SEQUENCE LISTING

<110> UCB Pharma SA

<120> Antibody molecules having specificity for human OX40

<130> G0160 WO01

<150> US 61/558,545
<151> 2011-11-11

<160> 28

<170> PatentIn version 3.5

<210> 1
<211> 5
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<213> Artificial

<220>
<223> CDRH1

<400> 1

Asn Tyr Gly Ile His
1 5

<210> 2
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<223> CDRH2

<400> 2

Ser Ile Ser Pro Ser Gly Gly Leu Thr Tyr Tyr Arg Asp Ser Val Lys
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Gly

<210> 3
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<212> PRT
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<223> CDRH3

<400> 3

Gly Gly Glu Gly Ile Phe Asp Tyr
1 5

<210> 4
<211> 11

<212> PRT
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<220>
<223> CDRL1

<400> 4

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

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<223> CDRL2

<400> 5

Asn Ala Asn Thr Leu His Thr
1 5

<210> 6
<211> 9
<212> PRT
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<220>
<223> CDRL3

<400> 6

Gln Gln Tyr Tyr Asp Tyr Pro Leu Thr
1 5

<210> 7
<211> 108
<212> PRT
<213> Artificial

<220>
<223> Light chain variable region of antibody A26

<400> 7

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 Thr Gln Ser Ile Tyr Asn Ala
20 25 30

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

Tyr Asn Ala Asn Thr Leu His Thr Gly Val Pro Ser Arg Phe Ser Ala

50 55 60

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

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

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

<210> 8
<211> 117
<212> PRT
<213> Artificial

<220>
<223> Heavy chain variable region of antibody A26

<400> 8

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

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

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

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

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

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

Ala Thr Gly Gly Glu Gly Ile Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 9
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<212> PRT
<213> Artificial

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<223> Light chain of anti-OX40 antibody Fab component

<400> 9

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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 Thr Gln Ser Ile Tyr Asn Ala
            20                  25                  30

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

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

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

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

Thr Phe Gly Gly 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
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
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<213> Artificial

<220>
<223> Heavy chain of anti-OX40 antibody Fab component

<400> 10

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1               5                  10                  15

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

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

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

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

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

Ala Thr Gly Gly Glu Gly Ile Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

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

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

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

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

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

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

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220
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<210> 11
<211> 121
<212> PRT
<213> Artificial

<220>
<223> Heavy chain of anti-albumin Fv component

<400> 11

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 Val Ser Gly Ile Asp Leu Ser Asn Tyr
20 25 30

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

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

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 12
<211> 112
<212> PRT
<213> Artificial

<220>
<223> Light chain of anti-albumin Fv component

<400> 12

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

Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Pro Ser Val Trp Ser Asn
20 25 30

Phe Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
35 40 45

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

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

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gly Gly Tyr Ser Ser Ile
                85                  90                  95

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

<210> 13
<211> 16
<212> PRT
<213> Artificial

<220>
<223> Linker 1

<400> 13

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Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Gly Gly Gly Ser
1               5                   10                  15
```

<210> 14
<211> 15
<212> PRT
<213> Artificial

<220>
<223> Linker 2

<400> 14

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Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1               5                   10                  15
```

<210> 15
<211> 357
<212> PRT
<213> Artificial

<220>
<223> A26 Fab Heavy-(G4S,G4T,G4S)-645dsFv(gH5)

<400> 15

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

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

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

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

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

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

Ala Thr Gly Gly Glu Gly Ile Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

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

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

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

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

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

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

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

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

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

Ser Cys Ala Val Ser Gly Ile Asp Leu Ser Asn Tyr Ala Ile Asn Trp
            260                 265                 270

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

Ala Ser Gly Thr Thr Phe Tyr Ala Thr Trp Ala Lys Gly Arg Phe Thr
290 295 300

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

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Thr Val Pro
325 330 335

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

Val Thr Val Ser Ser
355

<210> 16
<211> 341
<212> PRT
<213> Artificial

<220>
<223> A26 Fab Light-(3xG4S)-645dsFv(gL4)

<400> 16

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 Thr Gln Ser Ile Tyr Asn Ala
20 25 30

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

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

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

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

Thr Phe Gly Gly 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

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```
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
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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    210                 215                 220

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

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Pro
                245                 250                 255

Ser Val Trp Ser Asn Phe Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys
            260                 265                 270

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

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

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gly
305                 310                 315                 320

Gly Tyr Ser Ser Ile Ser Asp Thr Thr Phe Gly Cys Gly Thr Lys Val
                325                 330                 335

Glu Ile Lys Arg Thr
            340
```

<210> 17
<211> 119
<212> PRT
<213> Artificial

<220>
<223> 645gH1 heavy chain variable domain

<400> 17

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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 Val Ser Gly Ile Asp Leu Ser Asn Tyr
            20                  25                  30

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

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

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

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

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

Thr Leu Val Thr Val Ser Ser
        115
```

<210> 18
<211> 110
<212> PRT
<213> Artificial

<220>
<223> 645gL1 light chain variable domain

<400> 18

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

Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Pro Ser Val Trp Ser Asn
            20                  25                  30

Phe Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45

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

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

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gly Gly Tyr Ser Ser Ile
85 90 95

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

<210> 19
<211> 355
<212> PRT
<213> Artificial

<220>
<223> A26 Fab Heavy-(3xG4S)-645dsFv(gH1)

<400> 19

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

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

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

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

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

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

Ala Thr Gly Gly Glu Gly Ile Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

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

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

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

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

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

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

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

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

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

Ser Cys Ala Val Ser Gly Ile Asp Leu Ser Asn Tyr Ala Ile Asn Trp
            260                 265                 270

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

Ala Ser Gly Thr Thr Phe Tyr Ala Thr Trp Ala Lys Gly Arg Phe Thr
    290                 295                 300

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

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Thr Val Pro Gly Tyr
                325                 330                 335

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

Val Ser Ser
        355


<210>  20
<211>  340
<212>  PRT
<213>  Artificial

<220>
<223>  A26 Fab Light-(3xG4S)-645dsFv(gL1)

<400>  20

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

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```
Asp Arg Val Thr Ile Thr Cys Arg Ala Thr Gln Ser Ile Tyr Asn Ala
            20                  25                  30

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

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

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

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

Thr Phe Gly Gly 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
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 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    210                 215                 220

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

Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ser Ser
                245                 250                 255

Pro Ser Val Trp Ser Asn Phe Leu Ser Trp Tyr Gln Gln Lys Pro Gly
            260                 265                 270
```

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

Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
290 295 300

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gly
305 310 315 320

Gly Gly Tyr Ser Ser Ile Ser Asp Thr Thr Phe Gly Cys Gly Thr Lys
325 330 335

Val Glu Ile Lys
340

<210> 21
<211> 1137
<212> DNA
<213> Artificial

<220>
<223> Heavy chain A26-645(gH5) including E.coli OmpA leader

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gctgaagttc agctggtcga gtctggaggc gggcttgtcc agcctggagg gagcctgcgt 120

ctctcttgtg cagcaagcgg tttcacgttc accaactacg gtatccactg gattcgtcag 180

gcaccaggta aaggtctgga atgggtagcc tctatctctc cgtctggtgg tctgacgtac 240

taccgtgact ctgtcaaagg tcgtttcacc atctctcgtg atgacgcgaa aaactctccg 300

tacctgcaaa tgaactctct gcgtgcagaa gataccgcag tgtactactg cgctactggt 360

ggtgaaggta tcttcgacta ctggggtcag ggtaccctgg taactgtctc gagcgcttct 420

acaaagggcc caagcgtttt cccactggct ccgtcctcta aatccacctc tggtggtacg 480

gctgcactgg gttgcctggt gaaagactac ttcccagaac cagttaccgt gtcttggaac 540

tctggtgcac tgacctctgg tgttcacacc tttccagcag ttctccagtc ttctggtctg 600

tactccctgt ctagcgtggt taccgttccg tcttcttctc tgggtactca gacctacatc 660

tgcaacgtca accacaaacc gtccaacacc aaggtcgaca aaaaagtcga gccgaaatcc 720

tgtagtggag gtgggggctc aggtggaggc gggaccggtg gaggtggcag cgaggttcaa 780

ctgcttgagt ctggaggagg cctagtccag cctggaggga gcctgcgtct ctcttgtgca 840

gtaagcggca tcgacctgag caattacgcc atcaactggg tgagacaagc tccggggaag 900

tgtttagaat ggatcggtat aatatgggcc agtgggacga ccttttatgc tacatgggcg 960

aaaggaaggt ttacaattag ccgggacaat agcaaaaaca ccgtgtatct ccaaatgaac 1020

tccttgcgag cagaggacac ggcggtgtac tattgtgctc gcactgtccc aggttatagc 1080

actgcaccct acttcgatct gtggggacaa gggaccctgg tgactgtttc aagttaa 1137

<210> 22
<211> 1074
<212> DNA
<213> Artificial

<220>
<223> Heavy chain A26-645(gH5)

<400> 22
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tcttgtgcag caagcggttt cacgttcacc aactacggta tccactggat tcgtcaggca 120

ccaggtaaag gtctggaatg ggtagcctct atctctccgt ctggtggtct gacgtactac 180

cgtgactctg tcaaaggtcg tttcaccatc tctcgtgatg acgcgaaaaa ctctccgtac 240

ctgcaaatga actctctgcg tgcagaagat accgcagtgt actactgcgc tactggtggt 300

gaaggtatct tcgactactg gggtcagggt accctggtaa ctgtctcgag cgcttctaca 360

aagggcccaa gcgttttccc actggctccg tcctctaaat ccacctctgg tggtacggct 420

gcactgggtt gcctggtgaa agactacttc ccagaaccag ttaccgtgtc ttggaactct 480

ggtgcactga cctctggtgt tcacaccttt ccagcagttc tccagtcttc tggtctgtac 540

tccctgtcta gcgtggttac cgttccgtct tcttctctgg gtactcagac ctacatctgc 600

aacgtcaacc acaaaccgtc caacaccaag gtcgacaaaa aagtcgagcc gaaatcctgt 660

agtggaggtg ggggctcagg tggaggcggg accggtggag gtggcagcga ggttcaactg 720

cttgagtctg gaggaggcct agtccagcct ggagggagcc tgcgtctctc ttgtgcagta 780

agcggcatcg acctgagcaa ttacgccatc aactgggtga gacaagctcc ggggaagtgt 840

ttagaatgga tcggtataat atgggccagt gggacgacct tttatgctac atgggcgaaa 900

ggaaggttta caattagccg ggacaatagc aaaaacaccg tgtatctcca aatgaactcc 960

ttgcgagcag aggacacggc ggtgtactat tgtgctcgca ctgtcccagg ttatagcact 1020

gcaccctact tcgatctgtg gggacaaggg accctggtga ctgtttcaag ttaa 1074

<210> 23
<211> 1089
<212> DNA
<213> Artificial

<220>
<223> Light chain A26-645(gL4) including E.coli OmpA leader

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gctgatatcc agatgaccca gagcccaagc agtctctccg ccagcgtagg cgatcgtgtg 120

actattacct gtcgtgcaac ccagagcatc tacaacgctc tggcttggta tcagcagaaa 180

ccgggtaaag cgccaaaact cctgatctac aacgcgaaca ctctgcatac tggtgttccg 240

tctcgtttct ctgcgtctgg ttctggtacg gactctactc tgaccatctc ctctctccag 300

ccggaagatt tcgcgaccta ctactgccag cagtactacg attacccact gacgtttggt 360

ggtggtacca aagttgagat caaacgtacg gttgcagctc catccgtctt catctttcca 420

ccgtctgacg aacagctcaa atctggtact gcttctgtcg tttgcctcct gaacaacttc 480

tatccgcgtg aagcgaaagt ccagtggaaa gtcgacaacg cactccagtc tggtaactct 540

caggaatctg tgaccgaaca ggactccaaa gactccacct actctctgtc tagcaccctg 600

actctgtcca aagcagacta cgagaaacac aaagtgtacg cttgcgaagt tacccatcag 660

ggtctgagct ctccggttac caaatccttt aatagagggg agtgtggtgg cggtggcagt 720

ggtggtggag gttccggagg tggcggttca gacatacaaa tgacccagag tccttcatcg 780

gtatccgcgt ccgttggcga tagggtgact attacatgtc aaagctctcc tagcgtctgg 840

agcaattttc tatcctggta tcaacagaaa ccggggaagg ctccaaaact tctgatttat 900

gaagcctcga aactcaccag tggagttccg tcaagattca gtggctctgg atcagggaca 960

gacttcacgt tgacaatcag ttcgctgcaa ccagaggact ttgcgaccta ctattgtggt 1020

ggaggttaca gtagcataag tgatacgaca tttgggtgcg gtactaaggt ggaaatcaaa 1080

cgtacctaa 1089

<210> 24
<211> 1026
<212> DNA
<213> Artificial

<220>
<223> Light chain A26-645(gL4)

<400> 24
gatatccaga tgacccagag cccaagcagt ctctccgcca gcgtaggcga tcgtgtgact 60

attacctgtc gtgcaaccca gagcatctac aacgctctgg cttggtatca gcagaaaccg 120

ggtaaagcgc caaaactcct gatctacaac gcgaacactc tgcatactgg tgttccgtct 180

cgtttctctg cgtctggttc tggtacggac tctactctga ccatctcctc tctccagccg 240

gaagatttcg cgacctacta ctgccagcag tactacgatt acccactgac gtttggtggt 300

ggtaccaaag ttgagatcaa acgtacggtt gcagctccat ccgtcttcat ctttccaccg 360

tctgacgaac agctcaaatc tggtactgct tctgtcgttt gcctcctgaa caacttctat 420

ccgcgtgaag cgaaagtcca gtggaaagtc gacaacgcac tccagtctgg taactctcag 480

gaatctgtga ccgaacagga ctccaaagac tccacctact ctctgtctag caccctgact 540

ctgtccaaag cagactacga gaaacacaaa gtgtacgctt gcgaagttac ccatcagggt 600

ctgagctctc cggttaccaa atcctttaat agaggggagt gtggtggcgg tggcagtggt 660

ggtggaggtt ccggaggtgg cggttcagac atacaaatga cccagagtcc ttcatcggta 720

tccgcgtccg ttggcgatag ggtgactatt acatgtcaaa gctctcctag cgtctggagc 780

aattttctat cctggtatca acagaaaccg gggaaggctc caaaacttct gatttatgaa 840

gcctcgaaac tcaccagtgg agttccgtca agattcagtg gctctggatc agggacagac 900

ttcacgttga caatcagttc gctgcaacca gaggactttg cgacctacta ttgtggtgga 960

ggttacagta gcataagtga tacgacattt gggtgcggta ctaaggtgga aatcaaacgt 1020

acctaa 1026

<210> 25
<211> 1131
<212> DNA
<213> Artificial

<220>
<223> Heavy chain A26-645(gH5) including B72.3 leader sequence

<400> 25
atggaatggt cctgggtctt cctgtttttc ctttctgtca caaccggggt gcacagcgag 60

gtgcagctcg tcgagtctgg aggcgggctt gtccagcctg gagggagcct gcgtctctct 120

tgtgcagcaa gcggtttcac gttcaccaac tacggtatcc actggattcg tcaggcacca 180

ggtaaaggtc tggaatgggt agcctctatc tctccgtctg gtggtctgac gtactaccgt 240

gactctgtca aaggtcgttt caccatctct cgtgatgacg cgaaaaactc tccgtacctg 300

cagatgaact ctctgcgtgc agaagatacc gcagtgtact actgcgctac tggtggtgaa 360

ggtatcttcg actactgggg tcagggtacc ctggtaactg tctcaagcgc ttctacaaag 420

ggcccatcgg tcttcccccc ggcaccctcc tccaagagca cctctggggg cacagcggcc 480

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 540

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctctgg actctactcc 600

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 660

gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttgagcccaa atcttgttcc 720

ggaggtggcg gttccggagg tggcggtacc ggtggcggtg gatccgaagt ccagctgctt 780

gaatccggag gcggactcgt gcagcccgga ggcagtcttc gcttgtcctg cgctgtatct 840

ggaatcgacc tgagcaatta cgccatcaac tgggtgagac aggcacctgg gaaatgcctc 900

gaatggatcg gcattatatg ggctagtggg acgacctttt atgctacatg ggcgaagggt 960

agattcacaa tctcacggga taatagtaag aacacagtgt acctgcagat gaactccctg 1020

cgagcagagg ataccgccgt ttactattgt gctcgcactg tcccaggtta tagcactgca 1080

ccctactttg atctgtgggg gcagggcact ctggtcaccg tctcgagttg a 1131

<210> 26
<211> 1074
<212> DNA
<213> Artificial

<220>
<223> Heavy chain A26-645(gH5)

<400> 26
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tcttgtgcag caagcggttt cacgttcacc aactacggta tccactggat tcgtcaggca 120

ccaggtaaag gtctggaatg ggtagcctct atctctccgt ctggtggtct gacgtactac 180

cgtgactctg tcaaaggtcg tttcaccatc tctcgtgatg acgcgaaaaa ctctccgtac 240

ctgcagatga actctctgcg tgcagaagat accgcagtgt actactgcgc tactggtggt 300

gaaggtatct tcgactactg gggtcagggt accctggtaa ctgtctcaag cgcttctaca 360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc tggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660

tccggaggtg gcggttccgg aggtggcggt accggtggcg gtggatccga agtccagctg 720

cttgaatccg gaggcggact cgtgcagccc ggaggcagtc ttcgcttgtc ctgcgctgta 780

tctggaatcg acctgagcaa ttacgccatc aactgggtga gacaggcacc tgggaaatgc 840

ctcgaatgga tcggcattat atgggctagt gggacgacct tttatgctac atgggcgaag 900

ggtagattca caatctcacg ggataatagt aagaacacag tgtacctgca gatgaactcc 960

ctgcgagcag aggataccgc cgtttactat tgtgctcgca ctgtcccagg ttatagcact 1020

gcaccctact ttgatctgtg ggggcagggc actctggtca ccgtctcgag ttga 1074

<210> 27
<211> 1086
<212> DNA
<213> Artificial

<220>
<223> Light chain A26-645(gL4) including B72.3 leader sequence

<400> 27
atgtcagttc ccacacaggt gctgggcctg cttctgttgt ggctcaccga tgctaggtgt 60

gatatccaga tgacccagag tccaagcagt ctctccgcca gcgtaggcga tcgtgtgact 120

attacctgtc gtgcaaccca gagcatctac aacgctctgg cttggtatca gcagaaaccg 180

ggtaaagcgc caaaactcct gatctacaac gcgaacactc tgcataccgg tgttccgtct 240

cgtttctctg cgtctggttc tggtacggac tctactctga ccatctcctc tctgcagccg 300

gaagatttcg cgacctacta ctgccagcag tactacgatt acccactgac gtttggtggt 360

ggtaccaaag ttgagatcaa acgtacggtg gctgcaccat ctgtcttcat cttccccca 420

tctgatgagc agttgaagtc tggcactgcc tctgttgtgt gcctgctgaa taacttctac 480

cctagagagg ccaaagtcca gtggaaggtg gataacgccc ttcaatccgg aaactcccag 540

gagagtgtca ctgagcagga ctcaaaggac tccacctata gccttagcag cacactgaca 600

ctgagcaagg ctgactacga gaaacacaag gtctacgcct gcgaagtgac acatcaaggc 660

ctgagctcac ccgtgacaaa gagctttaac aggggagagt gtggtggagg tggctctggc 720

ggtggtggct ccggaggcgg aggaagcgac atccagatga cccagagccc ttcctctgta 780

agcgccagtg tcggagacag agtgactatt acctgccaaa gctccccttc agtctggtcc 840

aattttctat cctggtacca gcaaaagccc ggaaaggctc ctaaattgct gatctacgaa 900

gcaagcaaac tcaccagcgg cgtgcccagc aggttcagcg gcagtgggtc tggaactgac 960

tttaccctga caatctcctc actccagccc gaggacttcg ccacctatta ctgcggtgga 1020

ggttacagta gcataagtga tacgacattt ggatgcggca ctaaagtgga aatcaagcgt 1080

acctga 1086

<210> 28
<211> 1026
<212> DNA
<213> Artificial

<220>
<223> Light chain A26-645(gL4)

<400> 28
gatatccaga tgacccagag tccaagcagt ctctccgcca gcgtaggcga tcgtgtgact 60

attacctgtc gtgcaaccca gagcatctac aacgctctgg cttggtatca gcagaaaccg 120

ggtaaagcgc caaaactcct gatctacaac gcgaacactc tgcataccgg tgttccgtct 180

cgtttctctg cgtctggttc tggtacggac tctactctga ccatctcctc tctgcagccg 240

gaagatttcg cgacctacta ctgccagcag tactacgatt acccactgac gtttggtggt 300

ggtaccaaag ttgagatcaa acgtacggtg gctgcaccat ctgtcttcat cttccccca 360

tctgatgagc agttgaagtc tggcactgcc tctgttgtgt gcctgctgaa taacttctac 420

cctagagagg ccaaagtcca gtggaaggtg gataacgccc ttcaatccgg aaactcccag 480

gagagtgtca ctgagcagga ctcaaaggac tccacctata gccttagcag cacactgaca 540

ctgagcaagg ctgactacga gaaacacaag gtctacgcct gcgaagtgac acatcaaggc 600

ctgagctcac ccgtgacaaa gagctttaac aggggagagt gtggtggagg tggctctggc 660

ggtggtggct ccggaggcgg aggaagcgac atccagatga cccagagccc ttcctctgta 720

agcgccagtg tcggagacag agtgactatt acctgccaaa gctccccttc agtctggtcc 780

aattttctat cctggtacca gcaaaagccc ggaaaggctc ctaaattgct gatctacgaa 840

gcaagcaaac tcaccagcgg cgtgcccagc aggttcagcg gcagtgggtc tggaactgac 900

tttaccctga caatctcctc actccagccc gaggacttcg ccacctatta ctgcggtgga 960

ggttacagta gcataagtga tacgacattt ggatgcggca ctaaagtgga aatcaagcgt 1020

acctga 1026