SEQUENCE LISTING

<110> BOEHRINGER INGELHEIM INTERNATIONAL GMBH

<120> BIPARATOPIC POLYPEPTIDES ANTAGONIZING WNT SIGNALING IN TUMOR CELLS

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<220>
<223> CDR1 of Wnt1-333E06mod

<400> 1
Thr Tyr Thr Val Gly
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<220>
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<400> 2
Ala Ile Arg Arg Arg Gly Ser Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15
Gly

<210> 3
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<400> 3
Asp Thr Arg Thr Val Ala Leu Leu Gln Tyr Arg Tyr Asp Tyr
1 5 10

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<220>
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<400> 4
Ser Tyr Ala Met Gly
1 5

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<220>
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<400> 5
Ala Ile Arg Arg Ser Gly Arg Arg Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15
Gly

<210> 6
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<400> 6
Ala Arg Arg Val Arg Ser Ser Thr Arg Tyr Asn Thr Gly Thr Trp Trp
1 5 10 15
Trp Glu Tyr

<210> 7
<211> 5
<212> PRT
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<220>
<223> CDR1 of Wnt1-332D03mod

<400> 7
Arg Tyr Thr Met Gly
1 5

<210> 8
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<213> Artificial Sequence

<220>

<223> CDR2 of Wnt1-332D03mod

<400> 8
Ala Ile Val Arg Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1   5   10   15
Gly

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

<220>
<223> CDR3 of Wnt1-332D03mod

<400> 9
Asp Arg Arg Gly Arg Gly Glu Asn Tyr Ile Leu Leu Tyr Ser Ser Gly
1   5   10   15
Arg Tyr Glu Tyr
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<210> 10
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<220>
<223> CDR1 of Wnt3a-093A01

<400> 10
Ser Tyr Ala Met Gly
1   5

<210> 11
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 of Wnt3a-093A01

<400> 11
Ala Ile Ser Trp Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1   5   10   15
Gly

<210> 12
<211> 17
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<213> Artificial Sequence

<220>

<223> CDR3 of Wnt3a-093A01

<400> 12
Ser Pro Ile Pro Tyr Gly Ser Leu Leu Arg Arg Arg Asn Asn Tyr Asp
1 5 10 15
Tyr

<210> 13
<211> 5
<212> PRT
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<220>
<223> CDR1 of Wnt3a-367B10

<400> 13
Ser Tyr Ala Met Gly
1 5

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

<220>
<223> CDR2 of Wnt3a-367B10

<400> 14
Ala Ile Ser Trp Arg Ser Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15
Gly

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

<220>
<223> CDR3 of Wnt3a-367B10

<400> 15
Asp Pro Arg Gly Tyr Gly Val Ala Tyr Val Ser Ala Tyr Tyr Glu Tyr
1 5 10 15

<210> 16
<211> 5
<212> PRT
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<220>

<223> CDR1 of Alb11

<400> 16
Ser Phe Gly Met Ser
1 5

<210> 17
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<220>
<223> CDR2 of Alb11

<400> 17
Ser Ile Ser Gly Ser Gly Ser Asp Thr Leu Tyr Ala Asp Ser Val Lys
1 5 10 15
Gly

<210> 18
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 of Alb11

<400> 18
Gly Gly Ser Leu Ser Arg
1 5

<210> 19
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH domain Wnt1-333E06mod

<400> 19
Ala 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 Arg Thr Phe Ser Thr Tyr
20 25 30
Thr Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
35 40 45
Ala Ala Ile Arg Arg Arg Gly Ser 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 Val Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Ala Asp Thr Arg Thr Val Ala Leu Leu Gln Tyr Arg Tyr Asp Tyr

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            100                 105                 110
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120

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<220>
<223> VHH domain Wnt1-333G06

<400> 20
Ala 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 Gly Thr Phe Ser Ser Tyr
            20                  25                  30
Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
        35                  40                  45
Ala Ala Ile Arg Arg Ser Gly Arg Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Ala Ala Arg Arg Val Arg Ser Ser Thr Arg Tyr Asn Thr Gly Thr
            100                 105                 110
Trp Trp Trp Glu Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125



<210> 21
<211> 129
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH domain Wnt1-332D03mod

<400> 21
Ala 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 Leu Thr Phe Ser Arg Tyr
            20                  25                  30
Thr Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
        35                  40                  45
Ala Ala Ile Val Arg 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 Val Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Ala Asp Arg Arg Gly Arg Gly Glu Asn Tyr Ile Leu Leu Tyr Ser
```

```
            100                 105                 110
Ser Gly Arg Tyr Glu Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
        115                 120                 125
Ser


<210> 22
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH domain Wnt3a-093A01

<400> 22
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 Arg Thr Phe Ser Ser Tyr
            20                  25                  30
Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
        35                  40                  45
Ala Ala Ile Ser Trp 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 Val Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Ala Ser Pro Ile Pro Tyr Gly Ser Leu Leu Arg Arg Arg Asn Asn
            100                 105                 110
Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125

<210> 23
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH domain Wnt3a-367B10

<400> 23
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 Gly Thr Phe Ser Ser Tyr
            20                  25                  30
Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
        35                  40                  45
Ala Ala Ile Ser Trp Arg Ser 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 Val Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Ala Asp Pro Arg Gly Tyr Gly Val Ala Tyr Val Ser Ala Tyr Tyr
```

```
            100                 105                 110
Glu Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125

<210> 24
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH domain Alb11

<400> 24
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
1               5                   10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe
            20                  25                  30
Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Ser Ile Ser Gly Ser Gly Ser Asp Thr Leu Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Thr Ile Gly Gly Ser Leu Ser Arg Ser Ser Gln Gly Thr Leu Val Thr
            100                 105                 110
Val Ser Ser
        115

<210> 25
<211> 435
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH construct F013500575

<400> 25
Ala 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 Arg Thr Phe Ser Thr Tyr
            20                  25                  30
Thr Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
        35                  40                  45
Ala Ala Ile Arg Arg Arg Gly Ser 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 Val Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Ala Asp Thr Arg Thr Val Ala Leu Leu Gln Tyr Arg Tyr Asp Tyr
            100                 105                 110
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
```

```
        115                 120                 125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    130                 135                 140
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val
145                 150                 155                 160
Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu
                165                 170                 175
Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe Gly Met
            180                 185                 190
Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser
        195                 200                 205
Ile Ser Gly Ser Gly Ser Asp Thr Leu Tyr Ala Asp Ser Val Lys Gly
    210                 215                 220
Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln
225                 230                 235                 240
Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile
                245                 250                 255
Gly Gly Ser Leu Ser Arg Ser Ser Gln Gly Thr Leu Val Thr Val Ser
            260                 265                 270
Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        275                 280                 285
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    290                 295                 300
Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
305                 310                 315                 320
Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr
                325                 330                 335
Phe Ser Ser Tyr Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu
            340                 345                 350
Arg Glu Phe Val Ala Ala Ile Ser Trp Ser Gly Gly Ser Thr Tyr Tyr
        355                 360                 365
Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
    370                 375                 380
Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala
385                 390                 395                 400
Val Tyr Tyr Cys Ala Ala Ser Pro Ile Pro Tyr Gly Ser Leu Leu Arg
                405                 410                 415
Arg Arg Asn Asn Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
            420                 425                 430
Ser Ser Ala
        435
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<210> 26
<211> 439
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH construct F013500571

<400> 26
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Ala 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 Gly Thr Phe Ser Ser Tyr
```

```
            20                  25                  30
Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
        35                  40                  45
Ala Ala Ile Arg Arg Ser Gly Arg Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Ala Ala Arg Arg Val Arg Ser Ser Thr Arg Tyr Asn Thr Gly Thr
            100                 105                 110
Trp Trp Trp Glu Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    130                 135                 140
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145                 150                 155                 160
Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
                165                 170                 175
Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
            180                 185                 190
Ser Ser Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        195                 200                 205
Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Ser Asp Thr Leu Tyr Ala
    210                 215                 220
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr
225                 230                 235                 240
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val
                245                 250                 255
Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Arg Ser Ser Gln Gly Thr
            260                 265                 270
Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        275                 280                 285
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    290                 295                 300
Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
305                 310                 315                 320
Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
                325                 330                 335
Ala Ser Gly Gly Thr Phe Ser Ser Tyr Ala Met Gly Trp Phe Arg Gln
            340                 345                 350
Ala Pro Gly Lys Glu Arg Glu Phe Val Ala Ala Ile Ser Trp Arg Ser
        355                 360                 365
Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
    370                 375                 380
Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Arg
385                 390                 395                 400
Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala Ala Asp Pro Arg Gly Tyr
                405                 410                 415
Gly Val Ala Tyr Val Ser Ala Tyr Tyr Glu Tyr Trp Gly Gln Gly Thr
            420                 425                 430
Leu Val Thr Val Ser Ser Ala
        435
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<210> 27
<211> 440
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH construct F013500720

<400> 27
Ala 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 Leu Thr Phe Ser Arg Tyr
            20   25   30
Thr Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
        35   40   45
Ala Ala Ile Val Arg 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 Val Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Ala Asp Arg Arg Gly Arg Gly Glu Asn Tyr Ile Leu Leu Tyr Ser
            100   105   110
Ser Gly Arg Tyr Glu Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
        115   120   125
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    130   135   140
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
145   150   155   160
Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
                165   170   175
Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
            180   185   190
Phe Ser Ser Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
        195   200   205
Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Ser Asp Thr Leu Tyr
    210   215   220
Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
225   230   235   240
Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala
                245   250   255
Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Arg Ser Ser Gln Gly
            260   265   270
Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        275   280   285
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    290   295   300
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu
305   310   315   320
Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
                325   330   335
Ala Ala Ser Gly Gly Thr Phe Ser Ser Tyr Ala Met Gly Trp Phe Arg
            340   345   350
Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ala Ala Ile Ser Trp Arg

```
        355                 360                 365
Ser Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile
    370                 375                 380
Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu
385                 390                 395                 400
Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala Ala Asp Pro Arg Gly
                405                 410                 415
Tyr Gly Val Ala Tyr Val Ser Ala Tyr Tyr Glu Tyr Trp Gly Gln Gly
            420                 425                 430
Thr Leu Val Thr Val Ser Ser Ala
        435                 440
```

<210> 28
<211> 149
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH domain F0129093A01

<400> 28

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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 Arg Thr Phe Ser Ser Tyr
            20                  25                  30
Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
        35                  40                  45
Ala Ala Ile Ser Trp 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 Val Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Ala Ser Pro Ile Pro Tyr Gly Ser Leu Leu Arg Arg Arg Asn Asn
            100                 105                 110
Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ala
        115                 120                 125
Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala His
    130                 135                 140
His His His His His
145
```

<210> 29
<211> 151
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH domain F0130333G06

<400> 29

```
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 Gly Thr Phe Ser Ser Tyr
```

```
            20                  25                  30
Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
        35                  40                  45
Ala Ala Ile Arg Arg Ser Gly Arg Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Ala Ala Arg Arg Val Arg Ser Ser Thr Arg Tyr Asn Thr Gly Thr
            100                 105                 110
Trp Trp Trp Glu Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125
Ala Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala
    130                 135                 140
Ala His His His His His His
145                 150
```

<210> 30
<211> 148
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH domain F0129093A03

<400> 30

```
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 Arg Thr Phe Ser Thr Tyr
            20                  25                  30
Val Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
        35                  40                  45
Ala Ala Ile Asn Trp Ser Gly Ser Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Ala Ser Arg Ser Ser Tyr Ala Gly Arg Thr Tyr Tyr Glu Leu Tyr
            100                 105                 110
Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ala Ala
        115                 120                 125
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala His His
    130                 135                 140
His His His His
145
```

<210> 31
<211> 146
<212> PRT
<213> Artificial Sequence

<220>

<223> VHH domain F0130333E06

<400> 31
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 Arg Thr Phe Ser Thr Tyr
            20   25   30
Thr Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
        35   40   45
Ala Ala Ile Arg Arg Arg Gly Ser Ser Thr Tyr Tyr Ser Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Ala Asp Thr Arg Thr Val Ala Leu Leu Gln Tyr Arg Tyr Asp Tyr
            100   105   110
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ala Ala Glu Gln
        115   120   125
Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala His His His His
    130   135   140
His His
145

<210> 32
<211> 152
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH domain F0130332D03

<400> 32
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 Leu Thr Phe Ser Arg Tyr
            20   25   30
Thr Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
        35   40   45
Ala Ala Ile Asn Arg Ser Gly Gly Ser Thr Tyr Tyr Ser Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Ala Asp Arg Arg Gly Arg Gly Glu Asn Tyr Ser Leu Leu Tyr Ser
            100   105   110
Ser Asn Arg Tyr Glu Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
        115   120   125
Ser Ala Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly
    130   135   140
Ala Ala His His His His His His
145   150

<210> 33
<211> 148
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH domain F0130367B10

<400> 33
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 Gly Thr Phe Ser Ser Tyr
            20   25   30
Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
        35   40   45
Ala Ala Ile Ser Trp Arg Ser 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 Val Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Pro Glu Gly Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Ala Asp Pro Arg Gly Tyr Gly Val Ala Tyr Val Ser Ala Tyr Tyr
            100   105   110
Glu Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ala Ala
        115   120   125
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala His His
    130   135   140
His His His His
145

<210> 34
<211> 149
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH domain F0130378B05

<400> 34
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 Val Ala Ser Gly Arg Thr Phe Ser Ser Tyr
            20   25   30
Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
        35   40   45
Ala Ala Ile Ser Arg Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Ala Asp Arg Arg Val Tyr Ser Thr Leu Pro Pro Thr Thr Ser Arg
            100   105   110
Tyr Asn Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ala

```
        115                 120                 125
Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala His
    130                 135                 140
His His His His His
145
```

<210> 35
<211> 147
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH domain F0130378A04

<400> 35

```
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 Arg Thr Phe Ser Ser Tyr
            20                  25                  30
Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
        35                  40                  45
Ala Ala Ile Thr Arg Thr Gly Arg Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Ala Asp Arg Arg Gly Tyr Tyr Tyr Tyr Asp Ser Ser Phe Tyr Asp
            100                 105                 110
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ala Ala Glu
        115                 120                 125
Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala His His His
    130                 135                 140
His His His
145
```

<210> 36
<211> 150
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH domain F0130372C08

<400> 36

```
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 Arg Thr Phe Ser Asp Tyr
            20                  25                  30
Gly Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
        35                  40                  45
Ala Ala Ile Ser Trp Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
```

65 70 75 80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Ala Lys Arg Arg Gly Arg Gly Ser Val Ser Pro Asn Ser Ser Ser
100 105 110
Arg Tyr Asn Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala
115 120 125
Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala
130 135 140
His His His His His His
145 150

<210> 37
<211> 462
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH construct F013500016

<400> 37
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 Leu Thr Phe Ser Arg Tyr
20 25 30
Thr Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
35 40 45
Ala Ala Ile Asn Arg Ser Gly Gly Ser Thr Tyr Tyr Ser Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Ala Asp Arg Arg Gly Arg Gly Glu Asn Tyr Ser Leu Leu Tyr Ser
100 105 110
Ser Asn Arg Tyr Glu Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
115 120 125
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
145 150 155 160
Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
165 170 175
Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
180 185 190
Phe Ser Ser Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
195 200 205
Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Ser Asp Thr Leu Tyr
210 215 220
Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
225 230 235 240
Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala
245 250 255
Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Arg Ser Ser Gln Gly

```
            260                 265                 270
Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        275                 280                 285
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    290                 295                 300
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu
305                 310                 315                 320
Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
                325                 330                 335
Ala Ala Ser Gly Gly Thr Phe Ser Ser Tyr Ala Met Gly Trp Phe Arg
            340                 345                 350
Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ala Ala Ile Ser Trp Arg
        355                 360                 365
Ser Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile
    370                 375                 380
Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu
385                 390                 395                 400
Arg Pro Glu Gly Thr Ala Val Tyr Tyr Cys Ala Ala Asp Pro Arg Gly
                405                 410                 415
Tyr Gly Val Ala Tyr Val Ser Ala Tyr Tyr Glu Tyr Trp Gly Gln Gly
            420                 425                 430
Thr Leu Val Thr Val Ser Ser Gly Ala Ala Glu Gln Lys Leu Ile Ser
        435                 440                 445
Glu Glu Asp Leu Asn Gly Ala Ala His His His His His His
    450                 455                 460
```

<210> 38
<211> 463
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH construct F013500018

<400> 38

```
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 Leu Thr Phe Ser Arg Tyr
            20                  25                  30
Thr Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
        35                  40                  45
Ala Ala Ile Asn Arg Ser Gly Gly Ser Thr Tyr Tyr Ser Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Ala Asp Arg Arg Gly Arg Gly Glu Asn Tyr Ser Leu Leu Tyr Ser
            100                 105                 110
Ser Asn Arg Tyr Glu Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
        115                 120                 125
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    130                 135                 140
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
```

145 150 155 160
Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
165 170 175
Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
180 185 190
Phe Ser Ser Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
195 200 205
Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Ser Asp Thr Leu Tyr
210 215 220
Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
225 230 235 240
Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala
245 250 255
Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Arg Ser Ser Gln Gly
260 265 270
Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
275 280 285
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
290 295 300
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu
305 310 315 320
Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
325 330 335
Val Ala Ser Gly Arg Thr Phe Ser Ser Tyr Ala Met Gly Trp Phe Arg
340 345 350
Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ala Ala Ile Ser Arg Ser
355 360 365
Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile
370 375 380
Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu
385 390 395 400
Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala Ala Asp Arg Arg Val
405 410 415
Tyr Ser Thr Leu Pro Pro Thr Thr Ser Arg Tyr Asn Tyr Trp Gly Gln
420 425 430
Gly Thr Leu Val Thr Val Ser Ser Gly Ala Ala Glu Gln Lys Leu Ile
435 440 445
Ser Glu Glu Asp Leu Asn Gly Ala Ala His His His His His His
450 455 460

<210> 39
<211> 461
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH construct F013500021

<400> 39
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 Gly Thr Phe Ser Ser Tyr
20 25 30
Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val

```
        35                  40                  45
Ala Ala Ile Arg Arg Ser Gly Arg Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Ala Ala Arg Arg Val Arg Ser Ser Thr Arg Tyr Asn Thr Gly Thr
            100                 105                 110
Trp Trp Trp Glu Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    130                 135                 140
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145                 150                 155                 160
Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
                165                 170                 175
Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
            180                 185                 190
Ser Ser Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        195                 200                 205
Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Ser Asp Thr Leu Tyr Ala
    210                 215                 220
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr
225                 230                 235                 240
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val
                245                 250                 255
Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Arg Ser Ser Gln Gly Thr
            260                 265                 270
Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        275                 280                 285
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    290                 295                 300
Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
305                 310                 315                 320
Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
                325                 330                 335
Ala Ser Gly Gly Thr Phe Ser Ser Tyr Ala Met Gly Trp Phe Arg Gln
            340                 345                 350
Ala Pro Gly Lys Glu Arg Glu Phe Val Ala Ala Ile Ser Trp Arg Ser
        355                 360                 365
Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
    370                 375                 380
Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Arg
385                 390                 395                 400
Pro Glu Gly Thr Ala Val Tyr Tyr Cys Ala Ala Asp Pro Arg Gly Tyr
                405                 410                 415
Gly Val Ala Tyr Val Ser Ala Tyr Tyr Glu Tyr Trp Gly Gln Gly Thr
            420                 425                 430
Leu Val Thr Val Ser Ser Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu
        435                 440                 445
Glu Asp Leu Asn Gly Ala Ala His His His His His His
    450                 455                 460
```

<210> 40
<211> 456
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH construct F013500026

<400> 40
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 Arg Thr Phe Ser Thr Tyr
            20   25   30
Thr Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
        35   40   45
Ala Ala Ile Arg Arg Arg Gly Ser Ser Thr Tyr Tyr Ser Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Ala Asp Thr Arg Thr Val Ala Leu Leu Gln Tyr Arg Tyr Asp Tyr
            100   105   110
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        115   120   125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    130   135   140
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val
145   150   155   160
Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu
                165   170   175
Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe Gly Met
            180   185   190
Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser
        195   200   205
Ile Ser Gly Ser Gly Ser Asp Thr Leu Tyr Ala Asp Ser Val Lys Gly
    210   215   220
Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln
225   230   235   240
Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile
                245   250   255
Gly Gly Ser Leu Ser Arg Ser Ser Gln Gly Thr Leu Val Thr Val Ser
            260   265   270
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        275   280   285
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    290   295   300
Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
305   310   315   320
Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Gly Thr
                325   330   335
Phe Ser Ser Tyr Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu
            340   345   350
Arg Glu Phe Val Ala Ala Ile Ser Trp Arg Ser Gly Ser Thr Tyr Tyr

```
        355                 360                 365
Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
    370                 375                 380
Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Gly Thr Ala
385                 390                 395                 400
Val Tyr Tyr Cys Ala Ala Asp Pro Arg Gly Tyr Gly Val Ala Tyr Val
                405                 410                 415
Ser Ala Tyr Tyr Glu Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
            420                 425                 430
Ser Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly
        435                 440                 445
Ala Ala His His His His His His
    450                 455
```

<210> 41
<211> 461
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH construct F013500030

<400> 41

```
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 Val Ala Ser Gly Arg Thr Phe Ser Ser Tyr
            20                  25                  30
Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
        35                  40                  45
Ala Ala Ile Ser Arg Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Ala Asp Arg Arg Val Tyr Ser Thr Leu Pro Pro Thr Thr Ser Arg
            100                 105                 110
Tyr Asn Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    130                 135                 140
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
145                 150                 155                 160
Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
                165                 170                 175
Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser
            180                 185                 190
Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
        195                 200                 205
Val Ser Ser Ile Ser Gly Ser Gly Ser Asp Thr Leu Tyr Ala Asp Ser
    210                 215                 220
Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu
225                 230                 235                 240
Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr
```

```
                245                 250                 255
Cys Thr Ile Gly Gly Ser Leu Ser Arg Ser Ser Gln Gly Thr Leu Val
            260                 265                 270
Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        275                 280                 285
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    290                 295                 300
Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
305                 310                 315                 320
Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
                325                 330                 335
Gly Arg Thr Phe Ser Asp Tyr Gly Met Gly Trp Phe Arg Gln Ala Pro
            340                 345                 350
Gly Lys Glu Arg Glu Phe Val Ala Ala Ile Ser Trp Ser Gly Gly Arg
        355                 360                 365
Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
    370                 375                 380
Asn Ser Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu
385                 390                 395                 400
Asp Thr Ala Val Tyr Tyr Cys Ala Ala Lys Arg Arg Gly Arg Gly Ser
                405                 410                 415
Val Ser Pro Asn Ser Ser Ser Arg Tyr Asn Tyr Trp Gly Gln Gly Thr
            420                 425                 430
Leu Val Thr Val Ser Ser Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu
        435                 440                 445
Glu Asp Leu Asn Gly Ala Ala His His His His His His
    450                 455                 460

<210> 42
<211> 460
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH construct F013500032

<400> 42
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 Arg Thr Phe Ser Ser Tyr
            20                  25                  30
Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
        35                  40                  45
Ala Ala Ile Thr Arg Thr Gly Arg Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Ala Asp Arg Arg Gly Tyr Tyr Tyr Tyr Asp Ser Ser Phe Tyr Asp
            100                 105                 110
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
        115                 120                 125
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
```

```
    130                 135                 140
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
145                 150                 155                 160
Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser
                165                 170                 175
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe Gly
            180                 185                 190
Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
        195                 200                 205
Ser Ile Ser Gly Ser Gly Ser Asp Thr Leu Tyr Ala Asp Ser Val Lys
    210                 215                 220
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu
225                 230                 235                 240
Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr
                245                 250                 255
Ile Gly Gly Ser Leu Ser Arg Ser Ser Gln Gly Thr Leu Val Thr Val
            260                 265                 270
Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        275                 280                 285
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    290                 295                 300
Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
305                 310                 315                 320
Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Gly
                325                 330                 335
Thr Phe Ser Ser Tyr Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys
            340                 345                 350
Glu Arg Glu Phe Val Ala Ala Ile Arg Arg Ser Gly Arg Arg Thr Tyr
        355                 360                 365
Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
    370                 375                 380
Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr
385                 390                 395                 400
Ala Val Tyr Tyr Cys Ala Ala Ala Arg Arg Val Arg Ser Ser Thr Arg
                405                 410                 415
Tyr Asn Thr Gly Thr Trp Trp Trp Glu Tyr Trp Gly Gln Gly Thr Leu
            420                 425                 430
Val Thr Val Ser Ser Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu
        435                 440                 445
Asp Leu Asn Gly Ala Ala His His His His His His
    450                 455                 460
```

<210> 43
<211> 462
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH construct F013500033

<400> 43

```
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 Val Ala Ser Gly Arg Thr Phe Ser Ser Tyr
```

```
            20                  25                  30
Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
        35                  40                  45
Ala Ala Ile Ser Arg Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Ala Asp Arg Arg Val Tyr Ser Thr Leu Pro Pro Thr Thr Ser Arg
            100                 105                 110
Tyr Asn Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    130                 135                 140
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
145                 150                 155                 160
Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
                165                 170                 175
Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser
            180                 185                 190
Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
        195                 200                 205
Val Ser Ser Ile Ser Gly Ser Gly Ser Asp Thr Leu Tyr Ala Asp Ser
    210                 215                 220
Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu
225                 230                 235                 240
Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr
                245                 250                 255
Cys Thr Ile Gly Gly Ser Leu Ser Arg Ser Ser Gln Gly Thr Leu Val
            260                 265                 270
Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        275                 280                 285
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    290                 295                 300
Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
305                 310                 315                 320
Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
                325                 330                 335
Gly Gly Thr Phe Ser Ser Tyr Ala Met Gly Trp Phe Arg Gln Ala Pro
            340                 345                 350
Gly Lys Glu Arg Glu Phe Val Ala Ala Ile Arg Arg Ser Gly Arg Arg
        355                 360                 365
Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
    370                 375                 380
Asn Ser Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu
385                 390                 395                 400
Asp Thr Ala Val Tyr Tyr Cys Ala Ala Ala Arg Arg Val Arg Ser Ser
                405                 410                 415
Thr Arg Tyr Asn Thr Gly Thr Trp Trp Trp Glu Tyr Trp Gly Gln Gly
            420                 425                 430
Thr Leu Val Thr Val Ser Ser Gly Ala Ala Glu Gln Lys Leu Ile Ser
        435                 440                 445
Glu Glu Asp Leu Asn Gly Ala Ala His His His His His His
```

450 455 460

<210> 44
<211> 456
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH construct F013500039

<400> 44
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 Arg Thr Phe Ser Thr Tyr
20 25 30
Val Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
35 40 45
Ala Ala Ile Asn Trp Ser Gly Ser Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Ala Ser Arg Ser Ser Tyr Ala Gly Arg Thr Tyr Tyr Glu Leu Tyr
100 105 110
Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
115 120 125
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145 150 155 160
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
165 170 175
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe
180 185 190
Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
195 200 205
Ser Ser Ile Ser Gly Ser Gly Ser Asp Thr Leu Tyr Ala Asp Ser Val
210 215 220
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr
225 230 235 240
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
245 250 255
Thr Ile Gly Gly Ser Leu Ser Arg Ser Ser Gln Gly Thr Leu Val Thr
260 265 270
Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
275 280 285
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
290 295 300
Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
305 310 315 320
Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
325 330 335
Arg Thr Phe Ser Thr Tyr Thr Val Gly Trp Phe Arg Gln Ala Pro Gly

```
            340                 345                 350
Lys Glu Arg Glu Phe Val Ala Ala Ile Arg Arg Arg Gly Ser Ser Thr
        355                 360                 365
Tyr Tyr Ser Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
    370                 375                 380
Ser Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp
385                 390                 395                 400
Thr Ala Val Tyr Tyr Cys Ala Ala Asp Thr Arg Thr Val Ala Leu Leu
                405                 410                 415
Gln Tyr Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
            420                 425                 430
Ser Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly
        435                 440                 445
Ala Ala His His His His His His
    450                 455

<210> 45
<211> 463
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH construct F013500046

<400> 45
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 Leu Thr Phe Ser Arg Tyr
            20                  25                  30
Thr Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
        35                  40                  45
Ala Ala Ile Asn Arg Ser Gly Gly Ser Thr Tyr Tyr Ser Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Ala Asp Arg Arg Gly Arg Gly Glu Asn Tyr Ser Leu Leu Tyr Ser
            100                 105                 110
Ser Asn Arg Tyr Glu Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
        115                 120                 125
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    130                 135                 140
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
145                 150                 155                 160
Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
                165                 170                 175
Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
            180                 185                 190
Phe Ser Ser Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
        195                 200                 205
Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Ser Asp Thr Leu Tyr
    210                 215                 220
Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
```

225 230 235 240
Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala
245 250 255
Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Arg Ser Ser Gln Gly
260 265 270
Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
275 280 285
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
290 295 300
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu
305 310 315 320
Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
325 330 335
Ala Ala Ser Gly Arg Thr Phe Ser Ser Tyr Ala Met Gly Trp Phe Arg
340 345 350
Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ala Ala Ile Ser Trp Ser
355 360 365
Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile
370 375 380
Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu
385 390 395 400
Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala Ala Ser Pro Ile Pro
405 410 415
Tyr Gly Ser Leu Leu Arg Arg Arg Asn Asn Tyr Asp Tyr Trp Gly Gln
420 425 430
Gly Thr Leu Val Thr Val Ser Ser Gly Ala Ala Glu Gln Lys Leu Ile
435 440 445
Ser Glu Glu Asp Leu Asn Gly Ala Ala His His His His His His
450 455 460

<210> 46
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH construct F013500047

<400> 46
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Thr Tyr
20 25 30
Thr Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
35 40 45
Ala Ala Ile Arg Arg Arg Gly Ser Ser Thr Tyr Tyr Ser Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Ala Asp Thr Arg Thr Val Ala Leu Leu Gln Tyr Arg Tyr Asp Tyr
100 105 110
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser

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        115                 120                 125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    130                 135                 140
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val
145                 150                 155                 160
Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu
                165                 170                 175
Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe Gly Met
            180                 185                 190
Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser
        195                 200                 205
Ile Ser Gly Ser Gly Ser Asp Thr Leu Tyr Ala Asp Ser Val Lys Gly
    210                 215                 220
Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln
225                 230                 235                 240
Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile
                245                 250                 255
Gly Gly Ser Leu Ser Arg Ser Ser Gln Gly Thr Leu Val Thr Val Ser
            260                 265                 270
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        275                 280                 285
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    290                 295                 300
Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
305                 310                 315                 320
Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr
                325                 330                 335
Phe Ser Ser Tyr Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu
            340                 345                 350
Arg Glu Phe Val Ala Ala Ile Ser Trp Ser Gly Gly Ser Thr Tyr Tyr
        355                 360                 365
Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
    370                 375                 380
Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala
385                 390                 395                 400
Val Tyr Tyr Cys Ala Ala Ser Pro Ile Pro Tyr Gly Ser Leu Leu Arg
                405                 410                 415
Arg Arg Asn Asn Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
            420                 425                 430
Ser Ser Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
        435                 440                 445
Gly Ala Ala His His His His His His
    450                 455
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<210> 47
<211> 462
<212> PRT
<213> Artificial Sequence

<220>
<223> VHH construct F013500053

<400> 47
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Ser Tyr
            20                  25                  30
Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
        35                  40                  45
Ala Ala Ile Ser Trp 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 Val Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Ala Ser Pro Ile Pro Tyr Gly Ser Leu Leu Arg Arg Arg Asn Asn
            100                 105                 110
Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    130                 135                 140
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
145                 150                 155                 160
Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
                165                 170                 175
Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser
            180                 185                 190
Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
        195                 200                 205
Val Ser Ser Ile Ser Gly Ser Gly Ser Asp Thr Leu Tyr Ala Asp Ser
    210                 215                 220
Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu
225                 230                 235                 240
Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr
                245                 250                 255
Cys Thr Ile Gly Gly Ser Leu Ser Arg Ser Ser Gln Gly Thr Leu Val
            260                 265                 270
Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        275                 280                 285
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    290                 295                 300
Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
305                 310                 315                 320
Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
                325                 330                 335
Gly Gly Thr Phe Ser Ser Tyr Ala Met Gly Trp Phe Arg Gln Ala Pro
            340                 345                 350
Gly Lys Glu Arg Glu Phe Val Ala Ala Ile Arg Arg Ser Gly Arg Arg
        355                 360                 365
Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
    370                 375                 380
Asn Ser Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu
385                 390                 395                 400
Asp Thr Ala Val Tyr Tyr Cys Ala Ala Ala Arg Arg Val Arg Ser Ser
                405                 410                 415
Thr Arg Tyr Asn Thr Gly Thr Trp Trp Trp Glu Tyr Trp Gly Gln Gly
            420                 425                 430
Thr Leu Val Thr Val Ser Ser Gly Ala Ala Glu Gln Lys Leu Ile Ser
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        435                 440                 445
Glu Glu Asp Leu Asn Gly Ala Ala His His His His His His
    450                 455                 460
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