SEQUENCE LISTING

<110> Phanes Therapeutics, Inc.

<120> Anti-DLL3 Antibodies and Uses Thereof

<130> 689204.17WO

<150> US62/787,815
<151> 2019-01-03

<150> US62/754,207
<151> 2018-11-01

<150> US62/668,427
<151> 2018-05-08

<160> 195

<170> PatentIn version 3.5

<210> 1
<211> 118
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<220>
<223> 13P9A Heavy Chain Variable Region

<400> 1

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

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

Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Pro Asp Trp Ile
35 40 45

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

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

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

```
Ala Arg Gly Gly Tyr Asp Tyr Asp Gly Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Thr Leu Thr Val Ser Ser
        115


<210>  2
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  13P9A Light Chain Variable Region

<400>  2

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


Asp Ser Ile Thr Ile Thr Cys His Ala Ser Gln Asn Ile Asn Val Trp
            20                  25                  30


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


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


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


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


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


<210>  3
<211>  122
<212>  PRT
<213>  Artificial Sequence
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<220>
<223> 5A16A Heavy Chain Variable Region

<400> 3

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

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

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

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

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

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

Ala Arg Asp Ser Ser Gly Tyr Gly Gly Ala Tyr Ala Met Asp Phe Trp
            100   105   110

Gly Gln Gly Thr Ser Val Thr Val Ser Ser
        115   120

<210> 4
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 5A16A Light Chain Variable Region

<400> 4

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

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr
            20   25   30

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105
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<210> 5
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> 14L22A Heavy Chain Variable Region

<400> 5

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

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

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

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

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

Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Leu Tyr Tyr Cys
```

85 90 95

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

Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 6
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> 14L22A Light Chain Variable Region

<400> 6

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

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

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

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

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

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

Tyr Leu Ser Ser Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 7
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> 10P18A Heavy Chain Variable Region

<400> 7

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

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

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

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

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

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

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

Thr Val Ser Ser
        115

<210> 8
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> 10P18A Light Chain Variable Region

<400> 8

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

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser

```
            20                  25                  30

Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45

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

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

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

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

<210> 9
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 13P11A Heavy Chain Variable Region

<400> 9

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

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

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

Trp Met Gly Tyr Ile Ser Ser Ser Gly Ser Thr Asp Ser Asn Pro Ser
    50                  55                  60

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

```
Phe Leu His Leu Asn Ser Val Thr Thr Glu Asp Ile Ala Thr Tyr Tyr
                85                  90                  95


Cys Ala Thr Thr Gly Thr Trp Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Thr Leu Thr Val Ser Ser
        115


<210>  10
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  13P11A Light Chain Variable Region

<400>  10

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


Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val Gly Thr Tyr
            20                  25                  30


Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45


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


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


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


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


<210>  11
<211>  118
<212>  PRT
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<213> Artificial Sequence

<220>
<223> 3C16A Heavy Chain Variable Region

<400> 11

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


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


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


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


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


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


Ala Arg Pro Ser Asn Trp Asp Glu Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Thr Leu Thr Val Ser Ser
        115
```

<210> 12
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 3C16A Light Chain Variable Region

<400> 12

```
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
1               5                   10                  15
```

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

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

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

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

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

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

<210> 13
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> 3I21A Heavy Chain Variable Region

<400> 13

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

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

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

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

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

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

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

Thr Val Ser Ala
115

<210> 14
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 3I21A Light Chain Variable Region

<400> 14

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

Gly Arg Val Thr Ile Thr Cys Lys Ala Ser Asp His Ile Asn Asn Trp
20 25 30

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

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

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

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

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

<210> 15
<211> 120

<212> PRT
<213> Artificial Sequence

<220>
<223> 8H5A Heavy Chain Variable Region

<400> 15

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

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

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

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

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

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

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

Gly Thr Thr Leu Thr Val Ser Ser
        115   120

<210> 16
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> 8H5A Light Chain Variable Region

<400> 16

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

```
Thr Ser Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu His Ser
            20                  25                  30

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

Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala Ser Gly Val Pro
    50                  55                  60

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

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

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

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

<220>
<223> 15K2A Heavy Chain Variable Region

<400> 17

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

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

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

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

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

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


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


Thr Thr Val Thr Val Ser Ser
        115


<210>  18
<211>  111
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  15K2A Light Chain Variable Region

<400>  18

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


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


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


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


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


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


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


<210>  19
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<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 5A24A Heavy Chain Variable Region

<400> 19

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

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

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

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

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

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

Ala Arg Trp Asp Tyr Gly Asn Phe Ala Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ala
115

<210> 20
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> 5A24A Light Chain Variable Region

<400> 20

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

```
Thr Ser Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu His Ser
            20                  25                  30

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

Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala Ser Gly Val Pro
    50                  55                  60

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

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

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

<210> 21
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 15P17A Heavy Chain Variable Region

<400> 21

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

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

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

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

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

65 70 75 80

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

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

Thr Thr Val Thr Val Ser Ser
115

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

<220>
<223> 15P17A Light Chain Variable Region

<400> 22

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

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

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

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

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

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

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

<210> 23
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> 15N21A Heavy Chain Variable Region

<400> 23

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

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

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

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

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

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

Ala Arg His Arg Gly Gly Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 24
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> 15N21A Light Chain Variable Region

<400> 24

Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser Val Gly

1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
20 25 30

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

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

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

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

Tyr Tyr Thr Tyr Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105 110

<210> 25
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 13P9A HC CDR1

<400> 25

Gly Tyr Thr Phe Thr Ser Tyr Val
1 5

<210> 26
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 13P9A HC CDR2

<400> 26

Ile Asn Pro Tyr Asn Asp Ala Thr
1 5

<210> 27
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 13P9A HC CDR3

<400> 27

Ala Arg Gly Gly Tyr Asp Tyr Asp Gly Asp Tyr
1 5 10

<210> 28
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 5A16A HC CDR1

<400> 28

Gly Tyr Thr Phe Thr Arg Tyr Ile
1 5

<210> 29
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 5A16A HC CDR2

<400> 29

Ile Asn Pro Tyr Asn Asp Gly Thr
1 5

<210> 30
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 5A16A HC CDR3

<400> 30

Ala Arg Asp Ser Ser Gly Tyr Gly Gly Ala Tyr Ala Met Asp Phe
1   5   10   15

<210> 31
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 14L22A HC CDR1

<400> 31

Gly Phe Thr Phe Ser Ser Tyr Ala
1   5

<210> 32
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 14L22A HC CDR2

<400> 32

Ile Asn Ser Asn Gly Gly Asn Thr
1   5

<210> 33
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 14L22A HC CDR3

<400> 33

Ala Arg His Arg Gly Gly Phe Tyr Tyr Ala Val Asp Tyr
1   5   10

<210> 34
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> 10P18A HC CDR1

<400> 34

Gly Tyr Ser Phe Thr Gly Tyr Tyr
1 5

<210> 35
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 10P18A HC CDR2

<400> 35

Ile Tyr Pro Ser Asn Gly Glu Thr
1 5

<210> 36
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 10P18A HC CDR3

<400> 36

Ala Arg Glu Ser Tyr Ala Met Asp Tyr
1 5

<210> 37
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 13P11A HC CDR1

<400> 37

Gly Tyr Ser Ile Thr Asn Gly Asn His Trp
1 5 10

<210> 38
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> 13P11A HC CDR2

<400> 38

Ile Ser Ser Ser Gly Ser Thr
1 5

<210> 39
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 13P11A HC CDR3

<400> 39

Ala Thr Thr Gly Thr Trp Gly Tyr Phe Asp Tyr
1 5 10

<210> 40
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 3C16A HC CDR1

<400> 40

Gly Tyr Thr Phe Thr Ser Tyr Val
1 5

<210> 41
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 3C16A HC CDR2

<400> 41

Val Ile Pro Tyr Asn Asp Gly Thr
1 5

<210> 42
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 3C16A HC CDR3

<400> 42

Ala Arg Pro Ser Asn Trp Asp Glu Phe Asp Tyr
1 5 10

<210> 43
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 3I21A HC CDR1

<400> 43

Gly Tyr Thr Phe Thr Asn Tyr Trp
1 5

<210> 44
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 3I21A HC CDR2

<400> 44

Ile His Pro Ser Asp Ser Glu Thr
1 5

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

<220>
<223> 3I21A HC CDR3

<400> 45

Ala Arg Tyr Asp Gly Tyr Phe Ala Tyr

1 5

<210> 46
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 8H5A HC CDR1

<400> 46

Gly Phe Ser Leu Ser Thr Phe Gly Met Gly
1 5 10

<210> 47
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 8H5A HC CDR2

<400> 47

Ile Trp Trp Asp Asp Asp Lys
1 5

<210> 48
<211> 12
<212> PRT
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<220>
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Ala Arg Thr Tyr Asp Tyr Asp Glu Tyr Phe Asp Tyr
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<400> 49

Gly Tyr Thr Phe Thr Ser Tyr Trp
1 5

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<400> 50

Ile His Pro Ser Asp Ser Glu Thr
1 5

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Ala Arg Glu Asp Gly Tyr Tyr Trp Tyr Phe Asp Val
1 5 10

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<400> 52

Gly Tyr Lys Phe Thr Asp Phe Asn
1 5

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<400> 53

Ile Asn Pro Asn Ser Gly Gly Thr
1   5

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Ala Arg Trp Asp Tyr Gly Asn Phe Ala Tyr
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Gly Tyr Thr Phe Thr Asn Tyr Trp
1   5

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Ile His Pro Ser Asp Ser Glu Thr
1   5

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<400> 57

Ala Arg Glu Asp Gly Tyr Tyr Trp Tyr Phe Asp Val
1 5 10

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Gly Phe Thr Phe Ser Ser Tyr Ala
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<400> 59

Ile Asn Ser Asn Gly Gly Arg Asn
1 5

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Ala Arg His Arg Gly Gly Tyr Tyr Tyr Ala Met Asp Tyr
1 5 10

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<400> 61

Gln Asn Ile Asn Val Trp
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<400> 62

Lys Ala Ser
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<400> 63

Gln Gln Gly Gln Ser Tyr Pro Phe Thr
1   5

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<400> 64

Gly Asn Ile His Asn Tyr
1   5

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Asn Ala Lys
1

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<400> 66

Gln His Phe Trp Thr Thr Pro Trp Thr
1   5

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Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr
1   5   10

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Trp Ala Ser
1

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His Gln Tyr Leu Ser Ser Arg Thr
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Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr
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Leu Ala Ser
1

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Glu Asn Val Gly Thr Tyr
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Gly Ala Ser
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Gly Gln Ser Tyr Ser Tyr Pro Phe Thr
1   5

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Leu Ala Ser
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Leu Gln His Trp Asn Tyr Pro Leu Thr
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<400> 80

Gly Ala Thr
1

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<400> 81

Gln Gln Tyr Trp Ser Ile Pro Phe Thr
1 5

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<400> 82

Lys Ser Leu Leu His Ser Asn Gly Ile Thr Tyr
1 5 10

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<400> 83

Gln Met Ser
1

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<400> 84

Ala Gln Asn Leu Glu Leu Pro Phe Thr
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<400> 85

Glu Ser Val Asp Ile Tyr Gly Asn Ser Phe
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<400> 86

Leu Ala Ser
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Gln Gln Asn Asn Glu Asp Pro Trp Thr
1   5

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<400> 88

Lys Ser Leu Leu His Ser Asn Gly Ile Thr Tyr
1   5   10

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<400> 89

Gln Met Ser
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<400> 90

Ala Gln Asn Leu Glu Leu Pro Leu Thr
1   5

<210> 91
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<400> 91

Glu Ser Val Asp Ser Tyr Gly Asn Ser Phe
1 5 10

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<400> 92

Leu Ala Ser
1

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<400> 93

Gln Gln Asn His Glu Asp Pro Trp Thr
1 5

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<400> 94

Gln Ser Leu Leu Tyr Ser Ser Asn Gln Lys Asn Tyr
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<400> 95

Trp Ala Ser
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<400> 96

Gln Gln Tyr Tyr Thr Tyr Leu Thr
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<210> 97
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<212> PRT
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<220>
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<400> 97

Ser Tyr Val Met His
1 5

<210> 98
<211> 17
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<213> Artificial Sequence

<220>
<223> 13P9A HC CDR2

<400> 98

Tyr Ile Asn Pro Tyr Asn Asp Ala Thr Lys Tyr Asn Glu Lys Phe Lys

1 5 10 15

Gly

<210> 99
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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<400> 99

Gly Gly Tyr Asp Tyr Asp Gly Asp Tyr
1 5

<210> 100
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<220>
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<400> 100

Arg Tyr Ile Leu His
1 5

<210> 101
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<213> Artificial Sequence

<220>
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<400> 101

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

Gly

<210> 102
<211> 13
<212> PRT
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<400> 102

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

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<400> 103

Ser Tyr Ala Met Ser
1 5

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<213> Artificial Sequence

<220>
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<400> 104

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

Asp

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<400> 105

His Arg Gly Gly Phe Tyr Tyr Ala Val Asp Tyr
1 5 10

<210> 106
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<220>
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<400> 106

Gly Tyr Tyr Ile Asp
1 5

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<220>
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<400> 107

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

Gly

<210> 108
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<220>
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<400> 108

Glu Ser Tyr Ala Met Asp Tyr
1 5

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<400> 109

Asn Gly Asn His Trp Trp Ser
1 5

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<220>
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<400> 110

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

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<400> 111

Thr Gly Thr Trp Gly Tyr Phe Asp Tyr
1 5

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<220>
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<400> 112

Ser Tyr Val Met His

1 5

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<213> Artificial Sequence

<220>
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<400> 113

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

Gly

<210> 114
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<400> 114

Pro Ser Asn Trp Asp Glu Phe Asp Tyr
1 5

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<400> 115

Asn Tyr Trp Met Asn
1 5

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<220>
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<400> 116

Arg Ile His Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe Lys
1   5   10   15

Thr

<210> 117
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<400> 117

Tyr Asp Gly Tyr Phe Ala Tyr
1   5

<210> 118
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<400> 118

Thr Phe Gly Met Gly Val Gly
1   5

<210> 119
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<213> Artificial Sequence

<220>
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<400> 119

His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ala Leu Lys Ser

1 5 10 15

<210> 120
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<212> PRT
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<220>
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<400> 120

Thr Tyr Asp Tyr Asp Glu Tyr Phe Asp Tyr
1 5 10

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<220>
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<400> 121

Ser Tyr Trp Met Asn
1 5

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<220>
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<400> 122

Arg Ile His Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe Arg
1 5 10 15

Thr

<210> 123
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<220>
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<400> 123

Glu Asp Gly Tyr Tyr Trp Tyr Phe Asp Val
1   5   10

<210> 124
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<212> PRT
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<220>
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<400> 124

Asp Phe Asn Met Asp
1   5

<210> 125
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<220>
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<400> 125

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

Gly

<210> 126
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<220>
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<400> 126

Trp Asp Tyr Gly Asn Phe Ala Tyr

1 5

<210> 127
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<220>
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<400> 127

Asn Tyr Trp Met Asn
1 5

<210> 128
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<220>
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<400> 128

Arg Ile His Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe Lys
1 5 10 15

Ser

<210> 129
<211> 10
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<220>
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<400> 129

Glu Asp Gly Tyr Tyr Trp Tyr Phe Asp Val
1 5 10

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<220>
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<400> 130

Ser Tyr Ala Met Ser
1   5

<210> 131
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<220>
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<400> 131

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

Asp

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<220>
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<400> 132

His Arg Gly Gly Tyr Tyr Tyr Ala Met Asp Tyr
1   5   10

<210> 133
<211> 11
<212> PRT
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<220>
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<400> 133

His Ala Ser Gln Asn Ile Asn Val Trp Leu Ser

1 5 10

<210> 134
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<212> PRT
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<220>
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<400> 134

Lys Ala Ser Asn Leu His Thr
1 5

<210> 135
<211> 9
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<220>
<223> 13P9A LC CDR3

<400> 135

Gln Gln Gly Gln Ser Tyr Pro Phe Thr
1 5

<210> 136
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<220>
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<400> 136

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

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<212> PRT
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<220>
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<400> 137

Asn Ala Lys Thr Leu Pro Tyr
1 5

<210> 138
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<220>
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<400> 138

Gln His Phe Trp Thr Thr Pro Trp Thr
1 5

<210> 139
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<220>
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<400> 139

Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu
1 5 10 15

Ala

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<220>
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<400> 140

Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 141

<211> 8
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<220>
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<400> 141

His Gln Tyr Leu Ser Ser Arg Thr
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<210> 142
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<220>
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<400> 142

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

<210> 143
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<212> PRT
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<220>
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<400> 143

Leu Ala Ser Asn Leu Glu Ser
1 5

<210> 144
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<220>
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<400> 144

Gln His Ser Arg Glu Leu Pro Tyr Thr
1 5

<210> 145
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<212> PRT
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<220>
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<400> 145

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

<210> 146
<211> 7
<212> PRT
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<220>
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<400> 146

Gly Ala Ser Asn Arg Phe Thr
1   5

<210> 147
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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<400> 147

Gly Gln Ser Tyr Ser Tyr Pro Phe Thr
1   5

<210> 148
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<220>
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<400> 148

Lys Ala Ser Gln Asn Val Arg Thr Ala Val Ala
1 5 10

<210> 149
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<400> 149

Leu Ala Ser Asn Arg His Thr
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<400> 150

Leu Gln His Trp Asn Tyr Pro Leu Thr
1 5

<210> 151
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<212> PRT
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<220>
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<400> 151

Lys Ala Ser Asp His Ile Asn Asn Trp Leu Ala
1 5 10

<210> 152
<211> 7
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<220>

<223> 3I21A LC CDR2

<400> 152

Gly Ala Thr Ser Leu Glu Thr
1   5

<210> 153
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<220>
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<400> 153

Gln Gln Tyr Trp Ser Ile Pro Phe Thr
1   5

<210> 154
<211> 16
<212> PRT
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<220>
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<400> 154

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

<210> 155
<211> 7
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<220>
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<400> 155

Gln Met Ser Asn Leu Ala Ser
1   5

<210> 156
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<220>
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<400> 156

Ala Gln Asn Leu Glu Leu Pro Phe Thr
1 5

<210> 157
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<220>
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<400> 157

Arg Ala Ser Glu Ser Val Asp Ile Tyr Gly Asn Ser Phe Met His
1 5 10 15

<210> 158
<211> 7
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<220>
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<400> 158

Leu Ala Ser Asn Leu Glu Ser
1 5

<210> 159
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<220>
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<400> 159

Gln Gln Asn Asn Glu Asp Pro Trp Thr
1 5

<210> 160
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<220>
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<400> 160

Arg Ser Ser Lys Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr
1 5 10 15

<210> 161
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<212> PRT
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<400> 161

Gln Met Ser Asn Leu Ala Ser
1 5

<210> 162
<211> 9
<212> PRT
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<220>
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<400> 162

Ala Gln Asn Leu Glu Leu Pro Leu Thr
1 5

<210> 163
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<400> 163

Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly Asn Ser Phe Met His

1 5 10 15

<210> 164
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<400> 164

Leu Ala Ser Asn Leu Glu Ser
1 5

<210> 165
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<212> PRT
<213> Artificial Sequence

<220>
<223> 15P17A LC CDR3

<400> 165

Gln Gln Asn His Glu Asp Pro Trp Thr
1 5

<210> 166
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 15N21A LC CDR1

<400> 166

Lys Ser Ser Gln Ser Leu Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 167
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 15N21A LC CDR2

<400> 167

Trp Ala Ser Thr Arg Glu Ser
1   5

<210> 168
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 15N21A LC CDR3

<400> 168

Gln Gln Tyr Tyr Thr Tyr Leu Thr
1   5

<210> 169
<211> 618
<212> PRT
<213> Homo sapiens

<400> 169

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

Ala Leu Ile Phe Leu Pro Gln Thr Arg Pro Ala Gly Val Phe Glu Leu
            20   25   30

Gln Ile His Ser Phe Gly Pro Gly Pro Gly Pro Gly Ala Pro Arg Ser
        35   40   45

Pro Cys Ser Ala Arg Leu Pro Cys Arg Leu Phe Phe Arg Val Cys Leu
    50   55   60

Lys Pro Gly Leu Ser Glu Glu Ala Ala Glu Ser Pro Cys Ala Leu Gly
65   70   75   80

Ala Ala Leu Ser Ala Arg Gly Pro Val Tyr Thr Glu Gln Pro Gly Ala
                85   90   95

```
Pro Ala Pro Asp Leu Pro Leu Pro Asp Gly Leu Leu Gln Val Pro Phe
            100                 105                 110

Arg Asp Ala Trp Pro Gly Thr Phe Ser Phe Ile Ile Glu Thr Trp Arg
        115                 120                 125

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

Arg Val Ala Gly Arg Arg Arg Leu Ala Ala Gly Gly Pro Trp Ala Arg
145                 150                 155                 160

Asp Ile Gln Arg Ala Gly Ala Trp Glu Leu Arg Phe Ser Tyr Arg Ala
                165                 170                 175

Arg Cys Glu Pro Pro Ala Val Gly Thr Ala Cys Thr Arg Leu Cys Arg
            180                 185                 190

Pro Arg Ser Ala Pro Ser Arg Cys Gly Pro Gly Leu Arg Pro Cys Ala
        195                 200                 205

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

Ser Pro Glu His Gly Phe Cys Glu Gln Pro Gly Glu Cys Arg Cys Leu
225                 230                 235                 240

Glu Gly Trp Thr Gly Pro Leu Cys Thr Val Pro Val Ser Thr Ser Ser
                245                 250                 255

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

Pro Gly Pro Gly Pro Cys Asp Gly Asn Pro Cys Ala Asn Gly Gly Ser
        275                 280                 285

Cys Ser Glu Thr Pro Arg Ser Phe Glu Cys Thr Cys Pro Arg Gly Phe
    290                 295                 300
```

```
Tyr Gly Leu Arg Cys Glu Val Ser Gly Val Thr Cys Ala Asp Gly Pro
305                 310                 315                 320

Cys Phe Asn Gly Gly Leu Cys Val Gly Gly Ala Asp Pro Asp Ser Ala
                325                 330                 335

Tyr Ile Cys His Cys Pro Pro Gly Phe Gln Gly Ser Asn Cys Glu Lys
            340                 345                 350

Arg Val Asp Arg Cys Ser Leu Gln Pro Cys Arg Asn Gly Gly Leu Cys
        355                 360                 365

Leu Asp Leu Gly His Ala Leu Arg Cys Arg Cys Arg Ala Gly Phe Ala
    370                 375                 380

Gly Pro Arg Cys Glu His Asp Leu Asp Asp Cys Ala Gly Arg Ala Cys
385                 390                 395                 400

Ala Asn Gly Gly Thr Cys Val Glu Gly Gly Gly Ala His Arg Cys Ser
                405                 410                 415

Cys Ala Leu Gly Phe Gly Gly Arg Asp Cys Arg Glu Arg Ala Asp Pro
            420                 425                 430

Cys Ala Ala Arg Pro Cys Ala His Gly Gly Arg Cys Tyr Ala His Phe
        435                 440                 445

Ser Gly Leu Val Cys Ala Cys Ala Pro Gly Tyr Met Gly Ala Arg Cys
    450                 455                 460

Glu Phe Pro Val His Pro Asp Gly Ala Ser Ala Leu Pro Ala Ala Pro
465                 470                 475                 480

Pro Gly Leu Arg Pro Gly Asp Pro Gln Arg Tyr Leu Leu Pro Pro Ala
                485                 490                 495

Leu Gly Leu Leu Val Ala Ala Gly Val Ala Gly Ala Ala Leu Leu Leu
            500                 505                 510
```

```
Val His Val Arg Arg Arg Gly His Ser Gln Asp Ala Gly Ser Arg Leu
        515                 520                 525

Leu Ala Gly Thr Pro Glu Pro Ser Val His Ala Leu Pro Asp Ala Leu
    530                 535                 540

Asn Asn Leu Arg Thr Gln Glu Gly Ser Gly Asp Gly Pro Ser Ser Ser
545                 550                 555                 560

Val Asp Trp Asn Arg Pro Glu Asp Val Asp Pro Gln Gly Ile Tyr Val
                565                 570                 575

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

Pro Pro Leu His Thr Gly Arg Ala Gly Gln Arg Gln His Leu Leu Phe
        595                 600                 605

Pro Tyr Pro Ser Ser Ile Leu Ser Val Lys
    610                 615
```

<210> 170
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> H1 Heavy Chain Variable Region

<400> 170

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

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

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

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

```
Gln Gly Arg Ala Thr Leu Thr Ser Asp Lys Tyr Ser Asp Thr Ala Phe
65                  70                  75                  80


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


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


Pro Val Thr Val Ser Ser
        115


<210>  171
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  L1 Light Chain Variable Region

<400>  171

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


Glu Arg Ala Thr Leu Ser Cys His Ala Ser Gln Asn Ile Asn Val Trp
            20                  25                  30


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


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


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


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


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

<210> 172
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> L2 Light Chain Variable Region

<400> 172

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

Glu Arg Ala Thr Leu Ser Cys His Ala Ser Gln Asn Ile Asn Val Trp
20 25 30

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

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

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

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

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

<210> 173
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> L3 Light Chain Variable Region

<400> 173

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

Glu Thr Ala Ile Ile Ser Cys His Ala Ser Gln Asn Ile Asn Val Trp
            20   25   30

Leu Ser Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35   40   45

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

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

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

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

<210> 174
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> L4 Light Chain Variable Region

<400> 174

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

Glu Thr Ala Ile Ile Ser Cys His Ala Ser Gln Asn Ile Asn Val Trp
            20   25   30

Leu Ser Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35   40   45

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

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

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

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

<210> 175
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> KH1 Heavy Chain Variable Region

<400> 175

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

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

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

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

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

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

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

Ser Ser

<210> 176

<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> KH2 Heavy Chain Variable Region

<400> 176

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

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

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

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

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

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

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

Ser Ser

<210> 177
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> KH3 Heavy Chain Variable Region

<400> 177

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

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

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

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

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

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

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

Ser Ser
```

<210> 178
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> KH2 HCDR1

<400> 178

```
Gly Tyr Thr Phe Thr Ser Tyr Trp
1               5
```

<210> 179
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> KH2 HCDR2

<400> 179

Ile Asp Pro Ser Asp Ser Glu Thr
1   5

<210> 180
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> KH2 HCDR3

<400> 180

Ala Gly Thr Asp Leu Ala Tyr
1   5

<210> 181
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> H1 HCDR1

<400> 181

Gly Tyr Thr Phe Thr Ser Tyr Val
1   5

<210> 182
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> H1 HCDR2

<400> 182

Ile Asn Pro Tyr Asn Asp Ala Thr
1   5

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

<220>

<223> H1 HCDR3

<400> 183

Ala Arg Gly Gly Tyr Asp Tyr Asp Gly Asp Tyr
1 5 10

<210> 184
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> L2 LCDR1

<400> 184

Gln Asn Ile Asn Val Trp
1 5

<210> 185
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> L2 LCDR2

<400> 185

Lys Ala Ser
1

<210> 186
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> L2 LCDR3

<400> 186

Gln Gln Gly Gln Ser Tyr Pro Phe Thr
1 5

<210> 187
<211> 5
<212> PRT

<213> Artificial Sequence

<220>
<223> KH2 HCDR1

<400> 187

Ser Tyr Trp Met His
1 5

<210> 188
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> KH2 HCDR2

<400> 188

Asn Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 189
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> KH2 HCDR3

<400> 189

Thr Asp Leu Ala Tyr
1 5

<210> 190
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> H1 HCDR1

<400> 190

Ser Tyr Val Met His
1   5

<210> 191
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> H1 HCDR2

<400> 191

Tyr Ile Asn Pro Tyr Asn Asp Ala Thr Lys Tyr Ala Arg Lys Phe Gln
1   5   10   15

Gly

<210> 192
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> H1 HCDR3

<400> 192

Gly Gly Tyr Asp Tyr Asp Gly Asp Tyr
1   5

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

<220>
<223> L2 LCDR1

<400> 193

His Ala Ser Gln Asn Ile Asn Val Trp Leu Ser
1   5   10

<210> 194
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> L2 LCDR2

<400> 194

Lys Ala Ser Asn Leu His Thr
1 5

<210> 195
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> L2 LCDR3

<400> 195

Gln Gln Gly Gln Ser Tyr Pro Phe Thr
1 5