala Thr Leu Ala Ile His
660 665 670

<210> 55
<211> 3229
<212> DNA
<213> Unknown

<220>
<223> LILRB1

<400> 55
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gaaatgactc agtggtgaga ccctgtggag tcccacccac aaccagcaca ctgtgaccca 180

ctgcacaaac ctctagccca cagctcactt cctcctttaa gaagagaaga gaaaagagga 240

gaggagagga ggaacagaaa agaaaagaaa agaaaaagtg ggaaacaaat aatctaagaa 300

tgaggagaaa gcaagaagag tgacccccct gtgggcactc cattggtttt atggcgcctc 360

tactttctgg agtttgtgta aaacaaaaat attatggtct ttgtgcacat ttacatcaag 420

ctcagcctgg gcggcacagc cagatgcgag atgcgtctct gctgatctga gtctgcctgc 480

agcatggacc tgggtcttcc ctgaagcatc tccagggctg gagggacgac tgccatgcac 540

cgagggctca tccatccaca gagcagggca gtgggaggag acgccatgac ccccatcctc 600

acggtcctga tctgtctcgg gctgagtctg ggcccccgga cccacgtgca ggcagggcac 660

ctccccaagc ccaccctctg ggctgaacca ggctctgtga tcacccaggg gagtcctgtg 720

accctcaggt gtcaggggg ccaggagacc caggagtacc gtctatatag agaaaagaaa 780

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caatgcctga actcccagcc ccatgcccgt gggtcgtccc gcgccatctt ctccgtgggc 1140

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gagtggtcgg cccccagcga ccccctggac atcctgatcg caggacagtt ctatgacaga 1560

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ggggctgtgg ggccagagcc cacagacaga ggcctgcagt ggaggtccag cccagctgcc 2160

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gagatggaca ctcggagccc acacgatgaa gacccccagg cagtgacgta tgccgaggtg 2280

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<210> 56
<211> 6
<212> PRT
<213> Unknown

<220>
<223> immunoreceptor tyrosine-based inhibitory motif

<400> 56

Asn Leu Tyr Ala Ala Val
1 5

<210> 57
<211> 6
<212> PRT
<213> Unknown

<220>
<223> immunoreceptor tyrosine-based inhibitory motif

<400> 57

Val Thr Tyr Ala Glu Val
1 5

<210> 58
<211> 6
<212> PRT
<213> Unknown

<220>
<223> immunoreceptor tyrosine-based inhibitory motif

<400> 58

Val Thr Tyr Ala Gln Leu
1 5

<210> 59
<211> 6
<212> PRT
<213> Unknown

<220>
<223> immunoreceptor tyrosine-based inhibitory motif

<400> 59

Ser Ile Tyr Ala Thr Leu
1 5

<210> 60
<211> 35
<212> PRT
<213> Unknown

<220>
<223> ITIM1-2

<400> 60

Asn Leu Tyr Ala Ala Val Lys His Thr Gln Pro Glu Asp Gly Val Glu
1 5 10 15

Met Asp Thr Arg Ser Pro His Asp Glu Asp Pro Gln Ala Val Thr Tyr
20 25 30

Ala Glu Val
35

<210> 61
<211> 58
<212> PRT
<213> Unknown

<220>
<223> ITIM2-3

<400> 61

Val Thr Tyr Ala Glu Val Lys His Ser Arg Pro Arg Arg Glu Met Ala
1 5 10 15

Ser Pro Pro Ser Pro Leu Ser Gly Glu Phe Leu Asp Thr Lys Asp Arg
            20   25   30

Gln Ala Glu Glu Asp Arg Gln Met Asp Thr Glu Ala Ala Ala Ser Glu
        35   40   45

Ala Pro Gln Asp Val Thr Tyr Ala Gln Leu
    50   55

<210> 62
<211> 36
<212> PRT
<213> Unknown

<220>
<223> ITIM3-4

<400> 62

Val Thr Tyr Ala Gln Leu His Ser Leu Thr Leu Arg Arg Glu Ala Thr
1   5   10   15

Glu Pro Pro Pro Ser Gln Glu Gly Pro Ser Pro Ala Val Pro Ser Ile
            20   25   30

Tyr Ala Thr Leu
        35

<210> 63
<211> 87
<212> PRT
<213> Unknown

<220>
<223> ITIM1-3

<400> 63

Asn Leu Tyr Ala Ala Val Lys His Thr Gln Pro Glu Asp Gly Val Glu
1   5   10   15

Met Asp Thr Arg Ser Pro His Asp Glu Asp Pro Gln Ala Val Thr Tyr
            20   25   30

Ala Glu Val Lys His Ser Arg Pro Arg Arg Glu Met Ala Ser Pro Pro

```
        35                  40                  45

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

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

Asp Val Thr Tyr Ala Gln Leu
                85
```

<210> 64
<211> 88
<212> PRT
<213> Unknown

<220>
<223> ITIM2-4

<400> 64

```
Val Thr Tyr Ala Glu Val Lys His Ser Arg Pro Arg Arg Glu Met Ala
1               5                   10                  15

Ser Pro Pro Ser Pro Leu Ser Gly Glu Phe Leu Asp Thr Lys Asp Arg
            20                  25                  30

Gln Ala Glu Glu Asp Arg Gln Met Asp Thr Glu Ala Ala Ala Ser Glu
        35                  40                  45

Ala Pro Gln Asp Val Thr Tyr Ala Gln Leu His Ser Leu Thr Leu Arg
    50                  55                  60

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

Val Pro Ser Ile Tyr Ala Thr Leu
                85
```

<210> 65
<211> 117
<212> PRT
<213> Unknown

<220>
<223> ITIM1-4

<400> 65

Asn Leu Tyr Ala Ala Val Lys His Thr Gln Pro Glu Asp Gly Val Glu
1   5   10   15

Met Asp Thr Arg Ser Pro His Asp Glu Asp Pro Gln Ala Val Thr Tyr
            20   25   30

Ala Glu Val Lys His Ser Arg Pro Arg Arg Glu Met Ala Ser Pro Pro
        35   40   45

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

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

Asp Val Thr Tyr Ala Gln Leu His Ser Leu Thr Leu Arg Arg Glu Ala
                85   90   95

Thr Glu Pro Pro Pro Ser Gln Glu Gly Pro Ser Pro Ala Val Pro Ser
            100   105   110

Ile Tyr Ala Thr Leu
        115

<210> 66
<211> 20
<212> PRT
<213> Unknown

<220>
<223> D3D4 domain

<400> 66

Tyr Gly Ser Gln Ser Ser Lys Pro Tyr Leu Leu Thr His Pro Ser Asp
1   5   10   15

Pro Leu Glu Leu
            20

<210> 67
<211> 43
<212> PRT
<213> Unknown

<220>
<223> Short hinge

<400> 67

Val Val Ser Gly Pro Ser Gly Gly Pro Ser Ser Pro Thr Thr Gly Pro
1   5   10   15

Thr Ser Thr Ser Gly Pro Glu Asp Gln Pro Leu Thr Pro Thr Gly Ser
            20   25   30

Asp Pro Gln Ser Gly Leu Gly Arg His Leu Gly
        35   40

<210> 68
<211> 86
<212> PRT
<213> Unknown

<220>
<223> Hinge-transmembrane

<400> 68

Tyr Gly Ser Gln Ser Ser Lys Pro Tyr Leu Leu Thr His Pro Ser Asp
1   5   10   15

Pro Leu Glu Leu Val Val Ser Gly Pro Ser Gly Gly Pro Ser Ser Pro
            20   25   30

Thr Thr Gly Pro Thr Ser Thr Ser Gly Pro Glu Asp Gln Pro Leu Thr
        35   40   45

Pro Thr Gly Ser Asp Pro Gln Ser Gly Leu Gly Arg His Leu Gly Val
    50   55   60

Val Ile Gly Ile Leu Val Ala Val Ile Leu Leu Leu Leu Leu Leu Leu
65   70   75   80

Leu Leu Phe Leu Ile Leu

85

<210> 69
<211> 190
<212> PRT
<213> Unknown

<220>
<223> Transmembrane-intracellular domain.

<400> 69

Val Val Ile Gly Ile Leu Val Ala Val Ile Leu Leu Leu Leu Leu
1 5 10 15

Leu Leu Leu Phe Leu Ile Leu Arg His Arg Arg Gln Gly Lys His Trp
20 25 30

Thr Ser Thr Gln Arg Lys Ala Asp Phe Gln His Pro Ala Gly Ala Val
35 40 45

Gly Pro Glu Pro Thr Asp Arg Gly Leu Gln Trp Arg Ser Ser Pro Ala
50 55 60

Ala Asp Ala Gln Glu Glu Asn Leu Tyr Ala Ala Val Lys His Thr Gln
65 70 75 80

Pro Glu Asp Gly Val Glu Met Asp Thr Arg Ser Pro His Asp Glu Asp
85 90 95

Pro Gln Ala Val Thr Tyr Ala Glu Val Lys His Ser Arg Pro Arg Arg
100 105 110

Glu Met Ala Ser Pro Pro Ser Pro Leu Ser Gly Glu Phe Leu Asp Thr
115 120 125

Lys Asp Arg Gln Ala Glu Glu Asp Arg Gln Met Asp Thr Glu Ala Ala
130 135 140

Ala Ser Glu Ala Pro Gln Asp Val Thr Tyr Ala Gln Leu His Ser Leu
145 150 155 160

Thr Leu Arg Arg Glu Ala Thr Glu Pro Pro Pro Ser Gln Glu Gly Pro

```
                165                 170                 175

Ser Pro Ala Val Pro Ser Ile Tyr Ala Thr Leu Ala Ile His
            180                 185                 190
```

<210> 70
<211> 167
<212> PRT
<213> Unknown

<220>
<223> LILRB1 intracellular domain

<400> 70

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

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

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

Leu Tyr Ala Ala Val Lys His Thr Gln Pro Glu Asp Gly Val Glu Met
    50                  55                  60

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

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

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

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

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

Glu Pro Pro Pro Ser Gln Glu Gly Pro Ser Pro Ala Val Pro Ser Ile
```

145 150 155 160

Tyr Ala Thr Leu Ala Ile His
165

<210> 71
<211> 253
<212> PRT
<213> Unknown

<220>
<223> LILRB1 hinge-transmembrane-intracellular domain

<400> 71

Tyr Gly Ser Gln Ser Ser Lys Pro Tyr Leu Leu Thr His Pro Ser Asp
1 5 10 15

Pro Leu Glu Leu Val Val Ser Gly Pro Ser Gly Gly Pro Ser Ser Pro
20 25 30

Thr Thr Gly Pro Thr Ser Thr Ser Gly Pro Glu Asp Gln Pro Leu Thr
35 40 45

Pro Thr Gly Ser Asp Pro Gln Ser Gly Leu Gly Arg His Leu Gly Val
50 55 60

Val Ile Gly Ile Leu Val Ala Val Ile Leu Leu Leu Leu Leu Leu Leu
65 70 75 80

Leu Leu Phe Leu Ile Leu Arg His Arg Arg Gln Gly Lys His Trp Thr
85 90 95

Ser Thr Gln Arg Lys Ala Asp Phe Gln His Pro Ala Gly Ala Val Gly
100 105 110

Pro Glu Pro Thr Asp Arg Gly Leu Gln Trp Arg Ser Ser Pro Ala Ala
115 120 125

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

Glu Asp Gly Val Glu Met Asp Thr Arg Ser Pro His Asp Glu Asp Pro

145 150 155 160

Gln Ala Val Thr Tyr Ala Glu Val Lys His Ser Arg Pro Arg Arg Glu
165 170 175

Met Ala Ser Pro Pro Ser Pro Leu Ser Gly Glu Phe Leu Asp Thr Lys
180 185 190

Asp Arg Gln Ala Glu Glu Asp Arg Gln Met Asp Thr Glu Ala Ala Ala
195 200 205

Ser Glu Ala Pro Gln Asp Val Thr Tyr Ala Gln Leu His Ser Leu Thr
210 215 220

Leu Arg Arg Glu Ala Thr Glu Pro Pro Pro Ser Gln Glu Gly Pro Ser
225 230 235 240

Pro Ala Val Pro Ser Ile Tyr Ala Thr Leu Ala Ile His
245 250

<210> 72
<211> 233
<212> PRT
<213> Unknown

<220>
<223> LILRB1 hinge-transmembrane-intracellular domain

<400> 72

Val Val Ser Gly Pro Ser Gly Gly Pro Ser Ser Pro Thr Thr Gly Pro
1 5 10 15

Thr Ser Thr Ser Gly Pro Glu Asp Gln Pro Leu Thr Pro Thr Gly Ser
20 25 30

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

Leu Val Ala Val Ile Leu Leu Leu Leu Leu Leu Leu Leu Leu Phe Leu
50 55 60

Ile Leu Arg His Arg Arg Gln Gly Lys His Trp Thr Ser Thr Gln Arg

65 70 75 80

Lys Ala Asp Phe Gln His Pro Ala Gly Ala Val Gly Pro Glu Pro Thr
85 90 95

Asp Arg Gly Leu Gln Trp Arg Ser Ser Pro Ala Ala Asp Ala Gln Glu
100 105 110

Glu Asn Leu Tyr Ala Ala Val Lys His Thr Gln Pro Glu Asp Gly Val
115 120 125

Glu Met Asp Thr Arg Ser Pro His Asp Glu Asp Pro Gln Ala Val Thr
130 135 140

Tyr Ala Glu Val Lys His Ser Arg Pro Arg Arg Glu Met Ala Ser Pro
145 150 155 160

Pro Ser Pro Leu Ser Gly Glu Phe Leu Asp Thr Lys Asp Arg Gln Ala
165 170 175

Glu Glu Asp Arg Gln Met Asp Thr Glu Ala Ala Ala Ser Glu Ala Pro
180 185 190

Gln Asp Val Thr Tyr Ala Gln Leu His Ser Leu Thr Leu Arg Arg Glu
195 200 205

Ala Thr Glu Pro Pro Pro Ser Gln Glu Gly Pro Ser Pro Ala Val Pro
210 215 220

Ser Ile Tyr Ala Thr Leu Ala Ile His
225 230

<210> 73
<211> 63
<212> PRT
<213> Unknown

<220>
<223> LILRB1 hinge domain

<400> 73

Tyr Gly Ser Gln Ser Ser Lys Pro Tyr Leu Leu Thr His Pro Ser Asp

1 5 10 15

Pro Leu Glu Leu Val Val Ser Gly Pro Ser Gly Gly Pro Ser Ser Pro
20 25 30

Thr Thr Gly Pro Thr Ser Thr Ser Gly Pro Glu Asp Gln Pro Leu Thr
35 40 45

Pro Thr Gly Ser Asp Pro Gln Ser Gly Leu Gly Arg His Leu Gly
50 55 60

<210> 74
<211> 23
<212> PRT
<213> Unknown

<220>
<223> LILRB1 transmembrane domain

<400> 74

Val Val Ile Gly Ile Leu Val Ala Val Ile Leu Leu Leu Leu Leu Leu
1 5 10 15

Leu Leu Leu Phe Leu Ile Leu
20

<210> 75
<211> 740
<212> PRT
<213> Homo sapiens

<400> 75

Met Arg Gln Thr Leu Pro Leu Leu Leu Leu Thr Val Leu Arg Pro Ser
1 5 10 15

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

Gln Gly Pro Trp Gly Ser Ser Gly Ser Asn Ala Thr Asp Ser Pro Cys
35 40 45

Glu Gly Leu Pro Ala Ala Asp Ala Thr Ala Leu Thr Leu Ala Asn Arg
50 55 60

```
Asn Leu Glu Arg Leu Pro Gly Cys Leu Pro Arg Thr Leu Arg Ser Leu
65                  70                  75                  80

Asp Ala Ser His Asn Leu Leu Arg Ala Leu Ser Thr Ser Glu Leu Gly
                85                  90                  95

His Leu Glu Gln Leu Gln Val Leu Thr Leu Arg His Asn Arg Ile Ala
            100                 105                 110

Ala Leu Arg Trp Gly Pro Gly Gly Pro Ala Gly Leu His Thr Leu Asp
        115                 120                 125

Leu Ser Tyr Asn Gln Leu Ala Ala Leu Pro Pro Cys Thr Gly Pro Ala
    130                 135                 140

Leu Ser Ser Leu Arg Ala Leu Ala Leu Ala Gly Asn Pro Leu Arg Ala
145                 150                 155                 160

Leu Gln Pro Arg Ala Phe Ala Cys Phe Pro Ala Leu Gln Leu Leu Asn
                165                 170                 175

Leu Ser Cys Thr Ala Leu Gly Arg Gly Ala Gln Gly Gly Ile Ala Glu
            180                 185                 190

Ala Ala Phe Ala Gly Glu Asp Gly Ala Pro Leu Val Thr Leu Glu Val
        195                 200                 205

Leu Asp Leu Ser Gly Thr Phe Leu Glu Arg Val Glu Ser Gly Trp Ile
    210                 215                 220

Arg Asp Leu Pro Lys Leu Thr Ser Leu Tyr Leu Arg Lys Met Pro Arg
225                 230                 235                 240

Leu Thr Thr Leu Glu Gly Asp Ile Phe Lys Met Thr Pro Asn Leu Gln
                245                 250                 255

Gln Leu Asp Cys Gln Asp Ser Pro Ala Leu Ala Ser Val Ala Thr His
            260                 265                 270
```

```
Ile Phe Gln Asp Thr Pro His Leu Gln Val Leu Leu Phe Gln Asn Cys
        275                 280                 285

Asn Leu Ser Ser Phe Pro Pro Trp Thr Leu Asp Ser Ser Gln Val Leu
    290                 295                 300

Ser Ile Asn Leu Phe Gly Asn Pro Leu Thr Cys Ser Cys Asp Leu Ser
305                 310                 315                 320

Trp Leu Leu Thr Asp Ala Lys Arg Thr Val Leu Ser Arg Ala Ala Asp
                325                 330                 335

Thr Met Cys Ala Pro Ala Ala Gly Ser Ser Gly Pro Phe Ser Ala Ser
            340                 345                 350

Leu Ser Leu Ser Gln Leu Pro Gly Val Cys Gln Ser Asp Gln Ser Thr
        355                 360                 365

Thr Leu Gly Ala Ser His Pro Pro Cys Phe Asn Arg Ser Thr Tyr Ala
    370                 375                 380

Gln Gly Thr Thr Val Ala Pro Ser Ala Ala Pro Ala Thr Arg Pro Ala
385                 390                 395                 400

Gly Asp Gln Gln Ser Val Ser Lys Ala Pro Asn Val Gly Ser Arg Thr
                405                 410                 415

Ile Ala Ala Trp Pro His Ser Asp Ala Arg Glu Gly Thr Ala Pro Ser
            420                 425                 430

Thr Thr Asn Ser Val Ala Gly His Ser Asn Ser Ser Val Phe Pro Arg
        435                 440                 445

Ala Ala Ser Thr Thr Arg Thr Gln His Arg Gly Glu His Ala Pro Glu
    450                 455                 460

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

Lys Leu Leu Gly Pro Phe Pro Thr Ser Trp Asp Arg Ser Ile Ser Ser
                485                 490                 495
```

```
Pro Gln Pro Gly Gln Arg Thr His Ala Thr Pro Gln Ala Pro Asn Pro
            500                 505                 510

Ser Leu Ser Glu Gly Glu Ile Pro Val Leu Leu Leu Asp Asp Tyr Ser
        515                 520                 525

Glu Glu Glu Glu Gly Arg Lys Glu Glu Val Gly Thr Pro His Gln Asp
    530                 535                 540

Val Pro Cys Asp Tyr His Pro Cys Lys His Leu Gln Thr Pro Cys Ala
545                 550                 555                 560

Glu Leu Gln Arg Arg Trp Arg Cys Arg Cys Pro Gly Leu Ser Gly Glu
                565                 570                 575

Asp Thr Ile Pro Asp Pro Pro Arg Leu Gln Gly Val Thr Glu Thr Thr
            580                 585                 590

Asp Thr Ser Ala Leu Val His Trp Cys Ala Pro Asn Ser Val Val His
        595                 600                 605

Gly Tyr Gln Ile Arg Tyr Ser Ala Glu Gly Trp Ala Gly Asn Gln Ser
    610                 615                 620

Val Val Gly Val Ile Tyr Ala Thr Ala Arg Gln His Pro Leu Tyr Gly
625                 630                 635                 640

Leu Ser Pro Gly Thr Thr Tyr Arg Val Cys Val Leu Ala Ala Asn Arg
                645                 650                 655

Ala Gly Leu Ser Gln Pro Arg Ser Ser Gly Trp Arg Ser Pro Cys Ala
            660                 665                 670

Ala Phe Thr Thr Lys Pro Ser Phe Ala Leu Leu Leu Ser Gly Leu Cys
        675                 680                 685

Ala Ala Ser Gly Leu Leu Leu Ala Ser Thr Val Val Leu Ser Ala Cys
    690                 695                 700
```

```
Leu Cys Arg Arg Gly Gln Thr Leu Gly Leu Gln Arg Cys Asp Thr His
705                 710                 715                 720


Leu Val Ala Tyr Lys Asn Pro Ala Phe Asp Asp Tyr Pro Leu Gly Leu
                725                 730                 735


Gln Thr Val Ser
            740
```

<210> 76
<211> 320
<212> PRT
<213> Homo sapiens

<400> 76

```
Met Gly Leu Pro Trp Gly Gln Pro His Leu Gly Leu Gln Met Leu Leu
1               5                   10                  15


Leu Ala Leu Asn Cys Leu Arg Pro Ser Leu Ser Leu Gly Glu Trp Gly
            20                  25                  30


Ser Trp Met Asp Ala Ser Ser Gln Thr Gln Gly Ala Gly Gly Pro Ala
        35                  40                  45


Gly Val Ile Gly Pro Trp Ala Pro Ala Pro Leu Arg Leu Gly Glu Ala
    50                  55                  60


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


Val Ala Thr Glu Leu Val Pro Tyr Thr Pro Gln Ile Thr Ala Trp Asp
                85                  90                  95


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


Cys Val Phe Asp Gly Leu Ala Ser Ala Ser Asp Thr Val Trp Leu Val
        115                 120                 125


Val Ala Phe Ser Asn Ala Ser Arg Gly Phe Gln Asn Pro Glu Thr Leu
    130                 135                 140
```

```
Ala Asp Ile Pro Ala Ser Pro Gln Leu Leu Thr Asp Gly His Tyr Met
145                 150                 155                 160


Thr Leu Pro Leu Ser Pro Asp Gln Leu Pro Cys Gly Asp Pro Met Ala
                165                 170                 175


Gly Ser Gly Gly Ala Pro Val Leu Arg Val Gly His Asp His Gly Cys
            180                 185                 190


His Gln Gln Pro Phe Cys Asn Ala Pro Leu Pro Gly Pro Gly Pro Tyr
        195                 200                 205


Arg Glu Asp Pro Arg Ile His Arg His Leu Ala Arg Ala Ala Lys Trp
    210                 215                 220


Gln His Asp Arg His Tyr Leu His Pro Leu Phe Ser Gly Arg Pro Pro
225                 230                 235                 240


Thr Leu Gly Leu Leu Gly Ser Leu Tyr His Ala Leu Leu Gln Pro Val
                245                 250                 255


Val Ala Gly Gly Gly Pro Gly Ala Ala Ala Asp Arg Leu Leu His Gly
            260                 265                 270


Gln Ala Leu His Asp Pro Pro His Pro Thr Gln Arg Gly Arg His Thr
        275                 280                 285


Ala Gly Gly Leu Gln Ala Trp Pro Gly Pro Pro Pro Gln Pro Gln Pro
    290                 295                 300


Leu Ala Trp Pro Leu Cys Met Gly Leu Gly Glu Met Gly Arg Arg Glu
305                 310                 315                 320


<210>  77
<211>  276
<212>  PRT
<213>  Homo sapiens

<400>  77

Met Gly Leu Pro Trp Gly Gln Pro His Leu Gly Leu Gln Met Leu Leu
1               5                   10                  15
```

```
Leu Ala Leu Asn Cys Leu Arg Pro Ser Leu Ser Leu Glu Leu Val Pro
            20                  25                  30

Tyr Thr Pro Gln Ile Thr Ala Trp Asp Leu Glu Gly Lys Val Thr Ala
        35                  40                  45

Thr Thr Phe Ser Leu Glu Gln Pro Arg Cys Val Phe Asp Gly Leu Ala
    50                  55                  60

Ser Ala Ser Asp Thr Val Trp Leu Val Val Ala Phe Ser Asn Ala Ser
65                  70                  75                  80

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

Gln Leu Leu Thr Asp Gly His Tyr Met Thr Leu Pro Leu Ser Pro Asp
            100                 105                 110

Gln Leu Pro Cys Gly Asp Pro Met Ala Gly Ser Gly Gly Ala Pro Val
        115                 120                 125

Leu Arg Val Gly His Asp His Gly Cys His Gln Gln Pro Phe Cys Asn
    130                 135                 140

Ala Pro Leu Pro Gly Pro Gly Pro Tyr Arg Val Lys Phe Leu Leu Met
145                 150                 155                 160

Asp Thr Arg Gly Ser Pro Arg Ala Glu Thr Lys Trp Ser Asp Pro Ile
                165                 170                 175

Thr Leu His Gln Gly Lys Thr Pro Gly Ser Ile Asp Thr Trp Pro Gly
            180                 185                 190

Arg Arg Ser Gly Ser Met Ile Val Ile Thr Ser Ile Leu Ser Ser Leu
        195                 200                 205

Ala Gly Leu Leu Leu Leu Ala Phe Leu Ala Ala Ser Thr Met Arg Phe
    210                 215                 220
```

```
Ser Ser Leu Trp Trp Pro Glu Glu Ala Pro Glu Gln Leu Arg Ile Gly
225                 230                 235                 240


Ser Phe Met Gly Lys Arg Tyr Met Thr His His Ile Pro Pro Ser Glu
                245                 250                 255


Ala Ala Thr Leu Pro Val Gly Cys Lys Pro Gly Leu Asp Pro Leu Pro
            260                 265                 270


Ser Leu Ser Pro
        275
```

<210> 78
<211> 265
<212> PRT
<213> Homo sapiens

<400> 78

```
Met Gly Leu Pro Trp Gly Gln Pro His Leu Gly Leu Gln Met Leu Leu
1               5                   10                  15


Leu Ala Leu Asn Cys Leu Arg Pro Ser Leu Ser Leu Glu Leu Val Pro
            20                  25                  30


Tyr Thr Pro Gln Ile Thr Ala Trp Asp Leu Glu Gly Lys Val Thr Ala
        35                  40                  45


Thr Thr Phe Ser Leu Glu Gln Pro Arg Cys Val Phe Asp Gly Leu Ala
    50                  55                  60


Ser Ala Ser Asp Thr Val Trp Leu Val Val Ala Phe Ser Asn Ala Ser
65                  70                  75                  80


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


Gln Leu Leu Thr Asp Gly His Tyr Met Thr Leu Pro Leu Ser Pro Asp
            100                 105                 110


Gln Leu Pro Cys Gly Asp Pro Met Ala Gly Ser Gly Gly Ala Pro Val
        115                 120                 125
```

```
Leu Arg Val Gly His Asp His Gly Cys His Gln Gln Pro Phe Cys Asn
    130                 135                 140

Ala Pro Leu Pro Gly Pro Gly Pro Tyr Arg Glu Asp Pro Arg Ile His
145                 150                 155                 160

Arg His Leu Ala Arg Ala Ala Lys Trp Gln His Asp Arg His Tyr Leu
                165                 170                 175

His Pro Leu Phe Ser Gly Arg Pro Pro Thr Leu Gly Leu Leu Gly Ser
            180                 185                 190

Leu Tyr His Ala Leu Leu Gln Pro Val Val Ala Gly Gly Gly Pro Gly
        195                 200                 205

Ala Ala Ala Asp Arg Leu Leu His Gly Gln Ala Leu His Asp Pro Pro
    210                 215                 220

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

Pro Gly Pro Pro Pro Gln Pro Gln Pro Leu Ala Trp Pro Leu Cys Met
                245                 250                 255

Gly Leu Gly Glu Met Gly Arg Arg Glu
            260                 265
```

<210> 79
<211> 276
<212> PRT
<213> Homo sapiens

<400> 79

```
Met Gly Leu Pro Trp Gly Gln Pro His Leu Gly Leu Gln Met Leu Leu
1               5                   10                  15

Leu Ala Leu Asn Cys Leu Arg Pro Ser Leu Ser Leu Glu Leu Val Pro
            20                  25                  30

Tyr Thr Pro Gln Ile Thr Ala Trp Asp Leu Glu Gly Lys Val Thr Ala
        35                  40                  45
```

```
Thr Thr Phe Ser Leu Glu Gln Pro Arg Cys Val Phe Asp Gly Leu Ala
    50                  55                  60

Ser Ala Ser Asp Thr Val Trp Leu Val Val Ala Phe Ser Asn Ala Ser
65                  70                  75                  80

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

Gln Leu Leu Thr Asp Gly His Tyr Met Thr Leu Pro Leu Ser Pro Asp
            100                 105                 110

Gln Leu Pro Cys Gly Asp Pro Met Ala Gly Ser Gly Gly Ala Pro Val
        115                 120                 125

Leu Arg Val Gly His Asp His Gly Cys His Gln Gln Pro Phe Cys Asn
    130                 135                 140

Ala Pro Leu Pro Gly Pro Gly Pro Tyr Arg Val Lys Phe Leu Leu Met
145                 150                 155                 160

Asp Thr Arg Gly Ser Pro Arg Ala Glu Thr Lys Trp Ser Asp Pro Ile
                165                 170                 175

Thr Leu His Gln Gly Lys Thr Pro Gly Ser Ile Asp Thr Trp Pro Gly
            180                 185                 190

Arg Arg Ser Gly Ser Met Ile Val Ile Thr Ser Ile Leu Ser Ser Leu
        195                 200                 205

Ala Gly Leu Leu Leu Leu Ala Phe Leu Ala Ala Ser Thr Met Arg Phe
    210                 215                 220

Ser Ser Leu Trp Trp Pro Glu Glu Ala Pro Glu Gln Leu Arg Ile Gly
225                 230                 235                 240

Ser Phe Met Gly Lys Arg Tyr Met Thr His His Ile Pro Pro Arg Glu
                245                 250                 255
```

Ala Ala Thr Leu Pro Val Gly Cys Lys Pro Gly Leu Asp Pro Leu Pro
            260   265   270

Ser Leu Ser Pro
        275

<210> 80
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 80

Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Glu Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
            20   25   30

Thr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
        35   40   45

Gly Leu Ile Thr Pro Tyr Asn Gly Ala Ser Ser Tyr Asn Gln Lys Phe
    50   55   60

Arg Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80

Met Asp Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85   90   95

Ala Arg Gly Gly Tyr Asp Gly Arg Gly Phe Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115   120   125

Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile
    130   135   140

```
Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser
145                 150                 155                 160


Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Ser Gly Thr Ser
                165                 170                 175


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


Gly Arg Phe Ser Gly Ser Gly Ser Gly Asn Ser Tyr Ser Leu Thr Ile
        195                 200                 205


Ser Ser Val Glu Ala Glu Asp Asp Ala Thr Tyr Tyr Cys Gln Gln Trp
    210                 215                 220


Ser Gly Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
225                 230                 235


<210>  81
<211>  64
<212>  PRT
<213>  Unknown

<220>
<223>  Hinge (iTIM hinge)

<400>  81

Tyr Gly Ser Gln Ser Ser Lys Pro Tyr Leu Leu Thr His Pro Ser Asp
1               5                   10                  15


Pro Leu Glu Leu Val Val Ser Gly Pro Ser Gly Gly Pro Ser Ser Pro
            20                  25                  30


Thr Thr Gly Pro Thr Ser Thr Ser Gly Pro Glu Asp Gln Pro Leu Thr
        35                  40                  45


Pro Thr Gly Ser Asp Pro Gln Ser Gly Leu Gly Arg His Leu Gly Val
    50                  55                  60


<210>  82
<211>  44
<212>  PRT
<213>  Unknown
```

<220>
<223> Short hinge 2

<400> 82

Val Val Ser Gly Pro Ser Gly Gly Pro Ser Ser Pro Thr Thr Gly Pro
1   5   10   15

Thr Ser Thr Ser Gly Pro Glu Asp Gln Pro Leu Thr Pro Thr Gly Ser
            20   25   30

Asp Pro Gln Ser Gly Leu Gly Arg His Leu Gly Val
        35   40

<210> 83
<211> 67
<212> PRT
<213> Unknown

<220>
<223> Long hinge 1

<400> 83

Ala Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Pro Val Pro Ser
1   5   10   15

Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser
            20   25   30

Gly Gly Ser Gly Asn Ser Ser Gly Ser Gly Gly Ser Pro Val Pro Ser
        35   40   45

Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser
    50   55   60

Ala Ser Val
65

<210> 84
<211> 75
<212> PRT
<213> Unknown

<220>

<223> Long hinge 2

<400> 84

Ala Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Pro Val Pro Ser
1   5   10   15

Thr Pro Pro Thr Asn Ser Ser Ser Thr Pro Pro Thr Pro Ser Pro Ser
            20   25   30

Pro Val Pro Ser Thr Pro Pro Thr Asn Ser Ser Ser Thr Pro Pro Thr
        35   40   45

Pro Ser Pro Ser Pro Val Pro Ser Thr Pro Pro Thr Asn Ser Ser Ser
    50   55   60

Thr Pro Pro Thr Pro Ser Pro Ser Ala Ser Val
65   70   75

<210> 85
<211> 407
<212> PRT
<213> Artificial Sequence

<220>
<223> PA2.1.14 (VL:VH) scFv LIR1 sHTICD

<400> 85

Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala
1   5   10   15

Thr Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Arg Thr Phe Gly Gln
            20   25   30

Gly Thr Lys Val Glu Val Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly
        35   40   45

Ser Gly Gly Gly Gly Ser Gly Gly Gln Val Gln Leu Val Gln Ser Gly
    50   55   60

Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala
65   70   75   80

```
Ser Gly Tyr Thr Phe Thr Ser Tyr His Ile His Trp Val Arg Gln Ala
                85                  90                  95

Pro Gly Gln Gly Leu Glu Trp Ile Gly Trp Ile Tyr Pro Gly Asn Val
            100                 105                 110

Asn Thr Glu Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Ile Thr Ala
        115                 120                 125

Asp Glu Ser Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser
    130                 135                 140

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Glu Ile Thr Tyr Ala
145                 150                 155                 160

Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Val Val
                165                 170                 175

Ser Gly Pro Ser Gly Gly Pro Ser Ser Pro Thr Thr Gly Pro Thr Ser
            180                 185                 190

Thr Ser Gly Pro Glu Asp Gln Pro Leu Thr Pro Thr Gly Ser Asp Pro
        195                 200                 205

Gln Ser Gly Leu Gly Arg His Leu Gly Val Val Ile Gly Ile Leu Val
    210                 215                 220

Ala Val Ile Leu Leu Leu Leu Leu Leu Leu Leu Leu Phe Leu Ile Leu
225                 230                 235                 240

Arg His Arg Arg Gln Gly Lys His Trp Thr Ser Thr Gln Arg Lys Ala
                245                 250                 255

Asp Phe Gln His Pro Ala Gly Ala Val Gly Pro Glu Pro Thr Asp Arg
            260                 265                 270

Gly Leu Gln Trp Arg Ser Ser Pro Ala Ala Asp Ala Gln Glu Glu Asn
        275                 280                 285

Leu Tyr Ala Ala Val Lys His Thr Gln Pro Glu Asp Gly Val Glu Met
    290                 295                 300
```

Asp Thr Arg Ser Pro His Asp Glu Asp Pro Gln Ala Val Thr Tyr Ala
305 310 315 320

Glu Val Lys His Ser Arg Pro Arg Arg Glu Met Ala Ser Pro Pro Ser
325 330 335

Pro Leu Ser Gly Glu Phe Leu Asp Thr Lys Asp Arg Gln Ala Glu Glu
340 345 350

Asp Arg Gln Met Asp Thr Glu Ala Ala Ala Ser Glu Ala Pro Gln Asp
355 360 365

Val Thr Tyr Ala Gln Leu His Ser Leu Thr Leu Arg Arg Glu Ala Thr
370 375 380

Glu Pro Pro Pro Ser Gln Glu Gly Pro Ser Pro Ala Val Pro Ser Ile
385 390 395 400

Tyr Ala Thr Leu Ala Ile His
405

<210> 86
<211> 500
<212> PRT
<213> Artificial Sequence

<220>
<223> PA2.1.14 (VL:VH) scFv LIR1 HTICD

<400> 86

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

Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Ile Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

```
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
65                  70                  75                  80

Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly
                85                  90                  95

Ser His Val Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys
            100                 105                 110

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

Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
    130                 135                 140

Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser
145                 150                 155                 160

Tyr His Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp
                165                 170                 175

Ile Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Glu Tyr Asn Glu Lys
            180                 185                 190

Phe Lys Gly Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala
        195                 200                 205

Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr
    210                 215                 220

Cys Ala Arg Glu Glu Ile Thr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
225                 230                 235                 240

Thr Leu Val Thr Val Ser Ser Tyr Gly Ser Gln Ser Ser Lys Pro Tyr
                245                 250                 255

Leu Leu Thr His Pro Ser Asp Pro Leu Glu Leu Val Val Ser Gly Pro
            260                 265                 270
```

```
Ser Gly Gly Pro Ser Ser Pro Thr Thr Gly Pro Thr Ser Thr Ser Gly
        275                 280                 285

Pro Glu Asp Gln Pro Leu Thr Pro Thr Gly Ser Asp Pro Gln Ser Gly
    290                 295                 300

Leu Gly Arg His Leu Gly Val Val Ile Gly Ile Leu Val Ala Val Ile
305                 310                 315                 320

Leu Leu Leu Leu Leu Leu Leu Leu Leu Phe Leu Ile Leu Arg His Arg
                325                 330                 335

Arg Gln Gly Lys His Trp Thr Ser Thr Gln Arg Lys Ala Asp Phe Gln
            340                 345                 350

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

Trp Arg Ser Ser Pro Ala Ala Asp Ala Gln Glu Glu Asn Leu Tyr Ala
    370                 375                 380

Ala Val Lys His Thr Gln Pro Glu Asp Gly Val Glu Met Asp Thr Arg
385                 390                 395                 400

Ser Pro His Asp Glu Asp Pro Gln Ala Val Thr Tyr Ala Glu Val Lys
                405                 410                 415

His Ser Arg Pro Arg Arg Glu Met Ala Ser Pro Pro Ser Pro Leu Ser
            420                 425                 430

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

Met Asp Thr Glu Ala Ala Ala Ser Glu Ala Pro Gln Asp Val Thr Tyr
    450                 455                 460

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

Pro Ser Gln Glu Gly Pro Ser Pro Ala Val Pro Ser Ile Tyr Ala Thr
                485                 490                 495
```

Leu Ala Ile His
            500

<210> 87
<211> 462
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN_SsI CD8_HT 41BB CD3z

<400> 87

Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Glu Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
            20   25   30

Thr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
        35   40   45

Gly Leu Ile Thr Pro Tyr Asn Gly Ala Ser Ser Tyr Asn Gln Lys Phe
    50   55   60

Arg Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80

Met Asp Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85   90   95

Ala Arg Gly Gly Tyr Asp Gly Arg Gly Phe Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115   120   125

Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile
    130   135   140

Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser
145   150   155   160

```
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Ser Gly Thr Ser
                165                 170                 175

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

Gly Arg Phe Ser Gly Ser Gly Ser Gly Asn Ser Tyr Ser Leu Thr Ile
        195                 200                 205

Ser Ser Val Glu Ala Glu Asp Asp Ala Thr Tyr Tyr Cys Gln Gln Trp
    210                 215                 220

Ser Gly Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Thr
225                 230                 235                 240

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
                245                 250                 255

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
            260                 265                 270

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
        275                 280                 285

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
    290                 295                 300

Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys
305                 310                 315                 320

Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys
                325                 330                 335

Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val
            340                 345                 350

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn
        355                 360                 365
```

```
Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
    370                 375                 380

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

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
                405                 410                 415

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

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

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
    450                 455                 460
```

<210> 88
<211> 480
<212> PRT
<213> Artificial Sequence

<220>
<223> PA2.1.14 scFv LIR1 sHTICD

<400> 88

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30

His Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Glu Tyr Asn Glu Lys Phe
    50                  55                  60

Lys Gly Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
65                  70                  75                  80
```

```
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Glu Ile Thr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser
    130                 135                 140

Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ser
145                 150                 155                 160

Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr
                165                 170                 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Val Ser
            180                 185                 190

Asn Arg Phe Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205

Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala
    210                 215                 220

Thr Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Arg Thr Phe Gly Gln
225                 230                 235                 240

Gly Thr Lys Val Glu Val Lys Val Val Ser Gly Pro Ser Gly Gly Pro
                245                 250                 255

Ser Ser Pro Thr Thr Gly Pro Thr Ser Thr Ser Gly Pro Glu Asp Gln
            260                 265                 270

Pro Leu Thr Pro Thr Gly Ser Asp Pro Gln Ser Gly Leu Gly Arg His
        275                 280                 285

Leu Gly Val Val Ile Gly Ile Leu Val Ala Val Ile Leu Leu Leu Leu
    290                 295                 300
```

```
Leu Leu Leu Leu Leu Phe Leu Ile Leu Arg His Arg Arg Gln Gly Lys
305                 310                 315                 320

His Trp Thr Ser Thr Gln Arg Lys Ala Asp Phe Gln His Pro Ala Gly
                325                 330                 335

Ala Val Gly Pro Glu Pro Thr Asp Arg Gly Leu Gln Trp Arg Ser Ser
            340                 345                 350

Pro Ala Ala Asp Ala Gln Glu Glu Asn Leu Tyr Ala Ala Val Lys His
        355                 360                 365

Thr Gln Pro Glu Asp Gly Val Glu Met Asp Thr Arg Ser Pro His Asp
    370                 375                 380

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

Arg Arg Glu Met Ala Ser Pro Pro Ser Pro Leu Ser Gly Glu Phe Leu
                405                 410                 415

Asp Thr Lys Asp Arg Gln Ala Glu Glu Asp Arg Gln Met Asp Thr Glu
            420                 425                 430

Ala Ala Ala Ser Glu Ala Pro Gln Asp Val Thr Tyr Ala Gln Leu His
        435                 440                 445

Ser Leu Thr Leu Arg Arg Glu Ala Thr Glu Pro Pro Pro Ser Gln Glu
    450                 455                 460

Gly Pro Ser Pro Ala Val Pro Ser Ile Tyr Ala Thr Leu Ala Ile His
465                 470                 475                 480
```

<210> 89
<211> 500
<212> PRT
<213> Artificial Sequence

<220>
<223> PA2.1.14 scFv LIR1 HTICD

<400> 89

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


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30


His Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Glu Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Gly Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Glu Glu Ile Thr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125


Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser
    130                 135                 140


Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ser
145                 150                 155                 160


Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr
                165                 170                 175


Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Val Ser
            180                 185                 190


Asn Arg Phe Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205
```

```
Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala
    210                 215                 220

Thr Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Arg Thr Phe Gly Gln
225                 230                 235                 240

Gly Thr Lys Val Glu Val Lys Tyr Gly Ser Gln Ser Ser Lys Pro Tyr
                245                 250                 255

Leu Leu Thr His Pro Ser Asp Pro Leu Glu Leu Val Val Ser Gly Pro
            260                 265                 270

Ser Gly Gly Pro Ser Ser Pro Thr Thr Gly Pro Thr Ser Thr Ser Gly
        275                 280                 285

Pro Glu Asp Gln Pro Leu Thr Pro Thr Gly Ser Asp Pro Gln Ser Gly
    290                 295                 300

Leu Gly Arg His Leu Gly Val Val Ile Gly Ile Leu Val Ala Val Ile
305                 310                 315                 320

Leu Leu Leu Leu Leu Leu Leu Leu Leu Phe Leu Ile Leu Arg His Arg
                325                 330                 335

Arg Gln Gly Lys His Trp Thr Ser Thr Gln Arg Lys Ala Asp Phe Gln
            340                 345                 350

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

Trp Arg Ser Ser Pro Ala Ala Asp Ala Gln Glu Glu Asn Leu Tyr Ala
    370                 375                 380

Ala Val Lys His Thr Gln Pro Glu Asp Gly Val Glu Met Asp Thr Arg
385                 390                 395                 400

Ser Pro His Asp Glu Asp Pro Gln Ala Val Thr Tyr Ala Glu Val Lys
                405                 410                 415

His Ser Arg Pro Arg Arg Glu Met Ala Ser Pro Pro Ser Pro Leu Ser
            420                 425                 430
```

```
Gly Glu Phe Leu Asp Thr Lys Asp Arg Gln Ala Glu Glu Asp Arg Gln
        435                 440                 445


Met Asp Thr Glu Ala Ala Ala Ser Glu Ala Pro Gln Asp Val Thr Tyr
    450                 455                 460


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


Pro Ser Gln Glu Gly Pro Ser Pro Ala Val Pro Ser Ile Tyr Ala Thr
                485                 490                 495


Leu Ala Ile His
            500


<210>  90
<211>  32
<212>  PRT
<213>  Unknown

<220>
<223>  Hinge (truncated)

<400>  90

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


Pro Thr Gly Ser Asp Pro Gln Ser Gly Leu Gly Arg His Leu Gly Val
            20                  25                  30


<210>  91
<211>  85
<212>  PRT
<213>  Unknown

<220>
<223>  2X short hinge

<400>  91

Val Val Ser Gly Pro Ser Gly Gly Pro Ser Ser Pro Thr Thr Gly Pro
1               5                   10                  15
```

Thr Ser Thr Ser Gly Pro Glu Asp Gln Pro Leu Thr Pro Thr Gly Ser
20 25 30

Asp Pro Gln Ser Gly Leu Gly Arg His Val Val Ser Gly Pro Ser Gly
35 40 45

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

Asp Gln Pro Leu Thr Pro Thr Gly Ser Asp Pro Gln Ser Gly Leu Gly
65 70 75 80

Arg His Leu Gly Val
85

<210> 92
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 CDR-H1

<400> 92

Ser Gly Gly Tyr Tyr Trp Ser
1 5

<210> 93
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 CDR-H1

<400> 93

Thr Ser Gly Val Gly Val Gly
1 5

<210> 94
<211> 5
<212> PRT
<213> Artificial Sequence

<220>

<223> anti-HLA-A*11 CDR-H1

<400> 94

Ser Tyr Ala Met His
1 5

<210> 95
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 CDR-H1

<400> 95

Ser Tyr Asp Met His
1 5

<210> 96
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 CDR-H1

<400> 96

Ser Tyr Trp Met His
1 5

<210> 97
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 CDR-H2

<400> 97

Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 98
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 CDR-H2

<400> 98

Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser Leu Lys Ser
1   5   10   15

<210> 99
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 CDR-H2

<400> 99

Trp Ile Asn Ala Gly Asn Gly Asn Thr Lys Tyr Ser Gln Lys Phe Gln
1   5   10   15

Gly

<210> 100
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 CDR-H2

<400> 100

Ala Ile Gly Thr Ala Gly Asp Thr Tyr Tyr Pro Gly Ser Val Lys Gly
1   5   10   15

<210> 101
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 CDR-H2

<400> 101

Arg Ile Asn Ser Asp Gly Ser Ser Thr Ser Tyr Ala Asp Ser Val Lys
1   5   10   15

Gly

<210> 102
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 CDR-H3

<400> 102

His Tyr Tyr Tyr Tyr Ser Met Asp Val
1 5

<210> 103
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 CDR-H3

<400> 103

His Tyr Tyr Tyr Tyr Tyr Leu Asp Val
1 5

<210> 104
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 CDR-H3

<400> 104

His Tyr Tyr Tyr Tyr Met Asp Val
1 5

<210> 105
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> anti-HLA-A*11 CDR-H3

<400> 105

His Tyr Tyr Tyr Tyr Tyr Met Asp Val
1 5

<210> 106
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 CDR-H3

<400> 106

Lys Thr Thr Ser Phe Tyr Phe Asp Tyr
1 5

<210> 107
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 CDR-H3

<400> 107

Arg His Met Arg Leu Ser Cys Phe Asp Tyr
1 5 10

<210> 108
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 CDR-H3

<400> 108

Glu Gly Asn Gly Ala Asn Pro Asp Ala Phe Asp Ile
1 5 10

<210> 109
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 CDR-H3

<400> 109

Asp Leu Pro Gly Ser Tyr Trp Tyr Phe Asp Leu
1   5   10

<210> 110
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 CDR-H3

<400> 110

Gly Val Leu Leu Tyr Asn Trp Phe Asp Pro
1   5   10

<210> 111
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 CDR1 LC

<400> 111

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
1   5   10

<210> 112
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 CDR2 LC

<400> 112

Ala Ala Ser Ser Leu Gln Ser
1   5

<210> 113
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 CDR3 LC

<400> 113

Gln Gln Ser Tyr Ser Thr Pro Leu Thr
1 5

<210> 114
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*11 antigen binding domain

<400> 114

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg His Tyr Tyr Tyr Tyr Ser Met Asp Val Trp Gly Lys Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro
130 135 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145 150 155 160

Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser
180 185 190

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys

<210> 115
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*11 antigen binding domain

<400> 115

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

```
Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
    50                  55                  60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala His Arg His Met Arg Leu Ser Cys Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser
    130                 135                 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys
                165                 170                 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln
            180                 185                 190

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220

Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240

Val Glu Ile Lys
```

<210> 116
<211> 245

<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*11 antigen binding domain

<400> 116

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


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30


Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asn Ala Gly Asn Gly Asn Thr Lys Tyr Ser Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Glu Gly Asn Gly Ala Asn Pro Asp Ala Phe Asp Ile Trp Gly
            100                 105                 110


Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125


Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln
    130                 135                 140


Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145                 150                 155                 160


Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln
                165                 170                 175


Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu
            180                 185                 190
```

```
Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
        195                 200                 205


Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
    210                 215                 220


Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr
225                 230                 235                 240


Lys Val Glu Ile Lys
                245


<210>  117
<211>  243
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HLA-A*11 antigen binding domain

<400>  117

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Asp Met His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Gly Thr Ala Gly Asp Thr Tyr Tyr Pro Gly Ser Val Lys
    50                  55                  60


Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn Ser Leu Tyr Leu
65                  70                  75                  80


Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Asp Leu Pro Gly Ser Tyr Trp Tyr Phe Asp Leu Trp Gly Arg Gly
            100                 105                 110
```

```
Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125


Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140


Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160


Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
                165                 170                 175


Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser
            180                 185                 190


Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205


Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220


Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240


Glu Ile Lys
```

<210> 118
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*11 antigen binding domain

<400> 118

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30
```

```
Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg His Tyr Tyr Tyr Tyr Tyr Leu Asp Val Trp Gly Lys Gly
            100                 105                 110

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160

Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser
            180                 185                 190

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240
```

Glu Ile Lys

<210> 119
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*11 antigen binding domain

<400> 119

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Val Trp Val
        35                  40                  45


Ser Arg Ile Asn Ser Asp Gly Ser Ser Thr Ser Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Cys Leu Gly Val Leu Leu Tyr Asn Trp Phe Asp Pro Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125


Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140


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

```
Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
                165                 170                 175


Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser
            180                 185                 190


Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205


Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220


Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240


Glu Ile Lys
```

<210> 120
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*11 antigen binding domain

<400> 120

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30


Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45


Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60


Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80
```

```
Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg His Tyr Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr
            100                 105                 110

Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser
    130                 135                 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160

Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
            180                 185                 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
225                 230                 235                 240

Ile Lys
```

<210> 121
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*11 antigen binding domain

<400> 121

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
            20                  25                  30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45

Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
    50                  55                  60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala His Lys Thr Thr Ser Phe Tyr Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160

Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser
            180                 185                 190

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220
```

Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys

<210> 122
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*11 antigen binding domain

<400> 122

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg His Tyr Tyr Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro
130 135 140

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


Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
                165                 170                 175


Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser
            180                 185                 190


Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205


Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220


Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240


Glu Ile Lys
```

<210> 123
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<223> HLA-A*11 antigen binding domain

<400> 123

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caggtgcagc tgcaggaaag cggccctggc ctggtgaaac ccagccagac cctgagcctg       60

acctgcacag tgtccggcgg ctcgatcagc agcggcggct actactggtc ctggatcaga      120

cagccccctg gcaagggcct ggaatggatc ggctacatct actacagcgg cagcacctac      180

tacaacccca gcctgaagtc cagagtgacc atcagcgtgg acaccagcaa gaaccagttc      240

agcctgaagc tgagcagcgt gacagccgcc gacaccgctg tgtattactg tgcgagacac      300

tactactact actccatgga cgtctggggc aaagggacca cggtcaccgt gtcctcaggc      360

ggaggtggaa gcggaggggg aggatctggc ggcggaggaa gcggaggcga catccagatg      420

acccagtctc catcctccct gtctgcatct gtaggagaca gagtcaccat cacttgccgg      480
```

gcaagtcaga gcattagcag ctatttaaat tggtatcagc agaaaccagg gaaagcccct 540

aagctcctga tctatgctgc atccagtttg caaagtgggg tcccatcaag gttcagtggc 600

agtggatctg ggacagattt cactctcacc atcagcagtc tgcaacctga agattttgca 660

acttactact gtcaacagag ttacagtacc cctctcactt tcggcggcgg aacaaaggtg 720

gagatcaag 729

<210> 124
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> HLA-A*11 antigen binding domain

<400> 124
cagatcaccc tgaaagagtc cggccccacc ctggtgaaac ccacccagac cctgaccctg 60

acatgcacct tcagcggctt cagcctgagc acctctggcg tgggcgtggg ctggatcaga 120

cagcctcccg gcaaggccct ggaatggctg gccctgatct actggaacga cgacaagcgg 180

tacagcccca gcctgaagtc ccggctgacc atcaccaagg acacctcgaa gaaccaggtg 240

gtgctgacca tgacaaacat ggaccccgtg gacaccgcca catattactg tgcacacaga 300

cacatgcgtt taagctgttt tgactactgg ggccagggaa ccctggtcac cgtgtcctca 360

ggcggaggtg gaagcggagg gggaggatct ggcggcggag gaagcggagg cgacatccag 420

atgacccagt ctccatcctc cctgtctgca tctgtaggag acagagtcac catcacttgc 480

cgggcaagtc agagcattag cagctattta aattggtatc agcagaaacc agggaaagcc 540

cctaagctcc tgatctatgc tgcatccagt ttgcaaagtg gggtcccatc aaggttcagt 600

ggcagtggat ctgggacaga tttcactctc accatcagca gtctgcaacc tgaagatttt 660

gcaacttact actgtcaaca gagttacagt acccctctca ctttcggcgg cggaacaaag 720

gtggagatca ag 732

<210> 125
<211> 735
<212> DNA
<213> Artificial Sequence

<220>

<223> HLA-A*11 antigen binding domain

<400> 125
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tcctgcaagg ccagcggcta caccttcacc agctacgcca tgcactgggt tcgacaggcc 120

cctggccaga gactggaatg gatgggctgg atcaacgccg gcaacggcaa caccaagtac 180

agccagaaat tccagggcag agtgaccatc acccgggaca ccagcgccag caccgcctac 240

atggaactga gcagcctgcg gagcgaggac accgctgtgt attactgtgc gagagaagga 300

aatggtgcca accctgatgc ttttgatatc tggggccaag ggacaatggt caccgtgtcc 360

tcaggcggag gtggaagcgg agggggagga tctggcggcg gaggaagcgg aggcgacatc 420

cagatgaccc agtctccatc ctccctgtct gcatctgtag gagacagagt caccatcact 480

tgccgggcaa gtcagagcat tagcagctat ttaaattggt atcagcagaa accagggaaa 540

gcccctaagc tcctgatcta tgctgcatcc agtttgcaaa gtggggtccc atcaaggttc 600

agtggcagtg gatctgggac agatttcact ctcaccatca gcagtctgca acctgaagat 660

tttgcaactt actactgtca acagagttac agtacccctc tcactttcgg cggcggaaca 720

aaggtggaga tcaag 735

<210> 126
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<223> HLA-A*11 antigen binding domain

<400> 126
gaagtgcagc tggtggaaag cggcggaggc ctggtgcagc ctggcggcag cctgagactg 60

tcttgcgccg ccagcggctt caccttcagc agctacgaca tgcactgggt ccgccaggcc 120

accggcaagg gactggaatg ggtgtccgcc atcggcacag ccggcgacac ttactacccc 180

ggcagcgtga agggccggtt caccatcagc agagagaacg ccaagaacag cctgtacctg 240

cagatgaaca gccttcgagc cggcgatacc gccgtgtatt actgtgcaag agatctccct 300

ggtagctact ggtacttcga tctctggggc cgtggcaccc tggtcactgt gtcctcaggc 360

ggaggtggaa gcggaggggg aggatctggc ggcggaggaa gcggaggcga catccagatg 420

acccagtctc catcctccct gtctgcatct gtaggagaca gagtcaccat cacttgccgg 480

gcaagtcaga gcattagcag ctatttaaat tggtatcagc agaaaccagg gaaagcccct 540

aagctcctga tctatgctgc atccagtttg caaagtgggg tcccatcaag gttcagtggc 600

agtggatctg ggacagattt cactctcacc atcagcagtc tgcaacctga agattttgca 660

acttactact gtcaacagag ttacagtacc cctctcactt tcggcggcgg aacaaaggtg 720

gagatcaag 729

<210> 127
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<223> HLA-A*11 antigen binding domain

<400> 127
caggtgcagc tgcaggaaag cggccctggc ctggtgaaac ccagccagac cctgagcctg 60

acctgcacag tgtccggcgg ctcgatcagc agcggcggct actactggtc ctggatcaga 120

cagccccctg gcaagggcct ggaatggatc ggctacatct actacagcgg cagcacctac 180

tacaacccca gcctgaagtc cagagtgacc atcagcgtgg acaccagcaa gaaccagttc 240

agcctgaagc tgagcagcgt gacagccgcc gacaccgctg tgtattactg tgcgagacac 300

tactactact actacctgga cgtctggggc aaagggacca cggtcaccgt gtcctcaggc 360

ggaggtggaa gcggaggggg aggatctggc ggcggaggaa gcggaggcga catccagatg 420

acccagtctc catcctccct gtctgcatct gtaggagaca gagtcaccat cacttgccgg 480

gcaagtcaga gcattagcag ctatttaaat tggtatcagc agaaaccagg gaaagcccct 540

aagctcctga tctatgctgc atccagtttg caaagtgggg tcccatcaag gttcagtggc 600

agtggatctg ggacagattt cactctcacc atcagcagtc tgcaacctga agattttgca 660

acttactact gtcaacagag ttacagtacc cctctcactt tcggcggcgg aacaaaggtg 720

gagatcaag 729

<210> 128
<211> 729
<212> DNA
<213> Artificial Sequence

<220>

<223> HLA-A*11 antigen binding domain

<400> 128
gaagtgcagc tggtggaaag cggcggaggc ctggtgcagc ctggcggcag cctgagactg 60

tcttgcgccg ccagcggctt caccttcagc agctactgga tgcactgggt ccgccaggcc 120

cctggcaagg gactggtctg ggtgtctcga atcaacagcg acggcagcag caccagctac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acgccaagaa caccctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt attactgttg tttgggtgtt 300

ttattataca actggttcga cccctggggc cagggaaccc tggtcaccgt gtcctcaggc 360

ggaggtggaa gcggaggggg aggatctggc ggcggaggaa gcggaggcga catccagatg 420

acccagtctc catcctccct gtctgcatct gtaggagaca gagtcaccat cacttgccgg 480

gcaagtcaga gcattagcag ctatttaaat tggtatcagc agaaaccagg gaaagcccct 540

aagctcctga tctatgctgc atccagtttg caaagtgggg tcccatcaag gttcagtggc 600

agtggatctg ggacagattt cactctcacc atcagcagtc tgcaacctga agattttgca 660

acttactact gtcaacagag ttacagtacc cctctcactt tcggcggcgg aacaaaggtg 720

gagatcaag 729

<210> 129
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> HLA-A*11 antigen binding domain

<400> 129
caggtgcagc tgcaggaaag cggccctggc ctggtgaaac ccagccagac cctgagcctg 60

acctgcacag tgtccggcgg ctcgatcagc agcggcggct actactggtc ctggatcaga 120

cagccccctg gcaagggcct ggaatggatc ggctacatct actacagcgg cagcacctac 180

tacaacccca gcctgaagtc cagagtgacc atcagcgtgg acaccagcaa gaaccagttc 240

agcctgaagc tgagcagcgt gacagccgcc gacaccgctg tgtattactg tgcgagacac 300

tactactact acatggacgt ctggggcaaa gggaccacgg tcaccgtgtc ctcaggcgga 360

ggtggaagcg gaggggggagg atctggcggc ggaggaagcg gaggcgacat ccagatgacc 420

cagtctccat cctccctgtc tgcatctgta ggagacagag tcaccatcac ttgccgggca 480

agtcagagca ttagcagcta tttaaattgg tatcagcaga aaccagggaa agcccctaag 540

ctcctgatct atgctgcatc cagtttgcaa agtggggtcc catcaaggtt cagtggcagt 600

ggatctggga cagatttcac tctcaccatc agcagtctgc aacctgaaga ttttgcaact 660

tactactgtc aacagagtta cagtacccct ctcactttcg gcggcggaac aaaggtggag 720

atcaag 726

<210> 130
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<223> HLA-A*11 antigen binding domain

<400> 130
cagatcaccc tgaaagagtc cggccccacc ctggtgaaac ccacccagac cctgaccctg 60

acatgcacct tcagcggctt cagcctgagc acctctggcg tgggcgtggg ctggatcaga 120

cagcctcccg gcaaggccct ggaatggctg gccctgatct actggaacga cgacaagcgg 180

tacagcccca gcctgaagtc ccggctgacc atcaccaagg acacctcgaa gaaccaggtg 240

gtgctgacca tgacaaacat ggaccccgtg gacaccgcca catattactg tgcacacaaa 300

acgacgtcgt tttactttga ctactggggc cagggaaccc tggtcaccgt gtcctcaggc 360

ggaggtggaa gcggaggggg aggatctggc ggcggaggaa gcggaggcga catccagatg 420

acccagtctc catcctccct gtctgcatct gtaggagaca gagtcaccat cacttgccgg 480

gcaagtcaga gcattagcag ctatttaaat tggtatcagc agaaaccagg gaaagccct 540

aagctcctga tctatgctgc atccagtttg caaagtgggg tcccatcaag gttcagtggc 600

agtggatctg ggacagattt cactctcacc atcagcagtc tgcaacctga agattttgca 660

acttactact gtcaacagag ttacagtacc cctctcactt tcggcggcgg aacaaaggtg 720

gagatcaag 729

<210> 131
<211> 729
<212> DNA
<213> Artificial Sequence

<220>

<223> HLA-A*11 antigen binding domain

<400> 131
caggtgcagc tgcaggaaag cggccctggc ctggtgaaac ccagccagac cctgagcctg 60

acctgcacag tgtccggcgg ctcgatcagc agcggcggct actactggtc ctggatcaga 120

cagccccctg gcaagggcct ggaatggatc ggctacatct actacagcgg cagcacctac 180

tacaacccca gcctgaagtc cagagtgacc atcagcgtgg acaccagcaa gaaccagttc 240

agcctgaagc tgagcagcgt gacagccgcc gacaccgctg tgtattactg tgcgagacac 300

tactactact actacatgga cgtctggggc aaagggacca cggtcaccgt gtcctcaggc 360

ggaggtggaa gcggaggggg aggatctggc ggcggaggaa gcggaggcga catccagatg 420

acccagtctc catcctccct gtctgcatct gtaggagaca gagtcaccat cacttgccgg 480

gcaagtcaga gcattagcag ctatttaaat tggtatcagc agaaaccagg gaaagccct 540

aagctcctga tctatgctgc atccagtttg caaagtgggg tcccatcaag gttcagtggc 600

agtggatctg ggacagattt cactctcacc atcagcagtc tgcaacctga agattttgca 660

acttactact gtcaacagag ttacagtacc cctctcactt tcggcggcgg aacaaaggtg 720

gagatcaag 729

<210> 132
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 heavy chain

<400> 132

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

```
Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80


Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95


Cys Ala Arg His Tyr Tyr Tyr Tyr Ser Met Asp Val Trp Gly Lys Gly
            100                 105                 110


Thr Thr Val Thr Val Ser Ser
        115


<210>  133
<211>  120
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  anti-HLA-A*11 heavy chain

<400>  133

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


Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
            20                  25                  30


Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45


Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
    50                  55                  60


Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80


Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95


Cys Ala His Arg His Met Arg Leu Ser Cys Phe Asp Tyr Trp Gly Gln
            100                 105                 110
```

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 134
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 heavy chain

<400> 134

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20   25   30

Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35   40   45

Gly Trp Ile Asn Ala Gly Asn Gly Asn Thr Lys Tyr Ser Gln Lys Phe
    50   55   60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Glu Gly Asn Gly Ala Asn Pro Asp Ala Phe Asp Ile Trp Gly
            100   105   110

Gln Gly Thr Met Val Thr Val Ser Ser
        115   120

<210> 135
<211> 119
<212> PRT
<213> Artificial Sequence

<220>

<223> anti-HLA-A*11 heavy chain

<400> 135

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Asp Met His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Gly Thr Ala Gly Asp Thr Tyr Tyr Pro Gly Ser Val Lys
    50                  55                  60


Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn Ser Leu Tyr Leu
65                  70                  75                  80


Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Asp Leu Pro Gly Ser Tyr Trp Tyr Phe Asp Leu Trp Gly Arg Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115
```

<210> 136
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 heavy chain

<400> 136

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30
```

```
Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg His Tyr Tyr Tyr Tyr Tyr Leu Asp Val Trp Gly Lys Gly
            100                 105                 110

Thr Thr Val Thr Val Ser Ser
        115
```

<210> 137
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 heavy chain

<400> 137

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Val Trp Val
        35                  40                  45

Ser Arg Ile Asn Ser Asp Gly Ser Ser Thr Ser Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65                  70                  75                  80
```

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Cys Leu Gly Val Leu Leu Tyr Asn Trp Phe Asp Pro Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210>  138
<211>  118
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  anti-HLA-A*11 heavy chain

<400>  138

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30


Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45


Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60


Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80


Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95


Cys Ala Arg His Tyr Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr
            100                 105                 110


Thr Val Thr Val Ser Ser
        115
```

<210> 139
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 heavy chain

<400> 139

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


Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
            20                  25                  30


Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45


Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
    50                  55                  60


Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80


Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95


Cys Ala His Lys Thr Thr Ser Phe Tyr Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115
```

<210> 140
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 heavy chain

<400> 140

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                  10                  15
```

```
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg His Tyr Tyr Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly
            100                 105                 110

Thr Thr Val Thr Val Ser Ser
        115
```

<210> 141
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 light chain

<400> 141

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
```

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 142
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 heavy chain

<400> 142
caggtgcagc tgcaggaaag cggccctggc ctggtgaaac ccagccagac cctgagcctg 60

acctgcacag tgtccggcgg ctcgatcagc agcggcggct actactggtc ctggatcaga 120

cagccccctg gcaagggcct ggaatggatc ggctacatct actacagcgg cagcacctac 180

tacaacccca gcctgaagtc cagagtgacc atcagcgtgg acaccagcaa gaaccagttc 240

agcctgaagc tgagcagcgt gacagccgcc gacaccgctg tgtattactg tgcgagacac 300

tactactact actccatgga cgtctggggc aaagggacca cggtcaccgt gtcctca 357

<210> 143
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 heavy chain

<400> 143
cagatcaccc tgaaagagtc cggccccacc ctggtgaaac ccacccagac cctgaccctg 60

acatgcacct tcagcggctt cagcctgagc acctctggcg tgggcgtggg ctggatcaga 120

cagcctcccg gcaaggccct ggaatggctg gccctgatct actggaacga cgacaagcgg 180

tacagcccca gcctgaagtc ccggctgacc atcaccaagg acacctcgaa gaaccaggtg 240

gtgctgacca tgacaaacat ggaccccgtg gacaccgcca catattactg tgcacacaga 300

cacatgcgtt taagctgttt tgactactgg ggccagggaa ccctggtcac cgtgtcctca 360

<210> 144
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 heavy chain

<400> 144
caggtgcagc tggtgcagtc tggcgccgaa gtgaagaaac ctggcgcctc cgtgaaggtg 60

tcctgcaagg ccagcggcta caccttcacc agctacgcca tgcactgggt tcgacaggcc 120

cctggccaga gactggaatg gatgggctgg atcaacgccg gcaacggcaa caccaagtac 180

agccagaaat tccagggcag agtgaccatc acccgggaca ccagcgccag caccgcctac 240

atggaactga gcagcctgcg gagcgaggac accgctgtgt attactgtgc gagagaagga 300

aatggtgcca accctgatgc ttttgatatc tggggccaag ggacaatggt caccgtgtcc 360

tca 363

<210> 145
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 heavy chain

<400> 145
gaagtgcagc tggtggaaag cggcggaggc ctggtgcagc ctggcggcag cctgagactg 60

tcttgcgccg ccagcggctt caccttcagc agctacgaca tgcactgggt ccgccaggcc 120

accggcaagg gactggaatg ggtgtccgcc atcggcacag ccggcgacac ttactacccc 180

ggcagcgtga agggccggtt caccatcagc agagagaacg ccaagaacag cctgtacctg 240

cagatgaaca gccttcgagc cggcgatacc gccgtgtatt actgtgcaag agatctccct 300

ggtagctact ggtacttcga tctctggggc cgtggcaccc tggtcactgt gtcctca 357

<210> 146
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 heavy chain

<400> 146
caggtgcagc tgcaggaaag cggccctggc ctggtgaaac ccagccagac cctgagcctg 60

acctgcacag tgtccggcgg ctcgatcagc agcggcggct actactggtc ctggatcaga 120

cagccccctg gcaagggcct ggaatggatc ggctacatct actacagcgg cagcacctac 180

tacaacccca gcctgaagtc cagagtgacc atcagcgtgg acaccagcaa gaaccagttc 240

agcctgaagc tgagcagcgt gacagccgcc gacaccgctg tgtattactg tgcgagacac 300

tactactact actacctgga cgtctggggc aaagggacca cggtcaccgt gtcctca 357

<210> 147
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 heavy chain

<400> 147
gaagtgcagc tggtggaaag cggcggaggc ctggtgcagc ctggcggcag cctgagactg 60

tcttgcgccg ccagcggctt caccttcagc agctactgga tgcactgggt ccgccaggcc 120

cctggcaagg gactggtctg ggtgtctcga atcaacagcg acggcagcag caccagctac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acgccaagaa caccctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt attactgttg tttgggtgtt 300

ttattataca actggttcga cccctggggc cagggaaccc tggtcaccgt gtcctca 357

<210> 148
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 heavy chain

<400> 148
caggtgcagc tgcaggaaag cggccctggc ctggtgaaac ccagccagac cctgagcctg 60

acctgcacag tgtccggcgg ctcgatcagc agcggcggct actactggtc ctggatcaga 120

cagccccctg gcaagggcct ggaatggatc ggctacatct actacagcgg cagcacctac 180

tacaacccca gcctgaagtc cagagtgacc atcagcgtgg acaccagcaa gaaccagttc 240

agcctgaagc tgagcagcgt gacagccgcc gacaccgctg tgtattactg tgcgagacac 300

tactactact acatggacgt ctggggcaaa gggaccacgg tcaccgtgtc ctca 354

<210> 149
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 heavy chain

<400> 149
cagatcaccc tgaaagagtc cggccccacc ctggtgaaac ccacccagac cctgaccctg 60

acatgcacct tcagcggctt cagcctgagc acctctggcg tgggcgtggg ctggatcaga 120

cagcctcccg gcaaggccct ggaatggctg gccctgatct actggaacga cgacaagcgg 180

tacagcccca gcctgaagtc ccggctgacc atcaccaagg acacctcgaa gaaccaggtg 240

gtgctgacca tgacaaacat ggaccccgtg gacaccgcca catattactg tgcacacaaa 300

acgacgtcgt tttactttga ctactggggc cagggaaccc tggtcaccgt gtcctca 357

<210> 150
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 heavy chain

<400> 150
caggtgcagc tgcaggaaag cggccctggc ctggtgaaac ccagccagac cctgagcctg 60

acctgcacag tgtccggcgg ctcgatcagc agcggcggct actactggtc ctggatcaga 120

cagcccctg gcaagggcct ggaatggatc ggctacatct actacagcgg cagcacctac 180

tacaacccca gcctgaagtc cagagtgacc atcagcgtgg acaccagcaa gaaccagttc 240

agcctgaagc tgagcagcgt gacagccgcc gacaccgctg tgtattactg tgcgagacac 300

tactactact actacatgga cgtctggggc aaagggacca cggtcaccgt gtcctca 357

<210> 151
<211> 321

<212> DNA
<213> Artificial Sequence

<220>
<223> anti-HLA-A*11 light chain

<400> 151
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta cccctctcac tttcggcggc 300

ggaacaaagg tggagatcaa g 321

<210> 152
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 152

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly

<210> 153
<211> 66
<212> PRT
<213> Unknown

<220>
<223> encodes signal sequence

<400> 153

Ala Thr Gly Gly Ala Cys Ala Thr Gly Ala Gly Gly Gly Thr Cys Cys
1 5 10 15

Cys Cys Gly Cys Thr Cys Ala Gly Cys Thr Cys Cys Thr Gly Gly Gly
20 25 30

Gly Cys Thr Cys Cys Thr Gly Cys Thr Ala Cys Thr Cys Thr Gly Gly
        35   40   45

Cys Thr Cys Cys Gly Ala Gly Gly Thr Gly Cys Cys Ala Gly Ala Thr
    50   55   60

Gly Thr
65

<210> 154
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 154

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Ala
            20   25   30

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

Gly Arg Ile Lys Ser Lys Thr Asp Gly Gly Thr Thr Asp Tyr Ala Ala
    50   55   60

Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65   70   75   80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85   90   95

Tyr Cys Thr Thr Asp Leu Pro Lys Leu Arg Asn Phe His Ile Trp Gly
            100   105   110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115   120   125

```
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln
    130                 135                 140

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145                 150                 155                 160

Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln
                165                 170                 175

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu
            180                 185                 190

Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
        195                 200                 205

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
    210                 215                 220

Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr
225                 230                 235                 240

Lys Val Glu Ile Lys
                245
```

<210> 155
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 155

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Tyr Val
        35                  40                  45
```

```
Ser Ala Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Ser Leu Glu Tyr His Gly Phe Arg Gln Tyr Gly Leu Arg Tyr Trp
            100                 105                 110

His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln
    130                 135                 140

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
145                 150                 155                 160

Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
                165                 170                 175

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala
            180                 185                 190

Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
        195                 200                 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
    210                 215                 220

Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly
225                 230                 235                 240

Gly Gly Thr Lys Val Glu Ile Lys
                245
```

<210> 156
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 156

```
Gln Leu Gln Leu Gln Glu Ser Gly Ser Gly Leu Val Lys Pro Ser Gln
1               5                  10                  15


Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30


Gly Tyr Ser Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45


Trp Ile Gly Tyr Ile Tyr His Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60


Leu Lys Ser Arg Val Thr Ile Ser Val Asp Arg Ser Lys Asn Gln Phe
65                  70                  75                  80


Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95


Cys Ala Ser Ile Lys Phe Trp Phe Ala Gly Ile Asn Tyr Phe Phe Pro
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        115                 120                 125


Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met
    130                 135                 140


Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145                 150                 155                 160


Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr
                165                 170                 175
```

```
Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser
            180                 185                 190


Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205


Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
    210                 215                 220


Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly
225                 230                 235                 240


Gly Thr Lys Val Glu Ile Lys
                245
```

<210> 157
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 157

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Val Trp Val
        35                  40                  45


Ser Arg Ile Asn Ser Asp Gly Ser Ser Thr Ser Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Ser Gly Phe Leu Gly Met Gly Ser Asn Phe Ile Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160

Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser
            180                 185                 190

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

Glu Ile Lys
```

<210> 158
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 158

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15
```

```
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Leu Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Ser Gly Asp Arg Ala Arg Tyr Phe Asp Leu Trp Gly Arg Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160

Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser
            180                 185                 190

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240
```

Glu Ile Lys

<210> 159
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 159

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Val Trp Val
        35                  40                  45

Ser Arg Ile Asn Ser Asp Gly Ser Ser Thr Ser Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Tyr Pro Arg Gly Tyr His Gln Met Val Asp Ala Phe Asp Ile
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met
    130                 135                 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145                 150                 155                 160
```

```
Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr
                165                 170                 175


Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser
            180                 185                 190


Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205


Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
    210                 215                 220


Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly
225                 230                 235                 240


Gly Thr Lys Val Glu Ile Lys
                245


<210>  160
<211>  250
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  MSLN scFv domain

<400>  160

Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser
            20                  25                  30


Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45


Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60


Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80
```

```
Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Val Arg Phe Leu Ala Ala Arg Thr Thr Ile Pro Glu Ala
            100                 105                 110

Asn Phe Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
        115                 120                 125

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

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
145                 150                 155                 160

Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu
                165                 170                 175

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
            180                 185                 190

Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
        195                 200                 205

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
    210                 215                 220

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr
225                 230                 235                 240

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
                245                 250
```

<210> 161
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 161

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Val Leu Ser Arg Ala Arg Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125


Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser
    130                 135                 140


Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160


Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175


Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
            180                 185                 190


Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205
```

```
Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
225                 230                 235                 240

Ile Lys
```

<210> 162
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 162

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ser Ile Ser Ser Ser Ser Ser Tyr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Leu Arg Gly Arg Val Phe Asp Pro Trp Gly Gln Gly Thr Leu
            100                 105                 110

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125
```

```
Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
    130                 135                 140

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145                 150                 155                 160

Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
                165                 170                 175

Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val
            180                 185                 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
        195                 200                 205

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
    210                 215                 220

Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
225                 230                 235                 240

Lys
```

<210> 163
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 163

```
Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser
            20                  25                  30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45
```

```
Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

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

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met
    130                 135                 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145                 150                 155                 160

Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr
                165                 170                 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser
            180                 185                 190

Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
    210                 215                 220

Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly
225                 230                 235                 240

Gly Thr Lys Val Glu Ile Lys
                245
```

<210> 164
<211> 246

<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 164

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


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30


Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asn Ala Gly Asn Gly Asn Thr Lys Tyr Ser Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Gly Gln Arg Trp Leu Tyr Leu Gly Gly Ile Arg Arg His Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125


Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr
    130                 135                 140


Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160


Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln
                165                 170                 175


Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser
            180                 185                 190
```

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 165
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 165

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

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

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

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

Arg Glu Trp Ile Pro Ser Arg Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

```
Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125


Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser
    130                 135                 140


Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160


Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys
                165                 170                 175


Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln
            180                 185                 190


Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205


Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220


Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240


Val Glu Ile Lys
```

<210> 166
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 166

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30
```

```
Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Glu Ser Thr Gly Thr Gly Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110

Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser
    130                 135                 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys
                165                 170                 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln
            180                 185                 190

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220

Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240
```

Val Glu Ile Lys

<210> 167
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 167

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
            20                  25                  30

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

Ser Gly Ile Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr His Cys
                85                  90                  95

Ala Arg Glu Arg Tyr Arg Arg Val Leu His Trp Tyr Phe Asp Leu Trp
            100                 105                 110

Gly Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr
    130                 135                 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160
```

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 168
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 168

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asp Ile Asn Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Met Asn Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe
50 55 60

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

```
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Pro Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
            100                 105                 110

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
    130                 135                 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
145                 150                 155                 160

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

Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro
            180                 185                 190

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
        195                 200                 205

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser
    210                 215                 220

Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
225                 230                 235                 240


<210>  169
<211>  246
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  MSLN scFv domain

<400>  169

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15
```

```
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Glu His Met Gly Thr Ile Pro Tyr Tyr Phe Asp Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr
    130                 135                 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln
                165                 170                 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser
            180                 185                 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
    210                 215                 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly
225                 230                 235                 240
```

Thr Lys Val Glu Ile Lys
245

<210> 170
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 170

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

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

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser
130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160

```
Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys
                165                 170                 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln
            180                 185                 190

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220

Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240

Val Glu Ile Lys
```

<210> 171
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 171

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30

Asp Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80
```

```
Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Glu Asp Val Val Lys Gly Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110

Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser
    130                 135                 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys
                165                 170                 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln
            180                 185                 190

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220

Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240

Val Glu Ile Lys
```

<210> 172
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 172

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Asp Phe Ser His Lys Leu Gly Tyr Phe Gln His Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln
    130                 135                 140

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145                 150                 155                 160

Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln
                165                 170                 175

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu
            180                 185                 190

Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
        195                 200                 205
```

```
Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
    210                 215                 220


Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr
225                 230                 235                 240


Lys Val Glu Ile Lys
                245


<210>  173
<211>  238
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  MSLN scFv domain

<400>  173

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Tyr Asp Tyr Val Trp Gly Gln Gly Thr Leu Val Thr Val
            100                 105                 110


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

```
Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
    130                 135                 140

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile
145                 150                 155                 160

Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
                165                 170                 175

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

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
        195                 200                 205

Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser
    210                 215                 220

Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
225                 230                 235


<210>  174
<211>  244
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  MSLN scFv domain

<400>  174

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30

Asp Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60
```

```
Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Asp Arg Arg Asp Trp Asp Trp Phe Asp Pro Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser
    130                 135                 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys
                165                 170                 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln
            180                 185                 190

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220

Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240

Val Glu Ile Lys
```

<210> 175
<211> 243
<212> PRT
<213> Artificial Sequence

<220>

<223> MSLN scFv domain

<400> 175

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gly
1               5                  10                  15


Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Ser Ser Ser
            20                  25                  30


Asn Trp Trp Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45


Ile Gly Glu Ile Tyr His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60


Lys Ser Arg Val Thr Ile Ser Val Asp Lys Ser Lys Asn Gln Phe Ser
65                  70                  75                  80


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


Ala Arg Asp Gln Gln Ala Leu Lys Tyr Arg Val Asp Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125


Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140


Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160


Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
                165                 170                 175


Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser
            180                 185                 190


Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205
```

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys

<210> 176
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 176

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Leu Thr Leu Gly Cys Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

```
Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser
    130                 135                 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160

Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
            180                 185                 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
225                 230                 235                 240

Ile Lys
```

<210> 177
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 177

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Ser Asn
            20                  25                  30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

```
Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
    50                  55                  60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Gly Ser Asn Ser Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser
    130                 135                 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160

Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
            180                 185                 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
225                 230                 235                 240

Ile Lys
```

<210> 178
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 178

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Ala Phe Leu Phe Leu Ser Phe Ser Val Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125


Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser
    130                 135                 140


Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160


Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175
```

```
Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
            180                 185                 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
225                 230                 235                 240

Ile Lys
```

<210> 179
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 179

```
Glu Val Gln Leu Val Glu Ser Gly Gly Val Val Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
            20                  25                  30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Leu Ile Ser Trp Asp Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95
```

```
Ala Lys Gly Ile Phe Tyr Ser Ser Lys Glu Asp Phe Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln
    130                 135                 140

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145                 150                 155                 160

Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln
                165                 170                 175

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu
            180                 185                 190

Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
        195                 200                 205

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
    210                 215                 220

Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr
225                 230                 235                 240

Lys Val Glu Ile Lys
                245
```

<210> 180
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 180

```
Glu Val Gln Leu Val Glu Ser Gly Gly Val Val Val Gln Pro Gly Gly
1               5                   10                  15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
            20                  25                  30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Leu Ile Ser Trp Asp Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95

Ala Lys Asp Ile Trp Ile Phe Tyr Ser Ser Asn Pro Lys Pro Thr Val
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln
    130                 135                 140

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
145                 150                 155                 160

Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
                165                 170                 175

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala
            180                 185                 190

Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
        195                 200                 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
    210                 215                 220

Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly
225                 230                 235                 240
```

Gly Gly Thr Lys Val Glu Ile Lys
245

<210> 181
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 181

Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Asn Thr Gly Asn Pro Thr Tyr Ala Gln Gly Phe
50 55 60

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

Leu Gln Ile Cys Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Lys Asp Gln Thr Leu Thr Tyr Gly Asn Trp Phe Asp Pro Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr
130 135 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145 150 155 160

```
Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln
                165                 170                 175


Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser
            180                 185                 190


Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205


Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
    210                 215                 220


Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly
225                 230                 235                 240


Thr Lys Val Glu Ile Lys
                245


<210>  182
<211>  242
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  MSLN scFv domain

<400>  182

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Ser Gly
            20                  25                  30


Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45


Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser
    50                  55                  60


Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80
```

```
Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Asp His Tyr Glu Arg Gly Leu Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser
    130                 135                 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160

Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
            180                 185                 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
225                 230                 235                 240

Ile Lys
```

<210> 183
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 183

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Tyr Met Tyr Asn Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125


Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser
    130                 135                 140


Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160


Ser Gln Gly Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175


Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
            180                 185                 190


Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205
```

```
Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Ala Asn Ser Phe Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
225                 230                 235                 240

Ile Lys
```

<210> 184
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 184

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Arg Arg Pro Ala Phe Asp Ile Trp Gly Gln Gly Thr Met
            100                 105                 110

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125
```

```
Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
    130                 135                 140

Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145                 150                 155                 160

Gln Gly Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
                165                 170                 175

Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val
            180                 185                 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
        195                 200                 205

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
    210                 215                 220

Ala Asn Ser Phe Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
225                 230                 235                 240

Lys
```

<210> 185
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 185

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

```
Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Val His Leu Lys Arg Arg Pro Tyr Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

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

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160

Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

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

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

Glu Ile Lys
```

<210> 186
<211> 242

<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 186

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                  10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Ser Val His Lys Lys Pro Ile Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125


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


Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160


Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175


Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu Glu Ser Gly
            180                 185                 190
```

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
210 215 220

Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
225 230 235 240

Ile Lys

<210> 187
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 187

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ser Thr Ser Arg Arg Cys Thr Phe Gln His Trp Gly Gln Gly Thr
100 105 110

```
Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

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

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160

Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175

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

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
225                 230                 235                 240

Ile Lys
```

<210> 188
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 188

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30
```

```
Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Ser Thr Ser Pro Arg Pro Leu Phe Gln His Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

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

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160

Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175

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

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
225                 230                 235                 240
```

Ile Lys

<210> 189
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 189

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Ser Pro Tyr Gln Val Arg Gly Val Tyr Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Ala Ile Gln Leu Thr Gln Ser
    130                 135                 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160
```

Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys
165 170 175

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

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
195 200 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
210 215 220

Cys Gln Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys
225 230 235 240

Val Glu Ile Lys

<210> 190
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 190

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Ser Pro Tyr Lys Lys Arg Arg Thr Val Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Ala Ile Gln Leu Thr Gln Ser
    130                 135                 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160

Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys
                165                 170                 175

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

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220

Cys Gln Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240

Val Glu Ile Lys
```

<210> 191
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 191

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Ser Leu Gln Arg Gly Leu Ala Leu Phe Gln His Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

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

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160

Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

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

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220
```

Gln Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys

<210> 192
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 192

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ser Ile Leu Ser Val Pro Tyr Phe Asp Leu Trp Gly Arg Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

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

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


Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175


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


Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205


Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220


Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
225                 230                 235                 240


Ile Lys



<210>  193
<211>  247
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  MSLN scFv domain

<400>  193

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Ser Gly Trp Ile Arg Val Pro Leu Arg Leu Pro Leu Phe Gln His
            100                 105                 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ala Ile Gln Leu
    130                 135                 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145                 150                 155                 160

Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr
                165                 170                 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser
            180                 185                 190

Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
    210                 215                 220

Thr Tyr Tyr Cys Gln Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly
225                 230                 235                 240

Gly Thr Lys Val Glu Ile Lys
                245
```

<210> 194
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 194

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Val Thr Ile Phe Ala Ile Phe Asp Ile Trp Gly Gln Gly Thr
            100                 105                 110


Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125


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


Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160


Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175


Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu Glu Ser Gly
            180                 185                 190
```

```
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205


Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220


Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
225                 230                 235                 240


Ile Lys
```

<210> 195
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 195

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Val Gly Arg Gly Phe Val His Phe Asp Leu Trp Gly Arg Gly
            100                 105                 110
```

```
Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125


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


Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160


Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175


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


Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205


Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220


Gln Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240


Glu Ile Lys
```

<210> 196
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 196

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30
```

```
Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Thr Ser Arg Gly Leu Cys Val Leu Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Ala Ile Gln Leu Thr Gln Ser
    130                 135                 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160

Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys
                165                 170                 175

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

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220

Cys Gln Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240

Val Glu Ile Lys
```

<210> 197
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 197

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Ser Gly Pro Ser Ser Tyr Trp Tyr Phe Asp Leu Trp Gly Arg
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125


Gly Ser Gly Gly Gly Gly Ser Gly Gly Ala Ile Gln Leu Thr Gln Ser
    130                 135                 140


Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160


Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys
                165                 170                 175
```

```
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu Glu
            180                 185                 190

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220

Cys Gln Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240

Val Glu Ile Lys
```

<210> 198
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 198

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Arg Asn Ile Tyr Met Gly Gly Ile Trp Phe Asp Pro Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125


Gly Ser Gly Gly Gly Gly Ser Gly Gly Ala Ile Gln Leu Thr Gln Ser
    130                 135                 140


Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160


Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys
                165                 170                 175


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


Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205


Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220


Cys Gln Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240


Val Glu Ile Lys
```

<210> 199
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 199

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Leu Thr Val Arg Thr Gly Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110

Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

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

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160

Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

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

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220
```

Gln Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys

<210> 200
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 200

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Leu Arg Thr Ala His Leu Asp Phe Asp Leu Trp Gly Arg Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

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

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


Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175


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


Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205


Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220


Gln Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240


Glu Ile Lys
```

<210> 201
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 201

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Leu Ile Phe Pro Val Val Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

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

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160

Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

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

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

Glu Ile Lys
```

<210> 202
<211> 246
<212> PRT
<213> Artificial Sequence

<220>

<223> MSLN scFv domain

<400> 202

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                  10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Gly Tyr Arg Lys Tyr Gly Tyr Val Phe Phe Asp Ile Trp
            100                 105                 110


Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125


Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ala Ile Gln Leu Thr
    130                 135                 140


Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160


Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln
                165                 170                 175


Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser
            180                 185                 190


Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205
```

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
    210   215   220

Tyr Tyr Cys Gln Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225   230   235   240

Thr Lys Val Glu Ile Lys
                245

<210> 203
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 203

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20   25   30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Asp Gly Arg Tyr Arg Arg Phe Trp His Ala Phe Asp Ile Trp
            100   105   110

Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115   120   125

```
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ala Ile Gln Leu Thr
    130                 135                 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160

Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln
                165                 170                 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser
            180                 185                 190

Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
    210                 215                 220

Tyr Tyr Cys Gln Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225                 230                 235                 240

Thr Lys Val Glu Ile Lys
                245
```

<210> 204
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 204

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

```
Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ala His Ile Arg Gly Tyr Phe Asp Leu Trp Gly Arg Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

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

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160

Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175

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

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
225                 230                 235                 240

Ile Lys
```

<210> 205
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 205

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                  10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


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


Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Thr Trp Met Gly Gly Gly Gly Arg Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110


Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125


Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ala Ile Gln Leu Thr Gln
    130                 135                 140


Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145                 150                 155                 160


Cys Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln
                165                 170                 175
```

```
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu
            180                 185                 190

Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
        195                 200                 205

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
    210                 215                 220

Tyr Cys Gln Gln Phe Asn Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr
225                 230                 235                 240

Lys Val Glu Ile Lys
                245
```

<210> 206
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 206

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Arg Thr Ser Arg Thr Thr Trp Tyr Phe Asp Leu Trp Gly Arg Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

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

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160

Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

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

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Phe Asn Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

Glu Ile Lys
```

<210> 207
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 207

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Trp Met Gly Gly Gly Gly Arg Leu Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ala Ile Gln Leu Thr Gln
    130                 135                 140

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145                 150                 155                 160

Cys Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln
                165                 170                 175

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu
            180                 185                 190

Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
        195                 200                 205

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
    210                 215                 220

Tyr Cys Gln Gln Phe Asn Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr
225                 230                 235                 240
```

Lys Val Glu Ile Lys
245

<210> 208
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 208

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Trp Gly Gly Arg Leu Tyr Trp Tyr Phe Asp Leu Trp Gly Arg
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Ala Ile Gln Leu Thr Gln Ser
130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160

```
Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys
                165                 170                 175


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


Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205


Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220


Cys Gln Gln Phe Asn Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240


Val Glu Ile Lys
```

<210> 209
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 209

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


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


Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
```

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Val Ile Arg Gln Leu Trp Tyr Phe Asp Leu Trp Gly Arg Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

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

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160

Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

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

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Phe Asn Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

Glu Ile Lys
```

<210> 210
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 210

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

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

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145 150 155 160

Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

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

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

```
Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Phe Asn Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

Glu Ile Lys
```

<210> 211
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 211

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Val Asp Arg Thr Thr Trp Tyr Phe Asp Leu Trp Gly Arg Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125
```

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

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145 150 155 160

Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

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

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Phe Asn Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys

<210> 212
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 212

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

```
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Arg Trp Gly Lys Asp Gly Pro Tyr Trp Tyr Phe Asp Leu Trp
            100                 105                 110

Gly Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ala Ile Gln Leu Thr
    130                 135                 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160

Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln
                165                 170                 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser
            180                 185                 190

Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
    210                 215                 220

Tyr Tyr Cys Gln Gln Phe Asn Asn Tyr Pro Leu Thr Phe Gly Gly Gly
225                 230                 235                 240

Thr Lys Val Glu Ile Lys
                245
```

<210> 213
<211> 246

<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 213

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Arg Arg Asp Ser Tyr Gly Pro Tyr Trp Tyr Phe Asp Leu Trp
100 105 110

Gly Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ala Ile Gln Leu Thr
130 135 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145 150 155 160

Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser
180 185 190

Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Gln Gln Phe Asn Asn Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 214
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 214

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Asn Arg Pro Pro Pro Gly Tyr Trp Tyr Phe Asp Leu Trp Gly
100 105 110

```
Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125


Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ala Ile Gln Leu Thr Gln
    130                 135                 140


Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145                 150                 155                 160


Cys Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln
                165                 170                 175


Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu
            180                 185                 190


Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
        195                 200                 205


Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
    210                 215                 220


Tyr Cys Gln Gln Phe Asn Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr
225                 230                 235                 240


Lys Val Glu Ile Lys
                245


<210>  215
<211>  243
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  MSLN scFv domain

<400>  215

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
```

```
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Gly Arg Arg Phe Ser Trp Tyr Phe Asp Leu Trp Gly Arg Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

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

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160

Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

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

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Phe Asn Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240
```

Glu Ile Lys

<210> 216
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 216

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Ala
            20                  25                  30


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


Gly Arg Ile Lys Ser Lys Thr Asp Gly Gly Thr Thr Asp Tyr Ala Ala
    50                  55                  60


Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65                  70                  75                  80


Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95


Tyr Cys Thr Thr Asp Leu Pro Lys Leu Arg Asn Phe His Ile Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 217
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 217

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Tyr Val
35 40 45

Ser Ala Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys
85 90 95

Ala Ser Leu Glu Tyr His Gly Phe Arg Gln Tyr Gly Leu Arg Tyr Trp
100 105 110

His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 218
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 218

Gln Leu Gln Leu Gln Glu Ser Gly Ser Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Ser Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr His Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50   55   60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Arg Ser Lys Asn Gln Phe
65   70   75   80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85   90   95

Cys Ala Ser Ile Lys Phe Trp Phe Ala Gly Ile Asn Tyr Phe Phe Pro
            100   105   110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 219
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 219

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30

Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Val Trp Val
        35   40   45

Ser Arg Ile Asn Ser Asp Gly Ser Ser Thr Ser Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Ser Gly Phe Leu Gly Met Gly Ser Asn Phe Ile Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 220
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 220

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Leu Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Ser Gly Asp Arg Ala Arg Tyr Phe Asp Leu Trp Gly Arg Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 221
<211> 123

<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 221

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30

Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Val Trp Val
        35   40   45

Ser Arg Ile Asn Ser Asp Gly Ser Ser Thr Ser Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Tyr Pro Arg Gly Tyr His Gln Met Val Asp Ala Phe Asp Ile
            100   105   110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115   120

<210> 222
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 222

Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1   5   10   15

```
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser
            20                  25                  30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Val Arg Phe Leu Ala Ala Arg Thr Thr Ile Pro Glu Ala
            100                 105                 110

Asn Phe Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125
```

<210> 223
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 223

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Val Leu Ser Arg Ala Arg Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210>  224
<211>  117
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  heavy chain variable fragment

<400>  224

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Ser Ser Ser Ser Tyr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Leu Arg Gly Arg Val Phe Asp Pro Trp Gly Gln Gly Thr Leu
            100                 105                 110
```

Val Thr Val Ser Ser
        115

<210> 225
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 225

Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1   5   10   15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser
            20   25   30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35   40   45

Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50   55   60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65   70   75   80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85   90   95

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

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 226
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 226

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Ala Gly Asn Gly Asn Thr Lys Tyr Ser Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gln Arg Trp Leu Tyr Leu Gly Gly Ile Arg Arg His Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 227
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 227

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

```
Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
    50                  55                  60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65                  70                  75                  80

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

Arg Glu Trp Ile Pro Ser Arg Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 228
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 228

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95
```

Cys Ala Arg Glu Ser Thr Gly Thr Gly Ala Phe Asp Ile Trp Gly Gln
100 105 110

Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 229
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 229

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

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

Ser Gly Ile Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr His Cys
85 90 95

Ala Arg Glu Arg Tyr Arg Arg Val Leu His Trp Tyr Phe Asp Leu Trp
100 105 110

Gly Arg Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 230
<211> 116

<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 230

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asp Ile Asn Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Met Asn Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe
50 55 60

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

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Pro Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
100 105 110

Thr Val Ser Ser
115

<210> 231
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 231

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

```
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Glu His Met Gly Thr Ile Pro Tyr Tyr Phe Asp Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 232
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 232

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60
```

```
Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80


Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95


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


Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 233
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 233

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30


Asp Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45


Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60


Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80


Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95


Cys Ala Arg Glu Asp Val Val Lys Gly Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110
```

Gly Thr Met Val Thr Val Ser Ser
        115   120

<210> 234
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 234

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Glu Asp Phe Ser His Lys Leu Gly Tyr Phe Gln His Trp Gly
            100   105   110

Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 235
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 235

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Tyr Asp Tyr Val Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

Ser Ser

<210> 236
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 236

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Asp Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

```
Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Asp Arg Arg Asp Trp Asp Trp Phe Asp Pro Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 237
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 237

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gly
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Ser Ser Ser
            20                  25                  30

Asn Trp Trp Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

Ile Gly Glu Ile Tyr His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Val Thr Ile Ser Val Asp Lys Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Arg Asp Gln Gln Ala Leu Lys Tyr Arg Val Asp Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210>  238
<211>  118
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  heavy chain variable fragment

<400>  238

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30


Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


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


Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Leu Thr Leu Gly Cys Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210>  239
<211>  118
```

<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 239

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Ser Asn
            20   25   30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
    50   55   60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65   70   75   80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85   90   95

Arg Asp Gly Ser Asn Ser Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr
            100   105   110

Leu Val Thr Val Ser Ser
        115

<210> 240
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 240

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1   5   10   15

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ala Phe Leu Phe Leu Ser Phe Ser Val Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser
        115


<210>  241
<211>  121
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  heavy chain variable fragment

<400>  241

Glu Val Gln Leu Val Glu Ser Gly Gly Val Val Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
            20                  25                  30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Leu Ile Ser Trp Asp Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Ile Phe Tyr Ser Ser Lys Glu Asp Phe Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  242
<211>  124
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  heavy chain variable fragment

<400>  242

Glu Val Gln Leu Val Glu Ser Gly Gly Val Val Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
            20                  25                  30


Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Leu Ile Ser Trp Asp Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95


Ala Lys Asp Ile Trp Ile Phe Tyr Ser Ser Asn Pro Lys Pro Thr Val
            100                 105                 110
```

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 243
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 243

Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Asn Thr Gly Asn Pro Thr Tyr Ala Gln Gly Phe
50 55 60

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

Leu Gln Ile Cys Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Lys Asp Gln Thr Leu Thr Tyr Gly Asn Trp Phe Asp Pro Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 244
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 244

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Ser Gly
20 25 30

Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Asp His Tyr Glu Arg Gly Leu Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 245
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 245

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

```
Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Tyr Met Tyr Asn Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210>  246
<211>  117
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  heavy chain variable fragment

<400>  246

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Arg Asp Arg Arg Pro Ala Phe Asp Ile Trp Gly Gln Gly Thr Met
            100                 105                 110


Val Thr Val Ser Ser
        115


<210>  247
<211>  119
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  heavy chain variable fragment

<400>  247

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Val His Leu Lys Arg Arg Pro Tyr Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210>  248
<211>  118
```

<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 248

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20   25   30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Ser Val His Lys Lys Pro Ile Phe Asp Tyr Trp Gly Gln Gly Thr
            100   105   110

Leu Val Thr Val Ser Ser
        115

<210> 249
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 249

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1   5   10   15

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Ser Thr Ser Arg Arg Cys Thr Phe Gln His Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser
        115


<210>  250
<211>  118
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  heavy chain variable fragment

<400>  250

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Ser Thr Ser Pro Arg Pro Leu Phe Gln His Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210>  251
<211>  120
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  heavy chain variable fragment

<400>  251

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Ser Pro Tyr Gln Val Arg Gly Val Tyr Phe Asp Tyr Trp Gly Gln
            100                 105                 110
```

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 252
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 252

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20   25   30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Ser Pro Tyr Lys Lys Arg Arg Thr Val Phe Asp Tyr Trp Gly Gln
            100   105   110

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 253
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 253

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ser Leu Gln Arg Gly Leu Ala Leu Phe Gln His Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 254
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 254

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

```
Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Ser Ile Leu Ser Val Pro Tyr Phe Asp Leu Trp Gly Arg Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210>  255
<211>  123
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  heavy chain variable fragment

<400>  255

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

Ala Ser Gly Trp Ile Arg Val Pro Leu Arg Leu Pro Leu Phe Gln His
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 256
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 256

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Val Thr Ile Phe Ala Ile Phe Asp Ile Trp Gly Gln Gly Thr
100 105 110

Met Val Thr Val Ser Ser
115

<210> 257
<211> 119

<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 257

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20   25   30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Val Gly Arg Gly Phe Val His Phe Asp Leu Trp Gly Arg Gly
            100   105   110

Thr Leu Val Thr Val Ser Ser
        115

<210> 258
<211> 1503
<212> DNA
<213> Artificial Sequence

<220>
<223> PA2.1.14 scFv LIR1 HTICD

<400> 258
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tcctgcaagg cttctggata caccttcact agctatcata tacattgggt gcgccaggcc   120

cccggacaag ggcttgagtg gatcggatgg atctaccctg gcaatgttaa cacagaatat   180

aatgagaagt tcaagggcaa agccaccatt accgcggacg aatccacgaa cacagcctac 240

atggagctga gcagcctgag atctgaagac acggctgtgt attactgtgc gagggaggaa 300

attacctacg ctatggacta ctggggccag ggaaccctgg tcaccgtgtc ctcaggcgga 360

ggtggaagcg gaggggggagg atctggcggc ggaggaagcg gaggcgacat tcaaatgacc 420

cagagcccat ccaccctgag cgcatctgta ggtgaccggg tcaccatcac ttgtagatcc 480

agtcagagta ttgtacacag taatgggaac acctatttgg aatggtatca gcagaaacca 540

ggtaaagccc caaaattgct catctacaaa gtctctaaca gatttagtgg tgtaccagcc 600

aggttcagcg gttccggaag tggtactgaa ttcaccctca cgatctcctc tctccagcca 660

gatgatttcg ccacttatta ctgttttcaa ggttcacatg tgccgcgcac attcggtcag 720

ggtactaaag tagaagtcaa atacggctca cagagctcca aaccctacct gctgactcac 780

cccagtgacc ccctggagct cgtggtctca ggaccgtctg ggggccccag ctccccgaca 840

acaggcccca cctccacatc tggccctgag gaccagcccc tcacccccac cgggtcggat 900

ccccagagtg gtctgggaag gcacctgggg gttgtgatcg gcatcttggt ggccgtcatc 960

ctactgctcc tcctcctcct cctcctcttc ctcatcctcc gacatcgacg tcagggcaaa 1020

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gagcccacag acagaggcct gcagtggagg tccagcccag ctgccgatgc ccaggaagaa 1140

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aggagagaaa tggcctctcc tccttcccca ctgtctgggg aattcctgga cacaaaggac 1320

agacaggcgg aagaggacag gcagatggac actgaggctg ctgcatctga agccccccag 1380

gatgtgacct acgcccagct gcacagcttg accctcagac gggaggcaac tgagcctcct 1440

ccatcccagg aagggccctc tccagctgtg cccagcatct acgccactct ggccatccac 1500

tag 1503

<210> 259
<211> 120
<212> PRT
<213> Artificial Sequence

<220>

<223> heavy chain variable fragment

<400> 259

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Thr Ser Arg Gly Leu Cys Val Leu Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 260
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 260

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30
```

```
Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Ser Gly Pro Ser Ser Tyr Trp Tyr Phe Asp Leu Trp Gly Arg
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  261
<211>  120
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  heavy chain variable fragment

<400>  261

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80
```

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asn Ile Tyr Met Gly Gly Ile Trp Phe Asp Pro Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  262
<211>  119
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  heavy chain variable fragment

<400>  262

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Leu Thr Val Arg Thr Gly Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110


Thr Met Val Thr Val Ser Ser
        115
```

<210> 263
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 263

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Leu Arg Thr Ala His Leu Asp Phe Asp Leu Trp Gly Arg Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115
```

<210> 264
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 264

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Leu Ile Phe Pro Val Val Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210>  265
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  heavy chain variable fragment

<400>  265

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Gly Tyr Arg Lys Tyr Gly Tyr Val Phe Phe Asp Ile Trp
            100                 105                 110


Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120
```

<210> 266
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 266

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Gly Arg Tyr Arg Arg Phe Trp His Ala Phe Asp Ile Trp
            100                 105                 110
```

Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115   120

<210> 267
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 267

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20   25   30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Ala His Ile Arg Gly Tyr Phe Asp Leu Trp Gly Arg Gly Thr
            100   105   110

Leu Val Thr Val Ser Ser
        115

<210> 268
<211> 121
<212> PRT
<213> Artificial Sequence

<220>

<223> heavy chain variable fragment

<400> 268

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


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


Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Thr Trp Met Gly Gly Gly Gly Arg Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110


Arg Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 269
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 269

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
```

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Thr Ser Arg Thr Thr Trp Tyr Phe Asp Leu Trp Gly Arg Gly
            100   105   110

Thr Leu Val Thr Val Ser Ser
        115

<210> 270
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 270

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Trp Met Gly Gly Gly Gly Arg Leu Tyr Phe Asp Leu Trp Gly
            100                 105                 110


Arg Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  271
<211>  120
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  heavy chain variable fragment

<400>  271

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


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


Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Trp Gly Gly Arg Leu Tyr Trp Tyr Phe Asp Leu Trp Gly Arg
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 272
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 272

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Val Ile Arg Gln Leu Trp Tyr Phe Asp Leu Trp Gly Arg Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 273
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 273

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

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

Thr Leu Val Thr Val Ser Ser
        115


<210>  274
<211>  119
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  heavy chain variable fragment

<400>  274

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Asp Arg Thr Thr Trp Tyr Phe Asp Leu Trp Gly Arg Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210>  275
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  heavy chain variable fragment

<400>  275

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


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


Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Arg Trp Gly Lys Asp Gly Pro Tyr Trp Tyr Phe Asp Leu Trp
            100                 105                 110
```

Gly Arg Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 276
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 276

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Lys Arg Arg Asp Ser Tyr Gly Pro Tyr Trp Tyr Phe Asp Leu Trp
            100   105   110

Gly Arg Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 277
<211> 121
<212> PRT
<213> Artificial Sequence

<220>

<223> heavy chain variable fragment

<400> 277

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                  10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


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


Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Asn Arg Pro Pro Pro Gly Tyr Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110


Arg Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 278
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable fragment

<400> 278

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                  10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
```

```
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Arg Arg Phe Ser Trp Tyr Phe Asp Leu Trp Gly Arg Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210>  279
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  light chain variable fragment

<400>  279

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


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
```

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 280
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain variable fragment

<400> 280

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 281
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain variable fragment

<400> 281

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Ala
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Phe Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 282
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain variable fragment

<400> 282

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Ala
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Phe Asn Asn Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 283
<211> 42
<212> PRT
<213> Unknown

<220>
<223> 4-1BB co-stimulatory domain

<400> 283

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
1 5 10 15

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
20 25 30

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
35 40

<210> 284
<211> 126
<212> DNA
<213> Unknown

<220>
<223> encodes 4-1BB co-stimulatory domain

<400> 284
aaacggggca gaaagaaact cctgtatata ttcaaacaac catttatgag gccagtacaa 60

actactcaag aggaagatgg ctgtagctgc cgatttccag aagaagaaga aggaggatgt 120

gaactg 126

<210> 285
<211> 195

<212> PRT
<213> Artificial Sequence

<220>
<223> CAR intracellular domain

<400> 285

```
Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
1               5                  10                  15


Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
            20                  25                  30


Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu
        35                  40                  45


Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln
    50                  55                  60


Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly
65                  70                  75                  80


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


Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
            100                 105                 110


Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
        115                 120                 125


Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
    130                 135                 140


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


Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
                165                 170                 175


Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
            180                 185                 190
```

Pro Pro Arg
195

<210> 286
<211> 512
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 286

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Ala
20 25 30

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

Gly Arg Ile Lys Ser Lys Thr Asp Gly Gly Thr Thr Asp Tyr Ala Ala
50 55 60

Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Thr Thr Asp Leu Pro Lys Leu Arg Asn Phe His Ile Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln
130 135 140

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145 150 155 160

```
Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln
                165                 170                 175

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu
            180                 185                 190

Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
        195                 200                 205

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
    210                 215                 220

Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr
225                 230                 235                 240

Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
                245                 250                 255

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
            260                 265                 270

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
        275                 280                 285

Cys Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr
    290                 295                 300

Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys
305                 310                 315                 320

Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg
                325                 330                 335

Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp
            340                 345                 350

Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile
        355                 360                 365
```

```
Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp
    370                 375                 380

Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
385                 390                 395                 400

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly
                405                 410                 415

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
            420                 425                 430

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
        435                 440                 445

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
    450                 455                 460

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
465                 470                 475                 480

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
                485                 490                 495

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505                 510
```

<210> 287
<211> 515
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 287

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
```

```
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Tyr Val
        35                  40                  45

Ser Ala Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Ser Leu Glu Tyr His Gly Phe Arg Gln Tyr Gly Leu Arg Tyr Trp
            100                 105                 110

His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln
    130                 135                 140

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
145                 150                 155                 160

Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
                165                 170                 175

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala
            180                 185                 190

Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
        195                 200                 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
    210                 215                 220

Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly
225                 230                 235                 240

Gly Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
                245                 250                 255
```

```
Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
            260                 265                 270

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
        275                 280                 285

Asp Phe Ala Cys Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu
    290                 295                 300

Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
305                 310                 315                 320

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
                325                 330                 335

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
            340                 345                 350

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu
        355                 360                 365

Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln
    370                 375                 380

Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly
385                 390                 395                 400

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

Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
            420                 425                 430

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
        435                 440                 445

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
    450                 455                 460
```

```
Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
465                 470                 475                 480


Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
                485                 490                 495


Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
            500                 505                 510


Pro Pro Arg
        515
```

<210> 288
<211> 514
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 288

```
Gln Leu Gln Leu Gln Glu Ser Gly Ser Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30


Gly Tyr Ser Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45


Trp Ile Gly Tyr Ile Tyr His Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60


Leu Lys Ser Arg Val Thr Ile Ser Val Asp Arg Ser Lys Asn Gln Phe
65                  70                  75                  80


Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95


Cys Ala Ser Ile Lys Phe Trp Phe Ala Gly Ile Asn Tyr Phe Phe Pro
            100                 105                 110
```

```
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met
    130                 135                 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145                 150                 155                 160

Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr
                165                 170                 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser
            180                 185                 190

Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
    210                 215                 220

Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly
225                 230                 235                 240

Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro
                245                 250                 255

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
            260                 265                 270

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
        275                 280                 285

Phe Ala Cys Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala
    290                 295                 300

Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg
305                 310                 315                 320

Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro
                325                 330                 335
```

```
Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
            340                 345                 350

Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu
        355                 360                 365

Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu
    370                 375                 380

Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys
385                 390                 395                 400

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

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
            420                 425                 430

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
        435                 440                 445

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
    450                 455                 460

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
465                 470                 475                 480

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
                485                 490                 495

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
            500                 505                 510

Pro Arg
```

<210> 289
<211> 510
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 289

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Val Trp Val
        35                  40                  45


Ser Arg Ile Asn Ser Asp Gly Ser Ser Thr Ser Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Ser Gly Phe Leu Gly Met Gly Ser Asn Phe Ile Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125


Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140


Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160


Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
                165                 170                 175


Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser
            180                 185                 190
```

```
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
                245                 250                 255

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
            260                 265                 270

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
        275                 280                 285

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
    290                 295                 300

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
305                 310                 315                 320

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
                325                 330                 335

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
            340                 345                 350

Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys
        355                 360                 365

Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys
    370                 375                 380

Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val
385                 390                 395                 400

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn
                405                 410                 415
```

```
Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
            420                 425                 430

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
        435                 440                 445

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
    450                 455                 460

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
465                 470                 475                 480

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
                485                 490                 495

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505                 510
```

<210> 290
<211> 510
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 290

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Leu Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80
```

```
Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Ser Gly Asp Arg Ala Arg Tyr Phe Asp Leu Trp Gly Arg Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160

Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser
            180                 185                 190

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
                245                 250                 255

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
            260                 265                 270

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
        275                 280                 285
```

```
Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
    290                 295                 300

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
305                 310                 315                 320

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
                325                 330                 335

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
            340                 345                 350

Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys
        355                 360                 365

Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys
    370                 375                 380

Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val
385                 390                 395                 400

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn
                405                 410                 415

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
            420                 425                 430

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
        435                 440                 445

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
    450                 455                 460

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
465                 470                 475                 480

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
                485                 490                 495

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505                 510
```

<210> 291
<211> 514
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 291

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Val Trp Val
        35                  40                  45


Ser Arg Ile Asn Ser Asp Gly Ser Ser Thr Ser Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Tyr Pro Arg Gly Tyr His Gln Met Val Asp Ala Phe Asp Ile
            100                 105                 110


Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        115                 120                 125


Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met
    130                 135                 140


Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145                 150                 155                 160


Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr
                165                 170                 175
```

```
Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser
            180                 185                 190

Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
    210                 215                 220

Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly
225                 230                 235                 240

Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro
                245                 250                 255

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
            260                 265                 270

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
        275                 280                 285

Phe Ala Cys Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala
    290                 295                 300

Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg
305                 310                 315                 320

Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro
                325                 330                 335

Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
            340                 345                 350

Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu
        355                 360                 365

Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu
    370                 375                 380
```

```
Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys
385                 390                 395                 400


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


Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
            420                 425                 430


Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
        435                 440                 445


Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
    450                 455                 460


Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
465                 470                 475                 480


Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
                485                 490                 495


Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
            500                 505                 510


Pro Arg
```

<210> 292
<211> 517
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 292

```
Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser
            20                  25                  30
```

```
Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Val Arg Phe Leu Ala Ala Arg Thr Thr Ile Pro Glu Ala
            100                 105                 110

Asn Phe Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
        115                 120                 125

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

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
145                 150                 155                 160

Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu
                165                 170                 175

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
            180                 185                 190

Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
        195                 200                 205

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
    210                 215                 220

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr
225                 230                 235                 240

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro
                245                 250                 255
```

```
Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
            260                 265                 270

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
        275                 280                 285

Gly Leu Asp Phe Ala Cys Asp Phe Trp Val Leu Val Val Val Gly Gly
    290                 295                 300

Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe
305                 310                 315                 320

Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn
                325                 330                 335

Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr
            340                 345                 350

Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys
        355                 360                 365

Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr
    370                 375                 380

Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu
385                 390                 395                 400

Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
                405                 410                 415

Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
            420                 425                 430

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
        435                 440                 445

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
    450                 455                 460
```

```
Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
465                 470                 475                 480


Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
                485                 490                 495


Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
            500                 505                 510


Ala Leu Pro Pro Arg
        515


<210>  293
<211>  509
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  single chain variable fragment

<400>  293

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Val Leu Ser Arg Ala Arg Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110
```

```
Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125


Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser
    130                 135                 140


Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160


Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175


Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
            180                 185                 190


Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205


Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220


Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
225                 230                 235                 240


Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
                245                 250                 255


Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
            260                 265                 270


Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe
        275                 280                 285


Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
    290                 295                 300


Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
305                 310                 315                 320


Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
                325                 330                 335
```

```
Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
            340                 345                 350

Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
        355                 360                 365

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
    370                 375                 380

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
385                 390                 395                 400

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln
                405                 410                 415

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
            420                 425                 430

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
        435                 440                 445

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
    450                 455                 460

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
465                 470                 475                 480

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
                485                 490                 495

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505
```

<210> 294
<211> 508
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 294

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Ser Ser Ser Ser Tyr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Leu Arg Gly Arg Val Phe Asp Pro Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
130 135 140

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145 150 155 160

Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
165 170 175

Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val
180 185 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

```
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
    210                 215                 220

Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
225                 230                 235                 240

Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
                245                 250                 255

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
            260                 265                 270

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe Trp
        275                 280                 285

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
    290                 295                 300

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu
305                 310                 315                 320

Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr
                325                 330                 335

Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr
            340                 345                 350

Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro
        355                 360                 365

Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys
    370                 375                 380

Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe
385                 390                 395                 400

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu
                405                 410                 415

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
            420                 425                 430
```

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
435 440 445

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
450 455 460

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
465 470 475 480

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
485 490 495

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
500 505

<210> 295
<211> 514
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 295

Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser
20 25 30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

```
Cys Ala Arg Ile Lys Phe Thr Ser Phe Leu Tyr Val His Gly Phe Leu
            100                 105                 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met
    130                 135                 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145                 150                 155                 160

Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr
                165                 170                 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser
            180                 185                 190

Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
    210                 215                 220

Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly
225                 230                 235                 240

Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro
                245                 250                 255

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
            260                 265                 270

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
        275                 280                 285

Phe Ala Cys Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala
    290                 295                 300
```

```
Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg
305                 310                 315                 320

Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro
                325                 330                 335

Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
            340                 345                 350

Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu
        355                 360                 365

Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu
    370                 375                 380

Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys
385                 390                 395                 400

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

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
            420                 425                 430

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
        435                 440                 445

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
    450                 455                 460

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
465                 470                 475                 480

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
                485                 490                 495

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
            500                 505                 510

Pro Arg
```

<210> 296
<211> 513
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 296

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


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30


Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asn Ala Gly Asn Gly Asn Thr Lys Tyr Ser Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Gly Gln Arg Trp Leu Tyr Leu Gly Gly Ile Arg Arg His Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125


Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr
    130                 135                 140


Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160


Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln
                165                 170                 175
```

```
Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser
            180                 185                 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
    210                 215                 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly
225                 230                 235                 240

Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
                245                 250                 255

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
            260                 265                 270

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
        275                 280                 285

Ala Cys Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys
    290                 295                 300

Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser
305                 310                 315                 320

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
                325                 330                 335

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
            340                 345                 350

Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr
        355                 360                 365

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
    370                 375                 380
```

```
Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
385                 390                 395                 400


Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln
                405                 410                 415


Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
            420                 425                 430


Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
        435                 440                 445


Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
    450                 455                 460


Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
465                 470                 475                 480


Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
                485                 490                 495


Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
            500                 505                 510


Arg
```

<210> 297
<211> 511
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 297

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
            20                  25                  30
```

```
Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45

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

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65                  70                  75                  80

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

Arg Glu Trp Ile Pro Ser Arg Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser
    130                 135                 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys
                165                 170                 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln
            180                 185                 190

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220

Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240

Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
                245                 250                 255
```

```
Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
            260                 265                 270

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
        275                 280                 285

Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
    290                 295                 300

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
305                 310                 315                 320

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
                325                 330                 335

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
            340                 345                 350

Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
        355                 360                 365

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
    370                 375                 380

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg
385                 390                 395                 400

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln
                405                 410                 415

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
            420                 425                 430

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
        435                 440                 445

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
    450                 455                 460
```

```
Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
465                 470                 475                 480


Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
                485                 490                 495


Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505                 510


<210>  298
<211>  511
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  single chain variable fragment

<400>  298

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30


Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45


Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60


Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80


Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95


Cys Ala Arg Glu Ser Thr Gly Thr Gly Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110


Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125
```

```
Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser
    130                 135                 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys
                165                 170                 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln
            180                 185                 190

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220

Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240

Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
                245                 250                 255

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
            260                 265                 270

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
        275                 280                 285

Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
    290                 295                 300

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
305                 310                 315                 320

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
                325                 330                 335

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
            340                 345                 350
```

```
Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
        355                 360                 365

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
    370                 375                 380

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg
385                 390                 395                 400

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln
                405                 410                 415

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
            420                 425                 430

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
        435                 440                 445

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
    450                 455                 460

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
465                 470                 475                 480

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
                485                 490                 495

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505                 510
```

<210> 299
<211> 513
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 299

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
1               5                   10                  15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
            20                  25                  30

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

Ser Gly Ile Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr His Cys
                85                  90                  95

Ala Arg Glu Arg Tyr Arg Arg Val Leu His Trp Tyr Phe Asp Leu Trp
            100                 105                 110

Gly Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr
    130                 135                 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln
                165                 170                 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser
            180                 185                 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
    210                 215                 220
```

```
Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly
225                 230                 235                 240

Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
                245                 250                 255

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
            260                 265                 270

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
        275                 280                 285

Ala Cys Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys
    290                 295                 300

Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser
305                 310                 315                 320

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
                325                 330                 335

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
            340                 345                 350

Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr
        355                 360                 365

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
    370                 375                 380

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
385                 390                 395                 400

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln
                405                 410                 415

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
            420                 425                 430

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
        435                 440                 445
```

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
450 455 460

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
465 470 475 480

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
485 490 495

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
500 505 510

Arg

<210> 300
<211> 507
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 300

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asp Ile Asn Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Met Asn Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe
50 55 60

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

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

```
Ala Arg Glu Pro Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
            100                 105                 110

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
    130                 135                 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
145                 150                 155                 160

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

Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro
            180                 185                 190

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
        195                 200                 205

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser
    210                 215                 220

Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
225                 230                 235                 240

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
                245                 250                 255

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
            260                 265                 270

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe Trp Val
        275                 280                 285

Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr
    290                 295                 300
```

```
Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu
305                 310                 315                 320


His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg
                325                 330                 335


Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg
            340                 345                 350


Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
        355                 360                 365


Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg
    370                 375                 380


Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser
385                 390                 395                 400


Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr
                405                 410                 415


Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
            420                 425                 430


Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
        435                 440                 445


Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
    450                 455                 460


Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
465                 470                 475                 480


His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
                485                 490                 495


Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505


<210>  301
<211>  513
```

<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 301

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                  10                  15


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30


Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45


Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60


Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80


Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95


Cys Ala Arg Glu His Met Gly Thr Ile Pro Tyr Tyr Phe Asp Tyr Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125


Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr
    130                 135                 140


Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160


Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln
                165                 170                 175


Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser
            180                 185                 190
```

```
Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
    210                 215                 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly
225                 230                 235                 240

Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
                245                 250                 255

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
            260                 265                 270

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
        275                 280                 285

Ala Cys Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys
    290                 295                 300

Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser
305                 310                 315                 320

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
                325                 330                 335

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
            340                 345                 350

Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr
        355                 360                 365

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
    370                 375                 380

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
385                 390                 395                 400
```

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln
405 410 415

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
420 425 430

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
435 440 445

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
450 455 460

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
465 470 475 480

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
485 490 495

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
500 505 510

Arg

<210> 302
<211> 511
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 302

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

```
Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

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

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser
    130                 135                 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys
                165                 170                 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln
            180                 185                 190

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220

Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240

Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
                245                 250                 255

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
            260                 265                 270
```

```
Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
        275                 280                 285

Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
    290                 295                 300

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
305                 310                 315                 320

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
                325                 330                 335

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
            340                 345                 350

Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
        355                 360                 365

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
    370                 375                 380

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg
385                 390                 395                 400

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln
                405                 410                 415

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
            420                 425                 430

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
        435                 440                 445

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
    450                 455                 460

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
465                 470                 475                 480
```

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
485 490 495

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
500 505 510

<210> 303
<211> 511
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 303

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Asp Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Glu Asp Val Val Lys Gly Ala Phe Asp Ile Trp Gly Gln
100 105 110

Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser
130 135 140

```
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys
                165                 170                 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln
            180                 185                 190

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220

Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240

Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
                245                 250                 255

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
            260                 265                 270

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
        275                 280                 285

Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
    290                 295                 300

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
305                 310                 315                 320

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
                325                 330                 335

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
            340                 345                 350

Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
        355                 360                 365
```

```
Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
    370                 375                 380

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg
385                 390                 395                 400

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln
                405                 410                 415

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
            420                 425                 430

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
        435                 440                 445

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
    450                 455                 460

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
465                 470                 475                 480

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
                485                 490                 495

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505                 510
```

<210> 304
<211> 512
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 304

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
```

```
Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Asp Phe Ser His Lys Leu Gly Tyr Phe Gln His Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln
    130                 135                 140

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145                 150                 155                 160

Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln
                165                 170                 175

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu
            180                 185                 190

Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
        195                 200                 205

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
    210                 215                 220

Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr
225                 230                 235                 240
```

```
Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
                245                 250                 255

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
            260                 265                 270

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
        275                 280                 285

Cys Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr
    290                 295                 300

Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys
305                 310                 315                 320

Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg
                325                 330                 335

Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp
            340                 345                 350

Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile
        355                 360                 365

Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp
    370                 375                 380

Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
385                 390                 395                 400

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly
                405                 410                 415

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
            420                 425                 430

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
        435                 440                 445

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
    450                 455                 460
```

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
465 470 475 480

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
485 490 495

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
500 505 510

<210> 305
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 305

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Tyr Asp Tyr Val Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

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

```
Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
    130                 135                 140

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile
145                 150                 155                 160

Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
                165                 170                 175

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

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
        195                 200                 205

Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser
    210                 215                 220

Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Thr Thr
225                 230                 235                 240

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
                245                 250                 255

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
            260                 265                 270

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe Trp Val Leu Val
        275                 280                 285

Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
    290                 295                 300

Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser
305                 310                 315                 320

Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His
                325                 330                 335
```

```
Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys
            340                 345                 350

Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg
        355                 360                 365

Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro
    370                 375                 380

Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser
385                 390                 395                 400

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

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
            420                 425                 430

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
        435                 440                 445

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
    450                 455                 460

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
465                 470                 475                 480

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
                485                 490                 495

Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505
```

<210> 306
<211> 511
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 306

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                  10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30

Asp Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Asp Arg Arg Asp Trp Asp Trp Phe Asp Pro Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser
    130                 135                 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys
                165                 170                 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln
            180                 185                 190

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220
```

```
Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240

Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
                245                 250                 255

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
            260                 265                 270

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
        275                 280                 285

Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
    290                 295                 300

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
305                 310                 315                 320

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
                325                 330                 335

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
            340                 345                 350

Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
        355                 360                 365

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
    370                 375                 380

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg
385                 390                 395                 400

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln
                405                 410                 415

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
            420                 425                 430
```

```
Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
        435                 440                 445

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
    450                 455                 460

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
465                 470                 475                 480

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
                485                 490                 495

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505                 510
```

<210> 307
<211> 510
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 307

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gly
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Ser Ser Ser
            20                  25                  30

Asn Trp Trp Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

Ile Gly Glu Ile Tyr His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Val Thr Ile Ser Val Asp Lys Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Arg Asp Gln Gln Ala Leu Lys Tyr Arg Val Asp Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160

Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser
            180                 185                 190

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
                245                 250                 255

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
            260                 265                 270

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
        275                 280                 285

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
    290                 295                 300

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
305                 310                 315                 320
```

```
Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
                325                 330                 335

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
            340                 345                 350

Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys
        355                 360                 365

Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys
    370                 375                 380

Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val
385                 390                 395                 400

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn
                405                 410                 415

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
            420                 425                 430

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
        435                 440                 445

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
    450                 455                 460

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
465                 470                 475                 480

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
                485                 490                 495

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505                 510
```

<210> 308
<211> 509
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 308

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


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30


Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


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


Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Leu Thr Leu Gly Cys Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125


Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser
    130                 135                 140


Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160


Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175


Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
            180                 185                 190
```

```
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
225                 230                 235                 240

Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
                245                 250                 255

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
            260                 265                 270

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe
        275                 280                 285

Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
    290                 295                 300

Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
305                 310                 315                 320

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
                325                 330                 335

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
            340                 345                 350

Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
        355                 360                 365

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
    370                 375                 380

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
385                 390                 395                 400

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln
                405                 410                 415
```

```
Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
            420                 425                 430

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
        435                 440                 445

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
    450                 455                 460

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
465                 470                 475                 480

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
                485                 490                 495

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505
```

<210> 309
<211> 509
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 309

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Ser Asn
            20                  25                  30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
    50                  55                  60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65                  70                  75                  80
```

```
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Gly Ser Asn Ser Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser
    130                 135                 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160

Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
            180                 185                 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
225                 230                 235                 240

Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
                245                 250                 255

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
            260                 265                 270

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe
        275                 280                 285
```

```
Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
    290                 295                 300

Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
305                 310                 315                 320

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
                325                 330                 335

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
            340                 345                 350

Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
        355                 360                 365

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
    370                 375                 380

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
385                 390                 395                 400

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln
                405                 410                 415

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
            420                 425                 430

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
        435                 440                 445

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
    450                 455                 460

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
465                 470                 475                 480

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
                485                 490                 495

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505
```

<210> 310
<211> 509
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 310

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Ala Phe Leu Phe Leu Ser Phe Ser Val Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125


Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser
    130                 135                 140


Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160


Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175
```

```
Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
            180                 185                 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
225                 230                 235                 240

Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
                245                 250                 255

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
            260                 265                 270

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe
        275                 280                 285

Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
    290                 295                 300

Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
305                 310                 315                 320

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
                325                 330                 335

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
            340                 345                 350

Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
        355                 360                 365

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
    370                 375                 380
```

```
Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
385                 390                 395                 400


Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln
                405                 410                 415


Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
            420                 425                 430


Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
        435                 440                 445


Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
    450                 455                 460


Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
465                 470                 475                 480


Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
                485                 490                 495


Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505


<210>  311
<211>  512
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  single chain variable fragment

<400>  311

Glu Val Gln Leu Val Glu Ser Gly Gly Val Val Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
            20                  25                  30


Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

```
Ser Leu Ile Ser Trp Asp Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95

Ala Lys Gly Ile Phe Tyr Ser Ser Lys Glu Asp Phe Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln
    130                 135                 140

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145                 150                 155                 160

Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln
                165                 170                 175

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu
            180                 185                 190

Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
        195                 200                 205

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
    210                 215                 220

Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr
225                 230                 235                 240

Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
                245                 250                 255

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
            260                 265                 270
```

```
Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
        275                 280                 285

Cys Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr
    290                 295                 300

Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys
305                 310                 315                 320

Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg
                325                 330                 335

Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp
            340                 345                 350

Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile
        355                 360                 365

Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp
    370                 375                 380

Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
385                 390                 395                 400

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly
                405                 410                 415

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
            420                 425                 430

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
        435                 440                 445

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
    450                 455                 460

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
465                 470                 475                 480
```

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
485 490 495

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
500 505 510

<210> 312
<211> 515
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 312

Glu Val Gln Leu Val Glu Ser Gly Gly Val Val Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Leu Ile Ser Trp Asp Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Ile Trp Ile Phe Tyr Ser Ser Asn Pro Lys Pro Thr Val
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln
130 135 140

```
Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
145                 150                 155                 160

Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
                165                 170                 175

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala
            180                 185                 190

Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
        195                 200                 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
    210                 215                 220

Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly
225                 230                 235                 240

Gly Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
                245                 250                 255

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
            260                 265                 270

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
        275                 280                 285

Asp Phe Ala Cys Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu
    290                 295                 300

Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
305                 310                 315                 320

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
                325                 330                 335

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
            340                 345                 350

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu
        355                 360                 365
```

```
Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln
    370                 375                 380

Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly
385                 390                 395                 400

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

Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
            420                 425                 430

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
        435                 440                 445

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
    450                 455                 460

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
465                 470                 475                 480

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
                485                 490                 495

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
            500                 505                 510

Pro Pro Arg
        515
```

<210> 313
<211> 513
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 313

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

```
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Ile Asn Thr Asn Thr Gly Asn Pro Thr Tyr Ala Gln Gly Phe
    50                  55                  60

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

Leu Gln Ile Cys Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Lys Asp Gln Thr Leu Thr Tyr Gly Asn Trp Phe Asp Pro Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr
    130                 135                 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln
                165                 170                 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser
            180                 185                 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
    210                 215                 220
```

```
Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly
225                 230                 235                 240

Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
                245                 250                 255

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
            260                 265                 270

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
        275                 280                 285

Ala Cys Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys
    290                 295                 300

Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser
305                 310                 315                 320

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
                325                 330                 335

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
            340                 345                 350

Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr
        355                 360                 365

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
    370                 375                 380

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
385                 390                 395                 400

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln
                405                 410                 415

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
            420                 425                 430

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
        435                 440                 445
```

```
Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
    450                 455                 460

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
465                 470                 475                 480

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
                485                 490                 495

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
            500                 505                 510

Arg
```

<210> 314
<211> 509
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 314

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Ser Gly
            20                  25                  30

Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95
```

```
Cys Ala Arg Asp His Tyr Glu Arg Gly Leu Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser
    130                 135                 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160

Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
            180                 185                 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
225                 230                 235                 240

Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
                245                 250                 255

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
            260                 265                 270

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe
        275                 280                 285

Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
    290                 295                 300
```

```
Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
305                 310                 315                 320

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
                325                 330                 335

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
            340                 345                 350

Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
        355                 360                 365

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
    370                 375                 380

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
385                 390                 395                 400

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln
                405                 410                 415

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
            420                 425                 430

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
        435                 440                 445

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
    450                 455                 460

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
465                 470                 475                 480

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
                485                 490                 495

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505
```

<210> 315
<211> 509

<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 315

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                  10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Tyr Met Tyr Asn Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125


Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser
    130                 135                 140


Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160


Ser Gln Gly Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175


Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
            180                 185                 190
```

```
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Ala Asn Ser Phe Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
225                 230                 235                 240

Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
                245                 250                 255

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
            260                 265                 270

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe
        275                 280                 285

Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
    290                 295                 300

Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
305                 310                 315                 320

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
                325                 330                 335

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
            340                 345                 350

Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
        355                 360                 365

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
    370                 375                 380

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
385                 390                 395                 400
```

```
Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln
                405                 410                 415


Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
            420                 425                 430


Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
        435                 440                 445


Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
    450                 455                 460


Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
465                 470                 475                 480


Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
                485                 490                 495


Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505


<210>  316
<211>  508
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  single chain variable fragment

<400>  316

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Arg Arg Pro Ala Phe Asp Ile Trp Gly Gln Gly Thr Met
            100                 105                 110

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
    130                 135                 140

Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145                 150                 155                 160

Gln Gly Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
                165                 170                 175

Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val
            180                 185                 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
        195                 200                 205

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
    210                 215                 220

Ala Asn Ser Phe Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
225                 230                 235                 240

Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
                245                 250                 255

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
            260                 265                 270

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe Trp
        275                 280                 285
```

```
Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
    290                 295                 300

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu
305                 310                 315                 320

Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr
                325                 330                 335

Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr
            340                 345                 350

Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro
        355                 360                 365

Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys
    370                 375                 380

Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe
385                 390                 395                 400

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu
                405                 410                 415

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
            420                 425                 430

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
        435                 440                 445

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
    450                 455                 460

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
465                 470                 475                 480

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
                485                 490                 495
```

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
500 505

<210> 317
<211> 510
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 317

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Val His Leu Lys Arg Arg Pro Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

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

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145 150 155 160

```
Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

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

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
                245                 250                 255

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
            260                 265                 270

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
        275                 280                 285

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
    290                 295                 300

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
305                 310                 315                 320

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
                325                 330                 335

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
            340                 345                 350

Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys
        355                 360                 365

Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys
    370                 375                 380
```

```
Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val
385                 390                 395                 400


Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn
                405                 410                 415


Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
            420                 425                 430


Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
        435                 440                 445


Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
    450                 455                 460


Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
465                 470                 475                 480


Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
                485                 490                 495


Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505                 510


<210>  318
<211>  509
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  single chain variable fragment

<400>  318

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

```
Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Ser Val His Lys Lys Pro Ile Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

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

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160

Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175

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

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
225                 230                 235                 240

Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
                245                 250                 255
```

```
Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
            260                 265                 270

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe
        275                 280                 285

Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
    290                 295                 300

Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
305                 310                 315                 320

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
                325                 330                 335

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
            340                 345                 350

Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
        355                 360                 365

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
    370                 375                 380

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
385                 390                 395                 400

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln
                405                 410                 415

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
            420                 425                 430

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
        435                 440                 445

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
    450                 455                 460

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
465                 470                 475                 480
```

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
485 490 495

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
500 505

<210> 319
<211> 509
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 319

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ser Thr Ser Arg Arg Cys Thr Phe Gln His Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

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

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

Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175

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

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
225                 230                 235                 240

Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
                245                 250                 255

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
            260                 265                 270

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe
        275                 280                 285

Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
    290                 295                 300

Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
305                 310                 315                 320

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
                325                 330                 335

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
            340                 345                 350
```

```
Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
        355                 360                 365

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
    370                 375                 380

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
385                 390                 395                 400

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln
                405                 410                 415

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
            420                 425                 430

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
        435                 440                 445

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
    450                 455                 460

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
465                 470                 475                 480

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
                485                 490                 495

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505
```

<210> 320
<211> 509
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 320

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Ser Thr Ser Pro Arg Pro Leu Phe Gln His Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

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

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160

Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175

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

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
225                 230                 235                 240
```

```
Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
                245                 250                 255

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
            260                 265                 270

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe
        275                 280                 285

Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
    290                 295                 300

Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
305                 310                 315                 320

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
                325                 330                 335

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
            340                 345                 350

Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
        355                 360                 365

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
    370                 375                 380

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
385                 390                 395                 400

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln
                405                 410                 415

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
            420                 425                 430

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
        435                 440                 445
```

```
Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
    450                 455                 460

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
465                 470                 475                 480

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
                485                 490                 495

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505
```

<210> 321
<211> 511
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 321

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Ser Pro Tyr Gln Val Arg Gly Val Tyr Phe Asp Tyr Trp Gly Gln
            100                 105                 110
```

```
Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Ala Ile Gln Leu Thr Gln Ser
    130                 135                 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160

Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys
                165                 170                 175

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

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220

Cys Gln Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240

Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
                245                 250                 255

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
            260                 265                 270

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
        275                 280                 285

Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
    290                 295                 300

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
305                 310                 315                 320

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
                325                 330                 335
```

```
Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
            340                 345                 350

Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
        355                 360                 365

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
    370                 375                 380

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg
385                 390                 395                 400

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln
                405                 410                 415

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
            420                 425                 430

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
        435                 440                 445

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
    450                 455                 460

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
465                 470                 475                 480

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
                485                 490                 495

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505                 510
```

<210> 322
<211> 511
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 322

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Ser Pro Tyr Lys Lys Arg Arg Thr Val Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125


Gly Ser Gly Gly Gly Gly Ser Gly Gly Ala Ile Gln Leu Thr Gln Ser
    130                 135                 140


Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160


Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys
                165                 170                 175


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


Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205
```

```
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220

Cys Gln Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240

Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
                245                 250                 255

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
            260                 265                 270

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
        275                 280                 285

Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
    290                 295                 300

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
305                 310                 315                 320

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
                325                 330                 335

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
            340                 345                 350

Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
        355                 360                 365

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
    370                 375                 380

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg
385                 390                 395                 400

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln
                405                 410                 415

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
            420                 425                 430
```

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
435 440 445

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
450 455 460

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
465 470 475 480

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
485 490 495

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
500 505 510

<210> 323
<211> 510
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 323

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

```
Ala Ser Leu Gln Arg Gly Leu Ala Leu Phe Gln His Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

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

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160

Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

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

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
                245                 250                 255

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
            260                 265                 270

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
        275                 280                 285

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
    290                 295                 300
```

```
Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
305                 310                 315                 320

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
                325                 330                 335

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
            340                 345                 350

Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys
        355                 360                 365

Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys
    370                 375                 380

Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val
385                 390                 395                 400

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn
                405                 410                 415

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
            420                 425                 430

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
        435                 440                 445

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
    450                 455                 460

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
465                 470                 475                 480

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
                485                 490                 495

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505                 510
```

<210> 324
<211> 509

<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 324

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                  10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Ser Ile Leu Ser Val Pro Tyr Phe Asp Leu Trp Gly Arg Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125


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


Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160


Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175


Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu Glu Ser Gly
            180                 185                 190
```

```
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
225                 230                 235                 240

Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
                245                 250                 255

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
            260                 265                 270

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe
        275                 280                 285

Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
    290                 295                 300

Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
305                 310                 315                 320

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
                325                 330                 335

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
            340                 345                 350

Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
        355                 360                 365

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
    370                 375                 380

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
385                 390                 395                 400
```

```
Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln
                405                 410                 415


Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
            420                 425                 430


Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
        435                 440                 445


Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
    450                 455                 460


Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
465                 470                 475                 480


Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
                485                 490                 495


Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505


<210>  325
<211>  514
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  single chain variable fragment

<400>  325

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Ser Gly Trp Ile Arg Val Pro Leu Arg Leu Pro Leu Phe Gln His
            100                 105                 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ala Ile Gln Leu
    130                 135                 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145                 150                 155                 160

Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr
                165                 170                 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser
            180                 185                 190

Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
    210                 215                 220

Thr Tyr Tyr Cys Gln Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly
225                 230                 235                 240

Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro
                245                 250                 255

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
            260                 265                 270

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
        275                 280                 285
```

```
Phe Ala Cys Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala
    290                 295                 300

Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg
305                 310                 315                 320

Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro
                325                 330                 335

Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
            340                 345                 350

Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu
        355                 360                 365

Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu
    370                 375                 380

Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys
385                 390                 395                 400

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

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
            420                 425                 430

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
        435                 440                 445

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
    450                 455                 460

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
465                 470                 475                 480

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
                485                 490                 495
```

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
500 505 510

Pro Arg

<210> 326
<211> 509
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 326

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Val Thr Ile Phe Ala Ile Phe Asp Ile Trp Gly Gln Gly Thr
100 105 110

Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

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

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


Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175


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


Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205


Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220


Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
225                 230                 235                 240


Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
                245                 250                 255


Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
            260                 265                 270


Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe
        275                 280                 285


Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
    290                 295                 300


Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
305                 310                 315                 320


Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
                325                 330                 335


Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
            340                 345                 350


Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
        355                 360                 365
```

```
Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
    370                 375                 380

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
385                 390                 395                 400

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln
                405                 410                 415

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
            420                 425                 430

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
        435                 440                 445

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
    450                 455                 460

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
465                 470                 475                 480

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
                485                 490                 495

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505


<210>  327
<211>  510
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  single chain variable fragment

<400>  327

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30
```

```
Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Val Gly Arg Gly Phe Val His Phe Asp Leu Trp Gly Arg Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

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

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160

Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

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

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240
```

```
Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
                245                 250                 255

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
            260                 265                 270

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
        275                 280                 285

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
    290                 295                 300

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
305                 310                 315                 320

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
                325                 330                 335

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
            340                 345                 350

Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys
        355                 360                 365

Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys
    370                 375                 380

Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val
385                 390                 395                 400

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn
                405                 410                 415

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
            420                 425                 430

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
        435                 440                 445

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
    450                 455                 460
```

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
465 470 475 480

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
485 490 495

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
500 505 510

<210> 328
<211> 511
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 328

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Thr Ser Arg Gly Leu Cys Val Leu Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

```
Gly Ser Gly Gly Gly Gly Ser Gly Gly Ala Ile Gln Leu Thr Gln Ser
    130                 135                 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160

Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys
                165                 170                 175

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

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220

Cys Gln Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240

Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
                245                 250                 255

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
            260                 265                 270

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
        275                 280                 285

Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
    290                 295                 300

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
305                 310                 315                 320

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
                325                 330                 335
```

```
Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
            340                 345                 350

Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
        355                 360                 365

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
    370                 375                 380

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg
385                 390                 395                 400

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln
                405                 410                 415

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
            420                 425                 430

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
        435                 440                 445

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
    450                 455                 460

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
465                 470                 475                 480

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
                485                 490                 495

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505                 510
```

<210> 329
<211> 511
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 329

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ser Gly Pro Ser Ser Tyr Trp Tyr Phe Asp Leu Trp Gly Arg
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Ala Ile Gln Leu Thr Gln Ser
    130                 135                 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160

Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys
                165                 170                 175

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

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220
```

```
Cys Gln Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240

Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
                245                 250                 255

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
            260                 265                 270

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
        275                 280                 285

Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
    290                 295                 300

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
305                 310                 315                 320

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
                325                 330                 335

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
            340                 345                 350

Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
        355                 360                 365

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
    370                 375                 380

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg
385                 390                 395                 400

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln
                405                 410                 415

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
            420                 425                 430
```

```
Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
        435                 440                 445

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
    450                 455                 460

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
465                 470                 475                 480

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
                485                 490                 495

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505                 510
```

<210> 330
<211> 511
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 330

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Arg Asn Ile Tyr Met Gly Gly Ile Trp Phe Asp Pro Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Ala Ile Gln Leu Thr Gln Ser
    130                 135                 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160

Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys
                165                 170                 175

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

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220

Cys Gln Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240

Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
                245                 250                 255

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
            260                 265                 270

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
        275                 280                 285

Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
    290                 295                 300

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
305                 310                 315                 320
```

```
Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
                325                 330                 335

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
            340                 345                 350

Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
        355                 360                 365

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
    370                 375                 380

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg
385                 390                 395                 400

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln
                405                 410                 415

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
            420                 425                 430

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
        435                 440                 445

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
    450                 455                 460

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
465                 470                 475                 480

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
                485                 490                 495

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505                 510
```

<210> 331
<211> 510
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 331

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Leu Thr Val Arg Thr Gly Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110


Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125


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


Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160


Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175


Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu Glu Ser
            180                 185                 190
```

```
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
                245                 250                 255

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
            260                 265                 270

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
        275                 280                 285

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
    290                 295                 300

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
305                 310                 315                 320

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
                325                 330                 335

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
            340                 345                 350

Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys
        355                 360                 365

Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys
    370                 375                 380

Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val
385                 390                 395                 400

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn
                405                 410                 415
```

```
Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
            420                 425                 430

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
        435                 440                 445

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
    450                 455                 460

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
465                 470                 475                 480

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
                485                 490                 495

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505                 510
```

<210> 332
<211> 510
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 332

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80
```

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Leu Arg Thr Ala His Leu Asp Phe Asp Leu Trp Gly Arg Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

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

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160

Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

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

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
                245                 250                 255

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
            260                 265                 270

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
        275                 280                 285
```

```
Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
    290                 295                 300

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
305                 310                 315                 320

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
                325                 330                 335

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
            340                 345                 350

Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys
        355                 360                 365

Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys
    370                 375                 380

Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val
385                 390                 395                 400

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn
                405                 410                 415

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
            420                 425                 430

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
        435                 440                 445

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
    450                 455                 460

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
465                 470                 475                 480

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
                485                 490                 495

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505                 510
```

<210> 333
<211> 510
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 333

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Leu Ile Phe Pro Val Val Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125


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


Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160


Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175
```

```
Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu Glu Ser
            180                 185                 190

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
                245                 250                 255

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
            260                 265                 270

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
        275                 280                 285

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
    290                 295                 300

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
305                 310                 315                 320

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
                325                 330                 335

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
            340                 345                 350

Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys
        355                 360                 365

Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys
    370                 375                 380
```

```
Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val
385                 390                 395                 400


Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn
                405                 410                 415


Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
            420                 425                 430


Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
        435                 440                 445


Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
    450                 455                 460


Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
465                 470                 475                 480


Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
                485                 490                 495


Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505                 510


<210>  334
<211>  513
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  single chain variable fragment

<400>  334

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

```
Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Gly Tyr Arg Lys Tyr Gly Tyr Val Phe Phe Asp Ile Trp
            100                 105                 110

Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ala Ile Gln Leu Thr
    130                 135                 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160

Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln
                165                 170                 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser
            180                 185                 190

Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
    210                 215                 220

Tyr Tyr Cys Gln Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225                 230                 235                 240

Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
                245                 250                 255

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
            260                 265                 270
```

```
Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
        275                 280                 285

Ala Cys Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys
    290                 295                 300

Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser
305                 310                 315                 320

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
                325                 330                 335

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
            340                 345                 350

Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr
        355                 360                 365

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
    370                 375                 380

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
385                 390                 395                 400

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln
                405                 410                 415

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
            420                 425                 430

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
        435                 440                 445

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
    450                 455                 460

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
465                 470                 475                 480
```

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
485 490 495

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
500 505 510

Arg

<210> 335
<211> 513
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 335

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Arg Tyr Arg Arg Phe Trp His Ala Phe Asp Ile Trp
100 105 110

Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125

```
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ala Ile Gln Leu Thr
    130                 135                 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160

Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln
                165                 170                 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser
            180                 185                 190

Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
    210                 215                 220

Tyr Tyr Cys Gln Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225                 230                 235                 240

Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
                245                 250                 255

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
            260                 265                 270

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
        275                 280                 285

Ala Cys Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys
    290                 295                 300

Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser
305                 310                 315                 320

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
                325                 330                 335

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
            340                 345                 350
```

```
Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr
        355                 360                 365

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
    370                 375                 380

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
385                 390                 395                 400

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln
                405                 410                 415

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
            420                 425                 430

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
        435                 440                 445

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
    450                 455                 460

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
465                 470                 475                 480

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
                485                 490                 495

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
            500                 505                 510

Arg
```

<210> 336
<211> 509
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 336

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Ala His Ile Arg Gly Tyr Phe Asp Leu Trp Gly Arg Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125


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


Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160


Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175


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


Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205
```

```
Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
225                 230                 235                 240

Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
                245                 250                 255

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
            260                 265                 270

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe
        275                 280                 285

Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
    290                 295                 300

Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
305                 310                 315                 320

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
                325                 330                 335

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
            340                 345                 350

Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
        355                 360                 365

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
    370                 375                 380

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
385                 390                 395                 400

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln
                405                 410                 415

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
            420                 425                 430
```

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
435 440 445

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
450 455 460

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
465 470 475 480

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
485 490 495

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
500 505

<210> 337
<211> 512
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 337

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

```
Ala Thr Trp Met Gly Gly Gly Gly Arg Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ala Ile Gln Leu Thr Gln
    130                 135                 140

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145                 150                 155                 160

Cys Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln
                165                 170                 175

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu
            180                 185                 190

Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
        195                 200                 205

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
    210                 215                 220

Tyr Cys Gln Gln Phe Asn Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr
225                 230                 235                 240

Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
                245                 250                 255

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
            260                 265                 270

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
        275                 280                 285

Cys Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr
    290                 295                 300
```

```
Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys
305                 310                 315                 320

Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg
                325                 330                 335

Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp
            340                 345                 350

Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile
        355                 360                 365

Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp
    370                 375                 380

Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
385                 390                 395                 400

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly
                405                 410                 415

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
            420                 425                 430

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
        435                 440                 445

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
    450                 455                 460

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
465                 470                 475                 480

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
                485                 490                 495

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505                 510
```

<210> 338
<211> 510

<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 338

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                  10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


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


Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Thr Ser Arg Thr Thr Trp Tyr Phe Asp Leu Trp Gly Arg Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125


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


Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160


Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175


Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu Glu Ser
            180                 185                 190
```

```
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Phe Asn Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
                245                 250                 255

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
            260                 265                 270

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
        275                 280                 285

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
    290                 295                 300

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
305                 310                 315                 320

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
                325                 330                 335

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
            340                 345                 350

Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys
        355                 360                 365

Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys
    370                 375                 380

Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val
385                 390                 395                 400
```

```
Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn
                405                 410                 415


Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
            420                 425                 430


Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
        435                 440                 445


Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
    450                 455                 460


Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
465                 470                 475                 480


Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
                485                 490                 495


Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505                 510


<210>  339
<211>  512
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  single chain variable fragment

<400>  339

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


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


Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Trp Met Gly Gly Gly Gly Arg Leu Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ala Ile Gln Leu Thr Gln
    130                 135                 140

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145                 150                 155                 160

Cys Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln
                165                 170                 175

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu
            180                 185                 190

Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
        195                 200                 205

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
    210                 215                 220

Tyr Cys Gln Gln Phe Asn Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr
225                 230                 235                 240

Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
                245                 250                 255

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
            260                 265                 270

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
        275                 280                 285
```

```
Cys Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr
    290                 295                 300

Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys
305                 310                 315                 320

Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg
                325                 330                 335

Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp
            340                 345                 350

Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile
        355                 360                 365

Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp
    370                 375                 380

Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
385                 390                 395                 400

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly
                405                 410                 415

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
            420                 425                 430

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
        435                 440                 445

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
    450                 455                 460

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
465                 470                 475                 480

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
                485                 490                 495
```

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
500 505 510

<210> 340
<211> 511
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 340

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Trp Gly Gly Arg Leu Tyr Trp Tyr Phe Asp Leu Trp Gly Arg
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Ala Ile Gln Leu Thr Gln Ser
130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160

```
Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys
                165                 170                 175

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

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220

Cys Gln Gln Phe Asn Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240

Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
                245                 250                 255

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
            260                 265                 270

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
        275                 280                 285

Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
    290                 295                 300

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
305                 310                 315                 320

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
                325                 330                 335

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
            340                 345                 350

Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
        355                 360                 365

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
    370                 375                 380
```

```
Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg
385                 390                 395                 400


Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln
                405                 410                 415


Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
            420                 425                 430


Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
        435                 440                 445


Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
    450                 455                 460


Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
465                 470                 475                 480


Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
                485                 490                 495


Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505                 510


<210>  341
<211>  510
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  single chain variable fragment

<400>  341

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

```
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Val Ile Arg Gln Leu Trp Tyr Phe Asp Leu Trp Gly Arg Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

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

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160

Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

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

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Phe Asn Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
                245                 250                 255
```

```
Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
            260                 265                 270

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
        275                 280                 285

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
    290                 295                 300

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
305                 310                 315                 320

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
                325                 330                 335

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
            340                 345                 350

Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys
        355                 360                 365

Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys
    370                 375                 380

Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val
385                 390                 395                 400

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn
                405                 410                 415

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
            420                 425                 430

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
        435                 440                 445

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
    450                 455                 460

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
465                 470                 475                 480
```

```
Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
                485                 490                 495


Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505                 510


<210>  342
<211>  510
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  single chain variable fragment

<400>  342

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


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


Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


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


Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125


Ser Gly Gly Gly Gly Ser Gly Gly Ala Ile Gln Leu Thr Gln Ser Pro
    130                 135                 140
```

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

Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

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

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Phe Asn Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
                245                 250                 255

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
            260                 265                 270

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
        275                 280                 285

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
    290                 295                 300

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
305                 310                 315                 320

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
                325                 330                 335

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
            340                 345                 350
```

```
Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys
        355                 360                 365

Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys
    370                 375                 380

Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val
385                 390                 395                 400

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn
                405                 410                 415

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
            420                 425                 430

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
        435                 440                 445

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
    450                 455                 460

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
465                 470                 475                 480

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
                485                 490                 495

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505                 510
```

<210> 343
<211> 510
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 343

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Val Asp Arg Thr Thr Trp Tyr Phe Asp Leu Trp Gly Arg Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

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

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160

Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

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

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Phe Asn Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240
```

```
Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
                245                 250                 255

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
            260                 265                 270

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
        275                 280                 285

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
    290                 295                 300

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
305                 310                 315                 320

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
                325                 330                 335

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
            340                 345                 350

Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys
        355                 360                 365

Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys
    370                 375                 380

Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val
385                 390                 395                 400

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn
                405                 410                 415

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
            420                 425                 430

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
        435                 440                 445
```

```
Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
    450                 455                 460

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
465                 470                 475                 480

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
                485                 490                 495

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505                 510
```

<210> 344
<211> 513
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 344

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Arg Trp Gly Lys Asp Gly Pro Tyr Trp Tyr Phe Asp Leu Trp
            100                 105                 110
```

```
Gly Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ala Ile Gln Leu Thr
    130                 135                 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160

Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln
                165                 170                 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser
            180                 185                 190

Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
    210                 215                 220

Tyr Tyr Cys Gln Gln Phe Asn Asn Tyr Pro Leu Thr Phe Gly Gly Gly
225                 230                 235                 240

Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
                245                 250                 255

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
            260                 265                 270

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
        275                 280                 285

Ala Cys Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys
    290                 295                 300

Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser
305                 310                 315                 320

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
                325                 330                 335
```

```
Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
            340                 345                 350

Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr
        355                 360                 365

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
    370                 375                 380

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
385                 390                 395                 400

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln
                405                 410                 415

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
            420                 425                 430

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
        435                 440                 445

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
    450                 455                 460

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
465                 470                 475                 480

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
                485                 490                 495

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
            500                 505                 510

Arg
```

<210> 345
<211> 513
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 345

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                  10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


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


Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Arg Arg Asp Ser Tyr Gly Pro Tyr Trp Tyr Phe Asp Leu Trp
            100                 105                 110


Gly Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125


Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ala Ile Gln Leu Thr
    130                 135                 140


Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160


Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln
                165                 170                 175


Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser
            180                 185                 190
```

```
Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
    210                 215                 220

Tyr Tyr Cys Gln Gln Phe Asn Asn Tyr Pro Leu Thr Phe Gly Gly Gly
225                 230                 235                 240

Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
                245                 250                 255

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
            260                 265                 270

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
        275                 280                 285

Ala Cys Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys
    290                 295                 300

Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser
305                 310                 315                 320

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
                325                 330                 335

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
            340                 345                 350

Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr
        355                 360                 365

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
    370                 375                 380

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
385                 390                 395                 400

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln
                405                 410                 415
```

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
420 425 430

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
435 440 445

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
450 455 460

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
465 470 475 480

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
485 490 495

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
500 505 510

Arg

<210> 346
<211> 512
<212> PRT
<213> Artificial Sequence

<220>
<223> single chain variable fragment

<400> 346

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Asn Arg Pro Pro Pro Gly Tyr Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ala Ile Gln Leu Thr Gln
    130                 135                 140

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145                 150                 155                 160

Cys Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln
                165                 170                 175

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu
            180                 185                 190

Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
        195                 200                 205

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
    210                 215                 220

Tyr Cys Gln Gln Phe Asn Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr
225                 230                 235                 240

Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
                245                 250                 255

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
            260                 265                 270
```

```
Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
        275                 280                 285

Cys Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr
    290                 295                 300

Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys
305                 310                 315                 320

Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg
                325                 330                 335

Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp
            340                 345                 350

Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile
        355                 360                 365

Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp
    370                 375                 380

Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
385                 390                 395                 400

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly
                405                 410                 415

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
            420                 425                 430

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
        435                 440                 445

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
    450                 455                 460

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
465                 470                 475                 480

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
                485                 490                 495
```

```
Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505                 510


<210>  347
<211>  510
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  single chain variable fragment

<400>  347

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


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


Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Lys Gly Arg Arg Phe Ser Trp Tyr Phe Asp Leu Trp Gly Arg Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125


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


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

```
Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

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

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Phe Asn Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
                245                 250                 255

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
            260                 265                 270

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
        275                 280                 285

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
    290                 295                 300

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
305                 310                 315                 320

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
                325                 330                 335

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
            340                 345                 350

Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys
        355                 360                 365
```

```
Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys
    370                 375                 380

Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val
385                 390                 395                 400

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn
                405                 410                 415

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
            420                 425                 430

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
        435                 440                 445

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
    450                 455                 460

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
465                 470                 475                 480

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
                485                 490                 495

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            500                 505                 510
```

<210> 348
<211> 500
<212> PRT
<213> Unknown

<220>
<223> inhibitory receptor

<400> 348

```
Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1               5                   10                  15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
            20                  25                  30
```

```
Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35                  40                  45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly
                85                  90                  95

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

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

Gly Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly
    130                 135                 140

Ala Ser Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser
145                 150                 155                 160

Tyr His Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp
                165                 170                 175

Ile Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Glu Tyr Asn Glu Lys
            180                 185                 190

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
        195                 200                 205

Tyr Met His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
    210                 215                 220

Cys Ala Arg Glu Glu Ile Thr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
225                 230                 235                 240

Thr Ser Val Thr Val Ser Ser Tyr Gly Ser Gln Ser Ser Lys Pro Tyr
                245                 250                 255
```

```
Leu Leu Thr His Pro Ser Asp Pro Leu Glu Leu Val Val Ser Gly Pro
            260                 265                 270

Ser Gly Gly Pro Ser Ser Pro Thr Thr Gly Pro Thr Ser Thr Ser Gly
        275                 280                 285

Pro Glu Asp Gln Pro Leu Thr Pro Thr Gly Ser Asp Pro Gln Ser Gly
    290                 295                 300

Leu Gly Arg His Leu Gly Val Val Ile Gly Ile Leu Val Ala Val Ile
305                 310                 315                 320

Leu Leu Leu Leu Leu Leu Leu Leu Leu Phe Leu Ile Leu Arg His Arg
                325                 330                 335

Arg Gln Gly Lys His Trp Thr Ser Thr Gln Arg Lys Ala Asp Phe Gln
            340                 345                 350

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

Trp Arg Ser Ser Pro Ala Ala Asp Ala Gln Glu Glu Asn Leu Tyr Ala
    370                 375                 380

Ala Val Lys His Thr Gln Pro Glu Asp Gly Val Glu Met Asp Thr Arg
385                 390                 395                 400

Ser Pro His Asp Glu Asp Pro Gln Ala Val Thr Tyr Ala Glu Val Lys
                405                 410                 415

His Ser Arg Pro Arg Arg Glu Met Ala Ser Pro Pro Ser Pro Leu Ser
            420                 425                 430

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

Met Asp Thr Glu Ala Ala Ala Ser Glu Ala Pro Gln Asp Val Thr Tyr
    450                 455                 460
```

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

Pro Ser Gln Glu Gly Pro Ser Pro Ala Val Pro Ser Ile Tyr Ala Thr
485 490 495

Leu Ala Ile His
500

<210> 349
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> B2M shRNA

<400> 349
gcactcaaag cttgttaaga tcgaaatctt aacaagcttt gagtgc 46

<210> 350
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> B2M shRNA

<400> 350
gttaacttcc aatttacata ccgaagtatg taaattggaa gttaac 46

<210> 351
<211> 21
<212> PRT
<213> Unknown

<220>
<223> T2A self-cleaving polypeptide

<400> 351

Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu
1 5 10 15

Glu Asn Pro Gly Pro
20

<210> 352
<211> 64
<212> PRT
<213> Unknown

<220>
<223> HLA-A*02 scFv LIR-1 inhibitory receptor

<400> 352

Tyr Gly Ser Gln Ser Ser Lys Pro Tyr Leu Leu Thr His Pro Ser Asp
1   5   10   15

Pro Leu Glu Leu Val Val Ser Gly Pro Ser Gly Gly Pro Ser Ser Pro
            20   25   30

Thr Thr Gly Pro Thr Ser Thr Ser Gly Pro Glu Asp Gln Pro Leu Thr
        35   40   45

Pro Thr Gly Ser Asp Pro Gln Ser Gly Leu Gly Arg His Leu Gly Val
    50   55   60

<210> 353
<211> 64
<212> PRT
<213> Unknown

<220>
<223> HLA-A*02 scFv LIR-1 inhibitory receptor

<400> 353

Tyr Gly Ser Gln Ser Ser Lys Pro Tyr Leu Leu Thr His Pro Ser Asp
1   5   10   15

Pro Leu Glu Leu Val Val Ser Gly Pro Ser Gly Gly Pro Ser Ser Pro
            20   25   30

Thr Thr Gly Pro Thr Ser Thr Ser Gly Pro Glu Asp Gln Pro Leu Thr
        35   40   45

Pro Thr Gly Ser Asp Pro Gln Ser Gly Leu Gly Arg His Leu Gly Val
    50   55   60

<210> 354
<211> 44

<212> PRT
<213> Unknown

<220>
<223> HLA-A*02 scFv LIR-1 inhibitory receptor

<400> 354

Val Val Ser Gly Pro Ser Gly Gly Pro Ser Ser Pro Thr Thr Gly Pro
1   5   10   15

Thr Ser Thr Ser Gly Pro Glu Asp Gln Pro Leu Thr Pro Thr Gly Ser
            20   25   30

Asp Pro Gln Ser Gly Leu Gly Arg His Leu Gly Val
        35   40

<210> 355
<211> 64
<212> PRT
<213> Unknown

<220>
<223> HLA-A*02 scFv LIR-1 inhibitory receptor

<400> 355

Tyr Gly Ser Gln Ser Ser Lys Pro Tyr Leu Leu Thr His Pro Ser Asp
1   5   10   15

Pro Leu Glu Leu Val Val Ser Gly Pro Ser Gly Gly Pro Ser Ser Pro
            20   25   30

Thr Thr Gly Pro Thr Ser Thr Ser Gly Pro Glu Asp Gln Pro Leu Thr
        35   40   45

Pro Thr Gly Ser Asp Pro Gln Ser Gly Leu Gly Arg His Leu Gly Val
    50   55   60

<210> 356
<211> 44
<212> PRT
<213> Unknown

<220>
<223> HLA-A*02 scFv LIR-1 inhibitory receptor

<400> 356

Val Val Ser Gly Pro Ser Gly Gly Pro Ser Ser Pro Thr Thr Gly Pro
1 5 10 15

Thr Ser Thr Ser Gly Pro Glu Asp Gln Pro Leu Thr Pro Thr Gly Ser
20 25 30

Asp Pro Gln Ser Gly Leu Gly Arg His Leu Gly Val
35 40

<210> 357
<211> 71
<212> PRT
<213> Unknown

<220>
<223> HLA-A*02 scFv LIR-1 inhibitory receptor

<400> 357

Ser Ser Tyr Gly Ser Gln Ser Ser Lys Pro Tyr Leu Leu Thr His Pro
1 5 10 15

Ser Asp Pro Leu Glu Leu Val Val Ser Gly Pro Ser Gly Gly Pro Ser
20 25 30

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

Leu Thr Pro Thr Gly Ser Asp Pro Gln Ser Gly Leu Gly Arg His Leu
50 55 60

Gly Val Val Ile Gly Ile Leu
65 70

<210> 358
<211> 39
<212> PRT
<213> Unknown

<220>
<223> HLA-A*02 scFv LIR-1 inhibitory receptor

<400> 358

Ser Ser Thr Thr Gly Pro Thr Ser Thr Ser Gly Pro Glu Asp Gln Pro
1   5   10   15

Leu Thr Pro Thr Gly Ser Asp Pro Gln Ser Gly Leu Gly Arg His Leu
            20   25   30

Gly Val Val Ile Gly Ile Leu
        35

<210> 359
<211> 74
<212> PRT
<213> Unknown

<220>
<223> HLA-A*02 scFv LIR-1 inhibitory receptor

<400> 359

Ser Ser Ala Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Pro Val
1   5   10   15

Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser
            20   25   30

Pro Ser Gly Gly Ser Gly Asn Ser Ser Gly Ser Gly Gly Ser Pro Val
        35   40   45

Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser
    50   55   60

Pro Ser Ala Ser Val Val Ile Gly Ile Leu
65   70

<210> 360
<211> 82
<212> PRT
<213> Unknown

<220>
<223> HLA-A*02 scFv LIR-1 inhibitory receptor

<400> 360

Ser Ser Ala Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Pro Val
1   5   10   15

```
Pro Ser Thr Pro Pro Thr Asn Ser Ser Ser Thr Pro Pro Thr Pro Ser
            20                  25                  30

Pro Ser Pro Val Pro Ser Thr Pro Pro Thr Asn Ser Ser Ser Thr Pro
        35                  40                  45

Pro Thr Pro Ser Pro Ser Pro Val Pro Ser Thr Pro Pro Thr Asn Ser
    50                  55                  60

Ser Ser Thr Pro Pro Thr Pro Ser Pro Ser Ala Ser Val Val Ile Gly
65                  70                  75                  80

Ile Leu
```

<210> 361
<211> 92
<212> PRT
<213> Unknown

<220>
<223> HLA-A*02 scFv LIR-1 inhibitory receptor

<400> 361

```
Ser Ser Val Val Ser Gly Pro Ser Gly Gly Pro Ser Ser Pro Thr Thr
1               5                   10                  15

Gly Pro Thr Ser Thr Ser Gly Pro Glu Asp Gln Pro Leu Thr Pro Thr
            20                  25                  30

Gly Ser Asp Pro Gln Ser Gly Leu Gly Arg His Val Val Ser Gly Pro
        35                  40                  45

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

Pro Glu Asp Gln Pro Leu Thr Pro Thr Gly Ser Asp Pro Gln Ser Gly
65                  70                  75                  80

Leu Gly Arg His Leu Gly Val Val Ile Gly Ile Leu
                85                  90
```

<210> 362
<211> 22
<212> PRT
<213> Unknown

<220>
<223> signal sequence

<400> 362

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

Leu Arg Gly Ala Arg Cys
            20

<210> 363
<211> 711
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 363
caggtgcagc tggtgcagtc tggggctgag gtggagaagc ctggggcctc agtgaaggtc   60

tcctgcaagg cttctggata caccttcacc gactactata tgcactgggt gcgacaggcc   120

cctggacaag ggcttgagtg gatgggatgg atcaacccta acagtggtgg cacaaactat   180

gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac   240

atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gtctggctgg   300

gactttgact actggggcca gggaaccctg gtcaccgtgt cctcaggcgg aggtggaagc   360

ggaggggggag gatctggcgg cggaggaagc ggaggcgaca tcgtgatgac ccagtcttcc   420

tccctgtctg catctgtcgg agacagagtc accatcactt gccgggccag tcagagcatt   480

aggtactatt taagttggta tcagcagaaa ccaggaaaag cccctaagct cctgatctat   540

actgcatcca ttttacaaaa tggggtccca tcaaggttca gtggcagtgg atctgggaca   600

gatttcactc tcaccatcag cagcctgcaa cctgaggatt ttgcaactta ttactgcctc   660

cagacttaca ctactccgga ctttggccca gggaccaagg tggaaatcaa a   711

<210> 364
<211> 738
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 364
caggtgcagc tggtgcagtc tggggctgag gtgagggcac ctggggcctc agtgaagatt 60

tcctgcaagg cttctggatt caccttcaga ggctactata tccactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaatc atcaacccta gtggtggtag cagagcctac 180

gcacagaagt tccagggcag ggtcaccatg accagggaca cttccacgag cacagtctac 240

atggagctga gcagcctgag atctgacgac acggccatgt attactgtgc gagaaccgca 300

agttgtggtg gtgactgcta ctaccttgac tactggggcc agggaaccct ggtcaccgtg 360

tcctcaggcg gaggtggaag cggaggggga ggatctggcg gcggaggaag cggaggcgac 420

atccagatga cccagtctcc tcccaccctg tctgcatctg taggagacag agtcaccatc 480

acttgccggg ccagtgagaa tgttaatatc tggttggcct ggtatcagca gaaaccaggg 540

aaagccccta agctcctgat ctataagtca tccagtttag caagtggggt cccatcaagg 600

ttcagtggca gtggatctgg ggcagaattc actctcacca tcagcagcct gcagcctgat 660

gattttgcaa cttattactg ccaacagtat caaagttacc ccctcacttt cggcggaggg 720

accaaggtgg aaatcaaa 738

<210> 365
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 365
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg cttctggata ctcattcacc ggctacacca tgaactgggt gaggcaggcc 120

cctggacaaa gacttgagtg gatgggactt atcacccctt acaatggtgc ttctagctac 180

aaccagaagt tcaggggcag ggtcacaatc actagagaca cgtcagccag cacagcctac 240

atggagctct ccagcctgag atctgaagac actgcagtct attactgtgc aaggggggggt 300

tacgacggga ggggttttga ctactggggc cagggaacca cggtcaccgt gtcctcaggc 360

ggaggtggaa gcggaggggg aggatctggc ggcggaggaa gcggaggcga catccagatg 420

acccagtctc cttcaagctt gtctgcatct gtaggagaca gggtcaccat cacttgcagt 480

gccagctcaa gtgtaagtta catgcactgg tatcagcaga aaccaggcaa ggcccctaag 540

agattgatct atgacacatc caaattagca agtggggtcc caagtcgctt cagtggcagt 600

ggatctggga ccgaattcac tctcaccatc agcagcttgc agcctgagga ttttgcaact 660

tattactgcc agcagtggag tggttaccct ctcacgttcg gtcaggggac aaagttggaa 720

atcaaa 726

<210> 366
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 366
caggtgcagc tgcagcagtc tgggcctgag ctggagaagc ctggggcctc agtgaagatt 60

tcctgcaagg cttctggata ctcattcacc ggctacacca tgaactgggt gaagcagagc 120

catggaaaaa gccttgagtg gattggactt atcacccctt acaatggtgc ttctagctac 180

aaccagaagt tcaggggcaa ggccacatta actgtagaca agtcatccag cacagcctac 240

atggacctcc tcagcctgac atctgaagac tctgcagtct atttctgtgc aaggggggggt 300

tacgacggga ggggttttga ctactggggc cagggaacca cggtcaccgt gtcctcaggc 360

ggaggtggaa gcggaggggg aggatctggc ggcggaggaa gcggaggcga catcgagctc 420

acccagtctc ctgcaatcat gtctgcatct ccaggagaga aggtcaccat gacttgcagt 480

gccagctcaa gtgtaagtta catgcactgg tatcagcaga aatcaggcac ctcccctaag 540

agatggatct atgacacatc caaattggca agtggggtcc caggtcgctt cagtggcagt 600

ggatctggga actcttactc tctcaccatc agcagcgtgg aggctgagga tgatgcaact 660

tattactgcc agcagtggag tggttaccct ctcacgttcg gtgctgggac aaagttggaa 720

atcaaa 726

<210> 367
<211> 735
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 367
gaagtgcagc tggtggaaag cggcggaggc ctggtgaaac ctggcggcag cctgagactg 60

agctgcgccg ccagcggctt caccttctcg aacgcctgga tgagctgggt ccgccaggcc 120

cctggcaagg gactggaatg ggtcggacgg atcaagagca agaccgacgg cggcaccacc 180

gactacgctg cccccgtgaa gggccggttc accatcagcc gggacgacag caagaacacc 240

ctgtacctgc agatgaacag cctgaaaacc gaggacaccg ccgtgtatta ctgtaccaca 300

gatcttccta agcttaggaa ttttcatatt tggggccagg gaaccctggt caccgtgtcc 360

tcaggcggag gtggaagcgg agggggagga tctggcggcg gaggaagcgg aggcgacatc 420

cagatgaccc agtctccatc ctccctgtct gcatctgtag gagacagagt caccatcact 480

tgccgggcaa gtcagagcat tagcagctat ttaaattggt atcagcagaa accagggaaa 540

gcccctaagc tcctgatcta tgctgcatcc agtttgcaaa gtggggtccc atcaaggttc 600

agtggcagtg gatctgggac agatttcact ctcaccatca gcagtctgca acctgaagat 660

tttgcaactt actactgtca acagagttac agtacccctc tcactttcgg cggcggaaca 720

aaggtggaga tcaag 735

<210> 368
<211> 744
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 368
gaagtgcagc tggtggaaag cggcggaggc ctggtgcagc ctggcggcag cctgagactg 60

tcttgcgccg ccagcggctt caccttcagc agctacgcca tgcactgggt ccgccaggcc 120

cctggcaagg gactggaata cgtgtccgcc atcagctcga acggcggcag cacctactac 180

gccaacagcg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac 240

ctgcagatgg gcagcctgcg ggccgaggat atggccgtgt attactgtgc gagcctagaa 300

taccatggct ttcgacaata tgggcttcgt tattggcatt ggggccaggg aaccctggtc 360

accgtgtcct caggcggagg tggaagcgga gggggaggat ctggcggcgg aggaagcgga 420

ggcgacatcc agatgaccca gtctccatcc tccctgtctg catctgtagg agacagagtc 480

accatcactt gccgggcaag tcagagcatt agcagctatt taaattggta tcagcagaaa 540

ccagggaaag cccctaagct cctgatctat gctgcatcca gtttgcaaag tggggtccca 600

tcaaggttca gtggcagtgg atctgggaca gatttcactc tcaccatcag cagtctgcaa 660

cctgaagatt ttgcaactta ctactgtcaa cagagttaca gtacccctct cactttcggc 720

ggcggaacaa aggtggagat caag 744

<210> 369
<211> 741
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 369
cagctgcagc tccaggaaag cggcagcggc ctggtgaaac ccagccagac cctgagcctg 60

acctgtgccg tgtccggcgg cagcatcagc agcggcggct acagctggtc ctggatcaga 120

cagccccctg gcaagggcct ggaatggatc ggctacatct accacagcgg ctcgacctac 180

tacaacccca gcctgaagtc cagagtgacc atcagcgtgg acagaagcaa gaaccagttc 240

agcctgaagc tgagcagcgt gacagccgcc gacaccgctg tgtattactg tgccagcata 300

aaattctggt ttgcggggat taattatttt tttccgtggg gccagggaac cctggtcacc 360

gtgtcctcag gcggaggtgg aagcggaggg ggaggatctg gcggcggagg aagcggaggc 420

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 480

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 540

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 600

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 660

gaagattttg caacttacta ctgtcaacag agttacagta cccctctcac tttcggcggc 720

ggaacaaagg tggagatcaa g 741

<210> 370
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 370
gaagtgcagc tggtggaaag cggcggaggc ctggtgcagc ctggcggcag cctgagactg 60

tcttgcgccg ccagcggctt caccttcagc agctactgga tgcactgggt ccgccaggcc 120

cctggcaagg gactggtctg ggtgtctcga atcaacagcg acggcagcag caccagctac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acgccaagaa caccctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt attactgtgc aagcggattt 300

ttgggaatgg gctcgaattt tatttggggc cagggaaccc tggtcaccgt gtcctcaggc 360

ggaggtggaa gcggaggggg aggatctggc ggcggaggaa gcggaggcga catccagatg 420

acccagtctc catcctccct gtctgcatct gtaggagaca gagtcaccat cacttgccgg 480

gcaagtcaga gcattagcag ctatttaaat tggtatcagc agaaaccagg gaaagcccct 540

aagctcctga tctatgctgc atccagtttg caaagtgggg tcccatcaag gttcagtggc 600

agtggatctg ggacagattt cactctcacc atcagcagtc tgcaacctga agattttgca 660

acttactact gtcaacagag ttacagtacc cctctcactt tcggcggcgg aacaaaggtg 720

gagatcaag 729

<210> 371
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 371
caggtgcagc tgcaggaaag cggccctggc ctggtgaaac ccagccagac cctgagcctg 60

acctgcacag tgtccggcgg cagcatcagc agcggcggct actactggtc ctggatcaga 120

cagcaccccg gcaagggcct ggaatggatc ggctacatct actacagcgg cagcacctac 180

tacaacccca gcctgaagtc cctggtgaca atctccgtcg ataccagcaa gaaccagttc 240

agcctgaagc tgagcagcgt gacagccgcc gacaccgctg tgtattactg tgcaagcggg 300

gacagggcac ggtacttcga tctctggggc cgtggcaccc tggtcactgt gtcctcaggc 360

ggaggtggaa gcggaggggg aggatctggc ggcggaggaa gcggaggcga catccagatg 420

acccagtctc catcctccct gtctgcatct gtaggagaca gagtcaccat cacttgccgg 480

gcaagtcaga gcattagcag ctatttaaat tggtatcagc agaaaccagg gaaagcccct 540

aagctcctga tctatgctgc atccagtttg caaagtgggg tcccatcaag gttcagtggc 600

agtggatctg ggacagattt cactctcacc atcagcagtc tgcaacctga agattttgca 660

acttactact gtcaacagag ttacagtacc cctctcactt tcggcggcgg aacaaaggtg 720

gagatcaag 729

<210> 372
<211> 741
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 372
gaagtgcagc tggtggaaag cggcggaggc ctggtgcagc ctggcggcag cctgagactg 60

tcttgcgccg ccagcggctt caccttcagc agctactgga tgcactgggt ccgccaggcc 120

cctggcaagg gactggtctg ggtgtctcga atcaacagcg acggcagcag caccagctac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acgccaagaa caccctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt attactgtgc aagatatcca 300

cgtggatatc atcagatggt tgatgctttt gatatctggg gccaagggac aatggtcacc 360

gtgtcctcag gcggaggtgg aagcggaggg ggaggatctg gcggcggagg aagcggaggc 420

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 480

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 540

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 600

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 660

gaagattttg caacttacta ctgtcaacag agttacagta cccctctcac tttcggcggc 720

ggaacaaagg tggagatcaa g 741

<210> 373
<211> 750
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 373
cagctgcagc tccaggaaag cggccctggc ctggtgaaac ccagcgagac actgagcctg 60

acctgcaccg tgtccggcgg cagcatcagc agcagcagct actactgggg ctggatcaga 120

cagccccctg gcaagggcct ggaatggatc ggctcgatct actacagcgg ctccacctac 180

tacaacccca gcctgaagtc cagagtgacc atcagcgtgg acaccagcaa gaaccagttc 240

agcctgaagc tgagcagcgt gacagccgcc gacaccgctg tgtattactg tgcgagagta 300

cgatttttgg ctgctcgcac tactattccg gaggcgaatt ttctttgggg ccagggaacc 360

ctggtcaccg tgtcctcagg cggaggtgga agcggagggg gaggatctgg cggcggagga 420

agcggaggcg acatccagat gacccagtct ccatcctccc tgtctgcatc tgtaggagac 480

agagtcacca tcacttgccg ggcaagtcag agcattagca gctatttaaa ttggtatcag 540

cagaaaccag ggaaagcccc taagctcctg atctatgctg catccagttt gcaaagtggg 600

gtcccatcaa ggttcagtgg cagtggatct gggacagatt tcactctcac catcagcagt 660

ctgcaacctg aagattttgc aacttactac tgtcaacaga gttacagtac ccctctcact 720

ttcggcggcg gaacaaaggt ggagatcaag 750

<210> 374
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 374
gaagtgcagc tggtggaaag cggcggaggc ctggtgcagc ctggcggcag cctgagactg 60

tcttgcgccg ccagcggctt caccttcagc agctacagca tgaactgggt ccgccaggcc 120

cctggcaagg gactggaatg ggtgtcctac atcagcagca gcagctccac catctactac 180

gccgacagcg tgaagggtcg attcaccatc agccgggaca acgccaagaa cagcctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt attactgtgc gagagtactc 300

tccagggcta ggtttgacta ctggggccag ggaaccctgg tcaccgtgtc ctcaggcgga 360

ggtggaagcg gaggggggagg atctggcggc ggaggaagcg gaggcgacat ccagatgacc 420

cagtctccat cctccctgtc tgcatctgta ggagacagag tcaccatcac ttgccgggca 480

agtcagagca ttagcagcta tttaaattgg tatcagcaga aaccagggaa agcccctaag 540

ctcctgatct atgctgcatc cagtttgcaa agtggggtcc catcaaggtt cagtggcagt 600

ggatctggga cagatttcac tctcaccatc agcagtctgc aacctgaaga ttttgcaact 660

tactactgtc aacagagtta cagtacccct ctcactttcg gcggcggaac aaaggtggag 720

atcaag 726

<210> 375
<211> 723
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 375
gaagtgcagc tggtggaaag cggcggaggc ctggtgaaac ctggcggcag cctgagactg 60

agctgcgccg ccagcggctt caccttcagc agctacagca tgaactgggt ccgccaggcc 120

cctggcaagg gactggaatg ggtgtcctcg atcagcagca gcagctccta catctactac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acgccaagaa cagcctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt attactgtgc gagattacga 300

gggagggtgt tcgacccctg gggccaggga accctggtca ccgtgtcctc aggcggaggt 360

ggaagcggag ggggaggatc tggcggcgga ggaagcggag gcgacatcca gatgacccag 420

tctccatcct ccctgtctgc atctgtagga gacagagtca ccatcacttg ccgggcaagt 480

cagagcatta gcagctattt aaattggtat cagcagaaac cagggaaagc ccctaagctc 540

ctgatctatg ctgcatccag tttgcaaagt ggggtcccat caaggttcag tggcagtgga 600

tctgggacag atttcactct caccatcagc agtctgcaac ctgaagattt tgcaacttac 660

tactgtcaac agagttacag tacccctctc actttcggcg gcggaacaaa ggtggagatc 720

aag 723

<210> 376
<211> 741
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 376
cagctgcagc tccaggaaag cggccctggc ctggtgaaac ccagcgagac actgagcctg 60

acctgcaccg tgtccggcgg cagcatcagc agcagcagct actactgggg ctggatcaga 120

cagccccctg gcaagggcct ggaatggatc ggctcgatct actacagcgg ctccacctac 180

tacaacccca gcctgaagtc cagagtgacc atcagcgtgg acaccagcaa gaaccagttc 240

agcctgaagc tgagcagcgt gacagccgcc gacaccgctg tgtattactg tgcgagaata 300

aaatttacca gctttttata tgttcatggt tttctgtggg gccagggaac cctggtcacc 360

gtgtcctcag gcggaggtgg aagcggaggg ggaggatctg gcggcggagg aagcggaggc 420

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 480

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 540

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 600

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 660

gaagattttg caacttacta ctgtcaacag agttacagta cccctctcac tttcggcggc 720

ggaacaaagg tggagatcaa g 741

<210> 377
<211> 738
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 377
caggtgcagc tggtgcagtc tggcgccgaa gtgaagaaac ctggcgcctc cgtgaaggtg 60

tcctgcaagg ccagcggcta caccttcacc agctacgcca tgcactgggt tcgacaggcc 120

cctggccaga gactggaatg gatgggctgg atcaacgccg gcaacggcaa caccaagtac 180

agccagaaat tccagggcag agtgaccatc acccgggaca ccagcgccag caccgcctac 240

atggaactga gcagcctgcg gagcgaggac accgctgtgt attactgtgc gagaggccag 300

agatggctgt acctcggggg gattcgtcgg cattggggcc agggaaccct ggtcaccgtg 360

tcctcaggcg gaggtggaag cggaggggga ggatctggcg gcggaggaag cggaggcgac 420

atccagatga cccagtctcc atcctccctg tctgcatctg taggagacag agtcaccatc 480

acttgccggg caagtcagag cattagcagc tatttaaatt ggtatcagca gaaaccaggg 540

aaagccccta agctcctgat ctatgctgca tccagtttgc aaagtggggt cccatcaagg 600

ttcagtggca gtggatctgg gacagatttc actctcacca tcagcagtct gcaacctgaa 660

gattttgcaa cttactactg tcaacagagt tacagtaccc ctctcacttt cggcggcgga 720

acaaaggtgg agatcaag 738

<210> 378
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 378
caggtgcagc tgcaggaaag cggccctggc ctggtgaaac ccagcgagac actgagcctg 60

acctgcaccg tgtccggcgg cagcatcagc agctactact ggtcctggat cagacagccc 120

cctggcaagg gcctggaatg gatcggctac atctactaca gcggcagcac caactacaac 180

cccagcctga agtccagagt gaccatctcc gtcgatacca gcaagaacca gttcagcctg 240

aagctgagca gcgtgacagc cgccgacacc gctgtgtatt actgtgcgag agaatggatt 300

cccagccgtc cgtactactt tgactactgg ggccagggaa ccctggtcac cgtgtcctca 360

ggcggaggtg gaagcggagg gggaggatct ggcggcggag gaagcggagg cgacatccag 420

atgacccagt ctccatcctc cctgtctgca tctgtaggag acagagtcac catcacttgc 480

cgggcaagtc agagcattag cagctattta aattggtatc agcagaaacc agggaaagcc 540

cctaagctcc tgatctatgc tgcatccagt ttgcaaagtg gggtcccatc aaggttcagt 600

ggcagtggat ctgggacaga tttcactctc accatcagca gtctgcaacc tgaagatttt 660

gcaacttact actgtcaaca gagttacagt acccctctca ctttcggcgg cggaacaaag 720

gtggagatca ag 732

<210> 379
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 379
caggtgcagc tgcaggaaag cggccctggc ctggtgaaac ccagccagac cctgagcctg 60

acctgcacag tgtccggcgg ctcgatcagc agcggcggct actactggtc ctggatcaga 120

cagccccctg gcaagggcct ggaatggatc ggctacatct actacagcgg cagcacctac 180

tacaacccca gcctgaagtc cagagtgacc atcagcgtgg acaccagcaa gaaccagttc 240

agcctgaagc tgagcagcgt gacagccgcc gacaccgctg tgtattactg tgcgagagaa 300

agtaccggta caggagcttt tgatatctgg ggccaaggga caatggtcac cgtgtcctca 360

ggcggaggtg gaagcggagg gggaggatct ggcggcggag gaagcggagg cgacatccag 420

atgacccagt ctccatcctc cctgtctgca tctgtaggag acagagtcac catcacttgc 480

cgggcaagtc agagcattag cagctattta aattggtatc agcagaaacc agggaaagcc 540

cctaagctcc tgatctatgc tgcatccagt ttgcaaagtg gggtcccatc aaggttcagt 600

ggcagtggat ctgggacaga tttcactctc accatcagca gtctgcaacc tgaagatttt 660

gcaacttact actgtcaaca gagttacagt acccctctca ctttcggcgg cggaacaaag 720

gtggagatca ag 732

<210> 380
<211> 738
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 380
gaagtgcagc tggtggaaag cggaggcgga gtggttcgac ctggcggaag cctgagactg 60

tcttgcgccg ccagcggctt cacctttgac gactacggca tgagctgggt ccgccaggcc 120

cctggcaagg gactggaatg ggtgtccggc atcaactgga acggcggcag caccggctac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acgccaagaa cagcctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccttgt atcactgtgc gagagagagg 300

tacaggcggg tactccactg gtacttcgat ctctggggcc gtggcaccct ggtcactgtg 360

tcctcaggcg gaggtggaag cggaggggga ggatctggcg gcggaggaag cggaggcgac 420

atccagatga cccagtctcc atcctccctg tctgcatctg taggagacag agtcaccatc 480

acttgccggg caagtcagag cattagcagc tatttaaatt ggtatcagca gaaaccaggg 540

aaagccccta agctcctgat ctatgctgca tccagtttgc aaagtggggt cccatcaagg 600

ttcagtggca gtggatctgg gacagatttc actctcacca tcagcagtct gcaacctgaa 660

gattttgcaa cttactactg tcaacagagt tacagtaccc ctctcacttt cggcggcgga 720

acaaaggtgg agatcaag 738

<210> 381
<211> 720
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 381
caggtgcagc tggtgcagtc tggcgccgaa gtgaagaaac ctggcgcctc cgtgaaggtg 60

tcctgcaagg ccagcggcta caccttcacc agctacgaca tcaactgggt ccgccaggcc 120

accggacagg gcctggaatg gatgggctgg atgaacccca acagcggcaa caccggctac 180

gcccagaaat tccagggcag agtgaccatg acccggaaca cctcgatcag caccgcctac 240

atggaactga gcagcctgcg gagcgaggac accgctgtgt attactgtgc gagagaaccg 300

gatgcttttg atatctgggg ccaagggaca atggtcaccg tgtcctcagg cggaggtgga 360

agcggagggg gaggatctgg cggcggagga agcggaggcg acatccagat gacccagtct 420

ccatcctccc tgtctgcatc tgtaggagac agagtcacca tcacttgccg ggcaagtcag 480

agcattagca gctatttaaa ttggtatcag cagaaaccag ggaaagcccc taagctcctg 540

atctatgctg catccagttt gcaaagtggg gtcccatcaa ggttcagtgg cagtggatct 600

gggacagatt tcactctcac catcagcagt ctgcaacctg aagattttgc aacttactac 660

tgtcaacaga gttacagtac ccctctcact ttcggcggcg gaacaaaggt ggagatcaag 720

<210> 382
<211> 738

<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 382
caggtgcagc tgcaggaaag cggccctggc ctggtgaaac ccagccagac cctgagcctg 60

acctgcacag tgtccggcgg ctcgatcagc agcggcggct actactggtc ctggatcaga 120

cagccccctg gcaagggcct ggaatggatc ggctacatct actacagcgg cagcacctac 180

tacaacccca gcctgaagtc cagagtgacc atcagcgtgg acaccagcaa gaaccagttc 240

agcctgaagc tgagcagcgt gacagccgcc gacaccgctg tgtattactg tgcgagagaa 300

catatgggga cgattccgta ctactttgac tactggggcc agggaaccct ggtcaccgtg 360

tcctcaggcg gaggtggaag cggagggggа ggatctggcg gcggaggaag cggaggcgac 420

atccagatga cccagtctcc atcctccctg tctgcatctg taggagacag agtcaccatc 480

acttgccggg caagtcagag cattagcagc tatttaaatt ggtatcagca gaaaccaggg 540

aaagccccta agctcctgat ctatgctgca tccagtttgc aaagtggggt cccatcaagg 600

ttcagtggca gtggatctgg gacagatttc actctcacca tcagcagtct gcaacctgaa 660

gattttgcaa cttactactg tcaacagagt tacagtaccc ctctcacttt cggcggcgga 720

acaaaggtgg agatcaag 738

<210> 383
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 383
caggtgcagc tgcaggaaag cggccctggc ctggtgaaac ccagccagac cctgagcctg 60

acctgcacag tgtccggcgg ctcgatcagc agcggcggct actactggtc ctggatcaga 120

cagccccctg gcaagggcct ggaatggatc ggctacatct actacagcgg cagcacctac 180

tacaacccca gcctgaagtc cagagtgacc atcagcgtgg acaccagcaa gaaccagttc 240

agcctgaagc tgagcagcgt gacagccgcc gacaccgctg tgtattactg tgcgagagaa 300

gagtttggtt atggggacgt cctctactgg ggccagggaa ccctggtcac cgtgtcctca 360

ggcggaggtg gaagcggagg gggaggatct ggcggcggag gaagcggagg cgacatccag 420

atgacccagt ctccatcctc cctgtctgca tctgtaggag acagagtcac catcacttgc 480

cgggcaagtc agagcattag cagctattta aattggtatc agcagaaacc agggaaagcc 540

cctaagctcc tgatctatgc tgcatccagt ttgcaaagtg gggtcccatc aaggttcagt 600

ggcagtggat ctgggacaga tttcactctc accatcagca gtctgcaacc tgaagatttt 660

gcaacttact actgtcaaca gagttacagt acccctctca ctttcggcgg cggaacaaag 720

gtggagatca ag 732

<210> 384
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 384
caggtgcagc tgcaggaaag cggccctggc ctggtgaaac ccagccagac cctgagcctg 60

acctgcacag tgtccggcgg cagcatcagc agcggcgact actactggtc ctggatcaga 120

cagccccctg gcaagggcct ggaatggatc ggctacatct actacagcgg cagcacctac 180

tacaacccca gcctgaagtc tcgagtgacc atcagcgtgg acaccagcaa gaaccagttc 240

agcctgaagc tgagcagcgt gacagccgcc gacaccgctg tgtattactg tgccagagag 300

gacgtagtca aaggcgcttt tgatatctgg ggccaaggga caatggtcac cgtgtcctca 360

ggcggaggtg gaagcggagg gggaggatct ggcggcggag gaagcggagg cgacatccag 420

atgacccagt ctccatcctc cctgtctgca tctgtaggag acagagtcac catcacttgc 480

cgggcaagtc agagcattag cagctattta aattggtatc agcagaaacc agggaaagcc 540

cctaagctcc tgatctatgc tgcatccagt ttgcaaagtg gggtcccatc aaggttcagt 600

ggcagtggat ctgggacaga tttcactctc accatcagca gtctgcaacc tgaagatttt 660

gcaacttact actgtcaaca gagttacagt acccctctca ctttcggcgg cggaacaaag 720

gtggagatca ag 732

<210> 385
<211> 735

<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 385
gaagtgcagc tggtggaaag cggcggaggc ctggtgcagc ctggcggcag cctgagactg 60

tcttgcgccg ccagcggctt caccttcagc agctacagca tgaactgggt ccgccaggcc 120

cctggcaagg gactggaatg ggtgtcctac atcagcagca gcagctccac catctactac 180

gccgacagcg tgaagggtcg attcaccatc agccgggaca acgccaagaa cagcctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt attactgtgc gagagaagac 300

ttctcgcata agctagggta cttccagcac tggggccagg gcaccctggt caccgtgtcc 360

tcaggcggag gtggaagcgg agggggagga tctggcggcg gaggaagcgg aggcgacatc 420

cagatgaccc agtctccatc ctccctgtct gcatctgtag gagacagagt caccatcact 480

tgccgggcaa gtcagagcat tagcagctat ttaaattggt atcagcagaa accagggaaa 540

gcccctaagc tcctgatcta tgctgcatcc agtttgcaaa gtggggtccc atcaaggttc 600

agtggcagtg gatctgggac agatttcact ctcaccatca gcagtctgca acctgaagat 660

tttgcaactt actactgtca acagagttac agtacccctc tcactttcgg cggcggaaca 720

aaggtggaga tcaag 735

<210> 386
<211> 714
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 386
caggtgcagc tggtggaaag cggcggaggc ctggtgaaac ctggcggcag cctgagactg 60

agctgcgccg ccagcggctt caccttcagc gactactaca tgagctggat cagacaggcc 120

cctggcaagg gactggaatg ggtgtcctac atcagcagca gcggctcgac catctactac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acgccaagaa cagcctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt attactgtgc gagagattac 300

gattacgtgt ggggccaggg aaccctggtc accgtgtcct caggcggagg tggaagcgga 360

ggggggaggat ctggcggcgg aggaagcgga ggcgacatcc agatgaccca gtctccatcc 420

tccctgtctg catctgtagg agacagagtc accatcactt gccgggcaag tcagagcatt 480

agcagctatt taaattggta tcagcagaaa ccagggaaag cccctaagct cctgatctat 540

gctgcatcca gtttgcaaag tggggtccca tcaaggttca gtggcagtgg atctgggaca 600

gatttcactc tcaccatcag cagtctgcaa cctgaagatt ttgcaactta ctactgtcaa 660

cagagttaca gtacccctct cactttcggc ggcggaacaa aggtggagat caag 714

<210> 387
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 387
caggtgcagc tgcaggaaag cggccctggc ctggtgaaac ccagccagac cctgagcctg 60

acctgcacag tgtccggcgg cagcatcagc agcggcgact actactggtc ctggatcaga 120

cagccccctg gcaagggcct ggaatggatc ggctacatct actacagcgg cagcacctac 180

tacaacccca gcctgaagtc tcgagtgacc atcagcgtgg acaccagcaa gaaccagttc 240

agcctgaagc tgagcagcgt gacagccgcc gacaccgctg tgtattactg tgccagagat 300

cgccgtgatt gggactggtt cgacccctgg ggccagggaa ccctggtcac cgtgtcctca 360

ggcggaggtg gaagcggagg gggaggatct ggcggcggag gaagcggagg cgacatccag 420

atgacccagt ctccatcctc cctgtctgca tctgtaggag acagagtcac catcacttgc 480

cgggcaagtc agagcattag cagctattta attggtatc agcagaaacc agggaaagcc 540

cctaagctcc tgatctatgc tgcatccagt ttgcaaagtg gggtcccatc aaggttcagt 600

ggcagtggat ctgggacaga tttcactctc accatcagca gtctgcaacc tgaagatttt 660

gcaacttact actgtcaaca gagttacagt acccctctca ctttcggcgg cggaacaaag 720

gtggagatca ag 732

<210> 388
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 388
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acctgtgccg tgtctggcgg cagcatcagc agcagcaact ggtggtcctg ggtccgccag 120

cctcccggca agggcctcga atggatcggc gagatctacc acagcggcag caccaactac 180

aaccccagcc tgaagtccag agtgaccatc agcgtggaca agagcaagaa ccagttcagc 240

ctgaagctga gcagcgtgac agccgccgac accgctgtgt attactgtgc gagagatcag 300

caggcgttga aataccgtgt ggattggggc cagggaaccc tggtcaccgt gtcctcaggc 360

ggaggtggaa gcggaggggg aggatctggc ggcggaggaa gcggaggcga catccagatg 420

acccagtctc catcctccct gtctgcatct gtaggagaca gagtcaccat cacttgccgg 480

gcaagtcaga gcattagcag ctatttaaat tggtatcagc agaaaccagg gaaagccct 540

aagctcctga tctatgctgc atccagtttg caaagtgggg tcccatcaag gttcagtggc 600

agtggatctg ggacagattt cactctcacc atcagcagtc tgcaacctga agattttgca 660

acttactact gtcaacagag ttacagtacc cctctcactt tcggcggcgg aacaaaggtg 720

gagatcaag 729

<210> 389
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 389
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tcctgcaagg ccagcggcta caccttcacc agctacggca tcagctgggt ccgccaggct 120

cctggacagg gactggaatg gatgggctgg atcagcgcct acaacggcaa caccaactac 180

gcccagaaac tgcagggcag agtgaccatg accaccgaca ccagcaccag caccgcctac 240

atggaacttc gaagcctgag aagcgacgac accgccgtgt attactgtgc gagagatctt 300

acgctaggat gctttgacta ctggggccag ggaaccctgg tcaccgtgtc ctcaggcgga 360

ggtggaagcg gagggggagg atctggcggc ggaggaagcg gaggcgacat ccagatgacc 420

cagtctccat cctccctgtc tgcatctgta ggagacagag tcaccatcac ttgccgggca 480

agtcagagca ttagcagcta tttaaattgg tatcagcaga aaccagggaa agcccctaag 540

ctcctgatct atgctgcatc cagtttgcaa agtggggtcc catcaaggtt cagtggcagt 600

ggatctggga cagatttcac tctcaccatc agcagtctgc aacctgaaga ttttgcaact 660

tactactgtc aacagagtta cagtacccct ctcactttcg gcggcggaac aaaggtggag 720

atcaag 726

<210> 390
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 390
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tcttgcgccg ccagcggctt caccgtgtcc agcaactaca tgagctgggt ccgccaggcc 120

cctggcaagg gactggaatg ggtgtccgtg atctacagcg gcggcagcac ctactacgcc 180

gacagcgtga agggtcgatt caccatcagc cgggacaaca gcaagaacac cctgtacctg 240

cagatgaaca gcctgcgggc cgaggacacc gccgtgtatt actgtgcgag agatgggtca 300

aactcttggt acttcgatct ctggggccgt ggcaccctgg tcactgtgtc ctcaggcgga 360

ggtggaagcg gaggggggagg atctggcggc ggaggaagcg gaggcgacat ccagatgacc 420

cagtctccat cctccctgtc tgcatctgta ggagacagag tcaccatcac ttgccgggca 480

agtcagagca ttagcagcta tttaaattgg tatcagcaga aaccagggaa agcccctaag 540

ctcctgatct atgctgcatc cagtttgcaa agtggggtcc catcaaggtt cagtggcagt 600

ggatctggga cagatttcac tctcaccatc agcagtctgc aacctgaaga ttttgcaact 660

tactactgtc aacagagtta cagtacccct ctcactttcg gcggcggaac aaaggtggag 720

atcaag 726

<210> 391
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 391
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agctgcgccg ccagcggctt caccttcagc agctacggca tgcactgggt ccgccaggcc 120

cctggcaagg gactggaatg ggtggccgtg atttggtacg acggcagcaa caagtactac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt attactgtgc gagggcattt 300

ttattcctgt ctttttcggt ttggggccag ggaaccctgg tcaccgtgtc ctcaggcgga 360

ggtggaagcg gagggggagg atctggcggc ggaggaagcg gaggcgacat ccagatgacc 420

cagtctccat cctccctgtc tgcatctgta ggagacagag tcaccatcac ttgccgggca 480

agtcagagca ttagcagcta tttaaattgg tatcagcaga aaccagggaa agcccctaag 540

ctcctgatct atgctgcatc cagtttgcaa agtggggtcc catcaaggtt cagtggcagt 600

ggatctggga cagatttcac tctcaccatc agcagtctgc aacctgaaga ttttgcaact 660

tactactgtc aacagagtta cagtacccct ctcactttcg gcggcggaac aaaggtggag 720

atcaag 726

<210> 392
<211> 735
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 392
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tcttgcgccg ccagcggctt caccttcgac gactacacca tgcactgggt ccgccaggcc 120

cctggcaagg gactggaatg ggtgtccctg atcagctggg acggcggctc tacctactac 180

gccgactccg tgaagggccg gttcaccatc agccgggaca acagcaagaa cagcctgtac 240

ctgcagatga acagcctgcg gaccgaggac accgccttgt attactgtgc aaaagggata 300

ttctactcga gtaaagagga ttttgactac tggggccagg gaaccctggt caccgtgtcc 360

tcaggcggag gtggaagcgg agggggagga tctggcggcg gaggaagcgg aggcgacatc 420

cagatgaccc agtctccatc ctccctgtct gcatctgtag gagacagagt caccatcact 480

tgccgggcaa gtcagagcat tagcagctat ttaaattggt atcagcagaa accagggaaa 540

gcccctaagc tcctgatcta tgctgcatcc agtttgcaaa gtggggtccc atcaaggttc 600

agtggcagtg gatctgggac agatttcact ctcaccatca gcagtctgca acctgaagat 660

tttgcaactt actactgtca acagagttac agtacccctc tcactttcgg cggcggaaca 720

aaggtggaga tcaag 735

<210> 393
<211> 744
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 393
gaagtgcagc tggtggaatc tggcggcgtg gtggtgcagc ctggcggcag cctgagactg 60

tcttgcgccg ccagcggctt caccttcgac gactacacca tgcactgggt ccgccaggcc 120

cctggcaagg gactggaatg ggtgtccctg atcagctggg acggcggctc tacctactac 180

gccgactccg tgaagggccg gttcaccatc agccgggaca acagcaagaa cagcctgtac 240

ctgcagatga acagcctgcg gaccgaggac accgccttgt attactgtgc aaaagatata 300

tggatattct actcgagtaa tccaaagccg acggtctact ggggccaggg aaccctggtc 360

accgtgtcct caggcggagg tggaagcgga gggggaggat ctggcggcgg aggaagcgga 420

ggcgacatcc agatgaccca gtctccatcc tccctgtctg catctgtagg agacagagtc 480

accatcactt gccgggcaag tcagagcatt agcagctatt taaattggta tcagcagaaa 540

ccagggaaag cccctaagct cctgatctat gctgcatcca gtttgcaaag tggggtccca 600

tcaaggttca gtggcagtgg atctgggaca gatttcactc tcaccatcag cagtctgcaa 660

cctgaagatt ttgcaactta ctactgtcaa cagagttaca gtacccctct cactttcggc 720

ggcggaacaa aggtggagat caag 744

<210> 394
<211> 738
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 394
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tcctgcaagg ccagcggcta caccttcacc agctacgcca tgaactgggt ccgccaggcc 120

ccaggccagg gactggaatg gatgggctgg atcaacacca acaccggcaa ccccacctac 180

gcccagggct tcaccggcag attcgtgttc agcttcgaca ccagcgtgtc caccgcctac 240

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cagacgctga cctacggaaa ctggttcgac ccctggggcc agggaaccct ggtcaccgtg 360

tcctcaggcg gaggtggaag cggagggggа ggatctggcg gcggaggaag cggaggcgac 420

atccagatga cccagtctcc atcctccctg tctgcatctg taggagacag agtcaccatc 480

acttgccggg caagtcagag cattagcagc tatttaaatt ggtatcagca gaaaccaggg 540

aaagccccta agctcctgat ctatgctgca tccagtttgc aaagtggggt cccatcaagg 600

ttcagtggca gtggatctgg gacagatttc actctcacca tcagcagtct gcaacctgaa 660

gattttgcaa cttactactg tcaacagagt tacagtaccc ctctcacttt cggcggcgga 720

acaaaggtgg agatcaag 738

<210> 395
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 395
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acctgcaccg tgtccggcgg ctctgtgtcc agcggctcct actactggtc ctggatcaga 120

cagccccctg gcaagggcct cgaatggatc ggctacatct actacagcgg cagcaccaac 180

tacaacccca gcctgaagtc cagagtgacc atcagcgtgg acaccagcaa gaaccagttc 240

agcctgaagc tgagcagcgt gacagccgcc gacaccgctg tgtattactg tgcgagagat 300

cattacgagc gggggctcta ctggggccag ggaaccctgg tcaccgtgtc ctcaggcgga 360

ggtggaagcg gagggggagg atctggcggc ggaggaagcg gaggcgacat ccagatgacc 420

cagtctccat cctccctgtc tgcatctgta ggagacagag tcaccatcac ttgccgggca 480

agtcagagca ttagcagcta tttaaattgg tatcagcaga aaccagggaa agcccctaag 540

ctcctgatct atgctgcatc cagtttgcaa agtggggtcc catcaaggtt cagtggcagt 600

ggatctggga cagatttcac tctcaccatc agcagtctgc aacctgaaga ttttgcaact 660

tactactgtc aacagagtta cagtacccct ctcactttcg gcggcggaac aaaggtggag 720

atcaag 726

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<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 396
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agctgcgccg ccagcggctt caccttcagc gactactaca tgagctggat cagacaggcc 120

cctggcaagg gactggaatg ggtgtcctac atcagcagca gcggctcgac catctactac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acgccaagaa cagcctgtac 240

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tataactggt acttcgatct ctggggccgt ggcaccctgg tcactgtgtc ctcaggcgga 360

ggtggaagcg gagggggagg atctggcggc ggaggaagcg gaggcgacat ccagatgacc 420

cagagcccca gcagcgtgtc cgccagcgtg ggcgatcgag tgaccatcac ctgtcgggcc 480

tcccagggca tcagcagctg gctggcctgg tatcagcaga agcccggcaa ggcccccaag 540

ctgctgatct acgccgccag cagcctgcag agcggcgtgc caagcagatt cagcggcagc 600

ggctccggca ccgacttcac cctgaccatc agctccctgc agcccgagga cttcgccacc 660

tactactgcc agcaggctaa cagtttccct ctcactttcg gcggcggaac aaaggtggag 720

atcaag 726

<210> 397
<211> 723
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 397
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agctgcgccg ccagcggctt caccttcagc gactactaca tgagctggat cagacaggcc 120

cctggcaagg gactggaatg ggtgtcctac atcagcagca gcggctcgac catctactac 180

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tccggcaccg acttcaccct gaccatcagc tccctgcagc ccgaggactt cgccacctac 660

tactgccagc aggctaacag tttccctctc actttcggcg gcggaacaaa ggtggagatc 720

aag 723

<210> 398
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 398
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agctgcgccg ccagcggctt caccttcagc gactactaca tgagctggat cagacaggcc 120

cctggcaagg gactggaatg ggtgtcctac atcagcagca gcggctcgac catctactac 180

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agcggctccg gcaccgactt caccctgacc atcagcagcc tgcagcccga ggacttcgcc 660

acctactact gccagcagtt taatagttac cctctcactt tcggcggcgg aacaaaggtg 720

gagatcaag 729

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<220>
<223> MSLN scFv domain

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agctgcgccg ccagcggctt caccttcagc gactactaca tgagctggat cagacaggcc 120

cctggcaagg gactggaatg ggtgtcctac atcagcagca gcggctcgac catctactac 180

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ggctccggca ccgacttcac cctgaccatc agcagcctgc agcccgagga cttcgccacc 660

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atcaag 726

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<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 400
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agctgcgccg ccagcggctt caccttcagc gactactaca tgagctggat cagacaggcc 120

cctggcaagg gactggaatg ggtgtcctac atcagcagca gcggctcgac catctactac 180

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cagagcccca gcagcctgag cgccagcgtg ggcgatagag tgaccatcac ctgtcgcgcc 480

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ggctccggca ccgacttcac cctgaccatc agcagcctgc agcccgagga cttcgccacc 660

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atcaag 726

<210> 401
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 401
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agctgcgccg ccagcggctt caccttcagc gactactaca tgagctggat cagacaggcc 120

cctggcaagg gactggaatg ggtgtcctac atcagcagca gcggctcgac catctactac 180

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cagagcccca gcagcctgag cgccagcgtg ggcgatagag tgaccatcac ctgtcgcgcc 480

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ggctccggca ccgacttcac cctgaccatc agcagcctgc agcccgagga cttcgccacc 660

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atcaag 726

<210> 402
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 402
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agctgcgccg ccagcggctt caccttcagc gactactaca tgagctggat cagacaggcc 120

cctggcaagg gactggaatg ggtgtcctac atcagcagca gcggctcgac catctactac 180

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ctgacccaga gccccagcag cctgagcgcc agcgtgggcg atagagtgac catcacctgt 480

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ggcagcggct ccggcaccga cttcaccctg accatcagca gcctgcagcc cgaggacttc 660

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gtggagatca ag 732

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<220>
<223> MSLN scFv domain

<400> 403
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agctgcgccg ccagcggctt caccttcagc gactactaca tgagctggat cagacaggcc 120

cctggcaagg gactggaatg ggtgtcctac atcagcagca gcggctcgac catctactac 180

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ggcggaggtg gaagcggagg gggaggatct ggcggcggag gaagcggagg cgccatccag 420

ctgacccaga gccccagcag cctgagcgcc agcgtgggcg atagagtgac catcacctgt 480

cgcgccagcc agggcatcag cagcgctctg gcctggtatc agcagaagcc cggcaaggcc 540

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ggcagcggct ccggcaccga cttcaccctg accatcagca gcctgcagcc cgaggacttc 660

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gtggagatca ag 732

<210> 404
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 404
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agctgcgccg ccagcggctt caccttcagc gactactaca tgagctggat cagacaggcc 120

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gccgacagcg tgaagggccg gttcaccatc agccgggaca acgccaagaa cagcctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt attactgtgc gtctttacag 300

cgcgggctgg ccctcttcca gcactggggc cagggcaccc tggtcaccgt gtcctcaggc 360

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acccagagcc ccagcagcct gagcgccagc gtgggcgata gagtgaccat cacctgtcgc 480

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agcggctccg gcaccgactt caccctgacc atcagcagcc tgcagcccga ggacttcgcc 660

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gagatcaag 729

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<220>
<223> MSLN scFv domain

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cctggcaagg gactggaatg ggtgtcctac atcagcagca gcggctcgac catctactac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acgccaagaa cagcctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt attactgtgc tagcatattg 300

tcagttccgt acttcgatct ctggggccgt ggcaccctgg tcactgtgtc ctcaggcgga 360

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cagagcccca gcagcctgag cgccagcgtg ggcgatagag tgaccatcac ctgtcgcgcc 480

agccagggca tcagcagcgc tctggcctgg tatcagcaga agcccggcaa ggcccccaag 540

ctgctgatct acgacgccag ctccctggaa agcggcgtgc ccagcagatt cagcggcagc 600

ggctccggca ccgacttcac cctgaccatc agcagcctgc agcccgagga cttcgccacc 660

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atcaag 726

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cctggcaagg gactggaatg ggtgtcctac atcagcagca gcggctcgac catctactac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acgccaagaa cagcctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt attactgtgc gagtgggtgg 300

attcgtgtac ctttacgatt gcccctcttc cagcactggg gccagggcac cctggtcacc 360

gtgtcctcag gcggaggtgg aagcggaggg ggaggatctg gcggcggagg aagcggaggc 420

gccatccagc tgacccagag ccccagcagc ctgagcgcca gcgtgggcga tagagtgacc 480

atcacctgtc gcgccagcca gggcatcagc agcgctctgg cctggtatca gcagaagccc 540

ggcaaggccc ccaagctgct gatctacgac gccagctccc tggaaagcgg cgtgcccagc 600

agattcagcg gcagcggctc cggcaccgac ttcaccctga ccatcagcag cctgcagccc 660

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ggaacaaagg tggagatcaa g 741

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agctgcgccg ccagcggctt caccttcagc gactactaca tgagctggat cagacaggcc 120

cctggcaagg gactggaatg ggtgtcctac atcagcagca gcggctcgac catctactac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acgccaagaa cagcctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt attactgtgc gagagtaacc 300

atatttgcga tatttgatat ctggggccaa gggacaatgg tcaccgtgtc ctcaggcgga 360

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cagagcccca gcagcctgag cgccagcgtg ggcgatagag tgaccatcac ctgtcgcgcc 480

agccagggca tcagcagcgc tctggcctgg tatcagcaga agcccggcaa ggcccccaag 540

ctgctgatct acgacgccag ctccctggaa agcggcgtgc ccagcagatt cagcggcagc 600

ggctccggca ccgacttcac cctgaccatc agcagcctgc agcccgagga cttcgccacc 660

tactactgcc agcagtttaa tagttaccct ctcactttcg gcggcggaac aaaggtggag 720

atcaag 726

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cctggcaagg gactggaatg ggtgtcctac atcagcagca gcggctcgac catctactac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acgccaagaa cagcctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt attactgtgc gagagtggga 300

cgtggattcg ttcattttga tctctggggc cgtggcaccc tggtcactgt gtcctcaggc 360

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aagctgctga tctacgacgc cagctccctg gaaagcggcg tgcccagcag attcagcggc 600

agcggctccg gcaccgactt caccctgacc atcagcagcc tgcagcccga ggacttcgcc 660

acctactact gccagcagtt taatagttac cctctcactt tcggcggcgg aacaaaggtg 720

gagatcaag 729

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cctggcaagg gactggaatg ggtgtcctac atcagcagca gcggctcgac catctactac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acgccaagaa cagcctgtac 240

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ctgacccaga gccccagcag cctgagcgcc agcgtgggcg atagagtgac catcacctgt 480

cgcgccagcc agggcatcag cagcgctctg gcctggtatc agcagaagcc cggcaaggcc 540

cccaagctgc tgatctacga cgccagctcc ctggaaagcg gcgtgcccag cagattcagc 600

ggcagcggct ccggcaccga cttcaccctg accatcagca gcctgcagcc cgaggacttc 660

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gtggagatca ag 732

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<223> MSLN scFv domain

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cctggcaagg gactggaatg ggtgtcctac atcagcagca gcggctcgac catctactac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acgccaagaa cagcctgtac 240

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ctgacccaga gccccagcag cctgagcgcc agcgtgggcg atagagtgac catcacctgt 480

cgcgccagcc agggcatcag cagcgctctg gcctggtatc agcagaagcc cggcaaggcc 540

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ggcagcggct ccggcaccga cttcaccctg accatcagca gcctgcagcc cgaggacttc 660

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gtggagatca ag 732

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agctgcgccg ccagcggctt caccttcagc gactactaca tgagctggat cagacaggcc 120

cctggcaagg gactggaatg ggtgtcctac atcagcagca gcggctcgac catctactac 180

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ctgacccaga gccccagcag cctgagcgcc agcgtgggcg atagagtgac catcacctgt 480

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ggcagcggct ccggcaccga cttcaccctg accatcagca gcctgcagcc cgaggacttc 660

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gtggagatca ag 732

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<213> Artificial Sequence

<220>
<223> MSLN scFv domain

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agctgcgccg ccagcggctt caccttcagc gactactaca tgagctggat cagacaggcc 120

cctggcaagg gactggaatg ggtgtcctac atcagcagca gcggctcgac catctactac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acgccaagaa cagcctgtac 240

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gtccgcactg gagcttttga tatctggggc caagggacaa tggtcaccgt gtcctcaggc 360

ggaggtggaa gcggaggggg aggatctggc ggcggaggaa gcggaggcgc catccagctg 420

acccagagcc ccagcagcct gagcgccagc gtgggcgata gagtgaccat cacctgtcgc 480

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aagctgctga tctacgacgc cagctccctg gaaagcggcg tgcccagcag attcagcggc 600

agcggctccg gcaccgactt caccctgacc atcagcagcc tgcagcccga ggacttcgcc 660

acctactact gccagcagtt taatagttac cctctcactt tcggcggcgg aacaaaggtg 720

gagatcaag 729

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cctggcaagg gactggaatg ggtgtcctac atcagcagca gcggctcgac catctactac 180

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agcggctccg gcaccgactt caccctgacc atcagcagcc tgcagcccga ggacttcgcc 660

acctactact gccagcagtt taatagttac cctctcactt tcggcggcgg aacaaaggtg 720

gagatcaag 729

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agctgcgccg ccagcggctt caccttcagc gactactaca tgagctggat cagacaggcc 120

cctggcaagg gactggaatg ggtgtcctac atcagcagca gcggctcgac catctactac 180

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agcggctccg gcaccgactt caccctgacc atcagcagcc tgcagcccga ggacttcgcc 660

acctactact gccagcagtt taatagttac cctctcactt tcggcggcgg aacaaaggtg 720

gagatcaag 729

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<220>
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cctggcaagg gactggaatg ggtgtcctac atcagcagca gcggctcgac catctactac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acgccaagaa cagcctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt attactgtgc gagagatgga 300

tatcgcaaat atggttacgt atttttttgat atctggggcc aagggacaat ggtcaccgtg 360

tcctcaggcg gaggtggaag cggaggggga ggatctggcg gcggaggaag cggaggcgcc 420

atccagctga cccagagccc cagcagcctg agcgccagcg tgggcgatag agtgaccatc 480

acctgtcgcg ccagccaggg catcagcagc gctctggcct ggtatcagca gaagcccggc 540

aaggccccca agctgctgat ctacgacgcc agctccctgg aaagcggcgt gcccagcaga 600

ttcagcggca gcggctccgg caccgacttc accctgacca tcagcagcct gcagcccgag 660

gacttcgcca cctactactg ccagcagttt aatagttacc ctctcacttt cggcggcgga 720

acaaaggtgg agatcaag 738

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cctggcaagg gactggaatg ggtgtcctac atcagcagca gcggctcgac catctactac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acgccaagaa cagcctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt attactgtgc gagagatggg 300

aggtacaggc ggttctggca tgcttttgat atctggggcc aagggacaat ggtcaccgtg 360

tcctcaggcg gaggtggaag cggaggggga ggatctggcg gcggaggaag cggaggcgcc 420

atccagctga cccagagccc cagcagcctg agcgccagcg tgggcgatag agtgaccatc 480

acctgtcgcg ccagccaggg catcagcagc gctctggcct ggtatcagca gaagcccggc 540

aaggccccca agctgctgat ctacgacgcc agctccctgg aaagcggcgt gcccagcaga 600

ttcagcggca gcggctccgg caccgacttc accctgacca tcagcagcct gcagcccgag 660

gacttcgcca cctactactg ccagcagttt aatagttacc ctctcacttt cggcggcgga 720

acaaaggtgg agatcaag 738

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cctggcaagg gactggaatg ggtgtcctac atcagcagca gcggctcgac catctactac 180

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ggctccggca ccgacttcac cctgaccatc agcagcctgc agcccgagga cttcgccacc 660

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atcaag 726

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cctggcaagg gactcgaatg ggtgtccgcc atcagcggca gcggcggcag cacctactac 180

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agcggcagcg gctccggcac cgacttcacc ctgaccatca gcagcctgca gcccgaggac 660

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aaggtggaga tcaag 735

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cctggcaagg gactcgaatg ggtgtccgcc atcagcggca gcggcggcag cacctactac 180

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gagatcaag 729

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tcttgcgccg ccagcggctt caccttcagc agctacgcca tgagctgggt ccgccaggcc 120

cctggcaagg gactcgaatg ggtgtccgcc atcagcggca gcggcggcag cacctactac 180

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agcggcagcg gctccggcac cgacttcacc ctgaccatca gcagcctgca gcccgaggac 660

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aaggtggaga tcaag 735

<210> 421
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

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tcttgcgccg ccagcggctt caccttcagc agctacgcca tgagctgggt ccgccaggcc 120

cctggcaagg gactcgaatg ggtgtccgcc atcagcggca gcggcggcag cacctactac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtat attactgtgc gaaatggggg 300

gggcggttgt actggtactt cgatctctgg ggccgtggca ccctggtcac tgtgtcctca 360

ggcggaggtg gaagcggagg gggaggatct ggcggcggag gaagcggagg cgccatccag 420

ctgacccaga gccccagcag cctgagcgcc agcgtgggcg acagagtgac catcacctgt 480

cgggccagcc agggcatcag cagcgctctg gcctggtatc agcagaagcc cggcaaggcc 540

cccaagctgc tgatctacga cgcgtcctcc ctggaaagcg gcgtgcccag cagattcagc 600

ggcagcggct ccggcaccga cttcaccctg accatcagca gcctgcagcc cgaggacttc 660

gccacctact actgccagca gtttaataat taccctctca ctttcggcgg cggaacaaag 720

gtggagatca ag 732

<210> 422
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
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<400> 422
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tcttgcgccg ccagcggctt caccttcagc agctacgcca tgagctgggt ccgccaggcc 120

cctggcaagg gactcgaatg ggtgtccgcc atcagcggca gcggcggcag cacctactac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtat attactgtgc gaaagttatt 300

cggcaactct ggtacttcga tctctggggc cgtggcaccc tggtcactgt gtcctcaggc 360

ggaggtggaa gcggaggggg aggatctggc ggcggaggaa gcggaggcgc catccagctg 420

acccagagcc ccagcagcct gagcgccagc gtgggcgaca gagtgaccat cacctgtcgg 480

gccagccagg gcatcagcag cgctctggcc tggtatcagc agaagcccgg caaggccccc 540

aagctgctga tctacgacgc gtcctccctg gaaagcggcg tgcccagcag attcagcggc 600

agcggctccg gcaccgactt caccctgacc atcagcagcc tgcagcccga ggacttcgcc 660

acctactact gccagcagtt taataattac cctctcactt tcggcggcgg aacaaaggtg 720

gagatcaag 729

<210> 423
<211> 729
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<220>
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<400> 423
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tcttgcgccg ccagcggctt caccttcagc agctacgcca tgagctgggt ccgccaggcc 120

cctggcaagg gactcgaatg ggtgtccgcc atcagcggca gcggcggcag cacctactac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtat attactgtgc gaaagttttc 300

gccaactcct ggtacttcga tctctggggc cgtggcaccc tggtcactgt gtcctcaggc 360

ggaggtggaa gcggaggggg aggatctggc ggcggaggaa gcggaggcgc catccagctg 420

acccagagcc ccagcagcct gagcgccagc gtgggcgaca gagtgaccat cacctgtcgg 480

gccagccagg gcatcagcag cgctctggcc tggtatcagc agaagcccgg caaggccccc 540

aagctgctga tctacgacgc gtcctccctg gaaagcggcg tgcccagcag attcagcggc 600

agcggctccg gcaccgactt caccctgacc atcagcagcc tgcagcccga ggacttcgcc 660

acctactact gccagcagtt taataattac cctctcactt tcggcggcgg aacaaaggtg 720

gagatcaag 729

<210> 424
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 424
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tcttgcgccg ccagcggctt caccttcagc agctacgcca tgagctgggt ccgccaggcc 120

cctggcaagg gactcgaatg ggtgtccgcc atcagcggca gcggcggcag cacctactac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtat attactgtgc gaaagtagat 300

aggactacct ggtacttcga tctctggggc cgtggcaccc tggtcactgt gtcctcaggc 360

ggaggtggaa gcggaggggg aggatctggc ggcggaggaa gcggaggcgc catccagctg 420

acccagagcc ccagcagcct gagcgccagc gtgggcgaca gagtgaccat cacctgtcgg 480

gccagccagg gcatcagcag cgctctggcc tggtatcagc agaagcccgg caaggccccc 540

aagctgctga tctacgacgc gtcctccctg gaaagcggcg tgcccagcag attcagcggc 600

agcggctccg gcaccgactt caccctgacc atcagcagcc tgcagcccga ggacttcgcc 660

acctactact gccagcagtt taataattac cctctcactt tcggcggcgg aacaaaggtg 720

gagatcaag 729

<210> 425
<211> 738
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 425
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tcttgcgccg ccagcggctt caccttcagc agctacgcca tgagctgggt ccgccaggcc 120

cctggcaagg gactcgaatg ggtgtccgcc atcagcggca gcggcggcag cacctactac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtat attactgtgc gaaacgatgg 300

ggtaaggatg gtccttactg gtacttcgat ctctggggcc gtggcaccct ggtcactgtg 360

tcctcaggcg gaggtggaag cggagggggа ggatctggcg gcggaggaag cggaggcgcc 420

atccagctga cccagagccc cagcagcctg agcgccagcg tgggcgacag agtgaccatc 480

acctgtcggg ccagccaggg catcagcagc gctctggcct ggtatcagca gaagcccggc 540

aaggccccca agctgctgat ctacgacgcg tcctccctgg aaagcggcgt gcccagcaga 600

ttcagcggca gcggctccgg caccgacttc accctgacca tcagcagcct gcagcccgag 660

gacttcgcca cctactactg ccagcagttt aataattacc ctctcacttt cggcggcgga 720

acaaaggtgg agatcaag 738

<210> 426
<211> 738
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 426
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tcttgcgccg ccagcggctt caccttcagc agctacgcca tgagctgggt ccgccaggcc 120

cctggcaagg gactcgaatg ggtgtccgcc atcagcggca gcggcggcag cacctactac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtat attactgtgc gaaaagaaga 300

gacagttatg gtccttactg gtacttcgat ctctggggcc gtggcaccct ggtcactgtg 360

tcctcaggcg gaggtggaag cggagggggga ggatctggcg gcggaggaag cggaggcgcc 420

atccagctga cccagagccc cagcagcctg agcgccagcg tgggcgacag agtgaccatc 480

acctgtcggg ccagccaggg catcagcagc gctctggcct ggtatcagca gaagcccggc 540

aaggccccca agctgctgat ctacgacgcg tcctccctgg aaagcggcgt gcccagcaga 600

ttcagcggca gcggctccgg caccgacttc accctgacca tcagcagcct gcagcccgag 660

gacttcgcca cctactactg ccagcagttt aataattacc ctctcacttt cggcggcgga 720

acaaaggtgg agatcaag 738

<210> 427
<211> 735
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 427
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tcttgcgccg ccagcggctt caccttcagc agctacgcca tgagctgggt ccgccaggcc 120

cctggcaagg gactcgaatg ggtgtccgcc atcagcggca gcggcggcag cacctactac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtat attactgtgc gaagaatcgt 300

cccccgcccg ggtactggta cttcgatctc tggggccgtg gcaccctggt cactgtgtcc 360

tcaggcggag gtggaagcgg agggggagga tctggcggcg gaggaagcgg aggcgccatc 420

cagctgaccc agagccccag cagcctgagc gccagcgtgg gcgacagagt gaccatcacc 480

tgtcgggcca gccagggcat cagcagcgct ctggcctggt atcagcagaa gcccggcaag 540

gcccccaagc tgctgatcta cgacgcgtcc tccctggaaa gcggcgtgcc cagcagattc 600

agcggcagcg gctccggcac cgacttcacc ctgaccatca gcagcctgca gcccgaggac 660

ttcgccacct actactgcca gcagtttaat aattaccctc tcactttcgg cggcggaaca 720

aaggtggaga tcaag 735

<210> 428
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN scFv domain

<400> 428
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tcttgcgccg ccagcggctt caccttcagc agctacgcca tgagctgggt ccgccaggcc 120

cctggcaagg gactcgaatg ggtgtccgcc atcagcggca gcggcggcag cacctactac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtat attactgtgc gaagggaaga 300

cgatttagct ggtacttcga tctctggggc cgtggcaccc tggtcactgt gtcctcaggc 360

ggaggtggaa gcggaggggg aggatctggc ggcggaggaa gcggaggcgc catccagctg 420

acccagagcc ccagcagcct gagcgccagc gtgggcgaca gagtgaccat cacctgtcgg 480

gccagccagg gcatcagcag cgctctggcc tggtatcagc agaagcccgg caaggccccc 540

aagctgctga tctacgacgc gtcctccctg gaaagcggcg tgcccagcag attcagcggc 600

agcggctccg gcaccgactt caccctgacc atcagcagcc tgcagcccga ggacttcgcc 660

acctactact gccagcagtt taataattac cctctcactt tcggcggcgg aacaaaggtg 720

gagatcaag 729

<210> 429
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR1

<400> 429

Asn Ala Trp Met Ser
1 5

<210> 430
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR1

<400> 430

Ser Tyr Ala Met His
1 5

<210> 431
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR1

<400> 431

Ser Gly Gly Tyr Ser Trp Ser
1 5

<210> 432
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR1

<400> 432

Ser Gly Gly Tyr Tyr Trp Ser
1 5

<210> 433
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR1

<400> 433

Ser Ser Ser Tyr Tyr Trp Gly
1 5

<210> 434
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR1

<400> 434

Ser Tyr Ser Met Asn
1 5

<210> 435
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR1

<400> 435

Ser Tyr Tyr Trp Ser
1   5

<210> 436
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR1

<400> 436

Asp Tyr Gly Met Ser
1   5

<210> 437
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR1

<400> 437

Ser Tyr Asp Ile Asn
1   5

<210> 438
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR1

<400> 438

Ser Gly Asp Tyr Tyr Trp Ser
1   5

<210> 439
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR1

<400> 439

Asp Tyr Tyr Met Ser
1 5

<210> 440
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR1

<400> 440

Ser Ser Asn Trp Trp Ser
1 5

<210> 441
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR1

<400> 441

Ser Tyr Gly Ile Ser
1 5

<210> 442
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR1

<400> 442

Ser Asn Tyr Met Ser
1 5

<210> 443
<211> 5
<212> PRT
<213> Artificial Sequence

<220>

<223> MSLN scFv domain HC CDR1

<400> 443

Ser Tyr Gly Met His
1 5

<210> 444
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR1

<400> 444

Asp Tyr Thr Met His
1 5

<210> 445
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
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<400> 445

Ser Tyr Ala Met Asn
1 5

<210> 446
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR1

<400> 446

Ser Gly Ser Tyr Tyr Trp Ser
1 5

<210> 447
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR1

<400> 447

Ser Tyr Ala Met Ser
1   5

<210> 448
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR1

<400> 448

Gly Tyr Thr Met Asn
1   5

<210> 449
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR1

<400> 449

Ser Tyr Trp Met His
1   5

<210> 450
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR2

<400> 450

Arg Ile Lys Ser Lys Thr Asp Gly Gly Thr Thr Asp Tyr Ala Ala Pro
1   5   10   15

Val Lys Gly

<210> 451
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR2

<400> 451

Ala Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asn Ser Val Lys
1 5 10 15

Gly

<210> 452
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR2

<400> 452

Tyr Ile Tyr His Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 453
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR2

<400> 453

Arg Ile Asn Ser Asp Gly Ser Ser Thr Ser Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 454
<211> 16

<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR2

<400> 454

Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Lys Ser
1   5   10   15

<210> 455
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR2

<400> 455

Ser Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Lys Ser
1   5   10   15

<210> 456
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR2

<400> 456

Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys
1   5   10   15

Gly

<210> 457
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR2

<400> 457

Ser Ile Ser Ser Ser Ser Ser Tyr Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 458
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR2

<400> 458

Trp Ile Asn Ala Gly Asn Gly Asn Thr Lys Tyr Ser Gln Lys Phe Gln
1 5 10 15

Gly

<210> 459
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR2

<400> 459

Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 460
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR2

<400> 460

Gly Ile Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 461
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR2

<400> 461

Trp Met Asn Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe Gln
1   5   10   15

Gly

<210> 462
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR2

<400> 462

Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys
1   5   10   15

Gly

<210> 463
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR2

<400> 463

Glu Ile Tyr His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys Ser
1   5   10   15

<210> 464
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR2

<400> 464

Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu Gln
1 5 10 15

Gly

<210> 465
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR2

<400> 465

Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 466
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR2

<400> 466

Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 467
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR2

<400> 467

Leu Ile Ser Trp Asp Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1   5   10   15

Gly

<210> 468
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR2

<400> 468

Trp Ile Asn Thr Asn Thr Gly Asn Pro Thr Tyr Ala Gln Gly Phe Thr
1   5   10   15

Gly

<210> 469
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR2

<400> 469

Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1   5   10   15

Gly

<210> 470
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR2

<400> 470

Leu Ile Thr Pro Tyr Asn Gly Ala Ser Ser Tyr Asn Gln Lys Phe Arg
1   5   10   15

Gly

<210> 471
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR3

<400> 471

Asp Leu Pro Lys Leu Arg Asn Phe His Ile
1   5   10

<210> 472
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR3

<400> 472

Leu Glu Tyr His Gly Phe Arg Gln Tyr Gly Leu Arg Tyr Trp His
1   5   10   15

<210> 473
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR3

<400> 473

Ile Lys Phe Trp Phe Ala Gly Ile Asn Tyr Phe Phe Pro
1   5   10

<210> 474
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR3

<400> 474

Gly Phe Leu Gly Met Gly Ser Asn Phe Ile
1 5 10

<210> 475
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR3

<400> 475

Gly Asp Arg Ala Arg Tyr Phe Asp Leu
1 5

<210> 476
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR3

<400> 476

Tyr Pro Arg Gly Tyr His Gln Met Val Asp Ala Phe Asp Ile
1 5 10

<210> 477
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR3

<400> 477

Val Arg Phe Leu Ala Ala Arg Thr Thr Ile Pro Glu Ala Asn Phe Leu
1   5   10   15

<210> 478
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR3

<400> 478

Val Leu Ser Arg Ala Arg Phe Asp Tyr
1   5

<210> 479
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR3

<400> 479

Leu Arg Gly Arg Val Phe Asp Pro
1   5

<210> 480
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR3

<400> 480

Ile Lys Phe Thr Ser Phe Leu Tyr Val His Gly Phe Leu
1   5   10

<210> 481
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR3

<400> 481

Gly Gln Arg Trp Leu Tyr Leu Gly Gly Ile Arg Arg His
1 5 10

<210> 482
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR3

<400> 482

Glu Trp Ile Pro Ser Arg Pro Tyr Tyr Phe Asp Tyr
1 5 10

<210> 483
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR3

<400> 483

Glu Ser Thr Gly Thr Gly Ala Phe Asp Ile
1 5 10

<210> 484
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN scFv domain HC CDR3

<400> 484

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Glu Asp Val Val Lys Gly Ala Phe Asp Ile
1   5   10

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Glu Asp Phe Ser His Lys Leu Gly Tyr Phe Gln His
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Asp Tyr Asp Tyr Val
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<400> 493

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<400> 494

Asp Gly Ser Asn Ser Trp Tyr Phe Asp Leu
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<400> 495

Ala Phe Leu Phe Leu Ser Phe Ser Val
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1   5   10

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Tyr Met Tyr Asn Trp Tyr Phe Asp Leu
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Thr Ser Pro Arg Pro Leu Phe Gln His
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Pro Tyr Gln Val Arg Gly Val Tyr Phe Asp Tyr
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Pro Tyr Lys Lys Arg Arg Thr Val Phe Asp Tyr
1 5 10

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Leu Gln Arg Gly Leu Ala Leu Phe Gln His
1 5 10

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<400> 510

Gly Trp Ile Arg Val Pro Leu Arg Leu Pro Leu Phe Gln His
1 5 10

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<400> 511

Val Thr Ile Phe Ala Ile Phe Asp Ile
1 5

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Val Gly Arg Gly Phe Val His Phe Asp Leu
1   5   10

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<400> 514

Ser Gly Pro Ser Ser Tyr Trp Tyr Phe Asp Leu
1   5   10

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<400> 515

Asn Ile Tyr Met Gly Gly Ile Trp Phe Asp Pro
1   5   10

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Leu Thr Val Arg Thr Gly Ala Phe Asp Ile
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Leu Arg Thr Ala His Leu Asp Phe Asp Leu
1   5   10

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Asp Leu Ile Phe Pro Val Val Phe Asp Tyr
1   5   10

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Asp Gly Tyr Arg Lys Tyr Gly Tyr Val Phe Phe Asp Ile
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<400> 521

Ala His Ile Arg Gly Tyr Phe Asp Leu
1 5

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Trp Met Gly Gly Gly Gly Arg Trp Tyr Phe Asp Leu
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Thr Ser Arg Thr Thr Trp Tyr Phe Asp Leu
1 5 10

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1 5 10

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Trp Gly Gly Arg Leu Tyr Trp Tyr Phe Asp Leu
1 5 10

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Val Ile Arg Gln Leu Trp Tyr Phe Asp Leu
1 5 10

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Val Phe Ala Asn Ser Trp Tyr Phe Asp Leu
1 5 10

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Val Asp Arg Thr Thr Trp Tyr Phe Asp Leu
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Arg Trp Gly Lys Asp Gly Pro Tyr Trp Tyr Phe Asp Leu
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Arg Arg Asp Ser Tyr Gly Pro Tyr Trp Tyr Phe Asp Leu
1 5 10

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<400> 531

Asn Arg Pro Pro Pro Gly Tyr Trp Tyr Phe Asp Leu
1 5 10

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<400> 532

Gly Arg Arg Phe Ser Trp Tyr Phe Asp Leu
1 5 10

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Cys Ala Arg Glu Asp Val Val Lys Gly Ala Phe Asp Ile Trp
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Gly Gly Tyr Asp Gly Arg Gly Phe Asp Tyr
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1 5 10

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<223> MSLN scFv domain LC CDR2

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<210> 542
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<400> 542

Gln Gln Ser Tyr Ser Thr Pro Leu Thr
1   5

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<400> 543

Gln Gln Ala Asn Ser Phe Pro Leu Thr
1   5

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Gln Gln Phe Asn Ser Tyr Pro Leu Thr
1   5

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<400> 545

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<210> 546
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<220>
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<220>
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<223> Xaa is Leu or Ile

<400> 546

Tyr Xaa Xaa Xaa
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<210> 547
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<220>
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<220>
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tacctgcaga aaccaggcca gtctccaaag ctcctgatct acaaagtttc caaccgattt 180

tctggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaagatc 240

agtagagtgg aggctgagga tctgggagtt tattactgct ttcaaggttc acatgttcct 300

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gcggtctatt tctgtgccag agaggagatt acctatgcta tggactactg gggtcaagga 720

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cccggacaag ggcttgagtg gatgggatgg atctaccctg gcaatgttaa cacagaatat 180

aatgagaagt tcaagggcaa agccaccatt accgcggaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggctgtgt attactgtgc gagggaggaa 300

attacctacg ctatggacta ctggggccag ggaaccacag tcaccgtgtc ctcaggcgga 360

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cagagcccag gcaccctgag cctctctcca ggagagcggg ccaccctcag ttgtagatcc 480

agtcagagta ttgtacacag taatgggaac acctatttgg aatggtatca gcagaaacca 540

ggtcaagccc caagattgct catctacaaa gtctctaaca gatttagtgg tattccagac 600

aggttcagcg gttccggaag tggtactgat ttcaccctca cgatctccag gctcgagcca 660

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ggtactaaag tagaaatcaa a 741

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cccggacaag ggcttgagtg gatgggatgg atctaccctg gcaatgttaa cacagaatat 180

aatgagaagt tcaagggcaa agccaccatt accgcggaca aatccacgag cacagcctac 240

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attacctacg ctatggacta ctggggccag ggaaccacag tcaccgtgtc ctcaggcgga 360

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ggtcaatccc cacaattgct catctacaaa gtctctaaca gatttagtgg tgtaccagac 600

aggttcagcg gttccggaag tggtactgat ttcaccctca agatctccag ggtcgaggca 660

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aatgagaagt tcaagggcag attcaccatt agcagggacg attccaagaa cacactctac 240

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ggtaaagccc caaaattgct catctacaaa gtctctaaca gatttagtgg tgtaccaagc 600

aggttcagcg gttccggaag tggtactgat ttcaccctca cgatctcctc tctccagcca 660

gaagatttcg ccacttatta ctgttttcaa ggttcacatg tgccgcgcac attcggtggg 720

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cccggacaag ggcttgagtg gatcggatgg atctaccctg gcaatgttaa cacagaatat 180

aatgagaagt tcaagggcaa agccaccatt accgcggacg aatccacgaa cacagcctac 240

atggagctga gcagcctgag atctgaagac acggctgtgt attactgtgc gagggaggaa 300

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cagagcccat ccaccctgag cgcatctgta ggtgaccggg tcaccatcac ttgtagatcc 480

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ggtaaagccc caaaattgct catctacaaa gtctctaaca gatttagtgg tgtaccagcc 600

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aatgagaagt tcaagggcaa agccaccctt accgcggaca aatccacgaa cacagcctac 240

atggagctga gcagcctgag atctgaagac acggctgtgt atttctgtgc gagggaggaa 300

attacctacg ctatggacta ctggggccag ggaaccctgg tcaccgtgtc ctcaggcgga 360

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aggttcagcg gttccggaag tggtactgaa ttcaccctca cgatctcctc tctccagcca 660

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cctggacaag ggcttgagtg gatcggatgg atctaccctg gcgatggtag tacacagtat 180

aatgagaagt tcaagggcaa aaccaccctt accgcggaca aatcctccag cacagcctac 240

atgttgctga gcagcctgac ctctgaagac tctgctatct atttctgtgc gagggagggg 300

acctactacg ctatggacta ctggggccag ggaacctcag tcaccgtgtc ctcaggcgga 360

ggtggaagcg gagggggagg atctggcggc ggaggaagcg gaggcgatgt tttgatgacc 420

cagactccac tctccctgcc tgtctctctt ggagaccaag tctccatctc ttgtagatcc 480

agtcagagta ttgtacacag taatgggaac acctatttag aatggtatct gcagaaacca 540

ggtcagtctc caaagttgct catctacaaa gtctctaaca gatttagtgg tgtaccagac 600

aggttcagcg gttccggaag tggtactgat ttcaccctca agatctcgag agtggaggct 660

gaggatctgg gagtttatta ctgttttcaa ggttcacatg tgccgcgcac attcggtgga 720

ggtactaaac tggaaatcaa a 741

<210> 555
<211> 741
<212> DNA
<213> Artificial Sequence

<220>
<223> HLA scFv binding domain

<400> 555
cagctgcagc tgcaggagtc tgggcccggg ctggtgaagc cttcggaaac gctgagcctc 60

acctgcacgg tttctggata caccttcacc agctatcata tccagtggat ccgacagccc 120

cctggaaaag ggcttgagtg gatcggatgg atctaccctg gcgatggttc aacacagtac 180

aatgagaagt tcaagggcag agccacgatt agcgtggaca catccaagaa ccaattctcc 240

ctgaacctgg acagcgtgag tgctgcggac acggccattt attactgtgc gagagaggga 300

acttactacg ctatggacta ctggggcaaa gggagcacgg tcaccgtgtc ctcaggcgga 360

ggtggaagcg gagggggagg atctggcggc ggaggaagcg gaggcgacat ccagatgacc 420

cagagcccaa gctccctgag tgcgtccgtg ggcgaccgcg tgaccatcac ttgcagatcc 480

tctcagtcca tcgtgcactc caacggcaac acgtacctcg agtggtacca gcagaagccc 540

gggaaggccc cgaaactgct catctacaag gtgagcaacc ggttctccgg cgtccccagc 600

cgcttctcag ggtccggctc ggggacggat ttcaccttca cgattagcag cttgcagccc 660

gaagacatcg ccacgtacta ctgctttcag ggaagtcacg tgccgcgtac cttcgggccg 720

ggcacgaaag tggatattaa g 741

<210> 556
<211> 741
<212> DNA
<213> Artificial Sequence

<220>
<223> HLA scFv binding domain

<400> 556
gaggtgcagc tggtgcagtc tggggccgag ctgaagaagc ctgggtcctc ggtgaaggtg 60

tcctgcaagg cttctggata caccttcacc agctatcata tccagtgggt aaaacaggcc 120

cctggacaag ggcttgagtg gatcggatgg atctaccctg gcgatggttc aacacagtac 180

aatgagaagt tcaagggcaa agccacgctt accgtggaca aatccacgaa cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtat attactgtgc gagagaggga 300

acttactacg ctatggacta ctggggccaa gggaccctgg tcaccgtgtc ctcaggcgga 360

ggtggaagcg gaggggggagg atctggcggc ggaggaagcg gaggcgacat ccagatgacc 420

cagagcccat ccaccctgag tgcgtccgtg ggcgaccgcg tgaccatcac ttgcagatcc 480

tctcagtcca tcgtgcactc caacggcaac acgtacctcg agtggtacca gcagaagccc 540

gggaaggccc cgaaactgct catctacaag gtgagcaacc ggttctccgg cgtccccagc 600

cgcttctcag ggtccggctc ggggacggat ttcaccctca cgattagcag cttgcagccc 660

gatgacttcg ccacgtacta ctgctttcag ggaagtcacg tgccgcgtac cttcgggcag 720

ggcacgaaag tggaagttaa g 741

<210> 557
<211> 741
<212> DNA
<213> Artificial Sequence

<220>
<223> HLA scFv binding domain

<400> 557
caggtgcagc tggtgcagtc tggggccgag gtgaagaagc ctgggtcctc ggtgaaggtg 60

tcctgcaagg cttctggata caccttcacc agctatcata tccagtgggt acgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atctaccctg gcgatggttc aacacagtac 180

aatgagaagt tcaagggcag agtcacgatt accgcggaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtat attactgtgc gagagaggga 300

acttactacg ctatggacta ctggggccaa gggaccacgg tcaccgtgtc ctcaggcgga 360

ggtggaagcg gaggggggagg atctggcggc ggaggaagcg gaggcgagat cgtcctgacc 420

cagagcccag ggaccctgag tttgtccccg ggcgagcgcg cgaccctcag ttgcagatcc 480

tctcagtcca tcgtgcactc caacggcaac acgtacctcg agtggtacca gcagaagccc 540

gggcaggccc cgcgactgct catctacaag gtgagcaacc ggttctccgg catccccgac 600

cgcttctcag ggtccggctc ggggacggat ttcaccctca cgattagccg cttggagccc 660

gaagacttcg ccgtgtacta ctgctttcag ggaagtcacg tgccgcgtac cttcgggggg 720

ggcacgaaag tggaaattaa g 741

<210> 558
<211> 741
<212> DNA
<213> Artificial Sequence

<220>
<223> HLA scFv binding domain

<400> 558
caggtgaccc tgaagcagtc tggggccgag gtgaagaagc ctgggtcctc ggtgaaggtg 60

tcctgcacgg cttctggata caccttcacc agctatcatg tcagctgggt acgacaggcc 120

cctggacaag ggcttgagtg gttgggaagg atctaccctg gcgatggttc aacacagtac 180

aatgagaagt tcaagggcaa agtcacgatt accgcggaca aatccatgga cacatccttc 240

atggagctga ccagcctgac atctgaggac acggccgtat attactgtgc gagagaggga 300

acttactacg ctatggacct ctggggccaa gggaccctgg tcaccgtgtc ctcaggcgga 360

ggtggaagcg gaggggggagg atctggcggc ggaggaagcg gaggcgagat cgtcctgacc 420

cagagcccag ggaccctgag tttgtccccg ggcgagcgcg cgaccctcag ttgcagatcc 480

tctcagtcca tcgtgcactc caacggcaac acgtacctcg cgtggtacca gcagaagccc 540

gggcaggccc cgcgactgct catctccaag gtgagcaacc ggttctccgg cgtccccgac 600

cgcttctcag ggtccggctc ggggacggat ttcaccctca cgattagccg cttggagccc 660

gaagacttcg ccgtgtacta ctgccaacag ggaagtcacg tgccgcgtac cttcgggggg 720

ggcacgaaag tggaaattaa g 741

<210> 559
<211> 741
<212> DNA
<213> Artificial Sequence

<220>
<223> HLA scFv binding domain

<400> 559
caggtgcagc tggtgcagtc tggggccgag gtgaagaagc ctggggcctc ggtgaaggtg 60

tcctgcaagg cttctggata caccttcacc agctatcata tgcactgggt acgacaggcc 120

cctggacaaa ggcttgagtg gatgggatgg atctaccctg gcgatggttc aacacagtac 180

aatgagaagt tcaagggcaa agtcacgatt acccgggaca catccgcgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtat attactgtgc gagagaggga 300

acttactacg ctatggacta ctggggccaa gggaccctgg tcaccgtgtc ctcaggcgga 360

ggtggaagcg gaggggggagg atctggcggc ggaggaagcg gaggcgacat cgtcatgacc 420

cagaccccac tgtccctgcc tgtgaccccg ggcgagcccg cgagcatcag ttgcagatcc 480

tctcagtcca tcgtgcactc caacggcaac acgtacctcg actggtacct gcagaagccc 540

gggcagtccc cgcaactgct catctacaag gtgagcaacc ggttctccgg cgtccccgac 600

cgcttctcag ggtccggctc ggggacggat ttcaccctca agattagccg cgtggaggcc 660

gaagacgtcg gcgtgtacta ctgcatgcag ggaagtcacg tgccgcgtac cttcgggggg 720

ggcacgaaag tggaaattaa g 741

<210> 560
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-B*07 antigen binding domain

<400> 560

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Ser Trp His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

Ile Gly Tyr Ile His Phe Ser Gly Ser Thr His Tyr His Pro Ser Leu
    50                  55                  60

Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

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

Ala Arg Gly Gly Val Val Ser His Tyr Ala Met Asp Cys Trp Gly Gln
            100                 105                 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser
    130                 135                 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160

Arg Ala Ser Glu Asn Ile Tyr Ser Asn Leu Ala Trp Tyr Gln Gln Lys
                165                 170                 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Thr Tyr Leu Pro
            180                 185                 190

Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220
```

Cys Gln His Phe Trp Val Thr Pro Tyr Thr Phe Gly Gly Gly Thr Lys
225 230 235 240

Val Glu Ile Lys

<210> 561
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-B*07 antigen binding domain

<400> 561

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Tyr Ser Trp His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
35 40 45

Val Ser Tyr Ile His Phe Ser Gly Ser Thr His Tyr His Pro Ser Leu
50 55 60

Lys Ser Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Val Val Ser His Tyr Ala Met Asp Cys Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser
130 135 140

```
Pro Ser Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160


Arg Ala Ser Glu Asn Ile Tyr Ser Asn Leu Ala Trp Tyr Gln Gln Lys
                165                 170                 175


Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Thr Tyr Leu Pro
            180                 185                 190


Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205


Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220


Cys Gln His Phe Trp Val Thr Pro Tyr Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240


Val Glu Ile Lys
```

<210> 562
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-B*07 antigen binding domain

<400> 562

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30


Tyr Ser Trp His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45


Val Gly Tyr Ile His Phe Ser Gly Ser Thr His Tyr His Pro Ser Leu
    50                  55                  60
```

```
Lys Ser Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Gly Val Val Ser His Tyr Ala Met Asp Cys Trp Gly Gln
            100                 105                 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Glu Ile Val Leu Thr Gln Ser
    130                 135                 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145                 150                 155                 160

Arg Ala Ser Glu Asn Ile Tyr Ser Asn Leu Ala Trp Tyr Gln Gln Lys
                165                 170                 175

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Ala Ala Thr Tyr Leu Pro
            180                 185                 190

Asp Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
    210                 215                 220

Cys Gln His Phe Trp Val Thr Pro Tyr Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240

Val Glu Ile Lys
```

<210> 563
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-B*07 antigen binding domain

<400> 563

```
Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                  10                  15


Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30


Tyr Ser Trp His Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp
        35                  40                  45


Leu Gly Tyr Ile His Phe Ser Gly Ser Thr His Tyr His Pro Ser Leu
    50                  55                  60


Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn Gln Phe Ser
65                  70                  75                  80


Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Gly Gly Val Val Ser His Tyr Ala Met Asp Cys Trp Gly Gln
            100                 105                 110


Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125


Gly Ser Gly Gly Gly Gly Ser Gly Gly Glu Ile Val Leu Thr Gln Ser
    130                 135                 140


Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145                 150                 155                 160


Arg Ala Ser Glu Asn Ile Tyr Ser Asn Leu Ala Trp Tyr Gln Gln Lys
                165                 170                 175


Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Ala Ala Thr Tyr Leu Pro
            180                 185                 190
```

Asp Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
195 200 205

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
210 215 220

Cys Gln His Phe Trp Val Thr Pro Tyr Thr Phe Gly Gly Gly Thr Lys
225 230 235 240

Val Glu Ile Lys

<210> 564
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-B*07 antigen binding domain

<400> 564

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Tyr Ser Trp His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
35 40 45

Val Gly Tyr Ile His Phe Ser Gly Ser Thr His Tyr His Pro Ser Leu
50 55 60

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

Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Val Val Ser His Tyr Ala Met Asp Cys Trp Gly Gln
100 105 110

```
Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125


Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser
    130                 135                 140


Pro Ser Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160


Arg Ala Ser Glu Asn Ile Tyr Ser Asn Leu Ala Trp Tyr Gln Gln Lys
                165                 170                 175


Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Thr Tyr Leu Pro
            180                 185                 190


Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205


Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220


Cys Gln His Phe Trp Val Thr Pro Tyr Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240


Val Glu Ile Lys
```

<210> 565
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-B*07 antigen binding domain

<400> 565

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30
```

```
Tyr Ser Trp His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

Val Ser Tyr Ile His Phe Ser Gly Ser Thr His Tyr His Pro Ser Leu
    50                  55                  60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Gly Val Val Ser His Tyr Ala Met Asp Cys Trp Gly Gln
            100                 105                 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser
    130                 135                 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160

Arg Ala Ser Glu Asn Ile Tyr Ser Asn Leu Ala Trp Tyr Gln Gln Lys
                165                 170                 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Thr Tyr Leu Pro
            180                 185                 190

Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220

Cys Gln His Phe Trp Val Thr Pro Tyr Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240

Val Glu Ile Lys
```

<210> 566
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-B*07 antigen binding domain

<400> 566

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30


Tyr Ser Trp His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45


Val Gly Tyr Ile His Phe Ser Gly Ser Thr His Tyr His Pro Ser Leu
    50                  55                  60


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


Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Gly Gly Val Val Ser His Tyr Ala Met Asp Cys Trp Gly Gln
            100                 105                 110


Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125


Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser
    130                 135                 140


Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160


Arg Ala Ser Glu Asn Ile Tyr Ser Asn Leu Ala Trp Tyr Gln Gln Lys
                165                 170                 175
```

```
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Thr Tyr Leu Pro
            180                 185                 190

Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220

Cys Gln His Phe Trp Val Thr Pro Tyr Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240

Val Glu Ile Lys
```

<210> 567
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-B*07 antigen binding domain

<400> 567

```
Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Ser Trp His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

Ile Gly Tyr Ile His Phe Ser Gly Ser Thr His Tyr His Pro Ser Leu
    50                  55                  60

Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Arg Gly Gly Val Val Ser His Tyr Ala Met Asp Cys Trp Gly Gln
            100                 105                 110


Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125


Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser
    130                 135                 140


Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160


Arg Ala Ser Glu Asn Ile Tyr Ser Asn Leu Ala Trp Tyr Gln Gln Lys
                165                 170                 175


Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Thr Tyr Leu Pro
            180                 185                 190


Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205


Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220


Cys Gln His Phe Trp Val Thr Pro Tyr Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240


Val Glu Ile Lys
```

<210> 568
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-B*07 antigen binding domain

<400> 568

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15
```

```
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Ser Trp His Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

Ile Gly Tyr Ile His Phe Ser Gly Ser Thr His Tyr His Pro Ser Leu
    50                  55                  60

Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

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

Ala Arg Gly Gly Val Val Ser His Tyr Ala Met Asp Cys Trp Gly Gln
            100                 105                 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser
    130                 135                 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160

Arg Ala Ser Glu Asn Ile Tyr Ser Asn Leu Ala Trp Tyr Gln Gln Lys
                165                 170                 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Thr Tyr Leu Pro
            180                 185                 190

Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220
```

Cys Gln His Phe Trp Val Thr Pro Tyr Thr Phe Gly Gly Gly Thr Lys
225 230 235 240

Val Glu Ile Lys

<210> 569
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-B*07 antigen binding domain

<400> 569

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Tyr Ser Trp His Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp
35 40 45

Leu Gly Tyr Ile His Phe Ser Gly Ser Thr His Tyr His Pro Ser Leu
50 55 60

Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Val Val Ser His Tyr Ala Met Asp Cys Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser
130 135 140

```
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160


Arg Ala Ser Glu Asn Ile Tyr Ser Asn Leu Ala Trp Tyr Gln Gln Lys
                165                 170                 175


Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Thr Tyr Leu Pro
            180                 185                 190


Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205


Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220


Cys Gln His Phe Trp Val Thr Pro Tyr Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240


Val Glu Ile Lys
```

<210> 570
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 570

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


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


Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Val Ser Phe Asp Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125


Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
    130                 135                 140


Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
145                 150                 155                 160


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


Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro
            180                 185                 190


Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
        195                 200                 205


Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser
    210                 215                 220


Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
225                 230                 235                 240


<210>  571
<211>  248
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HLA-C*07 antigen binding domain

<400>  571
```

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                  10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Glu Arg Ser Ile Ser Pro Tyr Tyr Tyr Tyr Tyr Met Asp
            100                 105                 110

Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln
    130                 135                 140

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
145                 150                 155                 160

Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
                165                 170                 175

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala
            180                 185                 190

Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
        195                 200                 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
    210                 215                 220
```

Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly
225 230 235 240

Gly Gly Thr Lys Val Glu Ile Lys
245

<210> 572
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 572

Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser
20 25 30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Asp Ser Val Ile Trp Tyr Trp Phe Asp Pro Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gln Ser Val Leu Thr Gln Pro
130 135 140

```
Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser
145                 150                 155                 160


Gly Ser Ser Ser Asn Ile Gly Ser Asn Thr Val Asn Trp Tyr Gln Gln
                165                 170                 175


Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ser Asn Asn Gln Arg
            180                 185                 190


Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser
        195                 200                 205


Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr
    210                 215                 220


Tyr Cys Ala Ala Trp Asp Asp Ser Leu Asn Gly Trp Val Phe Gly Gly
225                 230                 235                 240


Gly Thr Lys Leu Thr Val Leu
                245


<210>  573
<211>  249
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HLA-C*07 antigen binding domain

<400>  573

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30


Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45


Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60
```

```
Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Glu Glu Ile Leu Pro Arg Leu Ser Tyr Tyr Tyr Tyr Met
            100                 105                 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile
    130                 135                 140

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
145                 150                 155                 160

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
                165                 170                 175

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
            180                 185                 190

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
        195                 200                 205

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
    210                 215                 220

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe
225                 230                 235                 240

Gly Gly Gly Thr Lys Val Glu Ile Lys
                245
```

<210> 574
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 574

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


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30


Ala Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asn Thr Asn Thr Gly Asn Pro Thr Tyr Ala Gln Gly Phe
    50                  55                  60


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


Leu Gln Ile Cys Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Gly Gly Arg Ala His Ser Ser Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110


Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125


Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln
    130                 135                 140


Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145                 150                 155                 160


Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln
                165                 170                 175


Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu
            180                 185                 190
```

```
Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
        195                 200                 205

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
    210                 215                 220

Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr
225                 230                 235                 240

Lys Val Glu Ile Lys
                245
```

<210> 575
<211> 251
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 575

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Asp Arg Ile Lys Ile Leu Pro Arg Leu Gly Tyr Tyr Tyr
            100                 105                 110
```

```
Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly
        115                 120                 125


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


Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
145                 150                 155                 160


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
                165                 170                 175


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
            180                 185                 190


Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
        195                 200                 205


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
    210                 215                 220


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu
225                 230                 235                 240


Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
                245                 250


<210>  576
<211>  246
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HLA-C*07 antigen binding domain

<400>  576

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30
```

```
Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Asp Thr Val Ile His Tyr Tyr Tyr Tyr Met Asp Val Trp
            100                 105                 110

Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr
    130                 135                 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln
                165                 170                 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser
            180                 185                 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
    210                 215                 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly
225                 230                 235                 240

Thr Lys Val Glu Ile Lys
                245
```

<210> 577
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 577

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30


Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45


Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60


Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80


Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95


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


Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly
        115                 120                 125


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


Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
145                 150                 155                 160


Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu
                165                 170                 175
```

```
Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
            180                 185                 190


Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
        195                 200                 205


Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
    210                 215                 220


Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr
225                 230                 235                 240


Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
                245                 250


<210>  578
<211>  246
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HLA-C*07 antigen binding domain

<400>  578

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30


Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45


Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60


Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80


Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95
```

```
Cys Ala Arg Asp Ile Phe Ile His Tyr Tyr Tyr Tyr Met Asp Val Trp
            100                 105                 110

Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr
    130                 135                 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln
                165                 170                 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser
            180                 185                 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
    210                 215                 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly
225                 230                 235                 240

Thr Lys Val Glu Ile Lys
                245
```

<210> 579
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 579

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Gly Thr Phe Tyr Ser Tyr Ser Pro Tyr Tyr Phe Asp Tyr
            100                 105                 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met
    130                 135                 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145                 150                 155                 160

Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr
                165                 170                 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser
            180                 185                 190

Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
    210                 215                 220
```

Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly
225 230 235 240

Gly Thr Lys Val Glu Ile Lys
245

<210> 580
<211> 251
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 580

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Glu Trp Ile Lys Ile Leu Pro Arg Leu Gly Tyr Tyr Tyr
100 105 110

Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly
115 120 125

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

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
145                 150                 155                 160


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
                165                 170                 175


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
            180                 185                 190


Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
        195                 200                 205


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
    210                 215                 220


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu
225                 230                 235                 240


Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
                245                 250


<210>  581
<211>  246
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HLA-C*07 antigen binding domain

<400>  581

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30


Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45


Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60
```

```
Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Asp Arg Ser Leu Tyr Tyr Tyr Tyr Tyr Met Asp Val Trp
            100                 105                 110

Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr
    130                 135                 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln
                165                 170                 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser
            180                 185                 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
    210                 215                 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly
225                 230                 235                 240

Thr Lys Val Glu Ile Lys
                245
```

<210> 582
<211> 248
<212> PRT
<213> Artificial Sequence

<220>

<223> HLA-C*07 antigen binding domain

<400> 582

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                  10                  15


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30


Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45


Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60


Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80


Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95


Cys Ala Arg Asp Lys Ile Leu Ala Pro Asn Tyr Tyr Tyr Tyr Met Asp
            100                 105                 110


Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
        115                 120                 125


Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln
    130                 135                 140


Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
145                 150                 155                 160


Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
                165                 170                 175


Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala
            180                 185                 190


Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
        195                 200                 205
```

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
210 215 220

Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly
225 230 235 240

Gly Gly Thr Lys Val Glu Ile Lys
245

<210> 583
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 583

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Glu Lys Ser Trp Lys Tyr Phe Tyr Tyr Tyr Tyr Tyr Tyr
100 105 110

Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly
115 120 125

```
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp
    130                 135                 140


Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
145                 150                 155                 160


Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu
                165                 170                 175


Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
            180                 185                 190


Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
        195                 200                 205


Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
    210                 215                 220


Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr
225                 230                 235                 240


Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
                245                 250


<210>  584
<211>  249
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HLA-C*07 antigen binding domain

<400>  584

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30


Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45
```

```
Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Glu Asn Thr Ser Thr Ile Pro Tyr Tyr Tyr Tyr Tyr Met
            100                 105                 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile
    130                 135                 140

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
145                 150                 155                 160

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
                165                 170                 175

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
            180                 185                 190

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
        195                 200                 205

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
    210                 215                 220

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe
225                 230                 235                 240

Gly Gly Gly Thr Lys Val Glu Ile Lys
                245
```

<210> 585
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 585

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30


Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45


Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60


Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80


Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95


Cys Ala Arg Glu Asp Val Asp Lys Asn Thr Ser Thr Ile Tyr Tyr Tyr
            100                 105                 110


Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser
        115                 120                 125


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


Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
145                 150                 155                 160


Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser
                165                 170                 175
```

```
Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
            180                 185                 190

Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe
        195                 200                 205

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
    210                 215                 220

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr
225                 230                 235                 240

Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
                245                 250
```

<210> 586
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 586

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Arg Asp Gly Gly Asp Ile Val Ser Ser Ser Ala Ile Tyr Trp Tyr
            100                 105                 110

Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly
        115                 120                 125

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

Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
145                 150                 155                 160

Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu
                165                 170                 175

Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
            180                 185                 190

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

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
    210                 215                 220

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Phe Asn Ser Tyr Pro Leu Thr
225                 230                 235                 240

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
                245                 250


<210>  587
<211>  248
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HLA-C*07 antigen binding domain

<400>  587

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15
```

```
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Asp Leu Ile Leu Pro Pro Tyr Tyr Tyr Tyr Tyr Met Asp
            100                 105                 110

Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln
    130                 135                 140

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
145                 150                 155                 160

Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
                165                 170                 175

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala
            180                 185                 190

Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
        195                 200                 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
    210                 215                 220

Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly
225                 230                 235                 240
```

Gly Gly Thr Lys Val Glu Ile Lys
245

<210> 588
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 588

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Glu Thr Trp Ile Lys Ile Leu Pro Arg Tyr Tyr Tyr Tyr
100 105 110

Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser
115 120 125

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

Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
145 150 155 160

```
Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser
                165                 170                 175


Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
            180                 185                 190


Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe
        195                 200                 205


Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
    210                 215                 220


Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr
225                 230                 235                 240


Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
                245                 250


<210>  589
<211>  246
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HLA-C*07 antigen binding domain

<400>  589

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30


Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45


Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60


Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80
```

```
Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Asp Leu Ser Arg Tyr Tyr Tyr Tyr Tyr Met Asp Val Trp
            100                 105                 110

Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr
    130                 135                 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln
                165                 170                 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser
            180                 185                 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
    210                 215                 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly
225                 230                 235                 240

Thr Lys Val Glu Ile Lys
                245
```

<210> 590
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 590

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Glu His Ile Val Leu Cys Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125


Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser
    130                 135                 140


Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160


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


Lys Ala Pro Lys Ser Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
            180                 185                 190


Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205
```

```
Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Tyr Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
225                 230                 235                 240

Ile Lys
```

<210> 591
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 591

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Asp Lys Ile Leu Pro Arg Pro Tyr Tyr Tyr Tyr Tyr Met
            100                 105                 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
        115                 120                 125
```

```
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile
    130                 135                 140

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
145                 150                 155                 160

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
                165                 170                 175

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
            180                 185                 190

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
        195                 200                 205

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
    210                 215                 220

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe
225                 230                 235                 240

Gly Gly Gly Thr Lys Val Glu Ile Lys
                245
```

<210> 592
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 592

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45
```

```
Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Ser Asn Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu
            100                 105                 110

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gln Ser Ala Leu Thr Gln Pro Pro Ser Ala
    130                 135                 140

Ser Gly Ser Pro Gly Gln Ser Val Thr Ile Ser Cys Thr Gly Thr Ser
145                 150                 155                 160

Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln Gln His Pro
                165                 170                 175

Gly Lys Ala Pro Lys Leu Met Ile Tyr Glu Val Ser Lys Arg Pro Ser
            180                 185                 190

Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser
        195                 200                 205

Leu Thr Val Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
    210                 215                 220

Ser Ser Tyr Ala Gly Ser Asn Asn Trp Val Phe Gly Gly Gly Thr Lys
225                 230                 235                 240

Leu Thr Val Leu
```

<210> 593
<211> 242

<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 593

Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Asn Thr Gly Asn Pro Thr Tyr Ala Gln Gly Phe
50 55 60

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

Leu Gln Ile Cys Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Thr Ser Tyr Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser
130 135 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145 150 155 160

Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
165 170 175

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
210 215 220

Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
225 230 235 240

Ile Lys

<210> 594
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 594

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

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

```
Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
        115                 120                 125


Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln
    130                 135                 140


Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
145                 150                 155                 160


Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
                165                 170                 175


Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala
            180                 185                 190


Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
        195                 200                 205


Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
    210                 215                 220


Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly
225                 230                 235                 240


Gly Gly Thr Lys Val Glu Ile Lys
                245
```

<210> 595
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 595

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
```

```
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Val Asp Asp Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
    130                 135                 140

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145                 150                 155                 160

Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
                165                 170                 175

Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val
            180                 185                 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
        195                 200                 205

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
    210                 215                 220

Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
225                 230                 235                 240
```

Lys

<210> 596
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 596

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Val Trp Val
        35                  40                  45


Ser Arg Ile Asn Ser Asp Gly Ser Ser Thr Ser Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Trp Ser Thr Asn Ile Leu Leu Ser Tyr Thr Lys Ala Phe Asp Ile
            100                 105                 110


Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        115                 120                 125


Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met
    130                 135                 140


Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145                 150                 155                 160
```

```
Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr
                165                 170                 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser
            180                 185                 190

Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
    210                 215                 220

Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly
225                 230                 235                 240

Gly Thr Lys Val Glu Ile Lys
                245
```

<210> 597
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 597

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80
```

```
Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Asp Lys Thr Tyr Tyr Tyr Tyr Tyr Tyr Met Asp Val Trp
            100                 105                 110

Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr
    130                 135                 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln
                165                 170                 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser
            180                 185                 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
    210                 215                 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly
225                 230                 235                 240

Thr Lys Val Glu Ile Lys
                245
```

<210> 598
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 598

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Glu Lys Tyr Phe His Asp Lys Tyr Phe His Asp Tyr Tyr
            100                 105                 110

Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser
        115                 120                 125

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

Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
145                 150                 155                 160

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser
                165                 170                 175

Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
            180                 185                 190

Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe
        195                 200                 205

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
    210                 215                 220
```

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr
225 230 235 240

Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
245 250

<210> 599
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 599

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Asp Thr Ser Val Tyr Tyr Tyr Tyr Tyr Met Asp Val Trp
100 105 110

Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr
130 135 140

```
Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160


Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln
                165                 170                 175


Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser
            180                 185                 190


Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205


Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
    210                 215                 220


Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly
225                 230                 235                 240


Thr Lys Val Glu Ile Lys
                245
```

<210> 600
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 600

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30


Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45


Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60
```

```
Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Glu Lys Ile Leu Pro Tyr Tyr Tyr Tyr Tyr Tyr Met Asp
            100                 105                 110

Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln
    130                 135                 140

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
145                 150                 155                 160

Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
                165                 170                 175

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala
            180                 185                 190

Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
        195                 200                 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
    210                 215                 220

Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly
225                 230                 235                 240

Gly Gly Thr Lys Val Glu Ile Lys
                245
```

<210> 601
<211> 257
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 601

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Ile Gln Trp Ile Tyr Ile Tyr Ile Asn Pro Arg Gly Phe Ile Phe
            100                 105                 110


Leu His Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val
        115                 120                 125


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


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


Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile
                165                 170                 175


Gly Ser Asn Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro
            180                 185                 190
```

Lys Leu Leu Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp
195 200 205

Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser
210 215 220

Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp
225 230 235 240

Asp Ser Leu Asn Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val
245 250 255

Leu

<210> 602
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 602

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
20 25 30

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

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60

Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80

Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

```
Tyr Tyr Cys Ala Lys Glu Asp Val Asp Phe His His Asp Ala Phe Asp
            100                 105                 110

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln
    130                 135                 140

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
145                 150                 155                 160

Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
                165                 170                 175

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala
            180                 185                 190

Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
        195                 200                 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
    210                 215                 220

Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly
225                 230                 235                 240

Gly Gly Thr Lys Val Glu Ile Lys
                245
```

<210> 603
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 603

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15
```

```
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Glu Gly Val Asp Lys Asn Thr Ser Thr Ile Tyr Tyr Tyr
            100                 105                 110

Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser
        115                 120                 125

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

Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
145                 150                 155                 160

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser
                165                 170                 175

Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
            180                 185                 190

Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe
        195                 200                 205

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
    210                 215                 220

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr
225                 230                 235                 240
```

Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
245 250

<210> 604
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 604

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Arg Gly Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu
100 105 110

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
130 135 140

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145 150 155 160

```
Gln Gly Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Glu Lys
                165                 170                 175


Ala Pro Lys Ser Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val
            180                 185                 190


Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
        195                 200                 205


Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
    210                 215                 220


Tyr Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
225                 230                 235                 240


Lys



<210>  605
<211>  248
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HLA-C*07 antigen binding domain

<400>  605

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Thr Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30


Tyr Met His Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
        35                  40                  45


Gly Leu Val Asp Pro Glu Asp Gly Glu Thr Ile Tyr Ala Glu Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asp Thr Ala Tyr
65                  70                  75                  80
```

```
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Thr Gly Ile His Val Asp Ile Arg Ser Met Glu Asp Trp Phe Asp
            100                 105                 110

Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln
    130                 135                 140

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
145                 150                 155                 160

Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
                165                 170                 175

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala
            180                 185                 190

Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
        195                 200                 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
    210                 215                 220

Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly
225                 230                 235                 240

Gly Gly Thr Lys Val Glu Ile Lys
                245
```

<210> 606
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 606

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30


Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45


Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60


Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80


Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95


Cys Ala Arg Asp Ile Gly Thr Ser Tyr Tyr Tyr Tyr Met Asp Val Trp
            100                 105                 110


Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125


Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr
    130                 135                 140


Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160


Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln
                165                 170                 175


Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser
            180                 185                 190


Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205
```

```
Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
    210                 215                 220


Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly
225                 230                 235                 240


Thr Lys Val Glu Ile Lys
                245


<210>  607
<211>  249
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HLA-C*07 antigen binding domain

<400>  607

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30


Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45


Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60


Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80


Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95


Cys Ala Arg Glu Val Val Glu Val Phe Leu Tyr Tyr Tyr Tyr Tyr Met
            100                 105                 110


Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
        115                 120                 125
```

```
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile
    130                 135                 140

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
145                 150                 155                 160

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
                165                 170                 175

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
            180                 185                 190

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
        195                 200                 205

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
    210                 215                 220

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe
225                 230                 235                 240

Gly Gly Gly Thr Lys Val Glu Ile Lys
                245
```

<210> 608
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 608

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45
```

```
Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Asp Leu Tyr Tyr Tyr Tyr Tyr Tyr Tyr Met Asp Val Trp
            100                 105                 110

Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr
    130                 135                 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln
                165                 170                 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser
            180                 185                 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
    210                 215                 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly
225                 230                 235                 240

Thr Lys Val Glu Ile Lys
                245
```

<210> 609
<211> 256

<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 609

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Glu Ser Trp Lys Tyr Phe Tyr Pro Arg Gly Ser Ile Phe
100 105 110

Ile His Tyr Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val
115 120 125

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
145 150 155 160

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
165 170 175

Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
180 185 190

```
Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro
        195                 200                 205


Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
    210                 215                 220


Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser
225                 230                 235                 240


Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
                245                 250                 255


<210>  610
<211>  248
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HLA-C*07 antigen binding domain

<400>  610

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30


Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45


Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60


Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80


Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95


Cys Ala Arg Asp Arg Ile Val Glu Val Phe Tyr Tyr Tyr Tyr Met Asp
            100                 105                 110
```

```
Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
        115                 120                 125


Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln
    130                 135                 140


Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
145                 150                 155                 160


Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
                165                 170                 175


Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala
            180                 185                 190


Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
        195                 200                 205


Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
    210                 215                 220


Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly
225                 230                 235                 240


Gly Gly Thr Lys Val Glu Ile Lys
                245


<210>  611
<211>  250
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HLA-C*07 antigen binding domain

<400>  611

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30
```

```
Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Glu Lys Tyr Phe His Asp Trp Leu Tyr Tyr Tyr Tyr Tyr
            100                 105                 110

Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly
        115                 120                 125

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

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
145                 150                 155                 160

Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu
                165                 170                 175

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
            180                 185                 190

Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
        195                 200                 205

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
    210                 215                 220

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr
225                 230                 235                 240
```

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
245 250

<210> 612
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 612

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

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

Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly
115 120 125

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

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
145 150 155 160

```
Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu
                165                 170                 175

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
            180                 185                 190

Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
        195                 200                 205

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
    210                 215                 220

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr
225                 230                 235                 240

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
                245                 250
```

<210> 613
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 613

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

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

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80
```

```
Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Val Gln Asn Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu
            100                 105                 110

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gln Ser Ala Leu Thr Gln Pro Pro Ser Ala
    130                 135                 140

Ser Gly Ser Pro Gly Gln Ser Val Thr Ile Ser Cys Thr Gly Thr Ser
145                 150                 155                 160

Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln Gln His Pro
                165                 170                 175

Gly Lys Ala Pro Lys Leu Met Ile Tyr Glu Val Ser Lys Arg Pro Ser
            180                 185                 190

Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser
        195                 200                 205

Leu Thr Val Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
    210                 215                 220

Ser Ser Tyr Ala Gly Ser Asn Asn Trp Val Phe Gly Gly Gly Thr Lys
225                 230                 235                 240

Leu Thr Val Leu
```

<210> 614
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-C*07 antigen binding domain

<400> 614

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Thr Ala Asn Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110

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

Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser
    130                 135                 140

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly
145                 150                 155                 160

Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
                165                 170                 175

Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser
            180                 185                 190

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
        195                 200                 205

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn
    210                 215                 220
```

Ser Phe Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
225 230 235

<210> 615
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*03 scFv

<400> 615

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser
130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160

```
Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys
                165                 170                 175


Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln
            180                 185                 190


Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205


Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220


Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240


Val Glu Ile Lys
```

<210> 616
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*03 scFv

<400> 616

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30


Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80
```

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Asn Pro Asp Lys Asp Pro Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160

Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser
            180                 185                 190

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

Glu Ile Lys
```

<210> 617
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*03 scFv

<400> 617

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                  10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Ser Gly
            20                  25                  30

Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Asp Phe Tyr Cys Thr Asn Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln
    130                 135                 140

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145                 150                 155                 160

Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln
                165                 170                 175

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu
            180                 185                 190

Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
        195                 200                 205
```

```
Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
    210                 215                 220


Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr
225                 230                 235                 240


Lys Val Glu Ile Lys
                245


<210>  618
<211>  244
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HLA-A*03 scFv

<400>  618

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
            20                  25                  30


Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45


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


Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65                  70                  75                  80


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


Arg Glu Ser Ser Ser Gly Ser Tyr Trp Tyr Phe Asp Leu Trp Gly Arg
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125
```

```
Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser
    130                 135                 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys
                165                 170                 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln
            180                 185                 190

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220

Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240

Val Glu Ile Lys
```

<210> 619
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*03 scFv

<400> 619

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
            20                  25                  30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35                  40                  45
```

```
Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
    50                  55                  60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95

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

Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly
        115                 120                 125

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

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
145                 150                 155                 160

Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu
                165                 170                 175

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
            180                 185                 190

Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
        195                 200                 205

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
    210                 215                 220

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr
225                 230                 235                 240

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
                245                 250
```

<210> 620
<211> 249

<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*03 scFv

<400> 620

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asp Leu Ser His Tyr Tyr Tyr Tyr Met Asp Val Trp
100 105 110

Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gln Thr Val Val Thr
130 135 140

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

Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn Trp
165 170 175

Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Ala Leu Ile Tyr Ser Thr
180 185 190

```
Ser Asn Lys His Ser Trp Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
        195                 200                 205


Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
    210                 215                 220


Ala Glu Tyr Tyr Cys Leu Leu Tyr Tyr Gly Gly Ala Gln Trp Val Phe
225                 230                 235                 240


Gly Gly Gly Thr Lys Leu Thr Val Leu
                245


<210>  621
<211>  246
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HLA-A*03 scFv

<400>  621

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30


Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


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


Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Glu Asn Arg Arg Tyr Asn Ser Cys Tyr Tyr Phe Asp Tyr Trp
            100                 105                 110
```

```
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr
    130                 135                 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln
                165                 170                 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser
            180                 185                 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
    210                 215                 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly
225                 230                 235                 240

Thr Lys Val Glu Ile Lys
                245
```

<210> 622
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*03 scFv

<400> 622

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30
```

```
Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

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

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Gly Asp Leu Ser His Tyr Tyr Tyr Tyr Leu Asp Val Trp
            100                 105                 110

Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gln Thr Val Val Thr
    130                 135                 140

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

Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn Trp
                165                 170                 175

Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Ala Leu Ile Tyr Ser Thr
            180                 185                 190

Ser Asn Lys His Ser Trp Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
        195                 200                 205

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
    210                 215                 220

Ala Glu Tyr Tyr Cys Leu Leu Tyr Tyr Gly Gly Ala Gln Trp Val Phe
225                 230                 235                 240
```

Gly Gly Gly Thr Lys Leu Thr Val Leu
245

<210> 623
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*03 scFv

<400> 623

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Ala Thr Leu Leu Ser Leu Ser Tyr Asp Ala Phe Asp Ile Trp Gly
100 105 110

Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln
130 135 140

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145 150 155 160

```
Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln
                165                 170                 175


Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu
            180                 185                 190


Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
        195                 200                 205


Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
    210                 215                 220


Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr
225                 230                 235                 240


Lys Val Glu Ile Lys
                245
```

<210> 624
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*03 scFv

<400> 624

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


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30


Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


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


Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80
```

```
Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Gly Asp Leu Ser His Tyr Tyr Tyr Met Asp Val Trp Gly
            100                 105                 110

Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gln Thr Val Val Thr Gln
    130                 135                 140

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
145                 150                 155                 160

Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn Trp Phe
                165                 170                 175

Gln Gln Lys Pro Gly Gln Ala Pro Arg Ala Leu Ile Tyr Ser Thr Ser
            180                 185                 190

Asn Lys His Ser Trp Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly
        195                 200                 205

Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala
    210                 215                 220

Glu Tyr Tyr Cys Leu Leu Tyr Tyr Gly Gly Ala Gln Trp Val Phe Gly
225                 230                 235                 240

Gly Gly Thr Lys Leu Thr Val Leu
                245
```

<210> 625
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*03 scFv

<400> 625

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
            20                  25                  30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35                  40                  45

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

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95

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

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
    130                 135                 140

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145                 150                 155                 160

Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
                165                 170                 175

Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val
            180                 185                 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
        195                 200                 205

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
    210                 215                 220
```

Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
225 230 235 240

Lys

<210> 626
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*03 scFv

<400> 626

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gln Ser Ala Leu Thr Gln Pro
130 135 140

```
Pro Ser Ala Ser Gly Ser Pro Gly Gln Ser Val Thr Ile Ser Cys Thr
145                 150                 155                 160


Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln
                165                 170                 175


Gln His Pro Gly Lys Ala Pro Lys Leu Met Ile Tyr Glu Val Ser Lys
            180                 185                 190


Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Asn
        195                 200                 205


Thr Ala Ser Leu Thr Val Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp
    210                 215                 220


Tyr Tyr Cys Ser Ser Tyr Ala Gly Ser Asn Asn Trp Val Phe Gly Gly
225                 230                 235                 240


Gly Thr Lys Leu Thr Val Leu
                245


<210>  627
<211>  251
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HLA-A*03 scFv

<400>  627

Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser
            20                  25                  30


Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45


Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60
```

```
Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Glu Ala Tyr Cys Leu Ser Asp Ser Tyr Trp Tyr Phe Asp
            100                 105                 110

Leu Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gln Ser Val
    130                 135                 140

Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr
145                 150                 155                 160

Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Thr Val Asn
                165                 170                 175

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

Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys
        195                 200                 205

Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu Asp
    210                 215                 220

Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu Asn Gly Trp
225                 230                 235                 240

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
                245                 250
```

<210> 628
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*03 scFv

<400> 628

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30


Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45


Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60


Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80


Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95


Cys Ala Arg Glu Ser Trp Lys Tyr Phe Tyr Pro Arg Gly Tyr Met Asp
            100                 105                 110


Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
        115                 120                 125


Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln
    130                 135                 140


Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
145                 150                 155                 160


Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
                165                 170                 175


Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala
            180                 185                 190
```

```
Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
        195                 200                 205


Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
    210                 215                 220


Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly
225                 230                 235                 240


Gly Gly Thr Lys Val Glu Ile Lys
                245


<210>  629
<211>  248
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HLA-A*01 scFv

<400>  629

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30


Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


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


Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Gly Gly Trp Thr Ala Trp Tyr Tyr Tyr Met Asp Val Trp Gly
            100                 105                 110
```

```
Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125


Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gln Thr Val Val Thr Gln
    130                 135                 140


Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
145                 150                 155                 160


Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn Trp Phe
                165                 170                 175


Gln Gln Lys Pro Gly Gln Ala Pro Arg Ala Leu Ile Tyr Ser Thr Ser
            180                 185                 190


Asn Lys His Ser Trp Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly
        195                 200                 205


Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala
    210                 215                 220


Glu Tyr Tyr Cys Leu Leu Tyr Tyr Gly Gly Ala Gln Trp Val Phe Gly
225                 230                 235                 240


Gly Gly Thr Lys Leu Thr Val Leu
                245


<210>  630
<211>  244
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HLA-A*01 scFv

<400>  630

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
```

```
Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ala Lys Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr
            100                 105                 110

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

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

Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Ser
145                 150                 155                 160

Ser Asn Ile Gly Ser Asn Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly
                165                 170                 175

Thr Ala Pro Lys Leu Leu Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly
            180                 185                 190

Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu
        195                 200                 205

Ala Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala
    210                 215                 220

Ala Trp Asp Asp Ser Leu Asn Gly Trp Val Phe Gly Gly Gly Thr Lys
225                 230                 235                 240

Leu Thr Val Leu
```

<210> 631
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*01 scFv

<400> 631

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30


Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45


Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60


Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80


Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95


Cys Ala Arg Asp Gln Val Asp Lys Asn Thr Tyr Tyr Tyr Tyr Met Asp
            100                 105                 110


Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
        115                 120                 125


Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln
    130                 135                 140


Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
145                 150                 155                 160


Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
                165                 170                 175
```

```
Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala
            180                 185                 190


Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
        195                 200                 205


Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
    210                 215                 220


Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly
225                 230                 235                 240


Gly Gly Thr Lys Val Glu Ile Lys
                245


<210>  632
<211>  243
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HLA-A*01 scFv

<400>  632

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30


Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Arg Ala Cys Gln Leu Ala Glu Tyr Phe Gln His Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140

Ser Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160

Ala Ser Gln Gly Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser
            180                 185                 190

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Ala Asn Ser Phe Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240

Glu Ile Lys
```

<210> 633
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*01 scFv

<400> 633

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15
```

```
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Asp Arg Val Asp Lys Asn Thr Ser Tyr Tyr Tyr Met Asp
            100                 105                 110

Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln
    130                 135                 140

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
145                 150                 155                 160

Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
                165                 170                 175

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala
            180                 185                 190

Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
        195                 200                 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
    210                 215                 220
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Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly
225 230 235 240

Gly Gly Thr Lys Val Glu Ile Lys
245

<210> 634
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*01 scFv

<400> 634

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Asp
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Tyr Ser Ile Ser Ser Ser
20 25 30

Asn Trp Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
35 40 45

Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Val Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

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

Ala Arg Arg Val Gln Leu Lys Leu Val His Trp Phe Asp Pro Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln
130 135 140

```
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145                 150                 155                 160


Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln
                165                 170                 175


Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu
            180                 185                 190


Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
        195                 200                 205


Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
    210                 215                 220


Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr
225                 230                 235                 240


Lys Val Glu Ile Lys
                245


<210>  635
<211>  245
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HLA-A*01 scFv

<400>  635

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30


Asp Ile Asn Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Met Asn Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe
    50                  55                  60
```

```
Gln Gly Arg Val Thr Met Thr Arg Asn Thr Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Thr Tyr Tyr Asp Tyr Val Thr Val Phe Tyr Phe Gln His Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln
    130                 135                 140

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145                 150                 155                 160

Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln
                165                 170                 175

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu
            180                 185                 190

Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
        195                 200                 205

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
    210                 215                 220

Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr
225                 230                 235                 240

Lys Val Glu Ile Lys
                245
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<210> 636
<211> 245
<212> PRT
<213> Artificial Sequence

<220>

<223> HLA-A*01 scFv

<400> 636

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Gln Leu Gln Leu Gln Glu Ser Gly Ser Gly Leu Val Lys Pro Ser Gln
1               5                  10                  15


Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30


Gly Tyr Ser Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45


Trp Ile Gly Tyr Ile Tyr His Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60


Leu Lys Ser Arg Val Thr Ile Ser Val Asp Arg Ser Lys Asn Gln Phe
65                  70                  75                  80


Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95


Cys Ala Arg Glu Ser Tyr Pro Ser Phe Tyr Ala Phe Asp Ile Trp Gly
            100                 105                 110


Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125


Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile Gln Met Thr Gln
    130                 135                 140


Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145                 150                 155                 160


Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln
                165                 170                 175


Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu
            180                 185                 190


Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
        195                 200                 205
```

```
Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
    210                 215                 220


Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr
225                 230                 235                 240


Lys Val Glu Ile Lys
                245


<210>  637
<211>  249
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HLA-A*01 scFv

<400>  637

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


Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
            20                  25                  30


Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45


Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
    50                  55                  60


Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80


Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95


Cys Ala His Ser Asn Met Trp Ser Tyr Ser Leu Asn Asp Tyr Tyr Phe
            100                 105                 110


Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
        115                 120                 125
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```
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Ile
    130                 135                 140

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
145                 150                 155                 160

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
                165                 170                 175

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
            180                 185                 190

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
        195                 200                 205

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
    210                 215                 220

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe
225                 230                 235                 240

Gly Gly Gly Thr Lys Val Glu Ile Lys
                245
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<210> 638
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L1

<400> 638

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Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
1               5                   10
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<210> 639
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> CDR-L1

<400> 639

Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn
1 5 10

<210> 640
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L1

<400> 640

Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser
1 5 10

<210> 641
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L1

<400> 641

Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Thr Val Asn
1 5 10

<210> 642
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L1

<400> 642

Arg Ala Ser Glu Asn Ile Tyr Ser Asn Leu Ala
1 5 10

<210> 643
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L1

<400> 643

Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala
1   5   10

<210> 644
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L1

<400> 644

Arg Ala Ser Gln Gly Ile Ser Ser Trp Leu Ala
1   5   10

<210> 645
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L2

<400> 645

Ala Ala Ser Ser Leu Gln Ser
1   5

<210> 646
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L2

<400> 646

Ser Thr Ser Asn Lys His Ser
1   5

<210> 647
<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L2

<400> 647

Glu Val Ser Lys Arg Pro Ser
1   5

<210> 648
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L2

<400> 648

Ser Asn Asn Gln Arg Pro Ser
1   5

<210> 649
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L2

<400> 649

Ala Ala Thr Tyr Leu Pro Asp
1   5

<210> 650
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L3

<400> 650

Gln Gln Ser Tyr Ser Thr Pro Leu Thr
1   5

<210> 651
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L3

<400> 651

Leu Leu Tyr Tyr Gly Gly Ala Gln Trp Val
1   5   10

<210> 652
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L3

<400> 652

Ser Ser Tyr Ala Gly Ser Asn Asn Trp Val
1   5   10

<210> 653
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L3

<400> 653

Ala Ala Trp Asp Asp Ser Leu Asn Gly Trp Val
1   5   10

<210> 654
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L3

<400> 654

Gln His Phe Trp Val Thr Pro Tyr Thr
1   5

<210> 655
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L3

<400> 655

Gln Gln Tyr Asn Ser Tyr Pro Leu Thr
1 5

<210> 656
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-L3

<400> 656

Gln Gln Ala Asn Ser Phe Pro Leu Thr
1 5

<210> 657
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H1

<400> 657

Ser Tyr Gly Ile Ser
1 5

<210> 658
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H1

<400> 658

Ser Tyr Ser Met Asn
1   5

<210> 659
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H1

<400> 659

Ser Gly Ser Tyr Tyr Trp Ser
1   5

<210> 660
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H1

<400> 660

Ser Tyr Tyr Trp Ser
1   5

<210> 661
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H1

<400> 661

Ser Tyr Trp Ile Gly
1   5

<210> 662
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H1

<400> 662

Ser Asn Tyr Met Ser
1 5

<210> 663
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H1

<400> 663

Ser Ser Ser Tyr Tyr Trp Gly
1 5

<210> 664
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H1

<400> 664

Ser Gly Gly Tyr Tyr Trp Ser
1 5

<210> 665
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H1

<400> 665

Ser Gly Tyr Ser Trp His
1 5

<210> 666
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> CDR-H1

<400> 666

Thr Ser Gly Val Gly Val Gly
1   5

<210> 667
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H1

<400> 667

Ser Tyr Trp Met His
1   5

<210> 668
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H1

<400> 668

Ser Tyr Ala Met Ser
1   5

<210> 669
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H1

<400> 669

Ser Tyr Ala Met Asn
1   5

<210> 670
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H1

<400> 670

Asp Tyr Tyr Met Ser
1   5

<210> 671
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H1

<400> 671

Ser Asn Ser Ala Ala Trp Asn
1   5

<210> 672
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H1

<400> 672

Asp Tyr Tyr Met His
1   5

<210> 673
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H1

<400> 673

Ser Ser Asn Trp Trp Gly
1   5

<210> 674
<211> 5

<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H1

<400> 674

Ser Tyr Asp Ile Asn
1 5

<210> 675
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H1

<400> 675

Ser Gly Gly Tyr Ser Trp Ser
1 5

<210> 676
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H2

<400> 676

Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu Gln
1 5 10 15

Gly

<210> 677
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H2

<400> 677

Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 678
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H2

<400> 678

Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 679
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H2

<400> 679

Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln
1 5 10 15

Gly

<210> 680
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H2

<400> 680

Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 681
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H2

<400> 681

Ser Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 682
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H2

<400> 682

Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 683
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H2

<400> 683

Tyr Ile His Phe Ser Gly Ser Thr His Tyr His Pro Ser Leu Lys Ser
1 5 10 15

<210> 684
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H2

<400> 684

Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser Leu Lys Ser
1 5 10 15

<210> 685
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H2

<400> 685

Arg Ile Asn Ser Asp Gly Ser Ser Thr Ser Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 686
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H2

<400> 686

Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 687
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H2

<400> 687

Trp Ile Asn Thr Asn Thr Gly Asn Pro Thr Tyr Ala Gln Gly Phe Thr
1 5 10 15

Gly

<210> 688
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H2

<400> 688

Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 689
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H2

<400> 689

Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala Val Ser Val
1 5 10 15

Lys Ser

<210> 690
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H2

<400> 690

Leu Val Asp Pro Glu Asp Gly Glu Thr Ile Tyr Ala Glu Lys Phe Gln
1 5 10 15

Gly

<210> 691
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H2

<400> 691

Trp Met Asn Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 692
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H2

<400> 692

Tyr Ile Tyr His Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 693
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3

<400> 693

Glu Arg Val Ser Gln Arg Gly Ala Phe Asp Ile
1 5 10

<210> 694
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> CDR-H3

<400> 694

Gly Asn Pro Asp Lys Asp Pro Phe Asp Tyr
1   5   10

<210> 695
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3

<400> 695

Asp Phe Tyr Cys Thr Asn Trp Tyr Phe Asp Leu
1   5   10

<210> 696
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3

<400> 696

Glu Ser Ser Ser Gly Ser Tyr Trp Tyr Phe Asp Leu
1   5   10

<210> 697
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3

<400> 697

Asp Ser Gly Tyr Lys Tyr Asn Leu Tyr Tyr Tyr Tyr Tyr Tyr Met Asp
1   5   10   15

Val

<210> 698
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3

<400> 698

Gly Gly Asp Leu Ser His Tyr Tyr Tyr Tyr Met Asp Val
1 5 10

<210> 699
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3

<400> 699

Glu Asn Arg Arg Tyr Asn Ser Cys Tyr Tyr Phe Asp Tyr
1 5 10

<210> 700
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3

<400> 700

Gly Gly Asp Leu Ser His Tyr Tyr Tyr Tyr Leu Asp Val
1 5 10

<210> 701
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3

<400> 701

Ala Thr Leu Leu Ser Leu Ser Tyr Asp Ala Phe Asp Ile
1 5 10

<210> 702
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3

<400> 702

Gly Gly Asp Leu Ser His Tyr Tyr Tyr Met Asp Val
1 5 10

<210> 703
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3

<400> 703

Glu Arg Asp Arg Trp Phe Asp Pro
1 5

<210> 704
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3

<400> 704

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

<210> 705
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3

<400> 705

Glu Ala Tyr Cys Leu Ser Asp Ser Tyr Trp Tyr Phe Asp Leu
1   5   10

<210> 706
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3

<400> 706

Glu Ser Trp Lys Tyr Phe Tyr Pro Arg Gly Tyr Met Asp Val
1   5   10

<210> 707
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3

<400> 707

Gly Gly Val Val Ser His Tyr Ala Met Asp Cys
1   5   10

<210> 708
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3

<400> 708

Ser Phe Asp Trp Phe Asp Pro
1   5

<210> 709
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3

<400> 709

Glu Arg Ser Ile Ser Pro Tyr Tyr Tyr Tyr Tyr Met Asp Val
1 5 10

<210> 710
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3

<400> 710

Asp Ser Val Ile Trp Tyr Trp Phe Asp Pro
1 5 10

<210> 711
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3

<400> 711

Glu Glu Ile Leu Pro Arg Leu Ser Tyr Tyr Tyr Tyr Met Asp Val
1 5 10 15

<210> 712
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3

<400> 712

Gly Gly Arg Ala His Ser Ser Trp Tyr Phe Asp Leu
1 5 10

<210> 713
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

<223> CDR-H3

<400> 713

Asp Arg Ile Lys Ile Leu Pro Arg Leu Gly Tyr Tyr Tyr Tyr Met Asp
1 5 10 15

Val

<210> 714
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3

<400> 714

Asp Thr Val Ile His Tyr Tyr Tyr Tyr Met Asp Val
1 5 10

<210> 715
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3

<400> 715

Asp Val Ile Val Glu Val Phe Leu Ser Tyr Tyr Tyr Tyr Met Asp Val
1 5 10 15

<210> 716
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3

<400> 716

Asp Ile Phe Ile His Tyr Tyr Tyr Tyr Met Asp Val
1 5 10

<210> 717
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3

<400> 717

Asp Gly Thr Phe Tyr Ser Tyr Ser Pro Tyr Tyr Phe Asp Tyr
1 5 10

<210> 718
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3

<400> 718

Glu Trp Ile Lys Ile Leu Pro Arg Leu Gly Tyr Tyr Tyr Tyr Met Asp
1 5 10 15

Val

<210> 719
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3

<400> 719

Asp Arg Ser Leu Tyr Tyr Tyr Tyr Tyr Met Asp Val
1 5 10

<210> 720
<211> 14
<212> PRT
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<220>
<223> CDR-H3

<400> 720

Asp Lys Ile Leu Ala Pro Asn Tyr Tyr Tyr Tyr Met Asp Val
1 5 10

<210> 721
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3

<400> 721

Glu Lys Ser Trp Lys Tyr Phe Tyr Tyr Tyr Tyr Tyr Tyr Met Asp Val
1 5 10 15

<210> 722
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<212> PRT
<213> Artificial Sequence

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<400> 722

Glu Asn Thr Ser Thr Ile Pro Tyr Tyr Tyr Tyr Tyr Met Asp Val
1 5 10 15

<210> 723
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3

<400> 723

Glu Asp Val Asp Lys Asn Thr Ser Thr Ile Tyr Tyr Tyr Tyr Tyr Tyr
1 5 10 15

Met Asp Val

<210> 724
<211> 17

<212> PRT
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<220>
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<400> 724

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

Leu

<210> 725
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<400> 725

Asp Leu Ile Leu Pro Pro Tyr Tyr Tyr Tyr Tyr Met Asp Val
1   5   10

<210> 726
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<400> 726

Glu Thr Trp Ile Lys Ile Leu Pro Arg Tyr Tyr Tyr Tyr Tyr Tyr Tyr
1   5   10   15

Met Asp Val

<210> 727
<211> 12
<212> PRT
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<223> CDR-H3

<400> 727

Asp Leu Ser Arg Tyr Tyr Tyr Tyr Tyr Met Asp Val
1 5 10

<210> 728
<211> 9
<212> PRT
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<220>
<223> CDR-H3

<400> 728

Glu His Ile Val Leu Cys Phe Asp Tyr
1 5

<210> 729
<211> 15
<212> PRT
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<220>
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<400> 729

Asp Lys Ile Leu Pro Arg Pro Tyr Tyr Tyr Tyr Tyr Met Asp Val
1 5 10 15

<210> 730
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<220>
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<400> 730

Gly Ser Asn Glu Tyr Phe Gln His
1 5

<210> 731
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<400> 731

Gly Thr Ser Tyr Trp Tyr Phe Asp Leu
1   5

<210> 732
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<400> 732

Glu Glu Ile Val Glu Val Phe Tyr Tyr Tyr Tyr Met Asp Val
1   5   10

<210> 733
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<400> 733

Val Asp Asp Tyr Tyr Phe Asp Tyr
1   5

<210> 734
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<400> 734

Ser Thr Asn Ile Leu Leu Ser Tyr Thr Lys Ala Phe Asp Ile
1   5   10

<210> 735
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<220>
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<400> 735

Asp Lys Thr Tyr Tyr Tyr Tyr Tyr Tyr Met Asp Val
1   5   10

<210> 736
<211> 19
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<220>
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<400> 736

Glu Lys Tyr Phe His Asp Lys Tyr Phe His Asp Tyr Tyr Tyr Tyr Tyr
1   5   10   15

Met Asp Val

<210> 737
<211> 12
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<400> 737

Asp Thr Ser Val Tyr Tyr Tyr Tyr Tyr Met Asp Val
1   5   10

<210> 738
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<220>
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<400> 738

Glu Lys Ile Leu Pro Tyr Tyr Tyr Tyr Tyr Tyr Met Asp Val
1   5   10

<210> 739
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3

<400> 739

Gln Trp Ile Tyr Ile Tyr Ile Asn Pro Arg Gly Phe Ile Phe Leu His
1   5   10   15

Asp Ala Phe Asp Ile
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<210> 740
<211> 12
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<220>
<223> CDR-H3

<400> 740

Glu Asp Val Asp Phe His His Asp Ala Phe Asp Ile
1   5   10

<210> 741
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<223> CDR-H3

<400> 741

Glu Gly Val Asp Lys Asn Thr Ser Thr Ile Tyr Tyr Tyr Tyr Tyr Tyr
1   5   10   15

Met Asp Val

<210> 742
<211> 8
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<400> 742

Asp Arg Arg Gly Tyr Phe Asp Leu
1 5

<210> 743
<211> 15
<212> PRT
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<400> 743

Gly Ile His Val Asp Ile Arg Ser Met Glu Asp Trp Phe Asp Pro
1 5 10 15

<210> 744
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<400> 744

Asp Ile Gly Thr Ser Tyr Tyr Tyr Tyr Met Asp Val
1 5 10

<210> 745
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<220>
<223> CDR-H3

<400> 745

Glu Val Val Glu Val Phe Leu Tyr Tyr Tyr Tyr Tyr Met Asp Val
1 5 10 15

<210> 746
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<220>
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<400> 746

Asp Leu Tyr Tyr Tyr Tyr Tyr Tyr Tyr Met Asp Val
1 5 10

<210> 747
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR-H3

<400> 747

Glu Ser Trp Lys Tyr Phe Tyr Pro Arg Gly Ser Ile Phe Ile His Tyr
1 5 10 15

Tyr Tyr Tyr Met Asp Val
20

<210> 748
<211> 14
<212> PRT
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<220>
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<400> 748

Asp Arg Ile Val Glu Val Phe Tyr Tyr Tyr Tyr Met Asp Val
1 5 10

<210> 749
<211> 16
<212> PRT
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<220>

<223> CDR-H3

<400> 749

Glu Lys Tyr Phe His Asp Trp Leu Tyr Tyr Tyr Tyr Tyr Met Asp Val
1   5   10   15

<210> 750
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
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<400> 750

Asp Leu Val Asp Lys Asn Thr Ser Tyr Tyr Tyr Tyr Tyr Met Asp Val
1   5   10   15

<210> 751
<211> 8
<212> PRT
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<220>
<223> CDR-H3

<400> 751

Val Gln Asn Glu Tyr Phe Gln His
1   5

<210> 752
<211> 6
<212> PRT
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<220>
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<400> 752

Ala Asn Trp Phe Asp Pro
1   5

<210> 753
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<220>
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<400> 753

Gly Gly Trp Thr Ala Trp Tyr Tyr Tyr Met Asp Val
1   5   10

<210> 754
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<220>
<223> CDR-H3

<400> 754

Ala Lys Tyr Tyr Tyr Met Asp Val
1   5

<210> 755
<211> 14
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<400> 755

Asp Gln Val Asp Lys Asn Thr Tyr Tyr Tyr Tyr Met Asp Val
1   5   10

<210> 756
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<220>
<223> CDR-H3

<400> 756

Ala Cys Gln Leu Ala Glu Tyr Phe Gln His
1   5   10

<210> 757
<211> 14

<212> PRT
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<220>
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<400> 757

Asp Arg Val Asp Lys Asn Thr Ser Tyr Tyr Tyr Met Asp Val
1   5   10

<210> 758
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<220>
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<400> 758

Arg Val Gln Leu Lys Leu Val His Trp Phe Asp Pro
1   5   10

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<220>
<223> CDR-H3

<400> 759

Tyr Tyr Asp Tyr Val Thr Val Phe Tyr Phe Gln His
1   5   10

<210> 760
<211> 11
<212> PRT
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<220>
<223> CDR-H3

<400> 760

Glu Ser Tyr Pro Ser Phe Tyr Ala Phe Asp Ile
1   5   10

<210> 761
<211> 15
<212> PRT
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<220>
<223> CDR-H3

<400> 761

Ser Asn Met Trp Ser Tyr Ser Leu Asn Asp Tyr Tyr Phe Asp Tyr
1 5 10 15

<210> 762
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> extracellular ligand binding domain VL

<400> 762

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1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly
85 90 95

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

<210> 763
<211> 118

<212> PRT
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<220>
<223> extracellular ligand binding domain VH

<400> 763

Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1   5   10   15

Ser Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20   25   30

His Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Glu Tyr Asn Glu Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80

Met His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85   90   95

Ala Arg Glu Glu Ile Thr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
            100   105   110

Ser Val Thr Val Ser Ser
        115

<210> 764
<211> 18
<212> PRT
<213> Unknown

<220>
<223> T2A self-cleaving peptide

<400> 764

Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
1   5   10   15

Gly Pro

<210> 765
<211> 19
<212> PRT
<213> Unknown

<220>
<223> P2A self-cleaving peptide

<400> 765

Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn
1 5 10 15

Pro Gly Pro

<210> 766
<211> 20
<212> PRT
<213> Unknown

<220>
<223> E2A self-cleaving peptide

<400> 766

Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly Asp Val Glu Ser
1 5 10 15

Asn Pro Gly Pro
20

<210> 767
<211> 22
<212> PRT
<213> Unknown

<220>
<223> F2A self-cleaving peptide

<400> 767

Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val
1 5 10 15

Glu Ser Asn Pro Gly Pro
20

<210> 768
<211> 63
<212> DNA
<213> Unknown

<220>
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ccc 63

<210> 769
<211> 943
<212> RNA
<213> Homo sapiens

<400> 769
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gcgcuacucu cucuuucugg ccuggaggcu auccagcgua cuccaaagau ucagguuuac 120

ucacgucauc cagcagagaa uggaaaguca aauuuccuga auugcuaugu gucuggguuu 180

cauccauccg acauugaagu ugacuuacug aagaauggag agagaauuga aaaaguggag 240

cauucagacu ugucuuucag caaggacugg ucuuucuauc ucuuguacua cacugaauuc 300

acccccacug aaaaagauga guaugccugc cgugugaacc augugacuuu gucacagccc 360

aagauaguua agugggaucg agacauguaa gcagcaucau ggagguuuga agaugccgca 420

uuuggauugg augaauucca aauucugcuu gcuugcuuuu uaauauugau augcuuauac 480

acuuacacuu uaugcacaaa auguaggguu auaauaaugu uaacauggac augaucuucu 540

uuauaauucu acuuugagug cugucuccau guuugaugua ucugagcagg uugcuccaca 600

gguagcucua ggagggcugg caacuuagag gugggggagca gagaauucuc uuauccaaca 660

ucaacaucuu ggucagauuu gaacucuuca aucucuugca cucaaagcuu guuaagauag 720

uuaagcgugc auaaguuaac uuccaauuua cauacucugc uuagaauuug ggggaaaauu 780

uagaaauaua auugacagga uuauuggaaa uuuguuauaa ugaaugaaac auuuugucau 840

auaagauuca uauuuacuuc uuauacauuu gauaaaguaa ggcaugguug ugguuaaucu 900

gguuuauuuu uguuccacaa guuaaauaaa ucauaaaacu uga 943

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<211> 6654
<212> DNA
<213> Homo sapiens

<400> 770
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gcgtgagtct ctcctaccct cccgctctgg tccttcctct cccgctctgc accctctgtg 180

gccctcgctg tgctctctcg ctccgtgact tcccttctcc aagttctcct tggtggcccg 240

ccgtggggct agtccagggc tggatctcgg ggaagcggcg gggtggcctg ggagtgggga 300

agggggtgcg cacccgggac gcgcgctact tgccccctttc ggcggggagc aggggagacc 360

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tcctagcacc tctgggtcta tgtggggcca caccgtgggg aggaaacagc acgcgacgtt 720

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aaatcttatt ttgaaaattt ccaaagtaat acatgccatg catagaccat ttctggaaga 1920

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tttcttttct ccctctccca acctatgtag ggtccttctt cctggatact cacgacgcgg 180

acccagttct cactcccatt gggtgtcggg tttccagaga agccaatcag tgtcgtcgcg 240

gtcgcggttc taaagtccgc acgcacccac cgggactcag attctcccca gacgccgagg 300

atggccgtca tggcgccccg aaccctcgtc ctgctactct cgggggctct ggccctgacc 360

cagacctggg cgggctctca ctccatgagg tatttcttca catccgtgtc ccggcccggc 420

cgcggggagc cccgcttcat cgcagtgggc tacgtggacg acacgcagtt cgtgcggttc 480

gacagcgacg ccgcgagcca gaggatggag ccgcgggcgc cgtggataga gcaggagggt 540

ccggagtatt gggacgggga gacacggaaa gtgaaggccc actcacagac tcaccgagtg 600

gacctgggga ccctgcgcgg ctactacaac cagagcgagg ccggttctca caccgtccag 660

aggatgtatg gctgcgacgt ggggtcggac tggcgcttcc tccgcgggta ccaccagtac 720

gcctacgacg gcaaggatta catcgccctg aaagaggacc tgcgctcttg gaccgcggcg 780

gacatggcag ctcagaccac caagcacaag tgggaggcgg cccatgtggc ggagcagttg 840

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cttccttccc tattaaaa 1698

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gggcccgcct ggcgggggcg caggacccgg gaagccgcgc cgggaggagg gtcgggcggg 180

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gaggcccagg cgcctttacc cggtttcatt ttcagtttag gccaaaaatc cccccaggtt 660

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gatggggtaa ggagggagac gggggtgtca tgtcttttag ggaaagcagg agcctctctg 1920

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gtgcactgag ctgtaacttc ttccttccct attaaaa 3217

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ggcaccgagt cggtgctttt ttt 83

<210> 774
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<223> Guide Nucleic Acid Targeting Sequence

<400> 774
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<220>
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cagatacctg gagaacggga 20

<210> 776
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<220>
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tcccgttctc caggtatctg 20

<210> 777
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<220>
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ccgccgcggt ccaagagcgc 20

<210> 778
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<220>
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cctgcgctct tggaccgcgg 20

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ggacctgcgc tcttggaccg c 21

<210> 780
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<210> 781
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<210> 785
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ggatggagcc gcgggcgccg tgg 23

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gcgccgtgga tagagcagga ggg 23

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ctggttgtag tagccgcgca ggg 23

<210> 794
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<210> 795
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<220>
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<210> 798
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<210> 799
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<210> 801
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<400> 802
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<210> 806
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<210> 809
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<220>
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<400> 809
ccagtacgcc tacgacggca agg 23

<210> 810
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<400> 810
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<210> 811
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<400> 811
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<210> 812
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<210> 813
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<400> 813
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<210> 814
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<400> 814
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<210> 815
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<210> 816
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<400> 816
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<210> 817
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<220>
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<400> 817
tcagaccacc aagcacaagt ggg 23

<210> 818
<211> 23
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caccaagcac aagtgggagg cgg 23

<210> 819
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<223> Guide Nucleic Acid Targeting Sequence

<400> 819
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<210> 820
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<220>
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<400> 820
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<210> 821
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<210> 822
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<210> 823
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<210> 824
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<210> 825
<211> 23
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<210> 826
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<220>
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cggggagaca cggaaagtga agg 23

<210> 827
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agtattggga cggggagaca cgg 23

<210> 828
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<220>

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agggtccgga gtattgggac ggg 23

<210> 829
<211> 23
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<210> 830
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<210> 831
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<220>
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<210> 832
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<210> 833
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<220>
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<400> 833
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<210> 834
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<210> 835
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<210> 836
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<400> 836
ccactcggtg agtctgtgag tgg 23

<210> 837
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<400> 837
tcggactggc gcttcctccg cgg 23

<210> 838
<211> 23
<212> DNA
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<223> Guide Nucleic Acid Targeting Sequence

<400> 838
gcagccatac atcctctgga cgg 23

<210> 839
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<400> 1224
gccaatcagt gtcgtcgcg 19

<210> 1225
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<212> DNA
<213> Artificial Sequence

<220>
<223> target HLA sequence complement

<400> 1225
gaggacctgc gctcttgga 19

<210> 1226
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> target HLA sequence complement

<400> 1226
gtgtgagaca gctgccttg 19

<210> 1227
<211> 19
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<220>
<223> target HLA sequence complement

<400> 1227
ggcacctgca tgtgtctgt 19

<210> 1228
<211> 19
<212> DNA
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<220>
<223> target HLA sequence complement

<400> 1228
tcatctttcc tgttccaga 19

<210> 1229
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> target HLA sequence complement

<400> 1229
aggcacctgc atgtgtctg 19

<210> 1230
<211> 19
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<220>
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<400> 1230
agaggacctg cgctcttgg 19

<210> 1231
<211> 19
<212> DNA
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<220>
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<400> 1231
acgcatatga ctcaccacg 19

<210> 1232
<211> 2
<212> RNA
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<220>
<223> 5' Flank Sequence

<400> 1232
gg 2

<210> 1233
<211> 23
<212> RNA
<213> Artificial Sequence

<220>

<223> 5' Flank Sequence

<400> 1233
acaccauguu gccagucucu agg 23

<210> 1234
<211> 23
<212> RNA
<213> Artificial Sequence

<220>
<223> 5' Flank Sequence

<400> 1234
ugauagcaau gucagcagug ccu 23

<210> 1235
<211> 23
<212> RNA
<213> Artificial Sequence

<220>
<223> 5' Flank Sequence

<400> 1235
uauugcuguu gacagugagc gac 23

<210> 1236
<211> 21
<212> RNA
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<220>
<223> 3' Flank Sequence

<400> 1236
uggcgucugg cccaaccaca c 21

<210> 1237
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> 3' Flank Sequence

<400> 1237
guaagguuga ccauacucua c 21

<210> 1238
<211> 4
<212> RNA
<213> Artificial Sequence

<220>
<223> Loop Region Sequence

<400> 1238
cgaa 4

<210> 1239
<211> 7
<212> RNA
<213> Artificial Sequence

<220>
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<400> 1239
uucaaga 7

<210> 1240
<211> 7
<212> RNA
<213> Artificial Sequence

<220>
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<400> 1240
auauuca 7

<210> 1241
<211> 9
<212> RNA
<213> Artificial Sequence

<220>
<223> Loop Region Sequence

<400> 1241
ugugcuguc 9

<210> 1242
<211> 6
<212> RNA
<213> Artificial Sequence

<220>

<223> Loop Region Sequence

<400> 1242
cucgag 6

<210> 1243
<211> 12
<212> RNA
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<220>
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<400> 1243
cuuccuguca ga 12

<210> 1244
<211> 15
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<220>
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<400> 1244
cuucccuuug ucaga 15

<210> 1245
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<220>
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<400> 1245
guguuauucu ug 12

<210> 1246
<211> 12
<212> RNA
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<220>
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<400> 1246
gugucuuaau ug 12

<210> 1247
<211> 12
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<220>
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<400> 1247
guguuagucu ug 12

<210> 1248
<211> 7
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<220>
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<400> 1248
ucaagag 7

<210> 1249
<211> 12
<212> RNA
<213> Artificial Sequence

<220>
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<400> 1249
ggacauccag gg 12

<210> 1250
<211> 15
<212> RNA
<213> Artificial Sequence

<220>
<223> Loop Region Sequence

<400> 1250
gugaagccac agaug 15

<210> 1251
<211> 10
<212> RNA
<213> Artificial Sequence

<220>

<223> Loop Region Sequence

<400> 1251
gauucuaaaa 10

<210> 1252
<211> 1443
<212> DNA
<213> Artificial Sequence

<220>
<223> PA2.1.14 (VL:VH) scFv LIR1 sHTICD

<400> 1252
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atcacttgta gatccagtca gagtattgta cacagtaatg ggaacaccta tttggaatgg 120

tatcagcaga aaccaggtaa agccccaaaa ttgctcatct acaaagtctc taacagattt 180

agtggtgtac cagccaggtt cagcggttcc ggaagtggta ctgaattcac cctcacgatc 240

tcctctctcc agccagatga tttcgccact tattactgtt ttcaaggttc acatgtgccg 300

cgcacattcg gtcagggtac taaagtagaa gtcaaaggcg gaggtggaag cggaggggga 360

ggatctggcg gcggaggaag cggaggccag gtgcagctgg tgcagtctgg ggctgaggtg 420

aagaagcctg ggtcctcagt gaaggtttcc tgcaaggctt ctggatacac cttcactagc 480

tatcatatac attgggtgcg ccaggccccc ggacaagggc ttgagtggat cggatggatc 540

taccctggca atgttaacac agaatataat gagaagttca agggcaaagc caccattacc 600

gcggacgaat ccacgaacac agcctacatg gagctgagca gcctgagatc tgaagacacg 660

gctgtgtatt actgtgcgag ggaggaaatt acctacgcta tggactactg gggccaggga 720

accctggtca ccgtgtcctc agtggtctca ggaccgtctg ggggccccag ctccccgaca 780

acaggcccca cctccacatc tggccctgag gaccagcccc tcacccccac cgggtcggat 840

ccccagagtg gtctgggaag gcacctgggg gttgtgatcg gcatcttggt ggccgtcatc 900

ctactgctcc tcctcctcct cctcctcttc ctcatcctcc gacatcgacg tcagggcaaa 960

cactggacat cgacccagag aaaggctgat ttccaacatc ctgcaggggc tgtggggcca 1020

gagcccacag acagaggcct gcagtggagg tccagcccag ctgccgatgc ccaggaagaa 1080

aacctctatg ctgccgtgaa gcacacacag cctgaggatg gggtggagat ggacactcgg 1140

agcccacacg atgaagaccc ccaggcagtg acgtatgccg aggtgaaaca ctccagacct 1200

aggagagaaa tggcctctcc tccttcccca ctgtctgggg aattcctgga cacaaaggac 1260

agacaggcgg aagaggacag gcagatggac actgaggctg ctgcatctga agccccccag 1320

gatgtgacct acgcccagct gcacagcttg accctcagac gggaggcaac tgagcctcct 1380

ccatcccagg aagggccctc tccagctgtg cccagcatct acgccactct ggccatccac 1440

tag 1443

<210> 1253
<211> 1503
<212> DNA
<213> Artificial Sequence

<220>
<223> PA2.1.14 (VL:VH) scFv LIR1 HTICD

<400> 1253
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atcacttgta gatccagtca gagtattgta cacagtaatg ggaacaccta tttggaatgg 120

tatcagcaga aaccaggtaa agccccaaaa ttgctcatct acaaagtctc taacagattt 180

agtggtgtac cagccaggtt cagcggttcc ggaagtggta ctgaattcac cctcacgatc 240

tcctctctcc agccagatga tttcgccact tattactgtt ttcaaggttc acatgtgccg 300

cgcacattcg gtcagggtac taaagtagaa gtcaaaggcg gaggtggaag cggaggggga 360

ggatctggcg gcggaggaag cggaggccag gtgcagctgg tgcagtctgg ggctgaggtg 420

aagaagcctg ggtcctcagt gaaggtttcc tgcaaggctt ctggatacac cttcactagc 480

tatcatatac attgggtgcg ccaggccccc ggacaagggc ttgagtggat cggatggatc 540

taccctggca atgttaacac agaatataat gagaagttca agggcaaagc caccattacc 600

gcggacgaat ccacgaacac agcctacatg gagctgagca gcctgagatc tgaagacacg 660

gctgtgtatt actgtgcgag ggaggaaatt acctacgcta tggactactg gggccaggga 720

accctggtca ccgtgtcctc atacggctca cagagctcca aaccctacct gctgactcac 780

cccagtgacc ccctggagct cgtggtctca ggaccgtctg ggggccccag ctccccgaca 840

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aggagagaaa tggcctctcc tccttcccca ctgtctgggg aattcctgga cacaaaggac 1320

agacaggcgg aagaggacag gcagatggac actgaggctg ctgcatctga agccccccag 1380

gatgtgacct acgcccagct gcacagcttg accctcagac gggaggcaac tgagcctcct 1440

ccatcccagg aagggccctc tccagctgtg cccagcatct acgccactct ggccatccac 1500

tag 1503

<210> 1254
<211> 1386
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN_SsI CD8_HT 41BB CD3z

<400> 1254
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tcatgcaaag cctcaggcta ctcctttact ggatacacga tgaattgggt gaaacagtcg 120

catggaaagt cactggaatg gatcggtctg attacgccct acaacggcgc ctccagctac 180

aaccagaagt tcaggggaaa ggcgaccctt actgtcgaca agtcgtcaag caccgcctac 240

atggacctcc tgtccctgac ctccgaagat agcgcggtct acttttgtgc acgcggaggt 300

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ggcggaggga gcggaggagg aggcagcgga ggtggagggt cggatatcga actcactcag 420

tccccagcaa tcatgtccgc ttcaccggga gaaaaggtga ccatgacttg ctcggcctcc 480

tcgtccgtgt catacatgca ctggtaccaa caaaaatcgg ggacctcccc taagagatgg 540

atctacgata ccagcaaact ggcttcaggc gtgccgggac gcttctcggg ttcggggagc 600

ggaaattcgt attcgttgac catttcgtcc gtggaagccg aggacgacgc aacttattac 660

tgccaacagt ggtcaggcta cccgctcact ttcggagccg gcactaagct ggagatcacc 720

actaccccag caccgaggcc acccaccccg gctcctacca tcgcctccca gcctctgtcc 780

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tatagcgaga ttggtatgaa aggggaacgc agaagaggca aaggccacga cggactgtac 1320

cagggactca gcaccgccac caaggacacc tatgacgctc ttcacatgca ggccctgccg 1380

cctcgg 1386

<210> 1255
<211> 1443
<212> DNA
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<220>
<223> PA2.1.14 scFv LIR1 sHTICD

<400> 1255
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cccggacaag ggcttgagtg gatcggatgg atctaccctg gcaatgttaa cacagaatat 180

aatgagaagt tcaagggcaa agccaccatt accgcggacg aatccacgaa cacagcctac 240

atggagctga gcagcctgag atctgaagac acggctgtgt attactgtgc gagggaggaa 300

attacctacg ctatggacta ctggggccag ggaaccctgg tcaccgtgtc ctcaggcgga 360

ggtggaagcg gaggggggagg atctggcggc ggaggaagcg gaggcgacat tcaaatgacc 420

cagagcccat ccaccctgag cgcatctgta ggtgaccggg tcaccatcac ttgtagatcc 480

agtcagagta ttgtacacag taatgggaac acctatttgg aatggtatca gcagaaacca 540

ggtaaagccc caaaattgct catctacaaa gtctctaaca gatttagtgg tgtaccagcc 600

aggttcagcg gttccggaag tggtactgaa ttcaccctca cgatctcctc tctccagcca 660

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tag 1443