SEQUENCE LISTING

<110> Roche Glycart AG

<120> Bispecific T cell activating antigen binding molecules

<130> 31447

<150> EP 13156686.1
<151> 2013-02-26

<160> 122

<170> PatentIn version 3.5

<210> 1
<211> 455
<212> PRT
<213> Artificial Sequence

<220>
<223> HC CD3 CH2527 (VH_3-23(12))

<400> 1

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

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

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

Ser Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50                  55                  60

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

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
            100                 105                 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
        115                 120                 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
    130                 135                 140

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
145                 150                 155                 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
                165                 170                 175
```

```
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
            180                 185                 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
        195                 200                 205

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
    210                 215                 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
225                 230                 235                 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
                245                 250                 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
            260                 265                 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
        275                 280                 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
    290                 295                 300

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
305                 310                 315                 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
                325                 330                 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
            340                 345                 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
        355                 360                 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
    370                 375                 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
385                 390                 395                 400

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
                405                 410                 415

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

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


<210>  2
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  LC CD3 CH2527 (VL_7-46(13))

<400>  2

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


Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
            20                  25                  30


Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Gly Gln Ala Phe Arg Gly
        35                  40                  45


Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Thr Pro Ala Arg Phe
    50                  55                  60


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


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


Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
            100                 105                 110


Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu
        115                 120                 125


Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro
    130                 135                 140


Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala
145                 150                 155                 160


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


Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg
            180                 185                 190


Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr
        195                 200                 205


Val Ala Pro Thr Glu Cys Ser
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210 215

<210> 3
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> VH CD3 CH2527 (VH_3-23(12))

<400> 3

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

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

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

Ser Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

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

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 4
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> HCDR1 CD3 CH2527 (VH_3-23(12))

<400> 4

Thr Tyr Ala Met Asn
1 5

<210> 5
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> HCDR2 CD3 CH2527 (VH_3-23(12))

<400> 5

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

Val Lys Gly

<210> 6
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> HCDR3 CD3 CH2527 (VH_3-23(12))

<400> 6

His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr
1 5 10

<210> 7
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> VL CD3 CH2527 (VL_7-46(13))

<400> 7

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

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Gly Gln Ala Phe Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Thr Pro Ala Arg Phe
50 55 60

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

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

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 8
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> LCDR1 CD3 CH2527 (VL_7-46(13))

<400> 8

Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 9
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> LCDR2 CD3 CH2527 (VL_7-46(13))

<400> 9

Gly Thr Asn Lys Arg Ala Pro
1 5

<210> 10
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> LCDR3 CD3 CH2527 (VL_7-46(13))

<400> 10

Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 11
<211> 442
<212> PRT
<213> Artificial Sequence

<220>
<223> HC MCSP M4-3 (C1)$

<400> 11

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Thr Ser Gly
20 25 30

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

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

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

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

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

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
        115                 120                 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
    130                 135                 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
145                 150                 155                 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
                165                 170                 175

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
            180                 185                 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
        195                 200                 205

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
    210                 215                 220

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
225                 230                 235                 240

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
                245                 250                 255

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
            260                 265                 270

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
        275                 280                 285

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
    290                 295                 300

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
305                 310                 315                 320

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
                325                 330                 335

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
            340                 345                 350

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
        355                 360                 365
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Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
    370                 375                 380

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
385                 390                 395                 400

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
                405                 410                 415

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
            420                 425                 430

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440
```

<210> 12
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> LC MCSP ML2 (G3)

<400> 12

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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 Gly Ile Arg Asn Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Tyr Thr Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
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145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

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

Phe Asn Arg Gly Glu Cys
210

<210> 13
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> VH MCSP M4-3 (C1)

<400> 13

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Thr Ser Gly
20 25 30

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

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

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

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

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

<210> 14
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> HCDR1 MCSP M4-3 (C1)

<400> 14

Ser Gly Tyr Tyr Trp Asn

1 5

<210> 15
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> HCDR2 MCSP M4-3 (C1)

<400> 15

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

<210> 16
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> HCDR3 MCSP M4-3 (C1)

<400> 16

Phe Asp Tyr
1

<210> 17
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> VL MCSP ML2 (G3)

<400> 17

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 Gly Ile Arg Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Tyr Thr Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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

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

<210> 18
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> LCDR1 MCSP ML2 (G3)

<400> 18

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

<210> 19
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> LCDR2 MCSP ML2 (G3)

<400> 19

Tyr Thr Ser Ser Leu His Ser
1 5

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

<220>
<223> LCDR3 MCSP ML2 (G3)

<400> 20

Gln Gln Tyr Ser Ala Leu Pro Trp Thr
1 5

<210> 21
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> HC CEA CH1A1A 98-99

<400> 21

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 Glu Phe
20 25 30

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

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

```
Lys Gly Arg Val Thr Phe 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 Trp Asp Phe Ala Tyr Tyr Val Glu Ala Met Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335
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Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445

Pro Gly Lys
    450
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<210> 22
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> LC CEA 2F1

<400> 22

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

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

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Tyr Thr Tyr Pro Leu
                85                  90                  95

Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala
```

100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

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

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 23
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> VH CEA CH1A1A 98-99

<400> 23

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 Glu Phe
20 25 30

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 24
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> HCDR1 CEA CH1A1A 98-99

<400> 24

Glu Phe Gly Met Asn
1   5

<210> 25
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> HCDR2 CEA CH1A1A 98-99

<400> 25

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

Gly

<210> 26
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> HCDR3 CEA CH1A1A 98-99

<400> 26

Trp Asp Phe Ala Tyr Tyr Val Glu Ala Met Asp Tyr
1   5   10

<210> 27
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> VL CEA 2F1

<400> 27

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

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

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Tyr Thr Tyr Pro Leu
85 90 95

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

<210> 28
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> LCDR1 CEA 2F1

<400> 28

Lys Ala Ser Ala Ala Val Gly Thr Tyr Val Ala
1 5 10

<210> 29
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> LCDR2 CEA 2F1

<400> 29

Ser Ala Ser Tyr Arg Lys Arg
1 5

<210> 30
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> LCDR3 CEA 2F1

<400> 30

His Gln Tyr Tyr Thr Tyr Pro Leu Phe Thr
1 5 10

<210> 31
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> VL CD3 CH2527 (VL_7-43(11))

<400> 31

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


Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
            20                  25                  30


Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
        35                  40                  45


Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Thr Pro Ala Arg Phe
    50                  55                  60


Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
65                  70                  75                  80


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


Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Ser
            100                 105                 110
```

<210> 32
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> VH CD3 CH2527 (VHcomboA49SV93A)

<400> 32

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


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


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


Ser Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50                  55                  60


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


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


Tyr Cys Ala Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
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100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 33
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> VH CD3 CH2527 (VHcomboA49SV93AR94K)

<400> 33

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

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

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

Ser Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

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

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

Tyr Cys Ala Lys His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 34
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> VH MCSP M4-3 (D6)

<400> 34

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Thr Ser Gly
20 25 30

Tyr Tyr Trp Asn Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu Trp

35 40 45

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

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

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

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

<210> 35
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> HCDR2 MCSP M4-3 (D6)

<400> 35

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

<210> 36
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> VH MCSP M4-3 (A7)

<400> 36

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Thr Asp Gly
20 25 30

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

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

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

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

Ala Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

eolf-seql

100 105 110

<210> 37
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> HCDR1 MCSP M4-3 (A7)

<400> 37

Asp Gly Tyr Tyr Trp Asn
1 5

<210> 38
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> HCDR2 MCSP M4-3 (A7)

<400> 38

Ile Thr Phe Asp Gly Arg Asn Asn Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 39
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> VH MCSP M4-3 (B7)

<400> 39

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Thr Ser Gly
20 25 30

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

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

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

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

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

<210> 40
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> HCDR2 MCSP M4-3 (B7)

<400> 40

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

<210> 41
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> VH MCSP M4-3 (B8)

<400> 41

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Thr Ser Gly
20 25 30

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

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

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

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

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

<210> 42
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> VH MCSP M4-3

<400> 42

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Thr Ser Gly

20 25 30

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

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

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

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

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

<210> 43
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> VL MCSP ML2 (E10)

<400> 43

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 Tyr Gly Ile Arg Gly Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Tyr Thr Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr His Cys Gln Gln Tyr Ser Lys Leu Pro Trp
85 90 95

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

<210> 44
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> LCDR1 MCSP ML2 (E10)

<400> 44

Arg Ala Ser Tyr Gly Ile Arg Gly Tyr Leu Asn
1 5 10

<210> 45
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> LCDR3 MCSP ML2 (E10)

<400> 45

Gln Gln Tyr Ser Lys Leu Pro Trp Thr
1 5

<210> 46
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> VL MCSP ML2 (E10-G3)

<400> 46

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 Tyr Gly Ile Arg Gly Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Tyr Thr Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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

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

<210> 47
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> VL MCSP ML2 (C5)

<400> 47

```
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 Arg Gly Ile Arg Glu Tyr
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Tyr Thr Gly Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


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


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


<210>  48
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  LCDR1 MCSP ML2 (C5)

<400>  48

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


<210>  49
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  LCDR2 MCSP ML2 (C5)

<400>  49

Tyr Thr Gly Ser Leu His Ser
1               5


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

<220>
<223>  LCDR3 MCSP ML2 (C5)

<400>  50

Gln Gln Tyr Ser Glu Leu Pro Trp Thr
```

1 5

<210> 51
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> VL MCSP ML2 (C5-G3)

<400> 51

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 Arg Gly Ile Arg Glu Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Tyr Thr Gly Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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

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

<210> 52
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> VL MCSP ML2

<400> 52

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 Gly Ile Arg Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Tyr Thr Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

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

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

<210> 53
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> LC CD3 CH2527 (Crossfab, VL-CH1)

<400> 53

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

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Gly Gln Ala Phe Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Thr Pro Ala Arg Phe
50 55 60

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

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

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Ser Ala
100 105 110

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
115 120 125

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

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
165 170 175

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
180 185 190

```
Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
        195                 200                 205


Val Glu Pro Lys Ser Cys
    210


<210>  54
<211>  685
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  MCSP M4-3 (C1) (VH-CH1) - CD3 CH2527 (Crossfab VH-Ck) - Fc(knob)
       P329GLALA

<400>  54

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


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Thr Ser Gly
            20                  25                  30


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


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


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


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


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


Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
        115                 120                 125


Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
    130                 135                 140


Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
145                 150                 155                 160


Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
                165                 170                 175


Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
            180                 185                 190
```

```
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
        195                 200                 205

Lys Val Glu Pro Lys Ser Cys Asp Gly Gly Gly Gly Ser Gly Gly Gly
    210                 215                 220

Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro
225                 230                 235                 240

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
                245                 250                 255

Thr Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
            260                 265                 270

Trp Val Ser Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
        275                 280                 285

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
    290                 295                 300

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
305                 310                 315                 320

Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser
                325                 330                 335

Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala
            340                 345                 350

Ser Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
        355                 360                 365

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
    370                 375                 380

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
385                 390                 395                 400

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
                405                 410                 415

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
            420                 425                 430

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Asp Lys Thr His Thr Cys
    450                 455                 460
```

```
Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu
465                 470                 475                 480

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                485                 490                 495

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            500                 505                 510

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        515                 520                 525

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    530                 535                 540

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
545                 550                 555                 560

Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys
                565                 570                 575

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys
            580                 585                 590

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys
        595                 600                 605

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    610                 615                 620

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
625                 630                 635                 640

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                645                 650                 655

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            660                 665                 670

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        675                 680                 685


<210>  55
<211>  442
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  MCSP M4-3 (C1) (VH-CH1) - Fc(hole) P329GLALA

<400>  55

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

```
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Thr Ser Gly
            20                  25                  30

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

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

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

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

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

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
        115                 120                 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
    130                 135                 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
145                 150                 155                 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
                165                 170                 175

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
            180                 185                 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
        195                 200                 205

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
    210                 215                 220

Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
225                 230                 235                 240

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
                245                 250                 255

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
            260                 265                 270

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
        275                 280                 285
```

```
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
    290                 295                 300

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
305                 310                 315                 320

Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
                325                 330                 335

Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu
            340                 345                 350

Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr
        355                 360                 365

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
    370                 375                 380

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
385                 390                 395                 400

Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
                405                 410                 415

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
            420                 425                 430

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440
```

<210> 56
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> LC CD3 CH2527 (Crossfab, VL-CH1)

<400> 56

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

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
            20                  25                  30

Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Gly Gln Ala Phe Arg Gly
        35                  40                  45

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Thr Pro Ala Arg Phe
    50                  55                  60
```

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

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

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Ser Ala
100 105 110

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
115 120 125

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

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
165 170 175

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
180 185 190

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
195 200 205

Val Glu Pro Lys Ser Cys
210

<210> 57
<211> 694
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA CH1A1A 98/99 - CD3 CH2527 (Crossfab VH-Ck) - Fc(knob) P329GLALA

<400> 57

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 Glu Phe
20 25 30

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu
225                 230                 235                 240

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
                245                 250                 255

Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp Val
            260                 265                 270

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Arg Ile Arg Ser
        275                 280                 285

Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg
    290                 295                 300

Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met
305                 310                 315                 320

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His
                325                 330                 335

Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp Gly Gln
```

```
            340                 345                 350

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Val Ala Ala Pro Ser Val
        355                 360                 365

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

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
385                 390                 395                 400

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val
                405                 410                 415

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu
            420                 425                 430

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu
        435                 440                 445

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
    450                 455                 460

Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
465                 470                 475                 480

Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                485                 490                 495

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
            500                 505                 510

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
        515                 520                 525

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
    530                 535                 540

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
545                 550                 555                 560

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly
                565                 570                 575

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
            580                 585                 590

Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn
        595                 600                 605

Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
```

610 615 620

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
625 630 635 640

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
645 650 655

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
660 665 670

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
675 680 685

Ser Leu Ser Pro Gly Lys
690

<210> 58
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA CH1A1A 98/99 (VH-CH1) - Fc(hole) P329GLALA

<400> 58

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 Glu Phe
20 25 30

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

```
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
                405                 410                 415
```

```
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445

Pro Gly Lys
    450
```

<210> 59
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> LC DP47 GS

<400> 59

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

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

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

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

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

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

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
```

180 185 190

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

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 60
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> LC CD3 CH2527 (Crossfab, VL-CH1)

<400> 60

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

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Gly Gln Ala Phe Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Thr Pro Ala Arg Phe
50 55 60

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

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

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Ser Ala
100 105 110

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
115 120 125

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

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
165 170 175

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
180 185 190

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
195 200 205

Val Glu Pro Lys Ser Cys
210

<210> 61
<211> 688
<212> PRT
<213> Artificial Sequence

<220>
<223> DP47 GS (VH-CH1) - CD3 CH2527 (Crossfab VH-Ck) - Fc(knob) P329GLALA

<400> 61

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

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

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

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

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
115 120 125

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
130 135 140

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
145 150 155 160

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
165 170 175

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
180 185 190

```
Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
        195                 200                 205

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Gly Gly Gly Gly Ser
    210                 215                 220

Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu
225                 230                 235                 240

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
                245                 250                 255

Thr Phe Ser Thr Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys
            260                 265                 270

Gly Leu Glu Trp Val Ser Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala
        275                 280                 285

Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
    290                 295                 300

Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu
305                 310                 315                 320

Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser
                325                 330                 335

Tyr Val Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
            340                 345                 350

Ser Ser Ala Ser Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
        355                 360                 365

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
    370                 375                 380

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
385                 390                 395                 400

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
                405                 410                 415

Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
            420                 425                 430

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

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Asp Lys Thr
    450                 455                 460
```

```
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
465                 470                 475                 480

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                485                 490                 495

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            500                 505                 510

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        515                 520                 525

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    530                 535                 540

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
545                 550                 555                 560

Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr
                565                 570                 575

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            580                 585                 590

Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys
        595                 600                 605

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    610                 615                 620

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
625                 630                 635                 640

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                645                 650                 655

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            660                 665                 670

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        675                 680                 685


<210>  62
<211>  445
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  DP47 GS (VH-CH1) - Fc(hole) P329GLALA

<400>  62

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15
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```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

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

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

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

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
        115                 120                 125

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
    130                 135                 140

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
145                 150                 155                 160

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
                165                 170                 175

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
            180                 185                 190

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
        195                 200                 205

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
    210                 215                 220

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

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                245                 250                 255

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            260                 265                 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        275                 280                 285
```

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys
325 330 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser
340 345 350

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys
355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385 390 395 400

Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 63
<211> 1365
<212> DNA
<213> Artificial Sequence

<220>
<223> HC CD3 CH2527 (VH_3-23(12))

<400> 63
gaggtgcagc tgctggaatc tggcggcgga ctggtgcagc ctggcggatc tctgagactg 60

agctgtgccg ccagcggctt caccttcagc acctacgcca tgaactgggt gcgccaggcc 120

cctggcaaag gcctggaatg ggtgtcccgg atcagaagca agtacaacaa ctacgccacc 180

tactacgccg acagcgtgaa gggccggttc accatcagcc gggacgacag caagaacacc 240

ctgtacctgc agatgaacag cctgcgggcc gaggacaccg ccgtgtacta ttgtgtgcgg 300

cacggcaact tcggcaacag ctatgtgtct tggtttgcct actggggcca gggcaccctc 360

gtgaccgtgt catctgctag caccaagggc ccatcggtct tccccctggc accctcctcc 420

aagagcacct ctgggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 480

ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct 540

gtcctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcagc 600

ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 660

aagaaagttg agcccaaatc ttgtgacaaa actcacacat gcccaccgtg cccagcacct 720

gaactcctgg ggggaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 780

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 840

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 900

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 960

tggctgaatg gcaaggagta caagtgcaag gtctccaaca aagccctccc agcccccatc 1020

gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1080

ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1140

tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1200

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1260

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1320

cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaa 1365

<210> 64
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> LC CD3 CH2527 (VL_7-46(13))

<400> 64
caggccgtcg tgacccagga acccagcctg acagtgtctc ctggcggcac cgtgaccctg 60

acatgtggca gttctacagg cgccgtgacc accagcaact acgccaactg ggtgcaggaa 120

aagcccggcc aggccttcag aggactgatc ggcggcacca acaagagagc ccctggcacc 180

cctgccagat tcagcggatc tctgctggga ggaaaggccg ccctgacact gtctggcgcc 240

cagccagaag atgaggccga gtactactgc gccctgtggt acagcaacct gtgggtgttc 300

ggcggaggca ccaagctgac agtcctaggt caacccaagg ctgcccccag cgtgaccctg 360

ttccccccca gcagcgagga actgcaggcc aacaaggcca ccctggtctg cctgatcagc 420

gacttctacc caggcgccgt gaccgtggcc tggaaggccg acagcagccc cgtgaaggcc 480

ggcgtggaga ccaccacccc cagcaagcag agcaacaaca agtacgccgc cagcagctac 540

ctgagcctga cccccgagca gtggaagagc cacaggtcct acagctgcca ggtgacccac 600

gagggcagca ccgtggagaa aaccgtggcc cccaccgagt gcagc 645

<210> 65
<211> 375
<212> DNA
<213> Artificial Sequence

<220>

<223> VH CD3 CH2527 (VH_3-23(12))

<400> 65
gaggtgcagc tgctggaatc tggcggcgga ctggtgcagc ctggcggatc tctgagactg 60

agctgtgccg ccagcggctt caccttcagc acctacgcca tgaactgggt gcgccaggcc 120

cctggcaaag gcctggaatg ggtgtcccgg atcagaagca agtacaacaa ctacgccacc 180

tactacgccg acagcgtgaa gggccggttc accatcagcc gggacgacag caagaacacc 240

ctgtacctgc agatgaacag cctgcgggcc gaggacaccg ccgtgtacta ttgtgtgcgg 300

cacggcaact tcggcaacag ctatgtgtct tggtttgcct actggggcca gggcaccctc 360

gtgaccgtgt catct 375

<210> 66
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> HCDR1 CD3 CH2527 (VH_3-23(12))

<400> 66
acctacgcca tgaac 15

<210> 67
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> HCDR2 CD3 CH2527 (VH_3-23(12))

<400> 67
cggatcagaa gcaagtacaa caactacgcc acctactacg ccgacagcgt gaagggc 57

<210> 68
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> HCDR3 CD3 CH2527 (VH_3-23(12))

<400> 68
cacggcaact tcggcaacag ctatgtgtct tggtttgcct ac 42

<210> 69
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> VL CD3 CH2527 (VL_7-46(13))

<400> 69
caggccgtcg tgacccagga acccagcctg acagtgtctc ctggcggcac cgtgaccctg 60

acatgtggca gttctacagg cgccgtgacc accagcaact acgccaactg ggtgcaggaa 120

aagcccggcc aggccttcag aggactgatc ggcggcacca acaagagagc ccctggcacc 180

cctgccagat tcagcggatc tctgctggga ggaaaggccg ccctgacact gtctggcgcc 240

cagccagaag atgaggccga gtactactgc gccctgtggt acagcaacct gtgggtgttc 300

ggcggaggca ccaagctgac agtccta 327

<210> 70
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> LCDR1 CD3 CH2527 (VL_7-46(13))

<400> 70
ggcagttcta caggcgccgt gaccaccagc aactacgcca ac 42

<210> 71
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> LCDR2 CD3 CH2527 (VL_7-46(13))

<400> 71
ggcaccaaca agagagcccc t 21

<210> 72
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> LCDR3 CD3 CH2527 (VL_7-46(13))

<400> 72
gccctgtggt acagcaacct gtgggtg 27

<210> 73
<211> 1326
<212> DNA
<213> Artificial Sequence

<220>
<223> HC MCSP M4-3 (C1)

<400> 73
caggtgcaat tgcaggaaag cggccctggc ctggtcaagc ccagccagac cctgagcctg 60

acctgcaccg tgtccggcgg cagcatcacc agcggctatt attggaactg gattcggcag 120

caccccggca agggcctgga atggatcggc tacatcactt tcgacggctc taacaactac 180

aaccccagcc tgaagtccag agtgaccatc agccgggaca ccagcaagaa ccagttcagc 240

ctgaagctgt ccagcgtgac agccgccgac accgccgtgt actactgcgc cgacttcgac 300

tactggggcc agggcaccct ggtcaccgtg tccagcgcta gcaccaaggg cccatcggtc 360

ttcccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 420

gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480

ggcgtgcaca ccttcccggc tgtcctacag tcctcaggac tctactccct cagcagcgtg 540

gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600

cccagcaaca ccaaggtgga caagaaagtt gagcccaaat cttgtgacaa aactcacaca 660

tgcccaccgt gcccagcacc tgaactcctg gggggaccgt cagtcttcct cttccccca 720

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 780

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 840

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 900

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggagt acaagtgcaa ggtctccaac 960

aaagccctcc cagccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1020

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg 1080

acctgcctgg tcaaaggctt ctatcccagc gacatcgccg tggagtggga gagcaatggg 1140

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1200

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 1260

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 1320

ggtaaa 1326

<210> 74
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> LC MCSP ML2 (G3)

<400> 74
gacatccaga tgacccagag ccccagcagc ctgagcgcca gcgtgggcga cagagtgacc 60

atcacctgcc gggccagcca gggcatccgg aactacctga actggtatca gcagaagccc 120

ggcaaggccc ccaagctgct gatctactac accagcagcc tgcacagcgg cgtgcctagc 180

cggtttagcg gcagcggctc cggcaccgac tacaccctga ccattagctc cctgcagccc 240

gaggacttcg ccacctacta ctgccagcag tactctgctc tgccgtggac cttcggccag 300

ggaacaaagg tggagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 75
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> VH MCSP M4-3 (C1)

<400> 75
caggtgcaat tgcaggaaag cggccctggc ctggtcaagc ccagccagac cctgagcctg 60

acctgcaccg tgtccggcgg cagcatcacc agcggctatt attggaactg gattcggcag 120

caccccggca agggcctgga atggatcggc tacatcactt tcgacggctc taacaactac 180

aaccccagcc tgaagtccag agtgaccatc agccgggaca ccagcaagaa ccagttcagc 240

ctgaagctgt ccagcgtgac agccgccgac accgccgtgt actactgcgc cgacttcgac 300

tactggggcc agggcaccct ggtcaccgtg tccagc 336

<210> 76
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> HCDR1 MCSP M4-3 (C1)

<400> 76
agcggctatt attggaac 18

<210> 77
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> HCDR2 MCSP M4-3 (C1)

<400> 77
tacatcactt tcgacggctc taacaactac aaccccagcc tgaagtcc 48

<210> 78
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> HCDR3 MCSP M4-3 (C1)

<400> 78
ttcgactac 9

<210> 79
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> VL MCSP ML2 (G3)

<400> 79
gacatccaga tgacccagag ccccagcagc ctgagcgcca gcgtgggcga cagagtgacc 60

atcacctgcc gggccagcca gggcatccgg aactacctga actggtatca gcagaagccc 120

ggcaaggccc ccaagctgct gatctactac accagcagcc tgcacagcgg cgtgcctagc 180

cggtttagcg gcagcggctc cggcaccgac tacaccctga ccattagctc cctgcagccc 240

gaggacttcg ccacctacta ctgccagcag tactctgctc tgccgtggac cttcggccag 300

ggaacaaagg tggagatcaa g 321

<210> 80
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> LCDR1 MCSP ML2 (G3)

<400> 80
cgggccagcc agggcatccg gaactacctg aac 33

<210> 81
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> LCDR2 MCSP ML2 (G3)

<400> 81
tacaccagca gcctgcacag c 21

<210> 82
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> LCDR3 MCSP ML2 (G3)

<400> 82
cagcagtact ctgctctgcc gtggacc 27

<210> 83
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> HC CEA CH1A1A 98-99

<400> 83
caggtgcagc tggtgcagtc tggcgccgaa gtgaagaaac ctggagctag tgtgaaggtg 60

tcctgcaagg ccagcggcta caccttcacc gagttcggca tgaactgggt ccgacaggct 120

ccaggccagg gcctcgaatg gatgggctgg atcaacacca agaccggcga ggccacctac 180

gtggaagagt tcaagggcag agtgaccttc accacggaca ccagcaccag caccgcctac 240

atggaactgc ggagcctgag aagcgacgac accgccgtgt actactgcgc cagatgggac 300

ttcgcctatt acgtggaagc catggactac tggggccagg gcaccaccgt gaccgtgtct 360

agcgctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

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aaggagtaca agtgcaaggt ctccaacaaa gccctcccag cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1200

gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1260

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acgcagaaga gcctctccct gtctccgggt aaa 1353

<210> 84
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> LC CEA 2F1

<400> 84
gatatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtgggaga cagagtcacc 60

atcacttgca aggccagtgc ggctgtgggt acgtatgttg cgtggtatca gcagaaacca 120

gggaaagcac ctaagctcct gatctattcg gcatcctacc gcaaaagggg agtcccatca 180

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gaagatttcg caacttacta ctgtcaccaa tattacacct atcctctatt cacgtttggc 300

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ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 645

<210> 85
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> VH CEA CH1A1A 98-99

<400> 85
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tcctgcaagg ccagcggcta caccttcacc gagttcggca tgaactgggt ccgacaggct 120

ccaggccagg gcctcgaatg gatgggctgg atcaacacca agaccggcga ggccacctac 180

gtggaagagt tcaagggcag agtgaccttc accacggaca ccagcaccag caccgcctac 240

atggaactgc ggagcctgag aagcgacgac accgccgtgt actactgcgc cagatgggac 300

ttcgcctatt acgtggaagc catggactac tggggccagg gcaccaccgt gaccgtgtct 360

agc 363

<210> 86
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> HCDR1 CEA CH1A1A 98-99

<400> 86
gagttcggca tgaac 15

<210> 87
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> HCDR2 CEA CH1A1A 98-99

<400> 87
tggatcaaca ccaagaccgg cgaggccacc tacgtggaag agttcaaggg c 51

<210> 88
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> HCDR3 CEA CH1A1A 98-99

<400> 88
tgggacttcg cctattacgt ggaagccatg gactac 36

<210> 89
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> VL CEA 2F1

<400> 89
gatatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtgggaga cagagtcacc 60

atcacttgca aggccagtgc ggctgtgggt acgtatgttg cgtggtatca gcagaaacca 120

gggaaagcac ctaagctcct gatctattcg gcatcctacc gcaaaagggg agtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagatttcg caacttacta ctgtcaccaa tattacacct atcctctatt cacgtttggc 300

cagggcacca agctcgagat caag 324

<210> 90
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> LCDR1 CEA 2F1

<400> 90
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<210> 91
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> LCDR2 CEA 2F1

<400> 91
tcggcatcct accgcaaaag g 21

<210> 92
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> LCDR3 CEA 2F1

<400> 92
caccaatatt acacctatcc tctattcacg 30

<210> 93
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> LC CD3 CH2527 (Crossfab, VL-CH1)

<400> 93
caggccgtcg tgacccagga acccagcctg acagtgtctc ctggcggcac cgtgaccctg 60

acatgtggca gttctacagg cgccgtgacc accagcaact acgccaactg ggtgcaggaa 120

aagcccggcc aggccttcag aggactgatc ggcggcacca acaagagagc ccctggcacc 180

cctgccagat tcagcggatc tctgctggga ggaaaggccg ccctgacact gtctggcgcc 240

cagccagaag atgaggccga gtactactgc gccctgtggt acagcaacct gtgggtgttc 300

ggcggaggca ccaagctgac agtgctgagc agcgcttcca ccaaaggccc ttccgtgttt 360

cctctggctc ctagctccaa gtccacctct ggaggcaccg ctgctctcgg atgcctcgtg 420

aaggattatt ttcctgagcc tgtgacagtg tcctggaata gcggagcact gacctctgga 480

gtgcatactt tccccgctgt gctgcagtcc tctggactgt acagcctgag cagcgtggtg 540

acagtgccca gcagcagcct gggcacccag acctacatct gcaacgtgaa ccacaagccc 600

agcaacacca aggtggacaa gaaggtggaa cccaagtctt gt 642

<210> 94
<211> 2055
<212> DNA
<213> Artificial Sequence

<220>
<223> MCSP M4-3 (C1) (VH-CH1) - CD3 CH2527 (Crossfab VH-Ck) - Fc(knob) P329GLALA

<400> 94
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acctgcaccg tgtccggcgg cagcatcacc agcggctatt attggaactg gattcggcag 120

caccccggca agggcctgga atggatcggc tacatcactt tcgacggctc taacaactac 180

aaccccagcc tgaagtccag agtgaccatc agccgggaca ccagcaagaa ccagttcagc 240

ctgaagctgt ccagcgtgac agccgccgac accgccgtgt actactgcgc cgacttcgac 300

tactggggcc agggcaccct ggtcaccgtg tccagcgcta gcacaaaggg ccccagcgtg 360

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tccggaggcg gaggatccga ggtgcagctg ctggaatctg gcggcggact ggtgcagcct 720

ggcggatctc tgagactgag ctgtgccgcc agcggcttca ccttcagcac ctacgccatg 780

aactgggtgc gccaggcccc tggcaaaggc ctggaatggg tgtcccggat cagaagcaag 840

tacaacaact acgccaccta ctacgccgac agcgtgaagg gccggttcac catcagccgg 900

gacgacagca agaacaccct gtacctgcag atgaacagcc tgcgggccga ggacaccgcc 960

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aacaattttt accctaggga agctaaagtg cagtggaaag tggataacgc actgcagtcc 1200

ggcaactccc aggaatctgt gacagaacag gactccaagg acagcaccta ctccctgtcc 1260

tccaccctga cactgtctaa ggctgattat gagaaacaca aagtctacgc ctgcgaagtc 1320

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acccacacct gtccccttg tcctgcccct gaagctgctg gcggcccttc tgtgttcctg 1440

ttccccccaa agcccaagga caccctgatg atcagccgga cccccgaagt gacctgcgtg 1500

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gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 1680

gtctccaaca aagccctcgg cgcccccatc gagaaaacca tctccaaagc caaagggcag 1740

ccccgagaac cacaggtgta caccctgccc ccatgccggg atgagctgac caagaaccag 1800

gtcagcctgt ggtgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 1860

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tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1980

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ctgtctccgg gtaaa 2055

<210> 95
<211> 1326
<212> DNA
<213> Artificial Sequence

<220>
<223> MCSP M4-3 (C1) (VH-CH1) - Fc(hole) P329GLALA

<400> 95
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acctgcaccg tgtccggcgg cagcatcacc agcggctatt attggaactg gattcggcag 120

caccccggca agggcctgga atggatcggc tacatcactt tcgacggctc taacaactac 180

aaccccagcc tgaagtccag agtgaccatc agccgggaca ccagcaagaa ccagttcagc 240

ctgaagctgt ccagcgtgac agccgccgac accgccgtgt actactgcgc cgacttcgac 300

tactggggcc agggcaccct ggtcaccgtg tccagcgcta gcaccaaggg cccctccgtg 360

ttcccctgg ccccagcag caagagcacc agcggcggca cagccgctct gggctgcctg 420

gtcaaggact acttccccga gcccgtgacc gtgtcctgga acagcggagc cctgacctcc 480

ggcgtgcaca ccttccccgc cgtgctgcag agttctggcc tgtatagcct gagcagcgtg 540

gtcaccgtgc cttctagcag cctgggcacc cagacctaca tctgcaacgt gaaccacaag 600

cccagcaaca ccaaggtgga caagaaggtg gagcccaaga gctgcgacaa aactcacaca 660

tgcccaccgt gcccagcacc tgaagctgca gggggaccgt cagtcttcct cttccccca 720

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 780

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 840

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 900

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggagt acaagtgcaa ggtctccaac 960

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ctcgtgagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 1260

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 1320

ggtaaa 1326

<210> 96
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> LC CD3 CH2527 (Crossfab, VL-CH1)

<400> 96
caggccgtcg tgacccagga acccagcctg acagtgtctc ctggcggcac cgtgaccctg 60

acatgtggca gttctacagg cgccgtgacc accagcaact acgccaactg ggtgcaggaa 120

aagcccggcc aggccttcag aggactgatc ggcggcacca acaagagagc ccctggcacc 180

cctgccagat tcagcggatc tctgctggga ggaaaggccg ccctgacact gtctggcgcc 240

cagccagaag atgaggccga gtactactgc gccctgtggt acagcaacct gtgggtgttc 300

ggcggaggca ccaagctgac agtgctgagc agcgcttcca ccaaaggccc ttccgtgttt 360

cctctggctc ctagctccaa gtccacctct ggaggcaccg ctgctctcgg atgcctcgtg 420

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agcaacacca aggtggacaa gaaggtggaa cccaagtctt gt 642

<210> 97
<211> 2082
<212> DNA
<213> Artificial Sequence

<220>
<223> CEA CH1A1A 98/99 - CD3 CH2527 (Crossfab VH-Ck) - Fc(knob) P329GLALA

<400> 97
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tcctgcaagg ccagcggcta caccttcacc gagttcggca tgaactgggt ccgacaggcc 120

cctggacagg gcctggaatg gatgggctgg atcaacacca agaccggcga ggccacctac 180

gtggaagagt tcaagggcag agtgaccttc accaccgaca ccagcaccag caccgcctac 240

atggaactgc ggagcctgag aagcgacgac accgccgtgt actactgcgc cagatgggac 300

ttcgcctact atgtggaagc catggactac tggggccagg gcaccaccgt gaccgtgtct 360

agtgctagca caaagggccc cagcgtgttc cctctggccc ctagcagcaa gagcacatct 420

ggcggaacag ccgccctggg ctgcctggtc aaggactact ttcccgagcc cgtgacagtg 480

tcctggaact ctggcgccct gacaagcggc gtgcacacct ttccagccgt gctgcagagc 540

agcggcctgt actctctgag cagcgtggtc accgtgccta gctctagcct gggcacccag 600

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ggcttcacct tcagcaccta cgccatgaac tgggtgcgcc aggcccctgg caaaggcctg 840

gaatgggtgt cccggatcag aagcaagtac aacaactacg ccacctacta cgccgacagc 900

gtgaagggcc ggttcaccat cagccgggac gacagcaaga acaccctgta cctgcagatg 960

aacagcctgc gggccgagga caccgccgtg tactattgtg tgcggcacgg caacttcggc 1020

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gctagcgtgg ccgctccctc cgtgtttatc tttcccccat ccgatgaaca gctgaaaagc 1140

ggcaccgcct ccgtcgtgtg tctgctgaac aatttttacc ctagggaagc taaagtgcag 1200

tggaaagtgg ataacgcact gcagtccggc aactcccagg aatctgtgac agaacaggac 1260

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tgccgggatg agctgaccaa gaaccaggtc agcctgtggt gcctggtcaa aggcttctat 1860

cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1920

acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac 1980

aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 2040

aaccactaca cgcagaagag cctctccctg tctccgggta aa 2082

<210> 98
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> CEA CH1A1A 98/99 (VH-CH1) - Fc(hole) P329GLALA

<400> 98
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tcctgcaagg ccagcggcta caccttcacc gagttcggca tgaactgggt ccgacaggct 120

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gtggaagagt tcaagggcag agtgaccttc accacggaca ccagcaccag caccgcctac 240

atggaactgc ggagcctgag aagcgacgac accgccgtgt actactgcgc cagatgggac 300

ttcgcctatt acgtggaagc catggactac tggggccagg gcaccaccgt gaccgtgtct 360

agcgctagca ccaagggccc ctccgtgttc cccctggccc ccagcagcaa gagcaccagc 420

ggcggcacag ccgctctggg ctgcctggtc aaggactact tccccgagcc cgtgaccgtg 480

tcctggaaca gcggagccct gacctccggc gtgcacacct tccccgccgt gctgcagagt 540

tctggcctgt atagcctgag cagcgtggtc accgtgcctt ctagcagcct gggcacccag 600

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aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960

aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtgca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctctcg tgcgcagtca aaggcttcta tcccagcgac 1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1200

gtgctggact ccgacggctc cttcttcctc gtgagcaagc tcaccgtgga caagagcagg 1260

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320

acgcagaaga gcctctccct gtctccgggt aaa 1353

<210> 99
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> LC DP47 GS

<400> 99
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ctctcttgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccgct gacgttcggc 300

caggggacca aagtggaaat caaacgtacg gtggctgcac catctgtctt catcttcccg 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 645

<210> 100
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> LC CD3 CH2527 (Crossfab, VL-CH1)

<400> 100
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acatgtggca gttctacagg cgccgtgacc accagcaact acgccaactg ggtgcaggaa 120

aagcccggcc aggccttcag aggactgatc ggcggcacca acaagagagc ccctggcacc 180

cctgccagat tcagcggatc tctgctggga ggaaaggccg ccctgacact gtctggcgcc 240

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gtgcatactt tccccgctgt gctgcagtcc tctggactgt acagcctgag cagcgtggtg 540

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agcaacacca aggtggacaa gaaggtggaa cccaagtctt gt 642

<210> 101
<211> 2064
<212> DNA
<213> Artificial Sequence

<220>
<223> DP47 GS (VH-CH1) - CD3 CH2527 (Crossfab VH-Ck) - Fc(knob) P329GLALA

<400> 101
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggcagc 300

ggatttgact actggggcca aggaaccctg gtcaccgtct cgagtgctag cacaaagggc 360

cccagcgtgt tccctctggc ccctagcagc aagagcacat ctggcggaac agccgccctg 420

ggctgcctcg tgaaggacta ctttcccgag cctgtgaccg tgtcctggaa ctctggcgcc 480

ctgacaagcg gcgtgcacac ctttccagcc gtgctgcaga gcagcggcct gtactctctg 540

agcagcgtgg tcaccgtgcc tagcagcagc ctgggcaccc agacctacat ctgcaacgtg 600

aaccacaagc ccagcaacac caaagtggac aagaaggtgg agcccaagag ctgtgatggc 660

ggaggagggt ccggaggcgg aggatccgag gtgcagctgc tggaatctgg cggcggactg 720

gtgcagcctg gcggatctct gagactgagc tgtgccgcca gcggcttcac cttcagcacc 780

tacgccatga actgggtgcg ccaggcccct ggcaaaggcc tggaatgggt gtcccggatc 840

agaagcaagt acaacaacta cgccacctac tacgccgaca gcgtgaaggg ccggttcacc 900

atcagccggg acgacagcaa gaacaccctg tacctgcaga tgaacagcct gcgggccgag 960

gacaccgccg tgtactattg tgtgcggcac ggcaacttcg gcaacagcta tgtgtcttgg 1020

tttgcctact ggggccaggg caccctcgtg accgtgtcaa gcgctagcgt ggccgctccc 1080

tccgtgttta tctttccccc atccgatgaa cagctgaaaa gcggcaccgc ctccgtcgtg 1140

tgtctgctga acaattttta ccctagggaa gctaaagtgc agtggaaagt ggataacgca 1200

ctgcagtccg gcaactccca ggaatctgtg acagaacagg actccaagga cagcacctac 1260

tccctgtcct ccaccctgac actgtctaag gctgattatg agaaacacaa agtctacgcc 1320

tgcgaagtca cccatcaggg cctgagctcg cccgtcacaa agagcttcaa caggggagag 1380

tgtgacaaga cccacacctg tccccccttgt cctgcccctg aagctgctgg cggcccttct 1440

gtgttcctgt tcccccccaaa gcccaaggac accctgatga tcagccggac ccccgaagtg 1500

acctgcgtgg tggtggatgt gtcccacgag gaccctgaag tgaagttcaa ttggtacgtg 1560

gacggcgtgg aagtgcacaa cgccaagaca aagccgcggg aggagcagta caacagcacg 1620

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 1680

aagtgcaagg tctccaacaa agccctcggc gcccccatcg agaaaaccat ctccaaagcc 1740

aaagggcagc cccgagaacc acaggtgtac accctgcccc catgccggga tgagctgacc 1800

aagaaccagg tcagcctgtg gtgcctggtc aaaggcttct atcccagcga catcgccgtg 1860

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1920

tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1980

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 2040

agcctctccc tgtctccggg taaa 2064

<210> 102
<211> 1335
<212> DNA
<213> Artificial Sequence

<220>
<223> DP47 GS (VH-CH1) - Fc(hole) P329GLALA

<400> 102
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggcagc 300

ggatttgact actggggcca aggaaccctg gtcaccgtct cgagtgctag caccaagggc 360

ccctccgtgt tccccctggc ccccagcagc aagagcacca gcggcggcac agccgctctg 420

ggctgcctgg tcaaggacta cttccccgag cccgtgaccg tgtcctggaa cagcggagcc 480

ctgacctccg gcgtgcacac cttccccgcc gtgctgcaga gttctggcct gtatagcctg 540

agcagcgtgg tcaccgtgcc ttctagcagc ctgggcaccc agacctacat ctgcaacgtg 600

aaccacaagc ccagcaacac caaggtggac aagaaggtgg agcccaagag ctgcgacaaa 660

actcacacat gcccaccgtg cccagcacct gaagctgcag ggggaccgtc agtcttcctc 720

ttccccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 780

gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 840

gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg 900

gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 960

gtctccaaca aagccctcgg cgcccccatc gagaaaacca tctccaaagc caaagggcag 1020

ccccgagaac cacaggtgtg caccctgccc ccatcccggg atgagctgac caagaaccag 1080

gtcagcctct cgtgcgcagt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 1140

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200

tccttcttcc tcgtgagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1260

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1320

ctgtctccgg gtaaa 1335

<210> 103
<211> 207
<212> PRT
<213> Homo sapiens

<400> 103

Met Gln Ser Gly Thr His Trp Arg Val Leu Gly Leu Cys Leu Leu Ser
1 5 10 15

Val Gly Val Trp Gly Gln Asp Gly Asn Glu Glu Met Gly Gly Ile Thr
20 25 30

Gln Thr Pro Tyr Lys Val Ser Ile Ser Gly Thr Thr Val Ile Leu Thr
35 40 45

Cys Pro Gln Tyr Pro Gly Ser Glu Ile Leu Trp Gln His Asn Asp Lys
50 55 60

Asn Ile Gly Gly Asp Glu Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp
65 70 75 80

```
His Leu Ser Leu Lys Glu Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr
                85                  90                  95

Val Cys Tyr Pro Arg Gly Ser Lys Pro Glu Asp Ala Asn Phe Tyr Leu
            100                 105                 110

Tyr Leu Arg Ala Arg Val Cys Glu Asn Cys Met Glu Met Asp Val Met
        115                 120                 125

Ser Val Ala Thr Ile Val Ile Val Asp Ile Cys Ile Thr Gly Gly Leu
    130                 135                 140

Leu Leu Leu Val Tyr Tyr Trp Ser Lys Asn Arg Lys Ala Lys Ala Lys
145                 150                 155                 160

Pro Val Thr Arg Gly Ala Gly Ala Gly Gly Arg Gln Arg Gly Gln Asn
                165                 170                 175

Lys Glu Arg Pro Pro Pro Val Pro Asn Pro Asp Tyr Glu Pro Ile Arg
            180                 185                 190

Lys Gly Gln Arg Asp Leu Tyr Ser Gly Leu Asn Gln Arg Arg Ile
        195                 200                 205


<210>  104
<211>  198
<212>  PRT
<213>  Macaca fascicularis

<400>  104

Met Gln Ser Gly Thr Arg Trp Arg Val Leu Gly Leu Cys Leu Leu Ser
1               5                   10                  15

Ile Gly Val Trp Gly Gln Asp Gly Asn Glu Glu Met Gly Ser Ile Thr
            20                  25                  30

Gln Thr Pro Tyr Gln Val Ser Ile Ser Gly Thr Thr Val Ile Leu Thr
        35                  40                  45

Cys Ser Gln His Leu Gly Ser Glu Ala Gln Trp Gln His Asn Gly Lys
    50                  55                  60

Asn Lys Glu Asp Ser Gly Asp Arg Leu Phe Leu Pro Glu Phe Ser Glu
65                  70                  75                  80

Met Glu Gln Ser Gly Tyr Tyr Val Cys Tyr Pro Arg Gly Ser Asn Pro
                85                  90                  95

Glu Asp Ala Ser His His Leu Tyr Leu Lys Ala Arg Val Cys Glu Asn
            100                 105                 110

Cys Met Glu Met Asp Val Met Ala Val Ala Thr Ile Val Ile Val Asp
```

115 120 125

Ile Cys Ile Thr Leu Gly Leu Leu Leu Leu Val Tyr Tyr Trp Ser Lys
130 135 140

Asn Arg Lys Ala Lys Ala Lys Pro Val Thr Arg Gly Ala Gly Ala Gly
145 150 155 160

Gly Arg Gln Arg Gly Gln Asn Lys Glu Arg Pro Pro Pro Val Pro Asn
165 170 175

Pro Asp Tyr Glu Pro Ile Arg Lys Gly Gln Gln Asp Leu Tyr Ser Gly
180 185 190

Leu Asn Gln Arg Arg Ile
195

<210> 105
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 105

Glu Pro Lys Ser Cys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 106
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 106

Glu Pro Lys Ser Cys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 107
<211> 227
<212> PRT
<213> Homo sapiens

<400> 107

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

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45

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

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95

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

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

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

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205

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

Pro Gly Lys
225

<210> 108
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> leader peptide

<400> 108

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Ala His Ser

<210> 109
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> leader peptide

<400> 109
atggactgga cctggagaat cctcttcttg gtggcagcag ccacaggagc ccactcc 57

<210> 110
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> leader peptide

<400> 110
atggactgga cctggaggat cctcttcttg gtggcagcag ccacaggagc ccactcc 57

<210> 111
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> leader peptide

<400> 111

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

Phe Pro Gly Ala Arg Cys
20

<210> 112
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> leader peptide

<400> 112
atggacatga gggtccccgc tcagctcctg ggcctcctgc tgctctggtt cccaggtgcc 60

aggtgt 66

<210> 113
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> leader peptide

<400> 113

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

Val His Ser

<210> 114
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> leader peptide

<400> 114
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctaccggtgt gcattcc 57

<210> 115
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> leader peptide

<400> 115
atgggctggt cctgcatcat cctgtttctg gtggctaccg ccactggagt gcattcc 57

<210> 116
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> leader peptide

<400> 116
atgggctggt cctgcatcat cctgtttctg gtcgccacag ccaccggcgt gcactct 57

<210> 117
<211> 643
<212> PRT
<213> Macaca fascicularis

<400> 117

Leu Ser Leu Glu Gly Ser Arg Thr Leu Thr Val Cys Pro Gly Ser Val
1 5 10 15

Gln Pro Leu Ser Ser Gln Thr Leu Arg Ala Ser Ser Ser Ala Gly Thr
20 25 30

Asp Pro Gln Leu Leu Leu Tyr Arg Val Val Arg Gly Pro Gln Leu Gly
35 40 45

Arg Leu Phe His Ala Gln Gln Asp Ser Thr Gly Glu Ala Leu Val Asn
50 55 60

Phe Thr Gln Ala Glu Val Tyr Ala Gly Asn Ile Leu Tyr Glu His Glu
65 70 75 80

```
Met Pro Thr Glu Pro Phe Trp Glu Ala His Asp Thr Leu Glu Leu Gln
                85                  90                  95

Leu Ser Ser Pro Pro Ala Arg Asp Val Ala Ala Thr Leu Ala Val Ala
            100                 105                 110

Val Ser Phe Glu Ala Ala Cys Pro Gln Arg Pro Ser His Leu Trp Lys
        115                 120                 125

Asn Lys Gly Leu Trp Val Pro Glu Gly Gln Arg Ala Lys Ile Thr Met
    130                 135                 140

Ala Ala Leu Asp Ala Ser Asn Leu Leu Ala Ser Val Pro Ser Pro Gln
145                 150                 155                 160

Arg Leu Glu His Asp Val Leu Phe Gln Val Thr Gln Phe Pro Ser Arg
                165                 170                 175

Gly Gln Leu Leu Val Ser Glu Glu Pro Leu His Ala Gly Gln Pro His
            180                 185                 190

Phe Leu Gln Ser Gln Leu Ala Ala Gly Gln Leu Val Tyr Ala His Gly
        195                 200                 205

Gly Gly Gly Thr Gln Gln Asp Gly Phe His Phe Arg Ala His Leu Gln
    210                 215                 220

Gly Pro Ala Gly Ala Thr Val Ala Gly Pro Gln Thr Ser Glu Ala Phe
225                 230                 235                 240

Ala Ile Thr Val Arg Asp Val Asn Glu Arg Pro Pro Gln Pro Gln Ala
                245                 250                 255

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

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

Tyr Glu Val Gln Arg Ala Pro His Asn Gly Phe Leu Ser Leu Val Gly
    290                 295                 300

Gly Gly Pro Gly Pro Val Thr His Phe Thr Gln Ala Asp Val Asp Ser
305                 310                 315                 320

Gly Arg Leu Ala Phe Val Ala Asn Gly Ser Ser Val Ala Gly Val Phe
                325                 330                 335

Gln Leu Ser Met Ser Asp Gly Ala Ser Pro Pro Leu Pro Met Ser Leu
            340                 345                 350
```

```
Ala Val Asp Ile Leu Pro Ser Ala Ile Glu Val Gln Leu Gln Ala Pro
        355                 360                 365

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

Leu Arg Val Val Ser Asp Arg Glu Glu Pro Glu Ala Ala Tyr Arg Leu
385                 390                 395                 400

Ile Gln Gly Pro Lys Tyr Gly His Leu Leu Val Gly Gly Arg Pro Ala
                405                 410                 415

Ser Ala Phe Ser Gln Leu Gln Ile Asp Gln Gly Glu Val Val Phe Ala
            420                 425                 430

Phe Thr Asn Phe Ser Ser Ser His Asp His Phe Arg Val Leu Ala Leu
        435                 440                 445

Ala Arg Gly Val Asn Ala Ser Ala Val Val Asn Ile Thr Val Arg Ala
    450                 455                 460

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

Arg Leu Asp Pro Thr Ile Leu Asp Ala Gly Glu Leu Ala Asn Arg Thr
                485                 490                 495

Gly Ser Val Pro His Phe Arg Leu Leu Glu Gly Pro Arg His Gly Arg
            500                 505                 510

Val Val Arg Val Pro Arg Ala Arg Thr Glu Pro Gly Gly Ser Gln Leu
        515                 520                 525

Val Glu Gln Phe Thr Gln Gln Asp Leu Glu Asp Gly Arg Leu Gly Leu
    530                 535                 540

Glu Val Gly Arg Pro Glu Gly Arg Ala Pro Ser Pro Thr Gly Asp Ser
545                 550                 555                 560

Leu Thr Leu Glu Leu Trp Ala Gln Gly Val Pro Pro Ala Val Ala Ser
                565                 570                 575

Leu Asp Phe Ala Thr Glu Pro Tyr Asn Ala Ala Arg Pro Tyr Ser Val
            580                 585                 590

Ala Leu Leu Ser Val Pro Glu Ala Thr Arg Met Glu Ala Gly Lys Pro
        595                 600                 605

Glu Ser Ser Thr Pro Thr Gly Glu Pro Gly Pro Met Ala Ser Ser Pro
    610                 615                 620
```

Val Pro Ala Val Ala Lys Gly Gly Phe Leu Gly Phe Leu Glu Ala Asn
625 630 635 640

Met Phe Ser

<210> 118
<211> 643
<212> PRT
<213> Homo sapiens

<400> 118

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

Gln Pro Leu Ser Ser Gln Thr Leu Arg Ala Ser Ser Ser Ala Gly Thr
20 25 30

Asp Pro Gln Leu Leu Leu Tyr Arg Val Val Arg Gly Pro Gln Leu Gly
35 40 45

Arg Leu Phe His Ala Gln Gln Asp Ser Thr Gly Glu Ala Leu Val Asn
50 55 60

Phe Thr Gln Ala Glu Val Tyr Ala Gly Asn Ile Leu Tyr Glu His Glu
65 70 75 80

Met Pro Pro Glu Pro Phe Trp Glu Ala His Asp Thr Leu Glu Leu Gln
85 90 95

Leu Ser Ser Pro Pro Ala Arg Asp Val Ala Ala Thr Leu Ala Val Ala
100 105 110

Val Ser Phe Glu Ala Ala Cys Pro Gln His Pro Ser His Leu Trp Lys
115 120 125

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

Ala Ala Leu Asp Ala Ser Asn Leu Leu Ala Ser Val Pro Ser Pro Gln
145 150 155 160

Arg Ser Glu His Asp Val Leu Phe Gln Val Thr Gln Phe Pro Ser Arg
165 170 175

Gly Gln Leu Leu Val Ser Glu Glu Pro Leu His Ala Gly Gln Pro His
180 185 190

Phe Leu Gln Ser Gln Leu Ala Ala Gly Gln Leu Val Tyr Ala His Gly
195 200 205

```
Gly Gly Gly Thr Gln Gln Asp Gly Phe His Phe Arg Ala His Leu Gln
    210                 215                 220

Gly Pro Ala Gly Ala Ser Val Ala Gly Pro Gln Thr Ser Glu Ala Phe
225                 230                 235                 240

Ala Ile Thr Val Arg Asp Val Asn Glu Arg Pro Pro Gln Pro Gln Ala
                245                 250                 255

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

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

Tyr Glu Val Gln Arg Ala Pro His Asn Gly Phe Leu Ser Leu Val Gly
    290                 295                 300

Gly Gly Leu Gly Pro Val Thr Arg Phe Thr Gln Ala Asp Val Asp Ser
305                 310                 315                 320

Gly Arg Leu Ala Phe Val Ala Asn Gly Ser Ser Val Ala Gly Ile Phe
                325                 330                 335

Gln Leu Ser Met Ser Asp Gly Ala Ser Pro Pro Leu Pro Met Ser Leu
            340                 345                 350

Ala Val Asp Ile Leu Pro Ser Ala Ile Glu Val Gln Leu Arg Ala Pro
        355                 360                 365

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

Leu Arg Val Val Ser Asp Arg Glu Glu Pro Glu Ala Ala Tyr Arg Leu
385                 390                 395                 400

Ile Gln Gly Pro Gln Tyr Gly His Leu Leu Val Gly Gly Arg Pro Thr
                405                 410                 415

Ser Ala Phe Ser Gln Phe Gln Ile Asp Gln Gly Glu Val Val Phe Ala
            420                 425                 430

Phe Thr Asn Phe Ser Ser Ser His Asp His Phe Arg Val Leu Ala Leu
        435                 440                 445

Ala Arg Gly Val Asn Ala Ser Ala Val Val Asn Val Thr Val Arg Ala
    450                 455                 460

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

Arg Leu Asp Pro Thr Val Leu Asp Ala Gly Glu Leu Ala Asn Arg Thr
485 490 495

Gly Ser Val Pro Arg Phe Arg Leu Leu Glu Gly Pro Arg His Gly Arg
500 505 510

Val Val Arg Val Pro Arg Ala Arg Thr Glu Pro Gly Gly Ser Gln Leu
515 520 525

Val Glu Gln Phe Thr Gln Gln Asp Leu Glu Asp Gly Arg Leu Gly Leu
530 535 540

Glu Val Gly Arg Pro Glu Gly Arg Ala Pro Gly Pro Ala Gly Asp Ser
545 550 555 560

Leu Thr Leu Glu Leu Trp Ala Gln Gly Val Pro Pro Ala Val Ala Ser
565 570 575

Leu Asp Phe Ala Thr Glu Pro Tyr Asn Ala Ala Arg Pro Tyr Ser Val
580 585 590

Ala Leu Leu Ser Val Pro Glu Ala Ala Arg Thr Glu Ala Gly Lys Pro
595 600 605

Glu Ser Ser Thr Pro Thr Gly Glu Pro Gly Pro Met Ala Ser Ser Pro
610 615 620

Glu Pro Ala Val Ala Lys Gly Gly Phe Leu Ser Phe Leu Glu Ala Asn
625 630 635 640

Met Phe Ser

<210> 119
<211> 428
<212> PRT
<213> Artificial Sequence

<220>
<223> NABA-avi-his

<400> 119

Gln Leu Thr Thr Glu Ser Met Pro Phe Asn Val Ala Glu Gly Lys Glu
1 5 10 15

Val Leu Leu Leu Val His Asn Leu Pro Gln Gln Leu Phe Gly Tyr Ser
20 25 30

Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Val Gly Tyr
35 40 45

Ala Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Asn Ser Gly Arg
50 55 60

```
Glu Thr Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Val Thr Gln
65                  70                  75                  80

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

Asn Glu Glu Ala Thr Gly Gln Phe His Val Tyr Pro Glu Leu Pro Lys
            100                 105                 110

Pro Ser Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys Asp Ala
        115                 120                 125

Met Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr Leu Trp
    130                 135                 140

Trp Ile Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln Leu Ser
145                 150                 155                 160

Asn Gly Asn Arg Thr Leu Thr Leu Leu Ser Val Thr Arg Asn Asp Thr
                165                 170                 175

Gly Pro Tyr Glu Cys Glu Ile Gln Asn Pro Val Ser Ala Asn Arg Ser
            180                 185                 190

Asp Pro Val Thr Leu Asn Val Thr Tyr Gly Pro Asp Thr Pro Thr Ile
        195                 200                 205

Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly Ala Asn Leu Asn Leu Ser
    210                 215                 220

Cys His Ser Ala Ser Asn Pro Ser Pro Gln Tyr Ser Trp Arg Ile Asn
225                 230                 235                 240

Gly Ile Pro Gln Gln His Thr Gln Val Leu Phe Ile Ala Lys Ile Thr
                245                 250                 255

Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe Val Ser Asn Leu Ala Thr
            260                 265                 270

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

Pro Val Val Ala Lys Pro Gln Ile Lys Ala Ser Lys Thr Thr Val Thr
    290                 295                 300

Gly Asp Lys Asp Ser Val Asn Leu Thr Cys Ser Thr Asn Asp Thr Gly
305                 310                 315                 320

Ile Ser Ile Arg Trp Phe Phe Lys Asn Gln Ser Leu Pro Ser Ser Glu
                325                 330                 335
```

```
Arg Met Lys Leu Ser Gln Gly Asn Ile Thr Leu Ser Ile Asn Pro Val
            340                 345                 350

Lys Arg Glu Asp Ala Gly Thr Tyr Trp Cys Glu Val Phe Asn Pro Ile
        355                 360                 365

Ser Lys Asn Gln Ser Asp Pro Ile Met Leu Asn Val Asn Tyr Asn Ala
    370                 375                 380

Leu Pro Gln Glu Asn Leu Ile Asn Val Asp Leu Glu Val Leu Phe Gln
385                 390                 395                 400

Gly Pro Gly Ser Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu
                405                 410                 415

Trp His Glu Ala Arg Ala His His His His His His
            420                 425


<210>  120
<211>  360
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD3e stalk-Fc(knob)-Avi

<400>  120

Gln Asp Gly Asn Glu Glu Met Gly Gly Ile Thr Gln Thr Pro Tyr Lys
1               5                   10                  15

Val Ser Ile Ser Gly Thr Thr Val Ile Leu Thr Cys Pro Gln Tyr Pro
            20                  25                  30

Gly Ser Glu Ile Leu Trp Gln His Asn Asp Lys Asn Ile Gly Gly Asp
        35                  40                  45

Glu Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp His Leu Ser Leu Lys
    50                  55                  60

Glu Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr Val Cys Tyr Pro Arg
65                  70                  75                  80

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

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

Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
        115                 120                 125
```

```
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
    130                 135                 140

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
145                 150                 155                 160

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
                165                 170                 175

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
            180                 185                 190

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

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
    210                 215                 220

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

Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys
                245                 250                 255

Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
            260                 265                 270

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
        275                 280                 285

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
    290                 295                 300

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
305                 310                 315                 320

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
                325                 330                 335

Leu Ser Leu Ser Pro Gly Lys Ser Gly Gly Leu Asn Asp Ile Phe Glu
            340                 345                 350

Ala Gln Lys Ile Glu Trp His Glu
        355                 360
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<210> 121
<211> 325
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3d stalk-Fc(hole)

<400> 121

Phe Lys Ile Pro Ile Glu Glu Leu Glu Asp Arg Val Phe Val Asn Cys
1 5 10 15

Asn Thr Ser Ile Thr Trp Val Glu Gly Thr Val Gly Thr Leu Leu Ser
20 25 30

Asp Ile Thr Arg Leu Asp Leu Gly Lys Arg Ile Leu Asp Pro Arg Gly
35 40 45

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

Val Gln Val His Tyr Arg Met Cys Arg Ser Glu Gln Leu Tyr Phe Gln
65 70 75 80

Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
85 90 95

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
100 105 110

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
115 120 125

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
130 135 140

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
145 150 155 160

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

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
180 185 190

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
195 200 205

Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
210 215 220

Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
225 230 235 240

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
245 250 255

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

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
275 280 285

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
290 295 300

Ser Pro Gly Lys Ser Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys
305 310 315 320

Ile Glu Trp His Glu
325

<210> 122
<211> 658
<212> PRT
<213> Mus musculus

<400> 122

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

Gln Pro Leu Ser Ser Gln Ser Leu Ser Ala Ser Ser Ser Thr Gly Ala
20 25 30

Asp Pro Arg His Leu Leu Tyr Arg Val Val Arg Gly Pro Gln Leu Gly
35 40 45

Arg Leu Leu His Ala Gln Gln Gly Ser Ala Glu Glu Val Leu Val Asn
50 55 60

Phe Thr Gln Ala Glu Val Asn Ala Gly Asn Ile Leu Tyr Glu His Glu
65 70 75 80

Met Ser Ser Glu Pro Phe Trp Glu Ala His Asp Thr Ile Gly Leu Leu
85 90 95

Leu Ser Ser Pro Pro Ala Arg Asp Leu Ala Ala Thr Leu Ala Val Met
100 105 110

Val Ser Phe Asp Ala Ala Cys Pro Gln Arg Pro Ser Arg Leu Trp Lys
115 120 125

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

Ala Ala Leu Asp Ala Ala Asn Leu Leu Ala Ser Val Pro Ala Ser Gln
145 150 155 160

Arg Ser Arg His Asp Val Leu Phe Gln Val Thr Gln Phe Pro Thr Arg
165 170 175

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Gly Gln Leu Leu Val Ser Glu Glu Pro Leu His Ala Arg Arg Pro Tyr
            180                 185                 190

Phe Leu Gln Ser Glu Leu Ala Ala Gly Gln Leu Val Tyr Ala His Gly
        195                 200                 205

Gly Gly Gly Thr Gln Gln Asp Gly Phe Arg Phe Arg Ala His Leu Gln
    210                 215                 220

Gly Pro Thr Gly Thr Ser Val Ala Gly Pro Gln Thr Ser Glu Ala Phe
225                 230                 235                 240

Val Ile Thr Val Arg Asp Val Asn Glu Arg Pro Pro Gln Pro Gln Ala
                245                 250                 255

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

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

Tyr Glu Val Gln Arg Ala Pro His Asn Gly Phe Leu Ser Leu Ala Gly
    290                 295                 300

Asp Asn Thr Gly Pro Val Thr His Phe Thr Gln Ala Asp Val Asp Ala
305                 310                 315                 320

Gly Arg Leu Ala Phe Val Ala Asn Gly Ser Ser Val Ala Gly Val Phe
                325                 330                 335

Gln Leu Ser Met Ser Asp Gly Ala Ser Pro Pro Ile Pro Met Ser Leu
            340                 345                 350

Ala Val Asp Val Leu Pro Ser Thr Ile Glu Val Gln Leu Arg Ala Pro
        355                 360                 365

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

Leu Gln Val Ile Ser Asp Arg Glu Glu Pro Asp Val Ala Tyr Arg Leu
385                 390                 395                 400

Thr Gln Gly Pro Leu Tyr Gly Gln Leu Leu Val Gly Gly Gln Pro Ala
                405                 410                 415

Ser Ala Phe Ser Gln Leu Gln Val Asp Gln Gly Asp Val Val Phe Val
            420                 425                 430

Phe Thr Asn Phe Ser Ser Ser Gln Asp His Phe Lys Val Val Ala Leu
        435                 440                 445
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Ala Arg Gly Val Asn Ala Ser Ala Thr Val Asn Val Thr Val Gln Ala
    450                 455                 460

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

Arg Leu Asp Pro Thr Val Leu Asp Ala Ser Glu Leu Ala Asn Arg Thr
                485                 490                 495

Gly Ser Met Pro His Phe Arg Leu Leu Ala Gly Pro Arg Tyr Gly Arg
            500                 505                 510

Val Val Arg Val Ser Gln Gly Arg Thr Glu Ser Arg Ser Asn Gln Leu
        515                 520                 525

Val Glu His Phe Thr Gln Arg Asp Leu Glu Glu Gly Gln Leu Gly Leu
    530                 535                 540

Glu Val Gly Lys Pro Glu Gly Arg Ser Thr Gly Pro Ala Gly Asp Arg
545                 550                 555                 560

Leu Thr Leu Glu Leu Trp Ala Lys Gly Val Pro Pro Ala Val Ala Leu
                565                 570                 575

Leu Asp Phe Ala Thr Glu Pro Tyr His Ala Ala Lys Ser Tyr Ser Val
            580                 585                 590

Ala Leu Leu Ser Val Pro Glu Ala Val Arg Thr Glu Thr Glu Lys Pro
        595                 600                 605

Gly Arg Ser Val Pro Thr Gly Gln Pro Gly Gln Ala Ala Ser Ser Pro
    610                 615                 620

Val Pro Thr Ala Ala Lys Gly Gly Val Asp Gly Leu Asn Asp Ile Phe
625                 630                 635                 640

Glu Ala Gln Lys Ile Glu Trp His Glu Ala Arg Ala His His His His
                645                 650                 655

His His
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