SEQUENCE LISTING

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<120> Deimmunized Serum-Binding Domains and their Use for Extending Serum Half-Life

<130> 1301.0007P9I

<150> US 61/488,725
<151> 2011-05-21

<160> 329

<170> PatentIn version 3.5

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Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
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Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro Arg Cys
1 5 10 15

Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
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Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu
35 40 45

Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg
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Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser
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Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
1 5 10 15

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
100 105 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
115 120 125

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
130 135 140

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145 150 155 160

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
165 170 175

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
180 185 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
195 200 205

Lys Ser Leu Ser Leu Ser Pro Gly Lys
210 215

<210> 6
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```
Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
1               5                  10                  15

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
            20                  25                  30

Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
        35                  40                  45

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
    50                  55                  60

Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln
65                  70                  75                  80

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
                85                  90                  95

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro
            100                 105                 110

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
        115                 120                 125

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
    130                 135                 140

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
145                 150                 155                 160

Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
                165                 170                 175

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
            180                 185                 190

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
        195                 200                 205

Ser Leu Ser Leu Ser Pro Gly Lys
    210                 215
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<210> 7
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<400> 7

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            20                  25                  30
```

```
Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr
        35                  40                  45

Val Asp Gly Val Gln Val His Asn Ala Lys Thr Lys Pro Arg Glu Gln
    50                  55                  60

Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His
65                  70                  75                  80

Gln Asn Trp Leu Asp Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                85                  90                  95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
            100                 105                 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
        115                 120                 125

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    130                 135                 140

Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
145                 150                 155                 160

Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
                165                 170                 175

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
            180                 185                 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
        195                 200                 205

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    210                 215
```

<210> 8
<211> 217
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<213> homo sapiens

<400> 8

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            20                  25                  30

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
        35                  40                  45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    50                  55                  60

Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65                  70                  75                  80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                85                  90                  95
```

```
Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            100                 105                 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
        115                 120                 125

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    130                 135                 140

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145                 150                 155                 160

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                165                 170                 175

Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val
            180                 185                 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        195                 200                 205

Lys Ser Leu Ser Leu Ser Leu Gly Lys
    210                 215
```

<210> 9
<211> 237
<212> PRT
<213> homo sapiens

<400> 9

```
Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1               5                   10                  15

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

Ile His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45

Lys Glu Val Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala
65                  70                  75                  80

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Thr Trp Pro Phe
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Ser Gly
            100                 105                 110

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

Pro Thr Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu
    130                 135                 140
```

```
Ser Thr Ser Gly Met Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys
145                 150                 155                 160

Ala Leu Glu Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Arg Tyr
                165                 170                 175

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

Asn Gln Val Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala
        195                 200                 205

Thr Tyr Tyr Cys Ala Gln Ile Asn Pro Ala Trp Phe Ala Tyr Trp Gly
    210                 215                 220

Gln Gly Thr Leu Val Thr Val Ser Ser Leu Gly Gly Cys
225                 230                 235
```

<210> 10
<211> 8
<212> PRT
<213> homo sapiens

<400> 10

```
Gly Gly Gly Ser Gly Gly Gly Gly
1               5
```

<210> 11
<211> 244
<212> PRT
<213> homo sapiens

<400> 11

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

Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Phe Asp
            20                  25                  30

Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45

Lys Leu Leu Ile Tyr Thr Thr Ser Asn Leu Glu Ser Gly Val Pro Asp
    50                  55                  60

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

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

Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly
            100                 105                 110

Gly Gly Ser Gly Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala
        115                 120                 125
```

```
Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    130                 135                 140

Gly Tyr Thr Phe Thr Asn Tyr Trp Ile His Trp Val Arg Gln Ala Pro
145                 150                 155                 160

Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Asp Pro Ser Asp Thr Tyr
                165                 170                 175

Pro Asn Tyr Asn Lys Lys Phe Lys Gly Arg Val Thr Met Thr Val Val
            180                 185                 190

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

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asn Gly Asp Ser Asp Tyr Tyr
    210                 215                 220

Ser Gly Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
225                 230                 235                 240

Leu Gly Gly Cys
```

<210> 12
<211> 240
<212> PRT
<213> homo sapiens

<400> 12

```
Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1               5                   10                  15

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

Ile His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45

Lys Glu Val Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala
65                  70                  75                  80

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Thr Trp Pro Phe
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Ser Gly
            100                 105                 110

Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
        115                 120                 125

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
    130                 135                 140

Thr Asn Tyr Trp Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
145                 150                 155                 160
```

```
Glu Trp Ile Gly Val Ile Asp Pro Ser Asp Thr Tyr Pro Asn Tyr Asn
                165                 170                 175

Lys Lys Phe Lys Gly Arg Val Thr Met Thr Val Val Val Ser Thr Ser
            180                 185                 190

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

Tyr Tyr Cys Ala Arg Asn Gly Asp Ser Asp Tyr Tyr Ser Gly Met Asp
    210                 215                 220

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Leu Gly Gly Cys
225                 230                 235                 240
```

<210> 13
<211> 241
<212> PRT
<213> homo sapiens

<400> 13

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

Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Phe Asp
            20                  25                  30

Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45

Lys Leu Leu Ile Tyr Thr Thr Ser Asn Leu Glu Ser Gly Val Pro Asp
    50                  55                  60

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

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

Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly
            100                 105                 110

Gly Gly Ser Gly Gly Gly Gly Gln Val Thr Leu Arg Glu Ser Gly Pro
        115                 120                 125

Ala Leu Val Lys Pro Thr Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser
    130                 135                 140

Gly Phe Ser Leu Ser Thr Ser Gly Met Gly Val Gly Trp Ile Arg Gln
145                 150                 155                 160

Pro Pro Gly Lys Ala Leu Glu Trp Leu Ala His Ile Trp Trp Asp Asp
                165                 170                 175

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

```
Asp Thr Ser Lys Asn Gln Val Val Leu Thr Met Thr Asn Met Asp Pro
        195                 200                 205

Val Asp Thr Ala Thr Tyr Tyr Cys Ala Gln Ile Asn Pro Ala Trp Phe
    210                 215                 220

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

Cys
```

<210> 14
<211> 470
<212> PRT
<213> homo sapiens

<400> 14

```
Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1               5                   10                  15

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

Ile His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45

Lys Glu Val Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala
65                  70                  75                  80

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Thr Trp Pro Phe
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Ser Gly
            100                 105                 110

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

Pro Thr Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu
    130                 135                 140

Ser Thr Ser Gly Met Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys
145                 150                 155                 160

Ala Leu Glu Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Arg Tyr
                165                 170                 175

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

Asn Gln Val Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala
        195                 200                 205

Thr Tyr Tyr Cys Ala Gln Ile Asn Pro Ala Trp Phe Ala Tyr Trp Gly
    210                 215                 220
```

```
Gln Gly Thr Leu Val Thr Val Ser Ser Leu Gly Gly Cys Val Glu Pro
225                 230                 235                 240

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
    290                 295                 300

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
            340                 345                 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
        355                 360                 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
    370                 375                 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            420                 425                 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    450                 455                 460

Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 15
<211> 477
<212> PRT
<213> homo sapiens

<400> 15

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

Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Phe Asp
20 25 30

Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Thr Thr Ser Asn Leu Glu Ser Gly Val Pro Asp
50 55 60

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

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

Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

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

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
130 135 140

Gly Tyr Thr Phe Thr Asn Tyr Trp Ile His Trp Val Arg Gln Ala Pro
145 150 155 160

Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Asp Pro Ser Asp Thr Tyr
165 170 175

Pro Asn Tyr Asn Lys Lys Phe Lys Gly Arg Val Thr Met Thr Val Val
180 185 190

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

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asn Gly Asp Ser Asp Tyr Tyr
210 215 220

Ser Gly Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
225 230 235 240

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

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
260 265 270

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
275 280 285

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
290 295 300

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
305 310 315 320

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
325 330 335

```
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
            340                 345                 350

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
        355                 360                 365

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
    370                 375                 380

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385                 390                 395                 400

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
                405                 410                 415

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
            420                 425                 430

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
        435                 440                 445

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
    450                 455                 460

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470                 475
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<210> 16
<211> 243
<212> PRT
<213> homo sapiens

<400> 16

```
Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1               5                   10                  15

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

Ile His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45

Lys Glu Val Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala
65                  70                  75                  80

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Thr Trp Pro Phe
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Ser Gly
            100                 105                 110

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

Pro Thr Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu
    130                 135                 140
```

```
Ser Thr Ser Gly Met Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys
145                 150                 155                 160

Ala Leu Glu Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Arg Tyr
                165                 170                 175

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

Asn Gln Val Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala
        195                 200                 205

Thr Tyr Tyr Cys Ala Gln Ile Asn Pro Ala Trp Phe Ala Tyr Trp Gly
    210                 215                 220

Gln Gly Thr Leu Val Thr Val Ser Ser Leu Gly Gly Cys Phe Asn Arg
225                 230                 235                 240

Gly Glu Cys
```

<210> 17
<211> 10
<212> PRT
<213> artificial

<220>
<223> linker plus C-terminus of human IgG-kappa chain

<400> 17

```
Leu Gly Gly Cys Phe Asn Arg Gly Glu Cys
1               5                   10
```

<210> 18
<211> 477
<212> PRT
<213> homo sapiens

<400> 18

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

Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Phe Asp
            20                  25                  30

Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45

Lys Leu Leu Ile Tyr Thr Thr Ser Asn Leu Glu Ser Gly Val Pro Asp
    50                  55                  60

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

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Ser Asn
                85                  90                  95
```

```
Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly
            100                 105                 110

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

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    130                 135                 140

Gly Tyr Thr Phe Thr Asn Tyr Trp Ile His Trp Val Arg Gln Ala Pro
145                 150                 155                 160

Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Asp Pro Ser Asp Thr Tyr
                165                 170                 175

Pro Asn Tyr Asn Lys Lys Phe Lys Gly Arg Val Thr Met Thr Val Val
            180                 185                 190

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

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asn Gly Asp Ser Asp Tyr Tyr
    210                 215                 220

Ser Gly Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
225                 230                 235                 240

Leu Gly Gly Cys Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
                245                 250                 255

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
            260                 265                 270

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
        275                 280                 285

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
    290                 295                 300

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
305                 310                 315                 320

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
                325                 330                 335

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
            340                 345                 350

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
        355                 360                 365

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
    370                 375                 380

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385                 390                 395                 400

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
                405                 410                 415
```

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
420 425 430

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
435 440 445

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
450 455 460

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 19
<211> 485
<212> PRT
<213> homo sapiens

<400> 19

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Ser Gly Gly Gly
225 230 235 240

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

Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Phe
260 265 270

Asp Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro
275 280 285

Pro Lys Leu Leu Ile Tyr Thr Thr Ser Asn Leu Glu Ser Gly Val Pro
290 295 300

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
305 310 315 320

Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Ser
325 330 335

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

Gly Gly Gly Ser Gly Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly
355 360 365

Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala
370 375 380

Ser Gly Tyr Thr Phe Thr Asn Tyr Trp Ile His Trp Val Arg Gln Ala
385 390 395 400

Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Asp Pro Ser Asp Thr
405 410 415

Tyr Pro Asn Tyr Asn Lys Lys Phe Lys Gly Arg Val Thr Met Thr Val
420 425 430

Val Val Ser Thr Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser
435 440 445

Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asn Gly Asp Ser Asp Tyr
450 455 460

Tyr Ser Gly Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
465 470 475 480

Ser Leu Gly Gly Cys
485

<210> 20
<211> 469
<212> PRT
<213> homo sapiens

<400> 20

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            20                  25                  30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        35                  40                  45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    50                  55                  60

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65                  70                  75                  80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                85                  90                  95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            100                 105                 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        115                 120                 125

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    130                 135                 140

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145                 150                 155                 160

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                165                 170                 175

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            180                 185                 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        195                 200                 205

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Ser Gly Gly Gly
    210                 215                 220

Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu
225                 230                 235                 240

Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Phe
                245                 250                 255

Asp Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro
            260                 265                 270

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

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
    290                 295                 300

Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Ser
305                 310                 315                 320
```

```
Asn Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
                325                 330                 335

Gly Gly Gly Ser Gly Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly
            340                 345                 350

Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala
        355                 360                 365

Ser Gly Tyr Thr Phe Thr Asn Tyr Trp Ile His Trp Val Arg Gln Ala
    370                 375                 380

Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Asp Pro Ser Asp Thr
385                 390                 395                 400

Tyr Pro Asn Tyr Asn Lys Lys Phe Lys Gly Arg Val Thr Met Thr Val
                405                 410                 415

Val Val Ser Thr Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser
            420                 425                 430

Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asn Gly Asp Ser Asp Tyr
        435                 440                 445

Tyr Ser Gly Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
    450                 455                 460

Ser Leu Gly Gly Cys
465
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<210> 21
<211> 466
<212> PRT
<213> homo sapiens

<400> 21

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Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1               5                   10                  15

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

Ile His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45

Lys Glu Val Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala
65                  70                  75                  80

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Thr Trp Pro Phe
                85                  90                  95

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Ser Gly
            100                 105                 110

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

```
Pro Thr Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu
    130                 135                 140

Ser Thr Ser Gly Met Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys
145                 150                 155                 160

Ala Leu Glu Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Arg Tyr
                165                 170                 175

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

Asn Gln Val Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala
        195                 200                 205

Thr Tyr Tyr Cys Ala Gln Ile Asn Pro Ala Trp Phe Ala Tyr Trp Gly
    210                 215                 220

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

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
                245                 250                 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            260                 265                 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
        275                 280                 285

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
    290                 295                 300

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
305                 310                 315                 320

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
                325                 330                 335

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
            340                 345                 350

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
        355                 360                 365

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
    370                 375                 380

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
385                 390                 395                 400

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
                405                 410                 415

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
            420                 425                 430

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
        435                 440                 445
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Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
450 455 460

Gly Lys
465

<210> 22
<211> 246
<212> PRT
<213> homo sapiens

<400> 22

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

Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Phe Asp
20 25 30

Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Thr Thr Ser Asn Leu Glu Ser Gly Val Pro Asp
50 55 60

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

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

Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

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

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
130 135 140

Gly Tyr Thr Phe Thr Asn Tyr Trp Ile His Trp Val Arg Gln Ala Pro
145 150 155 160

Gly Gln Cys Leu Glu Trp Ile Gly Val Ile Asp Pro Ser Asp Thr Tyr
165 170 175

Pro Asn Tyr Asn Lys Lys Phe Lys Gly Arg Val Thr Met Thr Val Val
180 185 190

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

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asn Gly Asp Ser Asp Tyr Tyr
210 215 220

Ser Gly Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
225 230 235 240

Phe Asn Arg Gly Glu Cys
245

<210> 23
<211> 6
<212> PRT
<213> homo sapiens

<400> 23

Phe Asn Arg Gly Glu Cys
1 5

<210> 24
<211> 5
<212> PRT
<213> artificial

<220>
<223> 2B6 heavy chain variable region CDR1

<400> 24

Asn Tyr Trp Ile His
1 5

<210> 25
<211> 5
<212> PRT
<213> artificial

<220>
<223> 3H7 Heavy chain variable region CDR1

<400> 25

Asp Ala Trp Met Asp
1 5

<210> 26
<211> 17
<212> PRT
<213> artificial

<220>
<223> 2B6 Heavy chain variable region CDR2

<400> 26

Val Ile Asp Pro Ser Asp Thr Tyr Pro Asn Tyr Asn Lys Lys Phe Lys
1 5 10 15

Gly

<210> 27
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> 3H7 Heavy chain variable region CDR2

<400> 27

Glu Ile Arg Asn Lys Ala Asn Asn Leu Ala Thr Tyr Tyr Ala Glu Ser
1 5 10 15

Val Lys Gly

<210> 28
<211> 12
<212> PRT
<213> artificial

<220>
<223> 2B6 Heavy chain variable region CDR3

<400> 28

Asn Gly Asp Ser Asp Tyr Tyr Ser Gly Met Asp Tyr
1 5 10

<210> 29
<211> 6
<212> PRT
<213> artificial

<220>
<223> 3H7 heavy chain variable region CDR3

<400> 29

Tyr Ser Pro Phe Ala Tyr
1 5

<210> 30
<211> 11
<212> PRT
<213> artificial

<220>
<223> 2B6 Light chain variable region CDR1

<400> 30

Arg Thr Ser Gln Ser Ile Gly Thr Asn Ile His
1 5 10

<210> 31
<211> 11
<212> PRT
<213> artificial

<220>
<223> 3H7 light chain variable region CDR1

<400> 31

Arg Ala Ser Gln Glu Ile Ser Gly Tyr Leu Ser
1 5 10

<210> 32
<211> 7
<212> PRT
<213> artificial

<220>
<223> 2B6 light chain variable region CDR2

<400> 32

Asn Val Ser Glu Ser Ile Ser
1 5

<210> 33
<211> 7
<212> PRT
<213> artificial

<220>
<223> 2B6 light chain variable region CDR2

<400> 33

Tyr Val Ser Glu Ser Ile Ser
1 5

<210> 34
<211> 7
<212> PRT
<213> artificial

<220>
<223> 2B6 light chain variable region CDR2

<400> 34

Tyr Ala Ser Glu Ser Ile Ser
1 5

<210> 35
<211> 7
<212> PRT
<213> artificial

<220>
<223> 3H7 light chain variable region CDR2

<400> 35

Ala Ala Ser Thr Leu Asp Ser
1 5

<210> 36
<211> 9
<212> PRT
<213> artificial

<220>
<223> 2B6 Light chain variable region CDR3

<400> 36

Gln Gln Ser Asn Thr Trp Pro Phe Thr
1 5

<210> 37
<211> 9
<212> PRT
<213> artificial

<220>
<223> 3H7 light chain variable region CDR3

<400> 37

Leu Gln Tyr Val Ser Tyr Pro Tyr Thr
1 5

<210> 38
<211> 121
<212> PRT
<213> artificial

<220>
<223> 2B6 heavy chain variable region

<400> 38

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 Asn Tyr
20 25 30

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

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

Lys 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 Asn Gly Asp Ser Asp Tyr Tyr Ser Gly Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 39
<211> 107
<212> PRT
<213> artificial

<220>
<223> 2B6 light chain variable region Hu2B6VL-1

<400> 39

Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1 5 10 15

Glu Lys Val Thr Ile Thr Cys Arg Thr Ser Gln Ser Ile Gly Thr Asn
20 25 30

Ile His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala
65 70 75 80

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Thr Trp Pro Phe
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 40
<211> 107
<212> PRT
<213> artificial

<220>
<223> Humanized 2B6 light chain variable region Hu2B6VL-2

<400> 40

Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1 5 10 15

Glu Lys Val Thr Ile Thr Cys Arg Thr Ser Gln Ser Ile Gly Thr Asn
20 25 30

Ile His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala
65 70 75 80

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Thr Trp Pro Phe
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 41
<211> 107
<212> PRT

<213> artificial

<220>
<223> Humanized 2B6 light chain variable region Hu2B6VL-3

<400> 41

Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1 5 10 15

Glu Lys Val Thr Ile Thr Cys Arg Thr Ser Gln Ser Ile Gly Thr Asn
20 25 30

Ile His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala
65 70 75 80

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Thr Trp Pro Phe
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 42
<211> 107
<212> PRT
<213> Mus sp.

<400> 42

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

Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Glu Ile Ser Gly Tyr
20 25 30

Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly Thr Ile Arg Arg Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly
50 55 60

Ser Trp Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
65 70 75 80

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

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 43
<211> 9
<212> PRT
<213> artificial

<220>
<223> IgG binding site of FcgammaRIIB receptor

<400> 43

Lys Lys Phe Ser Arg Ser Asp Pro Asn
1 5

<210> 44
<211> 9
<212> PRT
<213> artificial

<220>
<223> IgG binding site of FcgammaRIIB receptor

<400> 44

Gln Lys Phe Ser Arg Leu Asp Pro Asn
1 5

<210> 45
<211> 9
<212> PRT
<213> artificial

<220>
<223> IgG binding site of FcgammaRIIB receptor

<400> 45

Gln Lys Phe Ser Arg Leu Asp Pro Thr
1 5

<210> 46
<211> 9
<212> PRT
<213> artificial

<220>
<223> IgG binding site of FcgammaRIIB receptor

<400> 46

Lys Lys Phe Ser Arg Leu Asp Pro Thr
1 5

<210> 47
<211> 9
<212> PRT
<213> artificial

<220>
<223> IgG binding site of FcgammaRIIB receptor

<400> 47

Gln Lys Phe Ser His Leu Asp Pro Thr
1 5

<210> 48
<211> 9
<212> PRT
<213> artificial

<220>
<223> IgG binding site of FcgammaRIIB receptor

<400> 48

Lys Lys Phe Ser His Leu Asp Pro Thr
1 5

<210> 49
<211> 9
<212> PRT
<213> artificial

<220>
<223> IgG binding site of FcgammaRIIB receptor

<400> 49

Gln Lys Phe Ser Arg Leu Asp Pro Asn
1 5

<210> 50
<211> 9
<212> PRT
<213> artificial

<220>
<223> IgG binding site for FcgammaRIIB receptor

<400> 50

Lys Lys Phe Ser Arg Ser Asp Pro Asn
1 5

<210> 51
<211> 9
<212> PRT
<213> artificial

<220>
<223> IgG binding site of FcgammaRIIB receptor

<400> 51

Gln Lys Phe Ser Arg Leu Asp Pro Thr
1 5

<210> 52
<211> 9
<212> PRT
<213> artificial

<220>
<223> IgG binding site of FcgammaRIIB receptor

<400> 52

Gln Lys Phe Ser His Leu Asp Pro Thr
1 5

<210> 53
<211> 9
<212> PRT
<213> artificial

<220>
<223> IgG binding site of FcgammaRIIB receptor

<400> 53

Lys Lys Phe Ser Arg Leu Asp Pro Thr
1 5

<210> 54
<211> 9
<212> PRT
<213> artificial

<220>
<223> IgG binding site of FcgammaRIIB receptor

<400> 54

Lys Lys Phe Ser His Leu Asp Pro Thr
1 5

<210> 55
<211> 36
<212> DNA
<213> artificial

<220>
<223> Primer Lgh321F

<400> 55
cgagctagct ctagatgaga tcacagttct ctctac 36

<210> 56
<211> 47
<212> DNA
<213> artificial

<220>
<223> Primer Lgh318R

<400> 56
gcctccgcct ccggatccgc ctcctttgat ctccaccttg gtccctc 47

<210> 57
<211> 47
<212> DNA
<213> artificial

<220>

<223> Primer Lgh319F

<400> 57
ggaggcggat ccggaggcgg aggccaggtt cagctggtgc agtctgg 47

<210> 58
<211> 43
<212> DNA
<213> artificial

<220>
<223> Primer Lgh320R

<400> 58
tttgaattct agcagcctcc cagtgaggag acggtgaccg tgg 43

<210> 59
<211> 46
<212> DNA
<213> artificial

<220>
<223> Primer Lgh315R

<400> 59
gcctccgcct ccggatccgc ctcctttgat ctcaagcttg gtcccc 46

<210> 60
<211> 48
<212> DNA
<213> artificial

<220>
<223> Primer Lgh316F

<400> 60
ggaggcggat ccggaggcgg aggccaggtt accctgagag agtctggc 48

<210> 61
<211> 47
<212> DNA
<213> artificial

<220>
<223> Primer Lgh317R

<400> 61
tttgaattcc tagcagcctc ccagtgagct cacagtgacc agagtcc 47

<210> 62
<211> 27
<212> DNA
<213> artificial

<220>
<223> Primer Lgh339R

<400> 62
ctcaacgcag cctcccagtg agctcac 27

<210> 63
<211> 31
<212> DNA
<213> artificial

<220>
<223> Primer Lgh340R

<400> 63
aacgcagcct cccagtgagg agacggtgac c 31

<210> 64
<211> 27
<212> DNA
<213> artificial

<220>
<223> Primer Lgh366R

<400> 64
tttgaattct atttacccgg agacagg 27

<210> 65
<211> 33
<212> DNA
<213> artificial

<220>
<223> Primer Lhg367F

<400> 65
ctgggaggct gcgcagagcc caaatcttgt gac 33

<210> 66
<211> 33
<212> DNA
<213> artificial

<220>
<223> Primer Lgh368R

<400> 66
gtcacaagat ttgggctctg cgcagcctcc cag 33

<210> 67
<211> 50
<212> DNA
<213> artificial

<220>
<223> Primer Lgh369R

<400> 67
tttgaattct aacactctcc cctgttgaag cagcctccca gtgaggagac 50

<210> 68
<211> 118
<212> PRT
<213> artificial

<220>
<223> humanized anti-CD16A Heavy Chain Variable Region Hu3G8VH-1

<400> 68

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

Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ala
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser 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 Arg Ile Asn Pro Ala Trp Phe Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 69
<211> 118
<212> PRT
<213> artificial

<220>
<223> Humanized anti-CD16A heavy chain variable region Hu3G8VH-5

<400> 69

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

Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ala
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser 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 Gln Ile Asn Pro Ala Trp Phe Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 70
<211> 117
<212> PRT
<213> artificial

<220>
<223> Humanized anti-CD16A heavy chain variable region Hu3G8VH-22

<400> 70

Gln Val Thr Leu Arg Glu Ser Gly Pro Ala 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 His Ile Trp Trp Asp Asp Asp Lys Arg Tyr Ser Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser 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 Arg Ile Asn Pro Ala Tyr Phe Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser
115

<210> 71
<211> 111
<212> PRT
<213> artificial

<220>
<223> Humanized anti-CD16A light chain variable region Hu3G8VL-1

<400> 71

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

Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Phe Asp
20 25 30

Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Thr Thr Ser Asn Leu Glu Ser Gly Val Pro Asp
50 55 60

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

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

Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
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<210> 72
<211> 111
<212> PRT
<213> artificial

<220>
<223> Humanized anti-CD16A light chain variable region Hu3G8VL-43

<400> 72

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Asp Phe Asp
            20                  25                  30

Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45

Lys Leu Leu Ile Tyr Thr Thr Ser Ser Leu Glu Ser Gly Val Pro Asp
    50                  55                  60

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

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

Ser Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
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<210> 73
<211> 111
<212> PRT
<213> artificial

<220>
<223> Humanized anti-CD16A light chain variable region Hu3G8VL-22

<400> 73

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Asp Phe Asp
            20                  25                  30

Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45
```

Lys Leu Leu Ile Tyr Thr Thr Ser Asn Leu Glu Thr Gly Val Pro Asp
50 55 60

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

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

Ser Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 74
<211> 24
<212> DNA
<213> DNA sequence of SEQ ID NO:10

<400> 74
ggaggcggat ccggaggcgg aggc 24

<210> 75
<211> 18
<212> DNA
<213> homo sapiens

<400> 75
ttcaacaggg gagagtgt 18

<210> 76
<211> 30
<212> DNA
<213> artificial

<220>
<223> Linker plus C-terminus of human IgG kappa chain

<400> 76
ctgggaggct gcttcaacag gggagagtgt 30

<210> 77
<211> 6
<212> PRT
<213> homo sapiens

<400> 77

Val Glu Pro Lys Ser Cys
1 5

<210> 78
<211> 18
<212> DNA
<213> homo sapiens

<400> 78
gttgagccca aatcttgt 18

<210> 79
<211> 118
<212> PRT

<213> homo sapiens

<400> 79

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

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

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

Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ala
    50                  55                  60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Ser Asn Gln Val
65                  70                  75                  80

Phe Leu Lys Ile Ala Ser Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala Gln Ile Asn Pro Ala Trp Phe Ala Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser
        115
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<210> 80
<211> 354
<212> DNA
<213> homo sapiens

<400> 80

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caggttaccc tgaaagagtc tggccctggg atattgcagc cctcccagac cctcagtctg     60

acttgttctt tctctgggtt ttcactgagg acttctggta tgggtgtagg ctggattcgt    120

cagccttcag ggaagggtct agagtggctg gcacacattt ggtgggatga tgacaagcgc    180

tataatccag ccctgaagag ccgactgaca atctccaagg atacctccag caaccaggta    240

ttcctcaaaa tcgccagtgt ggacactgca gatactgcca catactactg tgctcaaata    300

aaccccgcct ggtttgctta ctggggccaa gggactctgg tcactgtgag ctca          354
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<210> 81
<211> 354
<212> DNA
<213> homo sapiens

<400> 81

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caggttaccc tgagagagtc tggccctgcg ctggtgaagc ccacacagac cctcacactg     60

acttgtacct tctctgggtt ttcactgagc acttctggta tgggtgtagg ctggattcgt    120

cagcctcccg ggaaggctct agagtggctg gcacacattt ggtgggatga tgacaagcgc    180

tataatccag ccctgaagag ccgactgaca atctccaagg atacctccaa aaaccaggta    240
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gtcctcacaa tgaccaacat ggaccctgtg gatactgcca catactactg tgctcaaata 300

aaccccgcct ggtttgctta ctggggccaa gggactctgg tcactgtgag ctca 354

<210> 82
<211> 111
<212> PRT
<213> homo sapiens

<400> 82

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

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Phe Asp
20 25 30

Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

Arg Phe Ser Ala Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

Pro Val Glu Glu Glu Asp Thr Ala Thr Tyr Tyr Cys Gln Gln Ser Asn
85 90 95

Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 83
<211> 333
<212> DNA
<213> homo sapiens

<400> 83
gacactgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 60

atctcctgca aggccagcca aagtgttgat tttgatggtg atagttttat gaactggtac 120

caacagaaac caggacagcc acccaaactc ctcatctata ctacatccaa tctagaatct 180

gggatcccag ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 240

cctgtggagg aggaggatac tgcaacctat tactgtcagc aaagtaatga ggatccgtac 300

acgttcggag gggggaccaa gctggaaata aaa 333

<210> 84
<211> 332
<212> DNA
<213> artificial

<220>
<223> Humanized anti-CD16A light chain variable region Hu3G8VL-1

<400> 84
gacatcgtga tgacccaatc tccagactct ttggctgtgt ctctagggga gagggccacc 60

atcaactgca aggccagcca aagtgttgat tttgatggtg atagttttat gaactggtac 120

caacagaaac caggacagcc acccaaactc ctcatctata ctacatccaa tctagaatct 180

ggggtcccag acaggtttag tggcagtggg tctgggacag acttcaccct caccatcagc 240

agcctgcagg ctgaggatgt ggcagtttat tactgtcagc aaagtaatga ggatccgtac 300

acgttcggac aggggaccaa gcttgagatc aa 332

<210> 85
<211> 121
<212> PRT
<213> artificial

<220>
<223> Humanized 2B6 heavy chain variable region

<400> 85

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 Asn Tyr
20 25 30

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

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

Lys Gly Arg Val Thr Met Thr Val Val Val 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 Asn Gly Asp Ser Asp Tyr Tyr Ser Gly Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 86
<211> 363
<212> DNA
<213> artificial

<220>
<223> humanized 2B6 heavy chain variable region

<400> 86
caggttcagc tggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggtta cacctttacc aactactgga tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gattggagtg attgatcctt ctgatactta tccaaattac 180

aataaaaagt tcaagggcag agtcaccatg accgtagtcg tatccacgag cacagcctac 240

atggagctga ggagcctgag atctgacgac acggccgtgt attactgtgc gagaaacggt 300

gattccgatt attactctgg tatggactac tgggggcaag ggaccacggt caccgtctcc 360

tca 363

<210> 87
<211> 111
<212> PRT
<213> artificial

<220>
<223> Humanized 2B6 light chain variable region

<400> 87

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

Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Phe Asp
20 25 30

Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Thr Thr Ser Asn Leu Glu Ser Gly Val Pro Asp
50 55 60

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

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

Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 88
<211> 321
<212> DNA
<213> artificial

<220>
<223> humanized 2B6 light chain variable region

<400> 88
gaaattgtgc tgactcagtc tccagacttt cagtctgtga ctccaaagga gaaagtcacc 60

ttcacctgca ggaccagtca gagcattggc acaaacatac actggtacca gcagaaacca 120

gatcagtctc caaagctcct catcaaggag gtttctgagt ctatctctgg agtcccatcg 180

aggttcagtg gcagtggatc tgggacagat ttcaccctca ccatcaatag cctggaagct 240

gaagatgctg caacgtatta ctgtcaacaa agtaatacct ggccgttcac gttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> 89
<211> 6
<212> PRT
<213> artificial

<220>
<223> thrombin cleavage recognition site

<400> 89

Leu Val Pro Arg Gly Ser
1 5

<210> 90
<211> 4
<212> PRT
<213> artificial

<220>
<223> Factor Xa cleavage recognition site

<220>
<221> VARIANT
<222> (2)..(2)
<223> Xaa=Glu or Asp

<400> 90

Ile Xaa Gly Arg
1

<210> 91
<211> 5
<212> PRT
<213> artificial

<220>
<223> enterokinase cleavage recognition site

<400> 91

Asp Asp Asp Asp Lys
1 5

<210> 92
<211> 4
<212> PRT
<213> artificial

<220>
<223> furin cleavage recognition site

<220>
<221> VARIANT
<222> (2)..(3)
<223> Xaa=any amino acid

<400> 92

Arg Xaa Xaa Arg

1

<210> 93
<211> 4
<212> PRT
<213> artificial

<220>
<223> preferred furin cleavage recognition site

<220>
<221> VARIANT
<222> (2)..(2)
<223> Xaa=any amino acid

<220>
<221> VARIANT
<222> (3)..(3)
<223> Xaa=Lys or Arg

<400> 93

Arg Xaa Xaa Arg
1

<210> 94
<211> 7
<212> PRT
<213> artificial

<220>
<223> AcTEV cleavage recognition site

<400> 94

Gln Asn Leu Tyr Phe Gln Gly
1 5

<210> 95
<211> 487
<212> PRT
<213> artificial

<220>
<223> covalent diabody polyprotein precursor

<400> 95

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

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Phe Asp
20 25 30

Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

Arg Phe Ser Ala Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

Pro Val Glu Glu Glu Asp Thr Ala Thr Tyr Tyr Cys Gln Gln Ser Asn
85 90 95

Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

Gly Gly Ser Gly Gly Gly Gly Glu Val Glu Leu Val Glu Ser Gly Gly
115 120 125

Gly Leu Val Gln Pro Gly Arg Ser Leu Lys Leu Ser Cys Ala Ala Ser
130 135 140

Gly Phe Thr Phe Ser Asp Tyr Tyr Met Ala Trp Val Arg Gln Ala Pro
145 150 155 160

Thr Thr Gly Leu Glu Trp Val Ala Ser Ile Ser Tyr Asp Gly Gly Asp
165 170 175

Thr His Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
180 185 190

Asn Ala Lys Ser Ser Leu Tyr Leu Gln Met Asp Ser Leu Arg Ser Glu
195 200 205

Asp Thr Ala Thr Tyr Tyr Cys Ala Thr Glu Thr Thr Gly Ile Pro Thr
210 215 220

Gly Val Met Asp Ala Trp Gly Gln Gly Val Ser Val Thr Val Ser Ser
225 230 235 240

Leu Gly Gly Cys Gly Gly Arg Ala Lys Arg Asp Val Gln Met Thr Gln
245 250 255

Ser Pro Ser Asn Leu Ala Ala Ser Pro Gly Glu Ser Val Ser Ile Asn
260 265 270

Cys Lys Ala Ser Glu Ser Ile Ser Lys Tyr Leu Ala Trp Tyr Leu Gln
275 280 285

Lys Pro Gly Lys Ala Asn Lys Leu Leu Met Tyr Asp Gly Ser Thr Leu
290 295 300

Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
305 310 315 320

Phe Thr Leu Thr Ile Arg Ser Leu Glu Pro Glu Asp Phe Gly Leu Tyr
325 330 335

Tyr Cys Gln Gln His Tyr Glu Tyr Pro Ala Thr Phe Gly Ser Gly Thr
340 345 350

Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly Gly Gly Gly Gln Val Thr
355 360 365

Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln Pro Ser Gln Thr Leu Ser
370 375 380

```
Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Arg Thr Ser Gly Met Gly
385                 390                 395                 400

Val Gly Trp Ile Arg Gln Pro Ser Gly Lys Gly Leu Glu Trp Leu Ala
                405                 410                 415

His Ile Trp Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ala Leu Lys Ser
            420                 425                 430

Arg Leu Thr Ile Ser Lys Asp Thr Ser Ser Asn Gln Val Phe Leu Lys
        435                 440                 445

Ile Ala Ser Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr Cys Ala Gln
    450                 455                 460

Ile Asn Pro Ala Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
465                 470                 475                 480

Val Ser Ser Leu Gly Gly Cys
                485
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<210> 96
<211> 1464
<212> DNA
<213> artificial

<220>
<223> DNA sequence of SEQ ID NO:97 (covalent diabody polyprotein precursor)

<400> 96

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gacactgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc     60

atctcctgca aggccagcca aagtgttgat tttgatggtg atagttttat gaactggtac    120

caacagaaac caggacagcc acccaaactc ctcatctata ctacatccaa tctagaatct    180

gggatcccag ccaggtttag tgccagtggg tctgggacag acttcaccct caacatccat    240

cctgtggagg aggaggatac tgcaacctat tactgtcagc aaagtaatga ggatccgtac    300

acgttcggag gggggaccaa gctggaaata aaaggaggcg gatccggagg cggaggcgag    360

gtggagctag tggagtctgg gggaggctta gtgcagcctg gaaggtccct gaaactctcg    420

tgtgcagcct caggattcac tttcagtgac tattacatgg cctgggtccg gcaggctcca    480

acgacgggtc tggagtgggt cgcatccatt agttatgatg gtggtgacac tcactatcga    540

gactccgtga agggccgatt tactatttcc agagataatg caaaaagcag cctatacctg    600

caaatggaca gtctgaggtc tgaggacacg gccacttatt actgtgcaac agagactacg    660

ggaataccta caggtgttat ggatgcctgg ggtcaaggag tttcagtcac tgtctcctca    720

ctgggaggct gcggcgggag agctaagagg gatgtccaga tgacccagtc tccatctaat    780

cttgctgcct ctcctggaga aagtgtttcc atcaattgca aggcaagtga gagcattagc    840

aagtatttag cctggtatct acagaaacct gggaaagcaa ataagcttct tatgtacgat    900
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gggtcaactt tgcaatctgg aattccatcg aggttcagtg gcagtggatc tggtacagat 960

ttcactctca ccatcagaag cctggagcct gaagattttg gactctatta ctgtcaacag 1020

cattatgaat atccagccac gttcggttct gggaccaagc tggagatcaa aggaggcgga 1080

tccggaggcg gaggccaggt taccctgaaa gagtctggcc ctgggatatt gcagccctcc 1140

cagaccctca gtctgacttg ttctttctct gggttttcac tgaggacttc tggtatgggt 1200

gtaggctgga ttcgtcagcc ttcagggaag ggtctagagt ggctggcaca catttggtgg 1260

gatgatgaca agcgctataa tccagccctg aagagccgac tgacaatctc caaggatacc 1320

tccagcaacc aggtattcct caaaatcgcc agtgtggaca ctgcagatac tgccacatac 1380

tactgtgctc aaataaaccc cgcctggttt gcttactggg gccaagggac tctggtcact 1440

gtgagctcac tgggaggctg ctag 1464

<210> 97
<211> 511
<212> PRT
<213> artificial

<220>
<223> covalent diabody polyprotein precursor

<400> 97

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

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Phe Asp
20 25 30

Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

Arg Phe Ser Ala Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

Pro Val Glu Glu Glu Asp Thr Ala Thr Tyr Tyr Cys Gln Gln Ser Asn
85 90 95

Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

Gly Gly Ser Gly Gly Gly Gly Glu Val Glu Leu Val Glu Ser Gly Gly
115 120 125

Gly Leu Val Gln Pro Gly Arg Ser Leu Lys Leu Ser Cys Ala Ala Ser
130 135 140

Gly Phe Thr Phe Ser Asp Tyr Tyr Met Ala Trp Val Arg Gln Ala Pro
145 150 155 160

Thr Thr Gly Leu Glu Trp Val Ala Ser Ile Ser Tyr Asp Gly Gly Asp
165 170 175

Thr His Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
180 185 190

Asn Ala Lys Ser Ser Leu Tyr Leu Gln Met Asp Ser Leu Arg Ser Glu
195 200 205

Asp Thr Ala Thr Tyr Tyr Cys Ala Thr Glu Thr Thr Gly Ile Pro Thr
210 215 220

Gly Val Met Asp Ala Trp Gly Gln Gly Val Ser Val Thr Val Ser Ser
225 230 235 240

Leu Gly Gly Cys Gly Gly Arg Ala Lys Arg Ala Pro Val Lys Gln Thr
245 250 255

Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro
260 265 270

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

Pro Gly Glu Ser Val Ser Ile Asn Cys Lys Ala Ser Glu Ser Ile Ser
290 295 300

Lys Tyr Leu Ala Trp Tyr Leu Gln Lys Pro Gly Lys Ala Asn Lys Leu
305 310 315 320

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

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Arg Ser Leu
340 345 350

Glu Pro Glu Asp Phe Gly Leu Tyr Tyr Cys Gln Gln His Tyr Glu Tyr
355 360 365

Pro Ala Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly
370 375 380

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

Leu Gln Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe
405 410 415

Ser Leu Arg Thr Ser Gly Met Gly Val Gly Trp Ile Arg Gln Pro Ser
420 425 430

Gly Lys Gly Leu Glu Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys
435 440 445

Arg Tyr Asn Pro Ala Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr
450 455 460

Ser Ser Asn Gln Val Phe Leu Lys Ile Ala Ser Val Asp Thr Ala Asp
465 470 475 480

Thr Ala Thr Tyr Tyr Cys Ala Gln Ile Asn Pro Ala Trp Phe Ala Tyr
485 490 495

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Leu Gly Gly Cys
500 505 510

<210> 98
<211> 1536
<212> DNA
<213> artificial

<220>
<223> DNA sequence of SEQ ID NO:99 (covalent diabody polyprotein precursor)

<400> 98
gacactgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 60

atctcctgca aggccagcca aagtgttgat tttgatggtg atagttttat gaactggtac 120

caacagaaac caggacagcc acccaaactc ctcatctata ctacatccaa tctagaatct 180

gggatcccag ccaggtttag tgccagtggg tctgggacag acttcaccct caacatccat 240

cctgtggagg aggaggatac tgcaacctat tactgtcagc aaagtaatga ggatccgtac 300

acgttcggag gggggaccaa gctggaaata aaaggaggcg gatccggagg cggaggcgag 360

gtggagctag tggagtctgg gggaggctta gtgcagcctg gaaggtccct gaaactctcg 420

tgtgcagcct caggattcac tttcagtgac tattacatgg cctgggtccg gcaggctcca 480

acgacgggtc tggagtgggt cgcatccatt agttatgatg gtggtgacac tcactatcga 540

gactccgtga agggccgatt tactatttcc agagataatg caaaaagcag cctatacctg 600

caaatggaca gtctgaggtc tgaggacacg gccacttatt actgtgcaac agagactacg 660

ggaataccta caggtgttat ggatgcctgg ggtcaaggag tttcagtcac tgtctcctca 720

ctgggaggct gcggcgggag agctaagagg gcccctgtga agcagaccct gaacttcgac 780

ctgctgaagc tggccggaga cgtggagagc aaccccggcc ccgatgtcca gatgacccag 840

tctccatcta atcttgctgc ctctcctgga gaaagtgttt ccatcaattg caaggcaagt 900

gagagcatta gcaagtattt agcctggtat ctacagaaac ctgggaaagc aaataagctt 960

cttatgtacg atgggtcaac tttgcaatct ggaattccat cgaggttcag tggcagtgga 1020

tctggtacag atttcactct caccatcaga agcctggagc ctgaagattt tggactctat 1080

tactgtcaac agcattatga atatccagcc acgttcggtt ctgggaccaa gctggagatc 1140

aaaggaggcg gatccggagg cggaggccag gttaccctga aagagtctgg ccctgggata 1200

ttgcagccct cccagaccct cagtctgact tgttctttct ctgggttttc actgaggact 1260

tctggtatgg gtgtaggctg gattcgtcag ccttcaggga agggtctaga gtggctggca 1320

cacatttggt gggatgatga caagcgctat aatccagccc tgaagagccg actgacaatc 1380

tccaaggata cctccagcaa ccaggtattc ctcaaaatcg ccagtgtgga cactgcagat 1440

actgccacat actactgtgc tcaaataaac cccgcctggt ttgcttactg gggccaaggg 1500

actctggtca ctgtgagctc actgggaggc tgctag 1536

<210> 99
<211> 239
<212> PRT
<213> homo sapiens

<400> 99

Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1 5 10 15

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

Ile His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
35 40 45

Lys Glu Val Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala
65 70 75 80

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Thr Trp Pro Phe
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Ser Gly
100 105 110

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

Pro Thr Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu
130 135 140

Ser Thr Ser Gly Met Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys
145 150 155 160

Ala Leu Glu Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Arg Tyr
165 170 175

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

Asn Gln Val Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala
195 200 205

Thr Tyr Tyr Cys Ala Gln Ile Asn Pro Ala Trp Phe Ala Tyr Trp Gly
210 215 220

Gln Gly Thr Leu Val Thr Val Ser Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 100
<211> 720
<212> DNA
<213> homo sapiens

<400> 100
gaaattgtgc tgactcagtc tccagacttt cagtctgtga ctccaaagga gaaagtcacc 60

ttcacctgca ggaccagtca gagcattggc acaaacatac actggtacca gcagaaacca 120

gatcagtctc caaagctcct catcaaggag gtttctgagt ctatctctgg agtcccatcg 180

aggttcagtg gcagtggatc tgggacagat ttcaccctca ccatcaatag cctggaagct 240

gaagatgctg caacgtatta ctgtcaacaa agtaatacct ggccgttcac gttcggcgga 300

gggaccaagg tggagatcaa aggaggcgga tccggaggcg gaggccaggt taccctgaga 360

gagtctggcc ctgcgctggt gaagcccaca cagaccctca cactgacttg taccttctct 420

gggttttcac tgagcacttc tggtatgggt gtaggctgga ttcgtcagcc tcccgggaag 480

gctctagagt ggctggcaca catttggtgg gatgatgaca agcgctataa tccagccctg 540

aagagccgac tgacaatctc caaggatacc tccaaaaacc aggtagtcct cacaatgacc 600

aacatggacc ctgtggatac tgccacatac tactgtgctc aaataaaccc cgcctggttt 660

gcttactggg gccaagggac tctggtcact gtgagctcat tcaacagggg agagtgttag 720

<210> 101
<211> 246
<212> PRT
<213> Homo sapiens

<400> 101

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

Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Phe Asp
20 25 30

Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Thr Thr Ser Asn Leu Glu Ser Gly Val Pro Asp
50 55 60

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

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

Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

Gly Gly Ser Gly Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala

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Gly Tyr Thr Phe Thr Asn Tyr Trp Ile His Trp Val Arg Gln Ala Pro
145                 150                 155                 160

Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Asp Pro Ser Asp Thr Tyr
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Pro Asn Tyr Asn Lys Lys Phe Lys Gly Arg Val Thr Met Thr Val Val
            180                 185                 190

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

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asn Gly Asp Ser Asp Tyr Tyr
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<400> 179

Lys Ser Ser Ser Asp Gly Asp Ser Phe Met Asn
1 5 10

<210> 180
<211> 11
<212> PRT

<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR1

<400> 180

Lys Ala Ser Ser Asp Gly Asp Ser Tyr Met Asn
1 5 10

<210> 181
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR1

<400> 181

Lys Ala Ser Ser Asp Gly Asp Ser Phe Leu Asn
1 5 10

<210> 182
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR1

<400> 182

Lys Ala Ser Ser Asp Gly Asp Ser Phe Met Ala
1 5 10

<210> 183
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR1

<400> 183

Lys Ala Ser Ser Asp Gly Asp Ser Tyr Leu Ala
1 5 10

<210> 184
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR1

<400> 184

Lys Ala Ser Val Asp Gly Asp Ser Phe Met Asn
1 5 10

<210> 185
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR1

<400> 185

Arg Ala Ser Val Asp Gly Asp Ser Phe Met Asn
1 5 10

<210> 186
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR1

<400> 186

Lys Ser Ser Val Asp Gly Asp Ser Phe Met Asn
1 5 10

<210> 187
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR1

<400> 187

Lys Ala Ser Val Asp Gly Asp Ser Tyr Met Asn
1 5 10

<210> 188
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR1

<400> 188

Lys Ala Ser Val Asp Gly Asp Ser Phe Leu Asn
1 5 10

<210> 189
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR1

<400> 189

Lys Ala Ser Val Asp Gly Asp Ser Phe Met Ala
1 5 10

<210> 190
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR1

<400> 190

Lys Ala Ser Val Asp Gly Asp Ser Tyr Leu Ala
1 5 10

<210> 191
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR1

<400> 191

Lys Ala Ser Asp Asp Gly Asp Ser Phe Met Asn
1 5 10

<210> 192
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR1

<400> 192

Arg Ala Ser Asp Asp Gly Asp Ser Phe Met Asn
1 5 10

<210> 193
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR1

<400> 193

Lys Ser Ser Asp Asp Gly Asp Ser Phe Met Asn
1 5 10

<210> 194
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR1

<400> 194

Lys Ala Ser Asp Asp Gly Asp Ser Tyr Met Asn
1 5 10

<210> 195
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR1

<400> 195

Lys Ala Ser Asp Asp Gly Asp Ser Phe Leu Asn
1 5 10

<210> 196
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR1

<400> 196

Lys Ala Ser Asp Asp Gly Asp Ser Phe Met Ala
1 5 10

<210> 197
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR1

<400> 197

Lys Ala Ser Asp Asp Gly Asp Ser Tyr Leu Ala
1 5 10

<210> 198
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR1

<400> 198

Lys Ala Ser Phe Asp Gly Asp Ser Phe Met Asn
1 5 10

<210> 199
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR1

<400> 199

Arg Ala Ser Phe Asp Gly Asp Ser Phe Met Asn
1 5 10

<210> 200
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR1

<400> 200

Lys Ser Ser Phe Asp Gly Asp Ser Phe Met Asn
1 5 10

<210> 201
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR1

<400> 201

Lys Ala Ser Phe Asp Gly Asp Ser Tyr Met Asn
1 5 10

<210> 202
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR1

<400> 202

Lys Ala Ser Phe Asp Gly Asp Ser Phe Leu Asn
1 5 10

<210> 203
<211> 11
<212> PRT

<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR1

<400> 203

Lys Ala Ser Phe Asp Gly Asp Ser Phe Met Ala
1 5 10

<210> 204
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR1

<400> 204

Lys Ala Ser Phe Asp Gly Asp Ser Tyr Leu Ala
1 5 10

<210> 205
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* FR2

<400> 205

Trp Tyr Gln Gln Lys Ala Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
1 5 10 15

<210> 206
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR2

<400> 206

Thr Thr Ser Asn Leu Glu Ser
1 5

<210> 207
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR2

<400> 207

Asp Ala Ser Asn Leu Glu Ser
1 5

<210> 208
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR2

<400> 208

Trp Ala Ser Asn Leu Glu Ser
1 5

<210> 209
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR2

<400> 209

Thr Thr Ser Asn Leu Glu Thr
1 5

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

<220>
<223> VL Sequences Derived from 3G8 VL* CDR2

<400> 210

Asp Ala Ser Asn Leu Glu Thr
1 5

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

<220>
<223> VL Sequences Derived from 3G8 VL* CDR2

<400> 211

Asp Ala Ser Asn Leu Ala Thr
1 5

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

<220>
<223> VL Sequences Derived from 3G8 VL* CDR2

<400> 212

Ser Ala Ser Asn Leu Gln Ser
1 5

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

<220>
<223> VL Sequences Derived from 3G8 VL* CDR2

<400> 213

Ser Thr Ser Asn Leu Glu Ser
1 5

<210> 214
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR2

<400> 214

Ser Thr Ser Asn Leu Gln Ser
1 5

<210> 215
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR2

<400> 215

Thr Thr Ser Asn Leu Gln Ser
1 5

<210> 216
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR2

<400> 216

Thr Thr Ser Ser Leu Gln Ser
1 5

<210> 217
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* FR3

<400> 217

Gly Ile Pro Ala Arg Phe Ser Ala Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Asn Ile His Pro Val Glu Glu Glu Asp Thr Ala Thr Tyr Tyr Cys
20 25 30

<210> 218
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* FR3

<400> 218

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
20 25 30

<210> 219
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR3

<400> 219

Gln Gln Ser Asn Glu Asp Pro Tyr Thr
1 5

<210> 220
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR3

<400> 220

Gln Gln Ser Tyr Ser Thr Pro Tyr Thr
1 5

<210> 221
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR3

<400> 221

Gln Gln Ser Tyr Glu Asp Pro Tyr Thr
1 5

<210> 222
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR3

<400> 222

Gln Gln Ser Asn Ser Asp Pro Tyr Thr
1 5

<210> 223
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* CDR3

<400> 223

Gln Gln Ser Asn Glu Thr Pro Tyr Thr
1 5

<210> 224
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* FR4

<400> 224

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
1 5 10

<210> 225
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Sequences Derived from 3G8 VL* FR4

<400> 225

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
1 5 10

<210> 226
<211> 714
<212> DNA
<213> Artificial Sequence

<220>
<223> H3G8VL-CB3.1VH

<400> 226
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atcaactgca aggccagcca aagtgttgat tttgatggtg atagttttat gaactggtac 120

caacagaaac caggacagcc acccaaactc ctcatctata ctacatccaa tctagaatct 180

ggggtcccag acaggtttag tggcagtggg tctgggacag acttcaccct caccatcagc 240

agcctgcagg ctgaggatgt ggcagtttat tactgtcagc aaagtaatga ggatccgtac 300

acgttcggac aggggaccaa gcttgagatc aaaggaggcg gatccggagg cggaggccag 360

gtccaactgc agcagcctgg ggctgagctg gtgaggcctg gggcttcagt gaagctgtcc 420

tgcaaggctt ctggctacac cttcaccagc tactggatga actgggtgaa gcagaggcct 480

ggacaaggcc ttgaatggat tggtatggtt gatccttcag acagtgaaac tcactacaat 540

caaatgttca aggacaaggc cacattgact gttgacaaat cctccagcac agcctacatg 600

cagctcagca gcctgacatc tgaggactct gcggtctatt actgtgcaag agctatgggc 660

tactggggtc aaggaacctc agtcaccgtc tcctcagttg agcccaaatc ttgt 714

<210> 227
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> H3G8VL-CB3.1VH

<400> 227

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

Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Phe Asp
20 25 30

Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Thr Thr Ser Asn Leu Glu Ser Gly Val Pro Asp
50 55 60

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

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

Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

Gly Gly Ser Gly Gly Gly Gly Gln Val Gln Leu Gln Gln Pro Gly Ala
115 120 125

Glu Leu Val Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser
130 135 140

Gly Tyr Thr Phe Thr Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro
145 150 155 160

Gly Gln Gly Leu Glu Trp Ile Gly Met Val Asp Pro Ser Asp Ser Glu
165 170 175

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

Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu
195 200 205

Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ala Met Gly Tyr Trp Gly Gln
210 215 220

Gly Thr Ser Val Thr Val Ser Ser Val Glu Pro Lys Ser Cys
225 230 235

<210> 228
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> CB3.1VL-h3G8VH

<400> 228
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atctcttgta agtcaagtca gagcctctta gatactgatg gaaagacata tttgaattgg 120

ttgttacaga ggccaggcca gtctccaaac cgcctaatct atctggtgtc taaactggac 180

tctggagtcc ctgacaggtt cactggcagt ggatcaggga cagatttcac actgaaaatc 240

agcagagtgg aggctgagga tttgggaatt tattattgct ggcaaggtac acattttccg 300

ctcacgttcg gtgctgggac caagctggag ctgaaaggag gcggatccgg aggcggaggc 360

caggttaccc tgagagagtc tggccctgcg ctggtgaagc ccacacagac cctcacactg 420

acttgtacct tctctgggtt ttcactgagc acttctggta tgggtgtagg ctggattcgt 480

cagcctcccg ggaaggctct agagtggctg gcacacattt ggtgggatga tgacaagcgc 540

tataatccag ccctgaagag ccgactgaca atctccaagg atacctccaa aaaccaggta 600

gtcctcacaa tgaccaacat ggaccctgtg gatactgcca catactactg tgctcaaata 660

aaccccgcct ggtttgctta ctggggccaa gggactctgg tcactgtgag ctcattcaac 720

aggggagagt gt 732

<210> 229
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> CB3.1VL-h3G8VH

<400> 229

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Thr
20 25 30

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

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

Asp Arg Phe Thr 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 Ile Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Phe Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105 110

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

Pro Ala Leu Val Lys Pro Thr Gln Thr Leu Thr Leu Thr Cys Thr Phe
130 135 140

Ser Gly Phe Ser Leu Ser Thr Ser Gly Met Gly Val Gly Trp Ile Arg
145 150 155 160

Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu Ala His Ile Trp Trp Asp
165 170 175

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

Lys Asp Thr Ser Lys Asn Gln Val Val Leu Thr Met Thr Asn Met Asp
195 200 205

Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala Gln Ile Asn Pro Ala Trp
210 215 220

Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Phe Asn
225 230 235 240

Arg Gly Glu Cys

<210> 230
<211> 702
<212> DNA
<213> Artificial Sequence

<220>
<223> 8B5-CB3.1-VEPKSC

<400> 230
gacattcaga tgacacagtc tccatcctcc ctacttgcgg cgctgggaga aagagtcagt 60

ctcacttgtc gggcaagtca ggaaattagt ggttacttaa gctggcttca gcagaaacca 120

gatggaacta ttaaacgcct gatctacgcc gcatccactt tagattctgg tgtcccaaaa 180

aggttcagtg gcagtgagtc tgggtcagat tattctctca ccatcagcag tcttgagtct 240

gaagattttg cagactatta ctgtctacaa tattttagtt atccgctcac gttcggtgct 300

gggaccaagc tggagctgaa aggaggcgga tccggaggcg gaggccaggt ccaactgcag 360

cagcctgggg ctgagctggt gaggcctggg gcttcagtga agctgtcctg caaggcttct 420

ggctacacct tcaccagcta ctggatgaac tgggtgaagc agaggcctgg acaaggcctt 480

gaatggattg gtatggttga tccttcagac agtgaaactc actacaatca aatgttcaag 540

gacaaggcca cattgactgt tgacaaatcc tccagcacag cctacatgca gctcagcagc 600

ctgacatctg aggactctgc ggtctattac tgtgcaagag ctatgggcta ctggggtcaa 660

ggaacctcag tcaccgtctc ctcagttgag cccaaatctt gt 702

<210> 231
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> 8B5-CB3.1-VEPKSC

<400> 231

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

Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Glu Ile Ser Gly Tyr
20 25 30

Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly Thr Ile Lys Arg Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly
50 55 60

Ser Glu Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
65 70 75 80

Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Phe Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Gly Gly Gly Ser Gly
100 105 110

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

Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
130 135 140

Thr Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
145 150 155 160

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

Gln Met Phe Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
180 185 190

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

Tyr Tyr Cys Ala Arg Ala Met Gly Tyr Trp Gly Gln Gly Thr Ser Val
210 215 220

Thr Val Ser Ser Val Glu Pro Lys Ser Cys
225 230

<210> 232
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> CB3.1-8B5-FNRGEC

<400> 232
gatgttgtga tgacccagac tccactcact ttgtcggtta acattggaca accagcctcc 60

atctcttgta agtcaagtca gagcctctta gatactgatg gaaagacata tttgaattgg 120

ttgttacaga ggccaggcca gtctccaaac cgcctaatct atctggtgtc taaactggac 180

tctggagtcc ctgacaggtt cactggcagt ggatcaggga cagatttcac actgaaaatc 240

agcagagtgg aggctgagga tttgggaatt tattattgct ggcaaggtac acattttccg 300

ctcacgttcg gtgctgggac caagctggag ctgaaaggag gcggatccgg aggcggaggc 360

gaagtgaagc ttgaggagtc tggaggaggc ttggtgcaac ctggaggatc catgaaactc 420

tcttgtgaag cctctggatt cacttttagt gacgcctgga tggactgggt ccgtcagtct 480

ccagagaagg ggcttgagtg ggttgctgaa attagaaaca aagctaaaaa tcatgcaaca 540

tactatgctg agtctgtgat agggaggttc accatctcaa gagatgattc caaaagtagt 600

gtctacctgc aaatgaacag cttaagagct gaagacactg gcatttatta ctgtggggct 660

ctgggccttg actactgggg ccaaggcacc actctcacag tctcctcgtt caacagggga 720

gagtgt 726

<210> 233
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> CB3.1-8B5-FNRGEC

<400> 233

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Thr
20 25 30

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

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

Asp Arg Phe Thr 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 Ile Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Phe Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Glu Val Lys Leu Glu Glu Ser Gly
115 120 125

Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu Ser Cys Glu Ala
130 135 140

Ser Gly Phe Thr Phe Ser Asp Ala Trp Met Asp Trp Val Arg Gln Ser
145 150 155 160

Pro Glu Lys Gly Leu Glu Trp Val Ala Glu Ile Arg Asn Lys Ala Lys
165 170 175

Asn His Ala Thr Tyr Tyr Ala Glu Ser Val Ile Gly Arg Phe Thr Ile
180 185 190

Ser Arg Asp Asp Ser Lys Ser Ser Val Tyr Leu Gln Met Asn Ser Leu
195 200 205

Arg Ala Glu Asp Thr Gly Ile Tyr Tyr Cys Gly Ala Leu Gly Leu Asp
210 215 220

Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Phe Asn Arg Gly
225 230 235 240

Glu Cys

<210> 234
<211> 696
<212> DNA
<213> Artificial Sequence

<220>
<223> 8B5VL-CB3.1VH-LGGC

<400> 234
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ctcacttgtc gggcaagtca ggaaattagt ggttacttaa gctggcttca gcagaaacca 120

gatggaacta ttaaacgcct gatctacgcc gcatccactt tagattctgg tgtcccaaaa 180

aggttcagtg gcagtgagtc tgggtcagat tattctctca ccatcagcag tcttgagtct 240

gaagattttg cagactatta ctgtctacaa tattttagtt atccgctcac gttcggtgct 300

gggaccaagc tggagctgaa aggaggcgga tccggaggcg gaggccaggt ccaactgcag 360

cagcctgggg ctgagctggt gaggcctggg gcttcagtga agctgtcctg caaggcttct 420

ggctacacct tcaccagcta ctggatgaac tgggtgaagc agaggcctgg acaaggcctt 480

gaatggattg gtatggttga tccttcagac agtgaaactc actacaatca aatgttcaag 540

gacaaggcca cattgactgt tgacaaatcc tccagcacag cctacatgca gctcagcagc 600

ctgacatctg aggactctgc ggtctattac tgtgcaagag ctatgggcta ctggggtcaa 660

ggaacctcag tcaccgtctc ctcactggga ggctgc 696

<210> 235
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> 8B5VL-CB3.1VH-LGGC

<400> 235

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

Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Glu Ile Ser Gly Tyr
20 25 30

Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly Thr Ile Lys Arg Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly
50 55 60

Ser Glu Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
65 70 75 80

Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Phe Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Gly Gly Gly Ser Gly
100 105 110

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

Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
130 135 140

Thr Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
145 150 155 160

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

Gln Met Phe Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
180 185 190

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

Tyr Tyr Cys Ala Arg Ala Met Gly Tyr Trp Gly Gln Gly Thr Ser Val
210 215 220

Thr Val Ser Ser Leu Gly Gly Cys
225 230

<210> 236
<211> 720
<212> DNA
<213> Artificial Sequence

<220>
<223> CB3.1-8B5-LGGC

<400> 236
gatgttgtga tgacccagac tccactcact ttgtcggtta acattggaca accagcctcc 60

atctcttgta agtcaagtca gagcctctta gatactgatg gaaagacata tttgaattgg 120

ttgttacaga ggccaggcca gtctccaaac cgcctaatct atctggtgtc taaactggac 180

tctggagtcc ctgacaggtt cactggcagt ggatcaggga cagatttcac actgaaaatc 240

agcagagtgg aggctgagga tttgggaatt tattattgct ggcaaggtac acattttccg 300

ctcacgttcg gtgctgggac caagctggag ctgaaaggag gcggatccgg aggcggaggc 360

gaagtgaagc ttgaggagtc tggaggaggc ttggtgcaac ctggaggatc catgaaactc 420

tcttgtgaag cctctggatt cacttttagt gacgcctgga tggactgggt ccgtcagtct 480

ccagagaagg ggcttgagtg ggttgctgaa attagaaaca aagctaaaaa tcatgcaaca 540

tactatgctg agtctgtgat agggaggttc accatctcaa gagatgattc caaaagtagt 600

gtctacctgc aaatgaacag cttaagagct gaagacactg gcatttatta ctgtggggct 660

ctgggccttg actactgggg ccaaggcacc actctcacag tctcctcgct gggaggctgc 720

<210> 237
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> CB3.1-8B5-LGGC

<400> 237

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Thr
20 25 30

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

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

Asp Arg Phe Thr 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 Ile Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Phe Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Glu Val Lys Leu Glu Glu Ser Gly
115 120 125

Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu Ser Cys Glu Ala
130 135 140

Ser Gly Phe Thr Phe Ser Asp Ala Trp Met Asp Trp Val Arg Gln Ser
145 150 155 160

Pro Glu Lys Gly Leu Glu Trp Val Ala Glu Ile Arg Asn Lys Ala Lys
165 170 175

Asn His Ala Thr Tyr Tyr Ala Glu Ser Val Ile Gly Arg Phe Thr Ile
180 185 190

Ser Arg Asp Asp Ser Lys Ser Ser Val Tyr Leu Gln Met Asn Ser Leu
195 200 205

Arg Ala Glu Asp Thr Gly Ile Tyr Tyr Cys Gly Ala Leu Gly Leu Asp
210 215 220

Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Leu Gly Gly Cys
225 230 235 240

<210> 238
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Lgh628F Primer

<400> 238
ggaggcggat ccggaggcgg aggccaggtc caactgcagc agcctgg 47

<210> 239
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Lgh629R Primer

<400> 239
tttgaattct aacaagattt gggctcaact gaggagacgg tgactgagg 49

<210> 240
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Lgh630R Primer

<400> 240
gcctccgcct ccggatccgc ctcctttcag ctccagcttg gtccc 45

<210> 241
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Lgh631F Primer

<400> 241
ggaggcggat ccggaggcgg aggcgaagtg aagcttgagg agtctgg 47

<210> 242
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Lgh640R Primer

<400> 242
tttgaattct aacactctcc cctgttgaac gaggagactg tgagagtgg 49

<210> 243
<211> 48

<212> DNA
<213> Artificial Sequence

<220>
<223> Lgh644R Primer

<400> 243
tttgtcgtca tcatcgtctt tgtagtcgga gtggacacct gtggagag 48

<210> 244
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Lgh646R Primer

<400> 244
tttgaattct agcagcctcc cagtgaggag acggtgactg ag 42

<210> 245
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Lgh647F Primer

<400> 245
caaagacgat gatgacgaca aagacattca gatgacacag tctcc 45

<210> 246
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Lgh648R Primer

<400> 246
tttgaattct agcagcctcc cagcgaggag actgtgagag tgg 43

<210> 247
<211> 1044
<212> DNA
<213> Artificial Sequence

<220>
<223> 2.4G2-3G8-hKappa

<400> 247
gatgtccaga tgacccagtc tccatctaat cttgctgcct ctcctggaga aagtgtttcc 60

atcaattgca aggcaagtga gagcattagc aagtatttag cctggtatct acagaaacct 120

gggaaagcaa ataagcttct tatgtacgat gggtcaactt tgcaatctgg aattccatcg 180

aggttcagtg gcagtggatc tggtacagat ttcactctca ccatcagaag cctggagcct 240

gaagattttg gactctatta ctgtcaacag cattatgaat atccagccac gttcggttct 300

gggaccaagc tggagatcaa aggaggcgga tccggaggcg gaggccaggt taccctgaaa 360

gagtctggcc ctgggatatt gcagccctcc cagaccctca gtctgacttg ttctttctct 420

gggttttcac tgaggacttc tggtatgggt gtaggctgga ttcgtcagcc ttcagggaag 480

ggtctagagt ggctggcaca catttggtgg gatgatgaca agcgctataa tccagccctg 540

aagagccgac tgacaatctc caaggatacc tccagcaacc aggtattcct caaaatcgcc 600

agtgtggaca ctgcagatac tgccacatac tactgtgctc aaataaaccc cgcctggttt 660

gcttactggg gccaagggac tctggtcact gtgagctcac tgggaggctg cggcggaggg 720

agccgtacgg tggctgcacc atcggtcttc atcttcccgc catctgatga gcagttgaaa 780

tctggaactg cctctgttgt gtgcctgctg aataacttct atcccagaga ggccaaagta 840

cagtggaagg tggataacgc cctccaatcg ggtaactccc aggagagtgt cacagagcag 900

gacagcaagg acagcaccta cagcctcagc agcaccctga cgctgagcaa agcagactac 960

gagaaacaca aagtctacgc ctgcgaagtc acccatcagg gcctgagctc gcccgtcaca 1020

aagagcttca acaggggaga gtgt 1044

<210> 248
<211> 348
<212> PRT
<213> Artificial Sequence

<220>
<223> 2.4G2-3G8-hKappa

<400> 248

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

Glu Ser Val Ser Ile Asn Cys Lys Ala Ser Glu Ser Ile Ser Lys Tyr
20 25 30

Leu Ala Trp Tyr Leu Gln Lys Pro Gly Lys Ala Asn Lys Leu Leu Met
35 40 45

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

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

Glu Asp Phe Gly Leu Tyr Tyr Cys Gln Gln His Tyr Glu Tyr Pro Ala
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly
100 105 110

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

```
Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
    130                 135                 140

Arg Thr Ser Gly Met Gly Val Gly Trp Ile Arg Gln Pro Ser Gly Lys
145                 150                 155                 160

Gly Leu Glu Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Arg Tyr
                165                 170                 175

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

Asn Gln Val Phe Leu Lys Ile Ala Ser Val Asp Thr Ala Asp Thr Ala
        195                 200                 205

Thr Tyr Tyr Cys Ala Gln Ile Asn Pro Ala Trp Phe Ala Tyr Trp Gly
    210                 215                 220

Gln Gly Thr Leu Val Thr Val Ser Ser Leu Gly Gly Cys Gly Gly Gly
225                 230                 235                 240

Ser Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
                245                 250                 255

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
            260                 265                 270

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
        275                 280                 285

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
    290                 295                 300

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
305                 310                 315                 320

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
                325                 330                 335

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
            340                 345
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<210> 249
<211> 1734
<212> DNA
<213> Artificial Sequence

<220>
<223> 3G8-2.4G2-hG1

<400> 249

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gacactgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc     60

atctcctgca aggccagcca aagtgttgat tttgatggtg atagttttat gaactggtac    120

caacagaaac caggacagcc acccaaactc ctcatctata ctacatccaa tctagaatct    180

gggatcccag ccaggtttag tgccagtggg tctgggacag acttcaccct caacatccat    240
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cctgtggagg aggaggatac tgcaacctat tactgtcagc aaagtaatga ggatccgtac 300

acgttcggag gggggaccaa gctggaaata aaaggaggcg gatccggagg cggaggcgag 360

gtggagctag tggagtctgg gggaggctta gtgcagcctg gaaggtccct gaaactctcg 420

tgtgcagcct caggattcac tttcagtgac tattacatgg cctgggtccg gcaggctcca 480

acgacgggtc tggagtgggt cgcatccatt agttatgatg gtggtgacac tcactatcga 540

gactccgtga agggccgatt tactatttcc agagataatg caaaaagcag cctatacctg 600

caaatggaca gtctgaggtc tgaggacacg gccacttatt actgtgcaac agagactacg 660

ggaataccta caggtgttat ggatgcctgg ggtcaaggag tttcagtcac tgtctcctca 720

ctgggaggct gcggcggagg gagcgcctcc accaagggcc catcggtctt ccccctggca 780

ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 840

ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 900

ttcccggctg tcctacagtc ctcaggactc tactccctca gcagcgtggt gaccgtgccc 960

tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 1020

aaggtggaca agagagttga gcccaaatct tgtgacaaaa ctcacacatg cccaccgtgc 1080

ccagcacctg aactcctggg gggaccgtca gtcttcctct tccccccaaa acccaaggac 1140

accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt gagccacgaa 1200

gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 1260

aagccgcggg aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg 1320

caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca 1380

gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac 1440

accctgcccc catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc 1500

aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1560

aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag 1620

ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1680

gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaa 1734

<210> 250
<211> 578
<212> PRT
<213> Artificial Sequence

<220>
<223> 3G8-2.4G2-hG1

<400> 250

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

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Phe Asp
            20                  25                  30

Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45

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

Arg Phe Ser Ala Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65                  70                  75                  80

Pro Val Glu Glu Glu Asp Thr Ala Thr Tyr Tyr Cys Gln Gln Ser Asn
                85                  90                  95

Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
            100                 105                 110

Gly Gly Ser Gly Gly Gly Gly Glu Val Glu Leu Val Glu Ser Gly Gly
        115                 120                 125

Gly Leu Val Gln Pro Gly Arg Ser Leu Lys Leu Ser Cys Ala Ala Ser
    130                 135                 140

Gly Phe Thr Phe Ser Asp Tyr Tyr Met Ala Trp Val Arg Gln Ala Pro
145                 150                 155                 160

Thr Thr Gly Leu Glu Trp Val Ala Ser Ile Ser Tyr Asp Gly Gly Asp
                165                 170                 175

Thr His Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
            180                 185                 190

Asn Ala Lys Ser Ser Leu Tyr Leu Gln Met Asp Ser Leu Arg Ser Glu
        195                 200                 205

Asp Thr Ala Thr Tyr Tyr Cys Ala Thr Glu Thr Thr Gly Ile Pro Thr
    210                 215                 220

Gly Val Met Asp Ala Trp Gly Gln Gly Val Ser Val Thr Val Ser Ser
225                 230                 235                 240

Leu Gly Gly Cys Gly Gly Gly Ser Ala Ser Thr Lys Gly Pro Ser Val
                245                 250                 255

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
            260                 265                 270

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
        275                 280                 285

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
    290                 295                 300

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
305                 310                 315                 320
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Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
325 330 335

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
340 345 350

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
355 360 365

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
370 375 380

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
385 390 395 400

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
405 410 415

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
420 425 430

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
435 440 445

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

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
465 470 475 480

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
500 505 510

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
515 520 525

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
530 535 540

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
545 550 555 560

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
565 570 575

Gly Lys

<210> 251
<211> 720
<212> DNA
<213> Artificial Sequence

<220>
<223> CD79VL-CD32BVH

<400> 251

gatgttgtga tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggcctcc 60

atctcctgca agtcaagtca gagcctctta gatagtgatg gaaagacata tttgaattgg 120

tttcagcaga ggccaggcca atctccaaac cgcctaattt atctggtgtc taaactggac 180

tctggggtcc cagacagatt cagcggcagt gggtcaggca ctgatttcac actgaaaatc 240

agcagggtgg aggctgagga tgttggggtt tattactgct ggcaaggtac acattttccg 300

ctcacgttcg gcggagggac caagcttgag atcaaaggag gcggatccgg aggcggaggc 360

gaagtgaagc ttgaggagtc tggaggaggc ttggtgcaac ctggaggatc catgaaactc 420

tcttgtgaag cctctggatt cacttttagt gacgcctgga tggactgggt ccgtcagtct 480

ccagagaagg ggcttgagtg ggttgctgaa attagaaaca aagctaaaaa tcatgcaaca 540

tactatgctg agtctgtgat agggaggttc accatctcaa gagatgattc caaaagtagt 600

gtctacctgc aaatgaacag cttaagagct gaagacactg gcatttatta ctgtggggct 660

ctgggccttg actactgggg ccaaggcacc actctcacag tctcctcgct gggaggctgc 720

<210> 252
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> CD79VL-CD32BVH

<400> 252

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Asn Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp 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 Val Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Phe Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

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

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
130 135 140

```
Ser Gly Phe Thr Phe Ser Asp Ala Trp Met Asp Trp Val Arg Gln Ala
145                 150                 155                 160

Pro Gly Lys Gly Leu Glu Trp Val Ala Glu Ile Arg Asn Lys Ala Lys
                165                 170                 175

Asn His Ala Thr Tyr Tyr Ala Glu Ser Val Ile Gly Arg Phe Thr Ile
            180                 185                 190

Ser Arg Asp Asp Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu
        195                 200                 205

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Gly Ala Leu Gly Leu Asp
    210                 215                 220

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Leu Gly Gly Cys
225                 230                 235                 240
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<210> 253
<211> 696
<212> DNA
<213> Artificial Sequence

<220>
<223> CD32BVL-CD79VH-1

<400> 253
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atcacttgtc gggcaagtca ggaaattagt ggttacttaa gctggctgca gcagaaacca 120

ggcaaggccc ctagacgcct gatctacgcc gcatccactt tagattctgg tgtcccatcc 180

aggttcagtg gcagtgagtc tgggaccgag ttcaccctca ccatcagcag ccttcagcct 240

gaagattttg caacctatta ctgtctacaa tattttagtt atccgctcac gttcggaggg 300

gggaccaagg tggaaataaa aggaggcgga tccggaggcg gaggccaggt tcagctggtg 360

cagtctggag ctgaggtgaa gaagcctggc gcctcagtga aggtctcctg caaggcttct 420

ggttacacct ttaccagcta ctggatgaac tgggtgcgac aggcccctgg acaagggctt 480

gagtggatcg gaatgattga tccttcagac agtgaaactc actacaatca aatgttcaag 540

gacagagtca ccatgaccac agacacatcc acgagcacag cctacatgga gctgaggagc 600

ctgagatctg acgacacggc cgtgtattac tgtgcgagag ctatgggcta ctgggggcaa 660

gggaccacgg tcaccgtctc ctcactggga ggctgc 696

<210> 254
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> CD32BVL-CD79VH-1

<400> 254

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 Glu Ile Ser Gly Tyr
20 25 30

Leu Ser Trp Leu Gln Gln Lys Pro Gly Lys Ala Pro Arg Arg Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Asp Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Glu Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Tyr Phe Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
115 120 125

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
130 135 140

Thr Ser Tyr Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
145 150 155 160

Glu Trp Ile Gly Met Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn
165 170 175

Gln Met Phe Lys Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
180 185 190

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

Tyr Tyr Cys Ala Arg Ala Met Gly Tyr Trp Gly Gln Gly Thr Thr Val
210 215 220

Thr Val Ser Ser Leu Gly Gly Cys
225 230

<210> 255
<211> 696
<212> DNA
<213> Artificial Sequence

<220>
<223> CD32BVL-CD79VH-2

<400> 255
gacatccaga tgacccagtc tccatcctcc ttatctgcct ctgtgggaga tagagtcacc 60

atcacttgtc gggcaagtca ggaaattagt ggttacttaa gctggctgca gcagaaacca 120

ggcaaggccc ctagacgcct gatctacgcc gcatccactt tagattctgg tgtcccatcc 180

aggttcagtg gcagtgagtc tgggaccgag ttcaccctca ccatcagcag ccttcagcct 240

gaagattttg caacctatta ctgtctacaa tattttagtt atccgctcac gttcggaggg 300

gggaccaagg tggaaataaa aggaggcgga tccggaggcg gaggccaggt tcagctggtg 360

cagtctggag ctgaggtgaa gaagcctggc gcctcagtga aggtctcctg caaggcttct 420

ggttacacct ttaccagcta ctggatgaac tgggtgcgac aggcccctgg acaagggctt 480

gagtggatcg gaatgattga tccttcagac agtgaaactc actacaatca aaagttcaag 540

gacagagtca ccatgaccac agacacatcc acgagcacag cctacatgga gctgaggagc 600

ctgagatctg acgacacggc cgtgtattac tgtgcgagag ctatgggcta ctgggggcaa 660

gggaccacgg tcaccgtctc ctcactggga ggctgc 696

<210> 256
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> CD32BVL-CD79VH-2

<400> 256

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 Glu Ile Ser Gly Tyr
20 25 30

Leu Ser Trp Leu Gln Gln Lys Pro Gly Lys Ala Pro Arg Arg Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Asp Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Glu Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Tyr Phe Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
115 120 125

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
130 135 140

Thr Ser Tyr Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
145 150 155 160

```
Glu Trp Ile Gly Met Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn
                165                 170                 175

Gln Lys Phe Lys Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
            180                 185                 190

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

Tyr Tyr Cys Ala Arg Ala Met Gly Tyr Trp Gly Gln Gly Thr Thr Val
    210                 215                 220

Thr Val Ser Ser Leu Gly Gly Cys
225                 230
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<210> 257
<211> 720
<212> DNA
<213> Artificial Sequence

<220>
<223> hHBCRCVL. R45N-h8B5VH-LGGC

<400> 257
gatgttgtga tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggcctcc 60

atctcctgca agtcaagtca gagcctctta gatagtgatg gaaagacata tttgaattgg 120

tttcagcaga ggccaggcca atctccaaac cgcctaattt atctggtgtc taaactggac 180

tctggggtcc cagacagatt cagcggcagt gggtcaggca ctgatttcac actgaaaatc 240

agcagggtgg aggctgagga tgttggggtt tattactgct ggcaaggtac acattttccg 300

ctcacgttcg gcggagggac caagcttgag atcaaaggag gcggatccgg aggcggaggc 360

gaagtgaagc ttgaggagtc tggaggaggc ttggtgcaac ctggaggatc catgaaactc 420

tcttgtgaag cctctggatt cacttttagt gacgcctgga tggactgggt ccgtcagtct 480

ccagagaagg ggcttgagtg ggttgctgaa attagaaaca aagctaaaaa tcatgcaaca 540

tactatgctg agtctgtgat agggaggttc accatctcaa gagatgattc caaaagtagt 600

gtctacctgc aaatgaacag cttaagagct gaagacactg gcatttatta ctgtggggct 660

ctgggccttg actactgggg ccaaggcacc actctcacag tctcctcgct gggaggctgc 720

<210> 258
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> hHBCRCVL. R45N-h8B5VH-LGGC

<400> 258

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

```
Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
            20                  25                  30

Asp Gly Lys Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
        35                  40                  45

Pro Asn Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp 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 Val Gly Val Tyr Tyr Cys Trp Gln Gly
                85                  90                  95

Thr His Phe Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110

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

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
    130                 135                 140

Ser Gly Phe Thr Phe Ser Asp Ala Trp Met Asp Trp Val Arg Gln Ala
145                 150                 155                 160

Pro Gly Lys Gly Leu Glu Trp Val Ala Glu Ile Arg Asn Lys Ala Lys
                165                 170                 175

Asn His Ala Thr Tyr Tyr Ala Glu Ser Val Ile Gly Arg Phe Thr Ile
            180                 185                 190

Ser Arg Asp Asp Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu
        195                 200                 205

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Gly Ala Leu Gly Leu Asp
    210                 215                 220

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Leu Gly Gly Cys
225                 230                 235                 240
```

<210> 259
<211> 696
<212> DNA
<213> Artificial Sequence

<220>
<223> H8B5VL-hHBCRCVH M48I-LGGC

<400> 259

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gacatccaga tgacccagtc tccatcctcc ttatctgcct ctgtgggaga tagagtcacc     60

atcacttgtc gggcaagtca ggaaattagt ggttacttaa gctggctgca gcagaaacca    120

ggcaaggccc ctagacgcct gatctacgcc gcatccactt tagattctgg tgtcccatcc    180

aggttcagtg gcagtgagtc tgggaccgag ttcaccctca ccatcagcag ccttcagcct    240
```

gaagattttg caacctatta ctgtctacaa tattttagtt atccgctcac gttcggaggg 300

gggaccaagg tggaaataaa aggaggcgga tccggaggcg gaggccaggt tcagctggtg 360

cagtctggag ctgaggtgaa gaagcctggc gcctcagtga aggtctcctg caaggcttct 420

ggttacacct ttaccagcta ctggatgaac tgggtgcgac aggcccctgg acaagggctt 480

gagtggatcg gaatgattga tccttcagac agtgaaactc actacaatca aatgttcaag 540

gacagagtca ccatgaccac agacacatcc acgagcacag cctacatgga gctgaggagc 600

ctgagatctg acgacacggc cgtgtattac tgtgcgagag ctatgggcta ctgggggcaa 660

gggaccacgg tcaccgtctc ctcactggga ggctgc 696

<210> 260
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> H8B5VL-HBCRCVH M48I-LGGC

<400> 260

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 Glu Ile Ser Gly Tyr
20 25 30

Leu Ser Trp Leu Gln Gln Lys Pro Gly Lys Ala Pro Arg Arg Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Asp Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Glu Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Tyr Phe Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
115 120 125

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
130 135 140

Thr Ser Tyr Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
145 150 155 160

Glu Trp Ile Gly Met Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn
165 170 175

```
Gln Met Phe Lys Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
            180                 185                 190

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

Tyr Tyr Cys Ala Arg Ala Met Gly Tyr Trp Gly Gln Gly Thr Thr Val
    210                 215                 220

Thr Val Ser Ser Leu Gly Gly Cys
225                 230
```

<210> 261
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Lgh321F Primer

<400> 261
cgagctagct ctagatgaga tcacagttct ctctac 36

<210> 262
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Lgh386R Primer

<400> 262
tttgaattct agcagcctcc cagtgaggag acggtgaccg tggtc 45

<210> 263
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Lgh784F Primer

<400> 263
ggcggatccg gaggcggagg ccaggttcag ctggtgcag 39

<210> 264
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Lgh785R Primer

<400> 264
cctccggatc cgcctccttt gatctcaagc ttggtccc 38

<210> 265
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Lgh786R Primer

<400> 265
tttgaattct agcagcctcc caggctggag acggtcacca gg 42

<210> 266
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Lgh787F Primer

<400> 266
ggaggcggat ccggaggcgg aggcgaagtg cagcttgtgg agtc 44

<210> 267
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 267

Leu Gly Gly Cys Gly Gly Gly Ser
1 5

<210> 268
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 268

Leu Glu Ile Lys
1

<210> 269
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 269

Thr Val Ser Ser
1

<210> 270
<211> 343
<212> PRT

<213> Artificial Sequence

<220>
<223> H8B5VL-hBCRCVH M48I, M62K_LGGCG3S_hKappa

<400> 270

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 Glu Ile Ser Gly Tyr
20 25 30

Leu Ser Trp Leu Gln Gln Lys Pro Gly Lys Ala Pro Arg Arg Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Asp Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Glu Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Tyr Phe Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
115 120 125

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
130 135 140

Thr Ser Tyr Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
145 150 155 160

Glu Trp Ile Gly Met Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn
165 170 175

Gln Lys Phe Lys Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
180 185 190

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

Tyr Tyr Cys Ala Arg Ala Met Gly Tyr Trp Gly Gln Gly Thr Thr Val
210 215 220

Thr Val Ser Ser Leu Gly Gly Cys Gly Gly Gly Ser Arg Thr Val Ala
225 230 235 240

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

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
260 265 270

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
275 280 285

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
290 295 300

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
305 310 315 320

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

Ser Phe Asn Arg Gly Glu Cys
340

<210> 271
<211> 1032
<212> DNA
<213> Artificial Sequence

<220>
<223> H8B5VL-hBCRCVH M48I, M62K_LGGCG3S_hKappa

<400> 271
gacatccaga tgacccagtc tccatcctcc ttatctgcct ctgtgggaga tagagtcacc 60

atcacttgtc gggcaagtca ggaaattagt ggttacttaa gctggctgca gcagaaacca 120

ggcaaggccc ctagacgcct gatctacgcc gcatccactt tagattctgg tgtcccatcc 180

aggttcagtg gcagtgagtc tgggaccgag ttcaccctca ccatcagcag ccttcagcct 240

gaagattttg caacctatta ctgtctacaa tattttagtt atccgctcac gttcggaggg 300

gggaccaagg tggaaataaa aggaggcgga tccggaggcg gaggccaggt tcagctggtg 360

cagtctggag ctgaggtgaa gaagcctggc gcctcagtga aggtctcctg caaggcttct 420

ggttacacct ttaccagcta ctggatgaac tgggtgcgac aggcccctgg acaagggctt 480

gagtggatcg gaatgattga tccttcagac agtgaaactc actacaatca aaagttcaag 540

gacagagtca ccatgaccac agacacatcc acgagcacag cctacatgga gctgaggagc 600

ctgagatctg acgacacggc cgtgtattac tgtgcgagag ctatgggcta ctgggggcaa 660

gggaccacgg tcaccgtctc ctcactggga ggctgcggcg gagggagccg aactgtggct 720

gcaccatcgg tcttcatctt cccgccatct gatgagcagt tgaaatctgg aactgcctct 780

gttgtgtgcc tgctgaataa cttctatccc agagaggcca aagtacagtg gaaggtggat 840

aacgccctcc aatcgggtaa ctcccaggag agtgtcacag agcaggacag caaggacagc 900

acctacagcc tcagcagcac cctgacgctg agcaaagcag actacgagaa acacaaagtc 960

tacgcctgcg aagtcaccca tcagggcctg agctcgcccg tcacaaagag cttcaacagg 1020

ggagagtgtt ag 1032

<210> 272
<211> 574

<212> PRT
<213> Artificial Sequence

<220>
<223> HBCRCVL R45N-h8B5VH_LGGCGGGS-hG1

<400> 272

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Asn Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp 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 Val Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Phe Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

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

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
130 135 140

Ser Gly Phe Thr Phe Ser Asp Ala Trp Met Asp Trp Val Arg Gln Ala
145 150 155 160

Pro Gly Lys Gly Leu Glu Trp Val Ala Glu Ile Arg Asn Lys Ala Lys
165 170 175

Asn His Ala Thr Tyr Tyr Ala Glu Ser Val Ile Gly Arg Phe Thr Ile
180 185 190

Ser Arg Asp Asp Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu
195 200 205

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Gly Ala Leu Gly Leu Asp
210 215 220

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Leu Gly Gly Cys
225 230 235 240

Gly Gly Gly Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
245 250 255

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
260 265 270

```
Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
        275                 280                 285

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
    290                 295                 300

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
305                 310                 315                 320

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
                325                 330                 335

Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
            340                 345                 350

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
        355                 360                 365

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
    370                 375                 380

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
385                 390                 395                 400

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
                405                 410                 415

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
            420                 425                 430

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
        435                 440                 445

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

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

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
                485                 490                 495

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
            500                 505                 510

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
        515                 520                 525

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
    530                 535                 540

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
545                 550                 555                 560

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                565                 570
```

<210> 273
<211> 1722
<212> DNA

<213> Artificial Sequence

<220>
<223> HBCRCVL R45N-h8B5VH_LGGCGGGS-hG1

<400> 273
gatgttgtga tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggcctcc 60

atctcctgca agtcaagtca gagcctctta gatagtgatg gaaagacata tttgaattgg 120

tttcagcaga ggccaggcca atctccaaac cgcctaattt atctggtgtc taaactggac 180

tctggggtcc cagacagatt cagcggcagt gggtcaggca ctgatttcac actgaaaatc 240

agcagggtgg aggctgagga tgttggggtt tattactgct ggcaaggtac acattttccg 300

ctcacgttcg gcggagggac caagcttgag atcaaaggag gcggatccgg aggcggaggc 360

gaagtgcagc ttgtggagtc tggaggaggc ttggtgcaac ctggaggatc cctgagactc 420

tcttgtgccg cctctggatt cacttttagt gacgcctgga tggactgggt ccgtcaggcc 480

ccaggcaagg ggcttgagtg ggttgctgaa attagaaaca aagctaaaaa tcatgcaaca 540

tactatgctg agtctgtgat agggaggttc accatctcaa gagatgacgc caaaaacagt 600

ctgtacctgc aaatgaacag cttaagagct gaagacactg ccgtgtatta ctgtggggct 660

ctgggccttg actactgggg ccaaggcacc ctggtgaccg tctccagcct gggaggctgc 720

ggcggaggga gcgcctccac caagggccca tcggtcttcc ccctggcacc ctcctccaag 780

agcacctctg ggggcacagc ggccctgggc tgcctggtca aggactactt ccccgaaccg 840

gtgacggtgt cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc 900

ctacagtcct caggactcta ctccctcagc agcgtggtga ccgtgccctc cagcagcttg 960

ggcacccaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag 1020

agagttgagc ccaaatcttg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 1080

ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc 1140

tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 1200

aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 1260

gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 1320

ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag 1380

aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 1440

tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat 1500

cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1560

acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac 1620

aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1680

aaccactaca cgcagaagag cctctccctg tctccgggta aa 1722

<210> 274
<211> 335
<212> PRT
<213> Artificial Sequence

<220>
<223> H8B5VL-HBCRCVH M48I, M62K_(-4)LEIK_hKappa

<400> 274

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 Glu Ile Ser Gly Tyr
20 25 30

Leu Ser Trp Leu Gln Gln Lys Pro Gly Lys Ala Pro Arg Arg Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Asp Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Glu Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Tyr Phe Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
115 120 125

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
130 135 140

Thr Ser Tyr Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
145 150 155 160

Glu Trp Ile Gly Met Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn
165 170 175

Gln Lys Phe Lys Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
180 185 190

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

Tyr Tyr Cys Ala Arg Ala Met Gly Tyr Trp Gly Gln Gly Thr Thr Val
210 215 220

Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
225 230 235 240

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
245 250 255

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
260 265 270

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
275 280 285

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
290 295 300

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
305 310 315 320

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
325 330 335

<210> 275
<211> 1005
<212> DNA
<213> Artificial Sequence

<220>
<223> H8B5VL-HBCRCVH M48I, M62K_(-4)LEIK_hKappa

<400> 275
gacatccaga tgacccagtc tccatcctcc ttatctgcct ctgtgggaga tagagtcacc 60

atcacttgtc gggcaagtca ggaaattagt ggttacttaa gctggctgca gcagaaacca 120

ggcaaggccc ctagacgcct gatctacgcc gcatccactt tagattctgg tgtcccatcc 180

aggttcagtg gcagtgagtc tgggaccgag ttcaccctca ccatcagcag ccttcagcct 240

gaagattttg caacctatta ctgtctacaa tattttagtt atccgctcac gttcggaggg 300

gggaccaagg tggaaataaa aggaggcgga tccggaggcg gaggccaggt tcagctggtg 360

cagtctggag ctgaggtgaa gaagcctggc gcctcagtga aggtctcctg caaggcttct 420

ggttacacct ttaccagcta ctggatgaac tgggtgcgac aggcccctgg acaagggctt 480

gagtggatcg gaatgattga tccttcagac agtgaaactc actacaatca aaagttcaag 540

gacagagtca ccatgaccac agacacatcc acgagcacag cctacatgga gctgaggagc 600

ctgagatctg acgacacggc cgtgtattac tgtgcgagag ctatgggcta ctgggggcaa 660

gggaccacgg tcctggagat caagcgaact gtggctgcac catcggtctt catcttcccg 720

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 780

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 840

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 900

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 960

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 1005

<210> 276
<211> 566
<212> PRT
<213> Artificial Sequence

<220>
<223> HBCRCVL R45N-h8B5VH_(-4)TVSS-hG1 = HBCRCVL R45N-h8B5VH_-hG1

<400> 276

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Asn Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp 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 Val Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Phe Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

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

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
130 135 140

Ser Gly Phe Thr Phe Ser Asp Ala Trp Met Asp Trp Val Arg Gln Ala
145 150 155 160

Pro Gly Lys Gly Leu Glu Trp Val Ala Glu Ile Arg Asn Lys Ala Lys
165 170 175

Asn His Ala Thr Tyr Tyr Ala Glu Ser Val Ile Gly Arg Phe Thr Ile
180 185 190

Ser Arg Asp Asp Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu
195 200 205

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Gly Ala Leu Gly Leu Asp
210 215 220

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

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
245 250 255

```
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
            260                 265                 270

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
        275                 280                 285

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
    290                 295                 300

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
305                 310                 315                 320

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro
                325                 330                 335

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
            340                 345                 350

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
        355                 360                 365

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
    370                 375                 380

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
385                 390                 395                 400

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
                405                 410                 415

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
            420                 425                 430

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
        435                 440                 445

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
    450                 455                 460

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

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
                485                 490                 495

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
            500                 505                 510

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
        515                 520                 525

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
    530                 535                 540

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
545                 550                 555                 560

Ser Leu Ser Pro Gly Lys
                565
```

<210> 277
<211> 1698
<212> DNA
<213> Artificial Sequence

<220>
<223> HBCRCVL R45N-h8B5VH_(-4)TVSS-hG1

<400> 277
gatgttgtga tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggcctcc 60

atctcctgca agtcaagtca gagcctctta gatagtgatg gaaagacata tttgaattgg 120

tttcagcaga ggccaggcca atctccaaac cgcctaattt atctggtgtc taaactggac 180

tctggggtcc cagacagatt cagcggcagt gggtcaggca ctgatttcac actgaaaatc 240

agcagggtgg aggctgagga tgttggggtt tattactgct ggcaaggtac acattttccg 300

ctcacgttcg gcggagggac caagcttgag atcaaaggag gcggatccgg aggcggaggc 360

gaagtgcagc ttgtggagtc tggaggaggc ttggtgcaac ctggaggatc cctgagactc 420

tcttgtgccg cctctggatt cacttttagt gacgcctgga tggactgggt ccgtcaggcc 480

ccaggcaagg ggcttgagtg ggttgctgaa attagaaaca aagctaaaaa tcatgcaaca 540

tactatgctg agtctgtgat agggaggttc accatctcaa gagatgacgc caaaaacagt 600

ctgtacctgc aaatgaacag cttaagagct gaagacactg ccgtgtatta ctgtggggct 660

ctgggccttg actactgggg ccaaggcacc ctggtgaccg tctccagcgc ctccaccaag 720

ggcccatcgg tcttcccccc ggcaccctcc tccaagagca cctctggggg cacagcggcc 780

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 840

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 900

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 960

gtgaatcaca agcccagcaa caccaaggtg gacaagagag ttgagcccaa atcttgtgac 1020

aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 1080

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 1140

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 1200

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 1260

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1320

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggg 1380

cagccccgag aaccacaggt gtacaccctg cccccatccc gggatgagct gaccaagaac 1440

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1500

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1560

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1620

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1680

tccctgtctc cgggtaaa 1698

<210> 278
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 278

Phe Asn Arg Gly Glu Cys Gly Gly Gly Ser
1 5 10

<210> 279
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 279

Phe Asn Arg Gly Glu Cys Leu Gln Val Tyr Tyr Arg Met
1 5 10

<210> 280
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 280

Leu Glu Gly Glu Glu Gly
1 5

<210> 281
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 281

Leu Glu Gly Glu Glu Gly Cys
1 5

<210> 282

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

<220>
<223> Linker

<400> 282

Leu Glu Ile Lys
1

<210> 283
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 283

Leu Gly Glu Glu Gly
1 5

<210> 284
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 284

Leu Gly Glu Glu Gly Cys
1 5

<210> 285
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 285

Leu Gly Gly Cys Gly Gly Gly Ser
1 5

<210> 286
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 286

Leu Gly Lys Lys Gly
1 5

<210> 287
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 287

Leu Gly Lys Lys Gly Cys
1 5

<210> 288
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 288

Leu Lys Gly Lys Lys Gly
1 5

<210> 289
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 289

Leu Lys Gly Lys Lys Gly Cys
1 5

<210> 290
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 290

Leu Gln Val Tyr Tyr Arg Met
1 5

<210> 291
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 291

Leu Gln Val Tyr Tyr Arg Met Cys
1 5

<210> 292
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 292

Thr Val Ser Ser
1

<210> 293
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 293

Val Glu Pro Lys Ser Cys Gly Gly Gly Ser
1 5 10

<210> 294
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 294

Val Glu Pro Lys Ser Cys Tyr Leu Tyr Leu Arg Ala Arg Val
1 5 10

<210> 295
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 295

Val Gln Val His Tyr Arg Met
1 5

<210> 296
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 296

Val Gln Val His Tyr Arg Met Cys
1 5

<210> 297
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 297

Tyr Leu Tyr Leu Arg Ala Arg Val
1 5

<210> 298
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 298

Tyr Leu Tyr Leu Arg Ala Arg Val Cys
1 5

<210> 299
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> E-coil Linker

<400> 299

Glu Val Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys Glu Val
1 5 10 15

Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys
20 25

<210> 300
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> K-coil Linker

<400> 300

Lys Val Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu Lys Val
1 5 10 15

Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu
20 25

<210> 301
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 301

Gly Gly Gly Asn Ser
1 5

<210> 302
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> YA2B6 light chain variable region

<400> 302

Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1 5 10 15

Glu Lys Val Thr Ile Thr Cys Arg Thr Ser Gln Ser Ile Gly Thr Asn
20 25 30

Ile His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala
65 70 75 80

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Thr Trp Pro Phe
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 303
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> YA2B6 hheavy chain variable region

<400> 303

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 Asn Tyr
20 25 30

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

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

Lys 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 Asn Gly Asp Ser Asp Tyr Tyr Ser Gly Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 304
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Albumin Binding Domain

<400> 304

Leu Ala Glu Ala Lys Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly
1 5 10 15

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

Gly Val Lys Ala Leu Ile Asp Glu Ile Leu Ala Ala Leu Pro
35 40 45

<210> 305
<211> 279
<212> PRT
<213> Artificial Sequence

<220>
<223> h3G8VL1-G3SG4-h2B6VH4-Kcoil-GGGNS

<400> 305

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

Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Phe Asp
            20                  25                  30

Gly Asp Ser Phe Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45

Lys Leu Leu Ile Tyr Thr Thr Ser Asn Leu Glu Ser Gly Val Pro Asp
    50                  55                  60

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

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

Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly
            100                 105                 110

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

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    130                 135                 140

Gly Tyr Thr Phe Thr Asn Tyr Trp Ile His Trp Val Arg Gln Ala Pro
145                 150                 155                 160

Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Asp Pro Ser Asp Thr Tyr
                165                 170                 175

Pro Asn Tyr Asn Lys Lys Phe Lys Gly Arg Val Thr Met Thr Val Val
            180                 185                 190

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

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asn Gly Asp Ser Asp Tyr Tyr
    210                 215                 220

Ser Gly Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
225                 230                 235                 240

Gly Gly Cys Gly Gly Gly Lys Val Ala Ala Leu Lys Glu Lys Val Ala
                245                 250                 255

Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu Lys Val Ala Ala Leu
            260                 265                 270

Lys Glu Gly Gly Gly Asn Ser
        275
```

<210> 306
<211> 837
<212> DNA
<213> Artificial Sequence

<220>

<223> h3G8VL1-G3SG4-h2B6VH4-Kcoil-GGGNS

<400> 306
gacatcgtga tgacccaatc tccagactct ttggctgtgt ctctagggga gagggccacc 60

atcaactgca aggccagcca aagtgttgat tttgatggtg atagttttat gaactggtac 120

caacagaaac caggacagcc acccaaactc ctcatctata ctacatccaa tctagaatct 180

ggggtcccag acaggtttag tggcagtggg tctgggacag acttcaccct caccatcagc 240

agcctgcagg ctgaggatgt ggcagtttat tactgtcagc aaagtaatga agatccgtac 300

acgttcggac aggggaccaa gcttgagatc aaaggaggcg gatccggcgg cggaggccag 360

gttcagctgg tgcagtctgg agctgaggtg aagaagcctg gggcctcagt gaaggtctcc 420

tgcaaggctt ctggttacac ctttaccaac tactggatac actgggtgcg acaggcccct 480

ggacaagggc ttgagtggat tggagtgatt gatccttctg atacttatcc aaattacaat 540

aaaaagttca agggcagagt caccatgacc gtagtcgtat ccacgagcac agcctacatg 600

gagctgagga gcctgagatc tgacgacacg gccgtgtatt actgtgcgag aaacggtgat 660

tccgattatt actctggtat ggactactgg gggcaaggga ccacggtcac cgtctcctcc 720

ggaggatgtg gcggtggaaa agtggccgca ctgaaggaga aagttgctgc tttgaaagag 780

aaggtcgccg cacttaagga aaaggtcgca gccctgaaag agggcggcgg gaattct 837

<210> 307
<211> 318
<212> PRT
<213> Artificial Sequence

<220>
<223> h2B6VL5-G3SG4-h3G8VH5-Ecoil-GGGNS-ABD

<400> 307

Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1 5 10 15

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

Ile His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
35 40 45

Lys Glu Val Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala
65 70 75 80

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Thr Trp Pro Phe
85 90 95

```
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Ser Gly
            100                 105                 110

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

Pro Thr Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu
    130                 135                 140

Ser Thr Ser Gly Met Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys
145                 150                 155                 160

Ala Leu Glu Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Arg Tyr
                165                 170                 175

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

Asn Gln Val Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala
        195                 200                 205

Thr Tyr Tyr Cys Ala Gln Ile Asn Pro Ala Trp Phe Ala Tyr Trp Gly
    210                 215                 220

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

Val Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys Glu Val Ala
                245                 250                 255

Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys Gly Gly Gly Asn Ser
            260                 265                 270

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

Val Ser Asp Tyr Tyr Lys Asn Leu Ile Asn Asn Ala Lys Thr Val Glu
    290                 295                 300

Gly Val Lys Ala Leu Ile Asp Glu Ile Leu Ala Ala Leu Pro
305                 310                 315
```

<210> 308
<211> 954
<212> DNA
<213> Artificial Sequence

<220>
<223> h2B6VL5-G3SG4-h3G8VH5-Ecoil-GGGNS-ABD

<400> 308

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gaaattgtgc tgactcagtc tccagacttt cagtctgtga ctccaaagga gaaagtcacc     60

ttcacctgca ggaccagtca gagcattggc acaaacatac actggtacca gcagaaacca    120

gatcagtctc caaagctcct catcaaggag gtttctgagt ctatctctgg agtcccatcg    180

aggttcagtg gcagtggatc tgggacagat ttcaccctca ccatcaatag cctggaagct    240

gaagatgctg caacgtatta ctgtcaacaa agtaatacct ggccgttcac gttcggcgga    300
```

gggaccaagg tggagatcaa aggaggcgga tccggcggcg gaggccaggt taccctgaga 360

gagtctggcc ctgcgctggt gaagcccaca cagaccctca cactgacttg taccttctct 420

gggttttcac tgagcacttc tggtatgggt gtaggctgga ttcgtcagcc tcccgggaag 480

gctctagagt ggctggcaca catttggtgg gatgatgaca agcgctataa tccagccctg 540

aagagccgac tgacaatctc caaggatacc tccaaaaacc aggtagtcct cacaatgacc 600

aacatggacc ctgtggatac tgccacatac tactgtgctc aaataaaccc cgcctggttt 660

gcttactggg gccaagggac tctggtcact gtgagctccg gaggatgtgg cggtggagaa 720

gtggccgcac tggagaaaga ggttgctgct ttggagaagg aggtcgctgc acttgaaaag 780

gaggtcgcag ccctggagaa aggcggcggg aattctctgg ccgaagcaaa agtgctggcc 840

aaccgcgaac tggataaata tggcgtgagc gattattata agaacctgat taacaacgca 900

aagaccgtgg aaggcgtgaa agcactgatt gatgaaattc tggccgccct gcct 954

<210> 309
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 309

Ala Pro Ser Ser Ser
1 5

<210> 310
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 310

Val Pro Ser Met Gly Ser Ser Ser
1 5

<210> 311
<211> 383
<212> PRT
<213> Homo sapiens

<400> 311

Met Gly Leu Gly Pro Val Phe Leu Leu Leu Ala Gly Ile Phe Pro Phe
1 5 10 15

```
Ala Pro Pro Gly Ala Ala Ala Glu Pro His Ser Leu Arg Tyr Asn Leu
            20                  25                  30

Thr Val Leu Ser Trp Asp Gly Ser Val Gln Ser Gly Phe Leu Thr Glu
        35                  40                  45

Val His Leu Asp Gly Gln Pro Phe Leu Arg Cys Asp Arg Gln Lys Cys
    50                  55                  60

Arg Ala Lys Pro Gln Gly Gln Trp Ala Glu Asp Val Leu Gly Asn Lys
65                  70                  75                  80

Thr Trp Asp Arg Glu Thr Arg Asp Leu Thr Gly Asn Gly Lys Asp Leu
                85                  90                  95

Arg Met Thr Leu Ala His Ile Lys Asp Gln Lys Glu Gly Leu His Ser
            100                 105                 110

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

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

Leu Glu Thr Lys Glu Trp Thr Met Pro Gln Ser Ser Arg Ala Gln Thr
145                 150                 155                 160

Leu Ala Met Asn Val Arg Asn Phe Leu Lys Glu Asp Ala Met Lys Thr
                165                 170                 175

Lys Thr His Tyr His Ala Met His Ala Asp Cys Leu Gln Glu Leu Arg
            180                 185                 190

Arg Tyr Leu Lys Ser Gly Val Val Leu Arg Arg Thr Val Pro Pro Met
        195                 200                 205

Val Asn Val Thr Arg Ser Glu Ala Ser Glu Gly Asn Ile Thr Val Thr
    210                 215                 220

Cys Arg Ala Ser Gly Phe Tyr Pro Trp Asn Ile Thr Leu Ser Trp Arg
225                 230                 235                 240

Gln Asp Gly Val Ser Leu Ser His Asp Thr Gln Gln Trp Gly Asp Val
                245                 250                 255

Leu Pro Asp Gly Asn Gly Thr Tyr Gln Thr Trp Val Ala Thr Arg Ile
            260                 265                 270

Cys Gln Gly Glu Glu Gln Arg Phe Thr Cys Tyr Met Glu His Ser Gly
        275                 280                 285

Asn His Ser Thr His Pro Val Pro Ser Gly Lys Val Leu Val Leu Gln
    290                 295                 300

Ser His Trp Gln Thr Phe His Val Ser Ala Val Ala Ala Ala Ala Ile
305                 310                 315                 320

Phe Val Ile Ile Ile Phe Tyr Val Arg Cys Cys Lys Lys Lys Thr Ser
                325                 330                 335
```

```
Ala Ala Glu Gly Pro Glu Leu Val Ser Leu Gln Val Leu Asp Gln His
            340                 345                 350

Pro Val Gly Thr Ser Asp His Arg Asp Ala Thr Gln Leu Gly Phe Gln
        355                 360                 365

Pro Leu Met Ser Asp Leu Gly Ser Thr Gly Ser Thr Glu Gly Ala
    370                 375                 380
```

<210> 312
<211> 305
<212> PRT
<213> Homo sapiens

<400> 312

```
Pro His Ser Leu Arg Tyr Asn Leu Met Val Leu Ser Gln Asp Gly Ser
1               5                   10                  15

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

Leu Arg Tyr Asp Arg Gln Lys Arg Arg Ala Lys Pro Gln Gly Gln Trp
        35                  40                  45

Ala Glu Asp Val Leu Gly Ala Lys Thr Trp Asp Thr Glu Thr Glu Asp
    50                  55                  60

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

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

Ile His Glu Asp Ser Ser Thr Arg Gly Ser Arg His Phe Tyr Tyr Asp
            100                 105                 110

Gly Glu Leu Phe Leu Ser Gln Asn Leu Glu Thr Gln Glu Ser Thr Val
        115                 120                 125

Pro Gln Ser Ser Arg Ala Gln Thr Leu Ala Met Asn Val Thr Asn Phe
    130                 135                 140

Trp Lys Glu Asp Ala Met Lys Thr Lys Thr His Tyr Arg Ala Met Gln
145                 150                 155                 160

Ala Asp Cys Leu Gln Lys Leu Gln Leu Pro Pro Met Val Asn Val Ile
                165                 170                 175

Cys Ser Glu Val Ser Glu Gly Asn Ile Thr Val Thr Cys Arg Ala Ser
            180                 185                 190

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

Ser Leu Ser His Asn Thr Gln Gln Trp Gly Asp Val Leu Pro Asp Gly
    210                 215                 220

Asn Gly Thr Tyr Gln Thr Trp Val Ala Thr Arg Ile Arg Gln Gly Glu
225                 230                 235                 240
```

```
Glu Gln Arg Phe Thr Cys Tyr Met Glu His Ser Gly Asn His Gly Thr
                245                 250                 255

His Pro Val Pro Ser Gly Lys Ala Leu Val Leu Gln Ser Gln Arg Thr
            260                 265                 270

Asp Phe Pro Tyr Val Ser Ala Ala Met Pro Cys Phe Val Ile Ile Ile
        275                 280                 285

Ile Leu Cys Val Pro Cys Cys Lys Lys Lys Thr Ser Ala Ala Glu Gly
    290                 295                 300

Pro
305
```

<210> 313
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 313

```
Gly Phe Asn Arg Gly Glu Cys
1               5
```

<210> 314
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 314

```
Gly Val Glu Pro Lys Ser Cys
1               5
```

<210> 315
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> TCRVL-HER2VH

<400> 315

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

Glu Arg Ala Thr Leu Ser Cys Ser Ala Thr Ser Ser Val Ser Tyr Met
            20                  25                  30

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
        35                  40                  45
```

```
Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50                  55                  60

Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
65                  70                  75                  80

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
                85                  90                  95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly Gly
            100                 105                 110

Gly Gly Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro
        115                 120                 125

Gly Ala Ser Leu Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys
    130                 135                 140

Asp Thr Tyr Ile His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu
145                 150                 155                 160

Trp Ile Gly Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Asp Pro
                165                 170                 175

Lys Phe Gln Asp Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr
            180                 185                 190

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

Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp
    210                 215                 220

Gly Gln Gly Ala Ser Val Thr Val Ser Ser Gly Phe Asn Arg Gly Glu
225                 230                 235                 240

Cys
```

<210> 316
<211> 723
<212> DNA
<213> Artificial Sequence

<220>
<223> TCRVL-HER2VH

<400> 316
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gtgccacctc aagtgtaagt tacatgcact ggtatcagca gaaaccaggg 120

aaagccccta agcgctggat ctatgacaca tccaaactgg cttctggggt cccatcaagg 180

ttcagcggca gtggatctgg gacagaattt actctcacaa tcagcagcct gcagcctgaa 240

gattttgcaa cttattactg tcagcagtgg agtagtaacc cgctcacgtt tggccagggg 300

accaagcttg agatcaaagg aggcggatcc ggcggcggag gccaggttca gctgcagcag 360

tctgggccag agcttgtgaa gccaggggcc tcactcaagt tgtcctgtac agcttctggc 420

ttcaacatta aagacaccta tatacactgg gtgaaacaga ggcctgaaca gggcctggaa 480

tggattggaa ggatttatcc tacgaatggt tatactagat atgacccgaa gttccaggac 540

aaggccacta taacagcaga cacatcctcc aacacagcct acctgcaggt cagccgcctg 600

acatctgagg acactgccgt ctattattgt tctagatggg gaggggacgg cttctatgct 660

atggactact ggggtcaagg agcctcggtc accgtgagct ccggattcaa caggggagag 720

tgt 723

<210> 317
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2VL-TCRVH

<400> 317

Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Asn Thr Ala
20 25 30

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

Tyr Ser Ala Ser Phe Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

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

Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
115 120 125

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Lys Phe
130 135 140

Thr Ser Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
145 150 155 160

Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Val Thr Lys Tyr Asn
165 170 175

Glu Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser
180 185 190

```
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
        195                 200                 205

His Tyr Cys Ala Arg Gly Ser Tyr Tyr Asp Tyr Asp Gly Phe Val Tyr
    210                 215                 220

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

Ser Cys
```

<210> 318
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> HER2VL-TCRVH

<400> 318

```
gacatcgtga tgacccagtc ccacaagttc atgtccacct ctgtgggcga tagggtcagc     60

atcacctgca aggccagcca ggatgtgaat actgctgtag cctggtatca gcagaaacca    120

ggacattctc ccaaactgct gatttactcc gcatccttcc ggtacactgg agtccctgat    180

cgcttcactg gcagcagatc tgggacagat ttcactttca ccatcagcag tgtgcaggct    240

gaagacctgg cagtttatta ctgtcagcaa cattatacta cacctcccac cttcggaggg    300

ggtaccaagg tggagatcaa aggaggcgga tccggcggcg gaggccaggt tcagctggtg    360

cagtctggag ctgaggtgaa gaagcctggg gcctcagtga aggtctcctg caaggccagc    420

ggttacaagt ttaccagcta cgtgatgcac tgggtgcgac aggcccctgg acaagggctt    480

gagtggatcg gatatattaa tccttacaat gatgttacta agtacaatga gaagttcaaa    540

ggcagagtca cgattaccgc ggacaaatcc acgagcacag cctacatgga gctgagcagc    600

ctgagatccg aggacacggc cgtgcactac tgtgcgagag ggagctacta tgattacgac    660

gggtttgttt actggggcca agggactctg gtcactgtga gctccggagt tgagcccaaa    720

tcttgt                                                               726
```

<210> 319
<211> 273
<212> PRT
<213> Artificial Sequence

<220>
<223> TCRVL-HER2VH-E coil

<400> 319

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

Glu Arg Ala Thr Leu Ser Cys Ser Ala Thr Ser Ser Val Ser Tyr Met
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

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

Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
65 70 75 80

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly Gly
100 105 110

Gly Gly Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro
115 120 125

Gly Ala Ser Leu Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys
130 135 140

Asp Thr Tyr Ile His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu
145 150 155 160

Trp Ile Gly Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Asp Pro
165 170 175

Lys Phe Gln Asp Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr
180 185 190

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

Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp
210 215 220

Gly Gln Gly Ala Ser Val Thr Val Ser Ser Gly Gly Cys Gly Gly Gly
225 230 235 240

Glu Val Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys Glu Val
245 250 255

Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys Gly Gly Gly Asn
260 265 270

Ser

<210> 320
<211> 819
<212> PRT
<213> Artificial Sequence

<220>
<223> TCRVL-HER2VH-E coil

<400> 320

Gly Ala Ala Ala Thr Thr Gly Thr Gly Thr Thr Gly Ala Cys Ala Cys
1 5 10 15

Ala Gly Thr Cys Thr Cys Cys Ala Gly Cys Cys Ala Cys Cys Cys Thr
20 25 30

Gly Thr Cys Thr Thr Thr Gly Thr Cys Thr Cys Cys Ala Gly Gly Gly
35 40 45

Gly Ala Ala Ala Gly Ala Gly Cys Cys Ala Cys Cys Cys Thr Cys Thr
50 55 60

Cys Cys Thr Gly Cys Ala Gly Thr Gly Cys Cys Ala Cys Cys Thr Cys
65 70 75 80

Ala Ala Gly Thr Gly Thr Ala Ala Gly Thr Thr Ala Cys Ala Thr Gly
85 90 95

Cys Ala Cys Thr Gly Gly Thr Ala Thr Cys Ala Gly Cys Ala Gly Ala
100 105 110

Ala Ala Cys Cys Ala Gly Gly Gly Ala Ala Ala Gly Cys Cys Cys Cys
115 120 125

Thr Ala Ala Gly Cys Gly Cys Thr Gly Gly Ala Thr Cys Thr Ala Thr
130 135 140

Gly Ala Cys Ala Cys Ala Thr Cys Cys Ala Ala Ala Cys Thr Gly Gly
145 150 155 160

Cys Thr Thr Cys Thr Gly Gly Gly Gly Thr Cys Cys Cys Ala Thr Cys
165 170 175

Ala Ala Gly Gly Thr Thr Cys Ala Gly Cys Gly Gly Cys Ala Gly Thr
180 185 190

Gly Gly Ala Thr Cys Thr Gly Gly Gly Ala Cys Ala Gly Ala Ala Thr
195 200 205

Thr Thr Ala Cys Thr Cys Thr Cys Ala Cys Ala Ala Thr Cys Ala Gly
210 215 220

Cys Ala Gly Cys Cys Thr Gly Cys Ala Gly Cys Cys Thr Gly Ala Ala
225 230 235 240

Gly Ala Thr Thr Thr Thr Gly Cys Ala Ala Cys Thr Thr Ala Thr Thr
245 250 255

Ala Cys Thr Gly Thr Cys Ala Gly Cys Ala Gly Thr Gly Gly Ala Gly
260 265 270

Thr Ala Gly Thr Ala Ala Cys Cys Cys Gly Cys Thr Cys Ala Cys Gly
275 280 285

Thr Thr Thr Gly Gly Cys Cys Ala Gly Gly Gly Gly Ala Cys Cys Ala
290 295 300

Ala Gly Cys Thr Thr Gly Ala Gly Ala Thr Cys Ala Ala Ala Gly Gly
305 310 315 320

Ala Gly Gly Cys Gly Gly Ala Thr Cys Cys Gly Gly Cys Gly Gly Cys
325 330 335

Gly Gly Ala Gly Gly Cys Cys Ala Gly Gly Thr Thr Cys Ala Gly Cys
340 345 350

Thr Gly Cys Ala Gly Cys Ala Gly Thr Cys Thr Gly Gly Gly Cys Cys
355 360 365

Ala Gly Ala Gly Cys Thr Thr Gly Thr Gly Ala Ala Gly Cys Cys Ala
370 375 380

Gly Gly Gly Gly Cys Cys Thr Cys Ala Cys Thr Cys Ala Ala Gly Thr
385 390 395 400

Thr Gly Thr Cys Cys Thr Gly Thr Ala Cys Ala Gly Cys Thr Thr Cys
405 410 415

Thr Gly Gly Cys Thr Thr Cys Ala Ala Cys Ala Thr Thr Ala Ala Ala
420 425 430

Gly Ala Cys Ala Cys Cys Thr Ala Thr Ala Thr Ala Cys Ala Cys Thr
435 440 445

Gly Gly Gly Thr Gly Ala Ala Ala Cys Ala Gly Ala Gly Gly Cys Cys
450 455 460

Thr Gly Ala Ala Cys Ala Gly Gly Gly Cys Cys Thr Gly Gly Ala Ala
465 470 475 480

Thr Gly Gly Ala Thr Thr Gly Gly Ala Ala Gly Gly Ala Thr Thr Thr
485 490 495

Ala Thr Cys Cys Thr Ala Cys Gly Ala Ala Thr Gly Gly Thr Thr Ala
500 505 510

Thr Ala Cys Thr Ala Gly Ala Thr Ala Thr Gly Ala Cys Cys Cys Gly
515 520 525

Ala Ala Gly Thr Thr Cys Cys Ala Gly Gly Ala Cys Ala Ala Gly Gly
530 535 540

Cys Cys Ala Cys Thr Ala Thr Ala Ala Cys Ala Gly Cys Ala Gly Ala
545 550 555 560

Cys Ala Cys Ala Thr Cys Cys Thr Cys Cys Ala Ala Cys Ala Cys Ala
565 570 575

Gly Cys Cys Thr Ala Cys Cys Thr Gly Cys Ala Gly Gly Thr Cys Ala
580 585 590

Gly Cys Cys Gly Cys Cys Thr Gly Ala Cys Ala Thr Cys Thr Gly Ala
595 600 605

Gly Gly Ala Cys Ala Cys Thr Gly Cys Cys Gly Thr Cys Thr Ala Thr
610 615 620

Thr Ala Thr Thr Gly Thr Thr Cys Thr Ala Gly Ala Thr Gly Gly Gly
625 630 635 640

Gly Ala Gly Gly Gly Gly Ala Cys Gly Gly Cys Thr Thr Cys Thr Ala
645 650 655

Thr Gly Cys Thr Ala Thr Gly Gly Ala Cys Thr Ala Cys Thr Gly Gly
660 665 670

Gly Gly Thr Cys Ala Ala Gly Gly Ala Gly Cys Cys Thr Cys Gly Gly
675 680 685

Thr Cys Ala Cys Cys Gly Thr Gly Ala Gly Cys Thr Cys Cys Gly Gly
690 695 700

Ala Gly Gly Ala Thr Gly Thr Gly Gly Cys Gly Gly Thr Gly Gly Ala
705 710 715 720

Gly Ala Ala Gly Thr Gly Gly Cys Cys Gly Cys Ala Cys Thr Gly Gly
725 730 735

Ala Gly Ala Ala Ala Gly Ala Gly Gly Thr Thr Gly Cys Thr Gly Cys
740 745 750

Thr Thr Thr Gly Gly Ala Gly Ala Ala Gly Gly Ala Gly Gly Thr Cys
755 760 765

Gly Cys Thr Gly Cys Ala Cys Thr Thr Gly Ala Ala Ala Ala Gly Gly
770 775 780

Ala Gly Gly Thr Cys Gly Cys Ala Gly Cys Cys Cys Thr Gly Gly Ala
785 790 795 800

Gly Ala Ala Ala Gly Gly Cys Gly Gly Cys Gly Gly Gly Ala Ala Thr
805 810 815

Thr Cys Thr

<210> 321
<211> 274
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2VL-TCRVH-K coil

<400> 321

Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Asn Thr Ala
20 25 30

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

Tyr Ser Ala Ser Phe Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

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

Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
115 120 125

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Lys Phe
130 135 140

Thr Ser Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
145 150 155 160

Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Val Thr Lys Tyr Asn
165 170 175

Glu Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser
180 185 190

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

His Tyr Cys Ala Arg Gly Ser Tyr Tyr Asp Tyr Asp Gly Phe Val Tyr
210 215 220

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Cys Gly Gly
225 230 235 240

Gly Lys Val Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu Lys
245 250 255

Val Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu Gly Gly Gly
260 265 270

Asn Ser

<210> 322
<211> 822
<212> DNA
<213> Artificial Sequence

<220>
<223> HER2VL-TCRVH-K coil

<400> 322
gacatcgtga tgacccagtc ccacaagttc atgtccacct ctgtgggcga tagggtcagc 60

atcacctgca aggccagcca ggatgtgaat actgctgtag cctggtatca gcagaaacca 120

ggacattctc ccaaactgct gatttactcc gcatccttcc ggtacactgg agtccctgat 180

cgcttcactg gcagcagatc tgggacagat ttcactttca ccatcagcag tgtgcaggct 240

gaagacctgg cagtttatta ctgtcagcaa cattatacta cacctcccac cttcggaggg 300

ggtaccaagg tggagatcaa aggaggcgga tccggcggcg gaggccaggt tcagctggtg 360

cagtctggag ctgaggtgaa gaagcctggg gcctcagtga aggtctcctg caaggccagc 420

ggttacaagt ttaccagcta cgtgatgcac tgggtgcgac aggcccctgg acaagggctt 480

gagtggatcg gatatattaa tccttacaat gatgttacta agtacaatga gaagttcaaa 540

ggcagagtca cgattaccgc ggacaaatcc acgagcacag cctacatgga gctgagcagc 600

ctgagatccg aggacacggc cgtgcactac tgtgcgagag ggagctacta tgattacgac 660

gggtttgttt actggggcca agggactctg gtcactgtga gctccggagg atgtggcggt 720

ggaaaagtgg ccgcactgaa ggagaaagtt gctgctttga aagagaaggt cgccgcactt 780

aaggaaaagg tcgcagccct gaaagagggc ggcgggaatt ct 822

<210> 323
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic ABD Construct

<400> 323

Leu Ala Glu Ala Lys Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly
1 5 10 15

Val Ser Asp Tyr Tyr Lys Asn Ala Ala Asn Asn Ala Lys Thr Val Glu
20 25 30

Gly Val Lys Ala Leu Ile Ala Glu Ile Leu Ala Ala Leu Pro
35 40 45

<210> 324
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic ABD Construct

<400> 324

Leu Ala Glu Ala Lys Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly
1 5 10 15

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

Gly Val Lys Ala Leu Ile Ala Glu Ile Leu Ala Ala Leu Pro
35 40 45

<210> 325
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial ABD Construct

<400> 325

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

Ala Leu Ile Asp Glu
20

<210> 326
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic ABD Construct (ABD Y60-E80 Variant N66D/T70S/V71A)

<400> 326

Tyr Tyr Lys Asn Leu Ile Asp Asn Ala Lys Ser Ala Glu Gly Val Lys
1 5 10 15

Ala Leu Ile Asp Glu
20

<210> 327
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic ABD Construct (ABD Y60-E80 Variant L64A/I65A/V71A)

<400> 327

Tyr Tyr Lys Asn Ala Ala Asn Asn Ala Lys Thr Ala Glu Gly Val Lys
1 5 10 15

Ala Leu Ile Asp Glu
20

<210> 328
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic ABD Construct (L64A/I65A/V71A ("ABD (AAA)"))

<400> 328

Leu Ala Glu Ala Lys Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly
1 5 10 15

Val Ser Asp Tyr Tyr Lys Asn Ala Ala Asn Asn Ala Lys Thr Ala Glu
20 25 30

Gly Val Lys Ala Leu Ile Asp Glu Ile Leu Ala Ala Leu Pro
35 40 45

<210> 329
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic ABD Construct (N66D/T70S/V71A ("ABD (DSA)"))

<400> 329

Leu Ala Glu Ala Lys Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly
1 5 10 15

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

Gly Val Lys Ala Leu Ile Asp Glu Ile Leu Ala Ala Leu Pro
35 40 45