SEQUENCE LISTING

<110> JOUNCE THERAPEUTICS, INC.

<120> ANTIBODIES TO ICOS

<130> 01140-0001-00PCT

<140> PCT/US16/23524
<141> 2016-03-22

<150> US 62/137,034
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<150> US 62/156,588
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<170> PatentIn version 3.5

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Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys
1 5 10 15

Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
20 25 30

Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
35 40 45

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Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
    50                  55                  60

Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
65                  70                  75                  80

Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
                85                  90                  95

Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
            100                 105                 110

Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
        115                 120                 125

His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
    130                 135                 140

Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
145                 150                 155                 160

Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
                165                 170                 175

Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser
            180                 185                 190

Arg Leu Thr Asp Val Thr Leu
        195
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<213> Homo sapiens

<400> 2

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

Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val Gln Gln Phe Lys
            20                  25                  30

Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp Leu Thr Lys Thr
        35                  40                  45

Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu Lys Phe Cys His
    50                  55                  60

Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu Tyr Asn Leu Asp
65                  70                  75                  80

His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser Ile Phe Asp Pro
                85                  90                  95

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

Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro Ile Gly Cys Ala
        115                 120                 125

Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu Ile Cys Trp Leu
    130                 135                 140

Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro Asn Gly Glu Tyr
145                 150                 155                 160

Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser Arg Leu Thr Asp
                165                 170                 175

Val Thr Leu
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<210> 3
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<400> 3

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Met Lys Pro Tyr Phe Cys Arg Val Phe Val Phe Cys Phe Leu Ile Arg
1               5                   10                  15


Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
            20                  25                  30


Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
        35                  40                  45


Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
    50                  55                  60


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


Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
                85                  90                  95


Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
            100                 105                 110


Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
        115                 120                 125


Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
    130                 135                 140


Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
145                 150                 155                 160


Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
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165 170 175

Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
180 185 190

Ser Arg Leu Ala Gly Val Thr Ser
195 200

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<213> Mus musculus

<400> 4

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

Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val Gln Gln Leu Lys
20 25 30

Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu Leu Thr Lys Thr
35 40 45

Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro Met Leu Cys Leu
50 55 60

Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu Asn Asn Pro Asp
65 70 75 80

Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser Ile Phe Asp Pro
85 90 95

Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr Leu His Ile Tyr
100 105 110

Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu Pro Val Gly Cys
115 120 125

```
Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile Leu Ile Ile Trp
    130                 135                 140

Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp Pro Asn Ser Glu
145                 150                 155                 160

Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys Ser Arg Leu Ala
                165                 170                 175

Gly Val Thr Ser
            180
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<213> Macaca fascicularis

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Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu His Met Lys
1               5                   10                  15

Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
            20                  25                  30

Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
        35                  40                  45

Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
    50                  55                  60

Leu Thr Lys Thr Lys Gly Ser Gly Asn Lys Val Ser Ile Lys Ser Leu
65                  70                  75                  80

Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
                85                  90                  95
```

```
Tyr Asn Leu Asp Arg Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
            100                 105                 110


Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
        115                 120                 125


His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
    130                 135                 140


Ile Gly Cys Ala Thr Phe Val Val Val Cys Ile Phe Gly Cys Ile Leu
145                 150                 155                 160


Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Thr Val His Asp Pro
                165                 170                 175


Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser
            180                 185                 190


Arg Leu Thr Gly Thr Thr Pro
        195


<210>  6
<211>  179
<212>  PRT
<213>  Macaca fascicularis

<400>  6

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


Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val Gln Gln Phe Lys
            20                  25                  30


Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp Leu Thr Lys Thr
        35                  40                  45
```

```
Lys Gly Ser Gly Asn Lys Val Ser Ile Lys Ser Leu Lys Phe Cys His
    50                  55                  60

Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu Tyr Asn Leu Asp
65                  70                  75                  80

Arg Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser Ile Phe Asp Pro
                85                  90                  95

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

Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro Ile Gly Cys Ala
        115                 120                 125

Thr Phe Val Val Val Cys Ile Phe Gly Cys Ile Leu Ile Cys Trp Leu
    130                 135                 140

Thr Lys Lys Lys Tyr Ser Ser Thr Val His Asp Pro Asn Gly Glu Tyr
145                 150                 155                 160

Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser Arg Leu Thr Gly
                165                 170                 175

Thr Thr Pro
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<210> 7
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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

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

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

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

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

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

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

Val Thr Val Ser Ser
115

<210> 11
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<213> Mesocricetus auratus

<400> 11

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

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Asp Lys Val Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Ser Gly
            20                  25                  30

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

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

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

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

Ser Thr Pro Pro Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
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<211> 10
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<213> Mesocricetus auratus

<400> 12

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Gly Phe Thr Phe Ser Asp Tyr Trp Met Asp
1               5                   10
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<210> 13
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<212> PRT
<213> Mesocricetus auratus

<400> 13

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

<210> 14
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<213> Mesocricetus auratus

<400> 14

Trp Gly Arg Tyr Ala Phe Asp Ser
1 5

<210> 15
<211> 15
<212> PRT
<213> Mesocricetus auratus

<400> 15

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

<210> 16
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<400> 16

Tyr Ala Ser Thr Arg His Thr
1 5

<210> 17
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<400> 17

Gln His His Tyr Ser Thr Pro Pro Thr
1 5

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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 Asp Tyr
20 25 30

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

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

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

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

Thr Arg Trp Gly Arg Phe Gly Phe Asp Ser Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 21

<211> 111
<212> PRT
<213> Mesocricetus auratus

<400> 21

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

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

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

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

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

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

Asn Ala Pro Pro Thr Phe Gly Pro Gly Thr Lys Leu Glu Leu Arg
100 105 110

<210> 22
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<213> Mesocricetus auratus

<400> 22

Gly Phe Thr Phe Ser Asp Tyr Trp Met Asp
1 5 10

<210> 23
<211> 17
<212> PRT

<213> Mesocricetus auratus

<400> 23

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

Gly

<210> 24
<211> 8
<212> PRT
<213> Mesocricetus auratus

<400> 24

Trp Gly Arg Phe Gly Phe Asp Ser
1 5

<210> 25
<211> 15
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<400> 25

Lys Ser Ser Gln Ser Leu Leu Ser Gly Ser Phe Asn Tyr Leu Thr
1 5 10 15

<210> 26
<211> 7
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<213> Mesocricetus auratus

<400> 26

Tyr Ala Ser Thr Arg His Thr
1 5

<210> 27
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<400> 27

His His His Tyr Asn Ala Pro Pro Thr
1 5

<210> 28
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<210> 29
<400> 29
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<210> 30
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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 Asp Tyr
20 25 30

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

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

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

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

Ser Arg Trp Gly Arg Phe Ala Phe Asp Ser Trp Gly Gln Gly Thr Leu

100 105 110

Val Thr Val Ser Ser
115

<210> 31
<211> 111
<212> PRT
<213> Mesocricetus auratus

<400> 31

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

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

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

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

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

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

Asn Ala Pro Pro Thr Phe Gly Pro Gly Thr Lys Leu Glu Leu Arg
100 105 110

<210> 32
<211> 10
<212> PRT
<213> Mesocricetus auratus

<400> 32

Gly Phe Thr Phe Ser Asp Tyr Trp Met Asp
1 5 10

<210> 33
<211> 17
<212> PRT
<213> Mesocricetus auratus

<400> 33

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

Gly

<210> 34
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<400> 34

Trp Gly Arg Phe Ala Phe Asp Ser
1 5

<210> 35
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<400> 35

Lys Ser Ser Gln Ser Leu Leu Ser Gly Ser Phe Asn Tyr Leu Thr
1 5 10 15

<210> 36
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<400> 36

Tyr Ala Ser Thr Arg His Thr
1 5

<210> 37
<211> 9
<212> PRT
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<400> 37

His His His Tyr Asn Ala Pro Pro Thr
1 5

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<400> 38
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<210> 39
<400> 39
000

<210> 40
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<212> PRT
<213> Mesocricetus auratus

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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 Asp Tyr
20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Val Lys Asn Ile Leu Tyr

65 70 75 80

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

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

Val Thr Val Ser Ser
115

<210> 41
<211> 111
<212> PRT
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<400> 41

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

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

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

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

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

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

Asn Ala Pro Pro Thr Phe Gly Pro Gly Thr Lys Leu Glu Leu Arg
100 105 110

<210> 42
<211> 10
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<400> 42

Gly Phe Thr Phe Ser Asp Tyr Trp Met Asp
1 5 10

<210> 43
<211> 17
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<400> 43

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

Gly

<210> 44
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<400> 44

Trp Gly Arg Phe Ala Phe Asp Ser
1 5

<210> 45
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<400> 45

Lys Ser Ser Gln Ser Leu Leu Ser Gly Ser Phe His Tyr Leu Thr
1 5 10 15

<210> 46
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<400> 46

Tyr Ala Ser Thr Arg His Thr
1 5

<210> 47
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<400> 47

His His His Tyr Asn Ala Pro Pro Thr
1 5

<210> 48
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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 Asp Tyr
20 25 30

Trp Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Gly Asn Ile Asp His Asp Gly Asn Ile Ile Asn Phe Ala Pro Ser Val
50 55 60

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

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

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

Val Thr Val Ser Ser
115

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<211> 111
<212> PRT
<213> Mesocricetus auratus

<400> 51

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

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

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

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

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

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

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

<210> 52
<211> 10
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<213> Mesocricetus auratus

<400> 52

Gly Phe Thr Phe Ser Asp Tyr Trp Met Asp
1 5 10

<210> 53
<211> 17
<212> PRT
<213> Mesocricetus auratus

<400> 53

Asn Ile Asp His Asp Gly Asn Ile Ile Asn Phe Ala Pro Ser Val Lys
1 5 10 15

Gly

<210> 54
<211> 8
<212> PRT
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<400> 54

Trp Gly His Tyr Ala Phe Asp Ser
1 5

<210> 55

<211> 15
<212> PRT
<213> Mesocricetus auratus

<400> 55

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

<210> 56
<211> 7
<212> PRT
<213> Mesocricetus auratus

<400> 56

Tyr Ala Ser Thr Arg His Thr
1 5

<210> 57
<211> 9
<212> PRT
<213> Mesocricetus auratus

<400> 57

Gln His His Tyr Ser Ser Pro Pro Thr
1 5

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<400> 60

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

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

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

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

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

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

Thr Arg Trp Gly Arg Phe Gly Phe Asp Ser Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

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<213> Artificial Sequence

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<223> 37A10S713 light chain variable region

<400> 61

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

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

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

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

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

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

Asn Ala Pro Pro Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100   105   110

<210> 62
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<220>
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<400> 62

Gly Phe Thr Phe Ser Asp Tyr Trp Met Asp
1   5   10

<210> 63
<211> 17
<212> PRT
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<220>
<223> 37A10S713 VH CDR2

<400> 63

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

Gly

<210> 64
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S713 VH CDR3

<400> 64

Trp Gly Arg Phe Gly Phe Asp Ser
1 5

<210> 65
<211> 15
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<213> Artificial Sequence

<220>
<223> 37A10S713 VL CDR1

<400> 65

Lys Ser Ser Gln Ser Leu Leu Ser Gly Ser Phe Asn Tyr Leu Thr
1 5 10 15

<210> 66
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S713 VL CDR2

<400> 66

Tyr Ala Ser Thr Arg His Thr
1 5

<210> 67
<211> 9
<212> PRT
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<223> 37A10S713 VL CDR3

<400> 67

His His His Tyr Asn Ala Pro Pro Thr
1 5

<210> 68
<400> 68
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<210> 69
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<210> 70
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<223> 37A10S714 heavy chain variable region

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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 Phe Thr Phe Ser Asp Tyr
20 25 30

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

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

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


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


Thr Arg Trp Gly Arg Phe Gly Phe Asp Ser Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210>  71
<211>  111
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  37A10S714 light chain variable region

<400>  71

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


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


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


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


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

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

Asn Ala Pro Pro Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105 110

<210> 72
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S714 VH CDR1

<400> 72

Gly Phe Thr Phe Ser Asp Tyr Trp Met Asp
1 5 10

<210> 73
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S714 VH CDR2

<400> 73

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

Gly

<210> 74
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S714 VH CDR3

<400> 74

Trp Gly Arg Phe Gly Phe Asp Ser
1 5

<210> 75
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S714 VL CDR1

<400> 75

Lys Ser Ser Gln Ser Leu Leu Ser Gly Ser Phe Asn Tyr Leu Thr
1 5 10 15

<210> 76
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S714 VL CDR2

<400> 76

Tyr Ala Ser Thr Arg Glu Thr
1 5

<210> 77
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S714 VL CDR3

<400> 77

His His His Tyr Asn Ala Pro Pro Thr
1 5

<210> 78
<400> 78
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<210> 79
<400> 79
000

<210> 80
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S715 heavy chain variable region

<400> 80

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

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

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

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

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

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

Thr Arg Trp Gly Arg Phe Gly Phe Asp Ser Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 81
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S715 light chain variable region

<400> 81

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

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

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

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

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

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

Asn Ala Pro Pro Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105 110

<210> 82
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S715 VH CDR1

<400> 82

Gly Phe Thr Phe Ser Asp Tyr Trp Met Asp
1 5 10

<210> 83
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S715 VH CDR2

<400> 83

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

Gly

<210> 84
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S715 VH CDR3

<400> 84

Trp Gly Arg Phe Gly Phe Asp Ser
1 5

<210> 85
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S715 VL CDR1

<400> 85

Lys Ser Ser Gln Ser Leu Leu Ser Gly Ser Phe Asn Tyr Leu Thr
1 5 10 15

<210> 86
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S715 VL CDR2

<400> 86

Tyr Ala Ser Thr Arg Gln Thr
1 5

<210> 87
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S715 VL CDR3

<400> 87

His His His Tyr Asn Ala Pro Pro Thr
1 5

<210> 88
<400> 88
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<210> 89
<400> 89
000

<210> 90
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S716 heavy chain variable region

<400> 90

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

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

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

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

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

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

Thr Arg Trp Gly Arg Phe Gly Phe Asp Ser Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 91
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S716 light chain variable region

<400> 91

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

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

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

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

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

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

Asn Ala Pro Pro Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100   105   110

<210> 92
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S716 VH CDR1

<400> 92

Gly Phe Thr Phe Ser Asp Tyr Trp Met Asp
1   5   10

<210> 93
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S716 VH CDR2

<400> 93

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

Gly

<210> 94
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S716 VH CDR3

<400> 94

Trp Gly Arg Phe Gly Phe Asp Ser
1 5

<210> 95
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S716 VL CDR1

<400> 95

Lys Ser Ser Gln Ser Leu Leu Ser Gly Ser Phe Asn Tyr Leu Thr
1 5 10 15

<210> 96
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S716 VL CDR2

<400> 96

Tyr Ala Ser Thr Arg His Thr
1 5

<210> 97
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S716 VL CDR3

<400> 97

His His His Tyr Asn Ala Pro Pro Thr
1 5

<210> 98
<400> 98
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<210> 99
<400> 99
000

<210> 100
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S717 heavy chain variable region

<400> 100

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

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

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

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

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


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


Thr Arg Trp Gly Arg Phe Gly Phe Asp Ser Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210>  101
<211>  111
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  37A10S717 light chain variable region

<400>  101

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


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


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


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


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

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

Asn Ala Pro Pro Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105 110

<210> 102
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S717 VH CDR1

<400> 102

Gly Phe Thr Phe Ser Asp Tyr Trp Met Asp
1 5 10

<210> 103
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S717 VH CDR2

<400> 103

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

Gly

<210> 104
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S717 VH CDR3

<400> 104

Trp Gly Arg Phe Gly Phe Asp Ser
1 5

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

<220>
<223> 37A10S717 VL CDR1

<400> 105

Lys Ser Ser Gln Ser Leu Leu Ser Gly Ser Phe Asn Tyr Leu Thr
1 5 10 15

<210> 106
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S717 VL CDR2

<400> 106

Tyr Ala Ser Thr Arg Glu Thr
1 5

<210> 107
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S717 VL CDR3

<400> 107

His His His Tyr Asn Ala Pro Pro Thr
1 5

<210> 108
<400> 108
000

<210> 109
<400> 109
000

<210> 110
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S718 heavy chain variable region

<400> 110

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

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

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

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

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

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

Thr Arg Trp Gly Arg Phe Gly Phe Asp Ser Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

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

<220>
<223> 37A10S718 light chain variable region

<400> 111

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

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

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

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

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

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

Asn Ala Pro Pro Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105 110

<210> 112
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S718 VH CDR1

<400> 112

Gly Phe Thr Phe Ser Asp Tyr Trp Met Asp
1 5 10

<210> 113
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S718 VH CDR2

<400> 113

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

Gly

<210> 114
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S718 VH CDR3

<400> 114

Trp Gly Arg Phe Gly Phe Asp Ser
1 5

<210> 115
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S718 VL CDR1

<400> 115

Lys Ser Ser Gln Ser Leu Leu Ser Gly Ser Phe Asn Tyr Leu Thr
1 5 10 15

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

<220>
<223> 37A10S718 VL CDR2

<400> 116

Tyr Ala Ser Thr Arg Gln Thr
1 5

<210> 117
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S718 VL CDR3

<400> 117

His His His Tyr Asn Ala Pro Pro Thr
1 5

<210> 118
<400> 118
000

<210> 119
<400> 119
000

<210> 120
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 16G10S71 heavy chain variable region

<400> 120

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

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

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

Ser Asn Ile Asp His Asp Gly Asn Ile Ile Asn Phe Ala Pro Ser Val
50 55 60

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

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

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

Val Thr Val Ser Ser
115

<210> 121
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> 16G10S71 light chain variable region

<400> 121

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Ser Ser
            20   25   30

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

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

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

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

Ser Ser Pro Pro Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100   105   110

<210> 122
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 16G10S71 VH CDR1

<400> 122

Gly Phe Thr Phe Ser Asp Tyr Trp Met Asp
1   5   10

<210> 123
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 16G10S71 VH CDR2

<400> 123

Asn Ile Asp His Asp Gly Asn Ile Ile Asn Phe Ala Pro Ser Val Lys
1 5 10 15

Gly

<210> 124
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 16G10S71 VH CDR3

<400> 124

Trp Gly His Tyr Ala Phe Asp Ser
1 5

<210> 125
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 16G10S71 VL CDR1

<400> 125

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

<210> 126
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 16G10S71 VL CDR2

<400> 126

Tyr Ala Ser Thr Arg His Thr
1 5

<210> 127
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 16G10S71 VL CDR3

<400> 127

Gln His His Tyr Ser Ser Pro Pro Thr
1 5

<210> 128
<400> 128
000

<210> 129
<400> 129
000

<210> 130
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 16G10S72 heavy chain variable region

<400> 130

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

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

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

Ser Asn Ile Asp His Asp Gly Asn Ile Ile Asn Phe Ala Pro Ser Val
50 55 60

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


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


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


Val Thr Val Ser Ser
        115


<210>  131
<211>  111
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  16G10S72 light chain variable region

<400>  131

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


Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Ser Ser
            20                  25                  30


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


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


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

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

Ser Ser Pro Pro Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105 110

<210> 132
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 16G10S72 VH CDR1

<400> 132

Gly Phe Thr Phe Ser Asp Tyr Trp Met Asp
1 5 10

<210> 133
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 16G10S72 VH CDR2

<400> 133

Asn Ile Asp His Asp Gly Asn Ile Ile Asn Phe Ala Pro Ser Val Lys
1 5 10 15

Gly

<210> 134
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 16G10S72 VH CDR3

<400> 134

Trp Gly His Tyr Ala Phe Asp Ser
1 5

<210> 135
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 16G10S72 VL CDR1

<400> 135

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

<210> 136
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 16G10S72 VL CDR2

<400> 136

Tyr Ala Ser Thr Arg Glu Thr
1 5

<210> 137
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 16G10S72 VL CDR3

<400> 137

Gln His His Tyr Ser Ser Pro Pro Thr
1 5

<210> 138
<400> 138
000

<210> 139
<400> 139
000

<210> 140
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 16G10S73 heavy chain variable region

<400> 140

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

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

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

Ser Asn Ile Asp His Asp Gly Asn Ile Ile Asn Phe Ala Pro Ser Val
50 55 60

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

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

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

Val Thr Val Ser Ser
115

<210> 141
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> 16G10S73 light chain variable region

<400> 141

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Ser Ser
20 25 30

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

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

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

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

Ser Ser Pro Pro Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105 110

<210> 142
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 16G10S73 VH CDR1

<400> 142

Gly Phe Thr Phe Ser Asp Tyr Trp Met Asp
1 5 10

<210> 143
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 16G10S73 VH CDR2

<400> 143

Asn Ile Asp His Asp Gly Asn Ile Ile Asn Phe Ala Pro Ser Val Lys
1 5 10 15

Gly

<210> 144
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 16G10S73 VH CDR3

<400> 144

Trp Gly His Tyr Ala Phe Asp Ser
1 5

<210> 145
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 16G10S73 VL CDR1

<400> 145

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

<210> 146
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 16G10S73 VL CDR2

<400> 146

Tyr Ala Ser Thr Arg Gln Thr
1 5

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

<220>
<223> 16G10S73 VL CDR3

<400> 147

Gln His His Tyr Ser Ser Pro Pro Thr
1 5

<210> 148
<400> 148
000

<210> 149
<400> 149
000

<210> 150
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 16G10S83 heavy chain variable region

<400> 150

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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 Phe Thr Phe Ser Asp Tyr
            20                  25                  30


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


Ser Asn Ile Asp His Asp Gly Asn Ile Ile Asn Phe Ala Pro Ser Val
    50                  55                  60


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


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


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


Val Thr Val Ser Ser
        115
```

<210> 151
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> 16G10S83 light chain variable region

<400> 151

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

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

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

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

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

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

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

<210> 152
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 16G10S83 VH CDR1

<400> 152

Gly Phe Thr Phe Ser Asp Tyr Trp Met Asp
1   5   10

<210> 153
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 16G10S83 VH CDR2

<400> 153

Asn Ile Asp His Asp Gly Asn Ile Ile Asn Phe Ala Pro Ser Val Lys
1 5 10 15

Gly

<210> 154
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 16G10S83 VH CDR3

<400> 154

Trp Gly His Tyr Ala Phe Asp Ser
1 5

<210> 155
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 16G10S83 VL CDR1

<400> 155

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

<210> 156
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 16G10S83 VL CDR2

<400> 156

Tyr Ala Ser Thr Arg Gln Thr
1 5

<210> 157
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 16G10S83 VL CDR3

<400> 157

Gln His His Tyr Ser Ser Pro Pro Thr
1 5

<210> 158
<400> 158
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<210> 159
<400> 159
000

<210> 160
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 35A9S79 heavy chain variable region

<400> 160

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

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

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

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

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


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


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


Val Thr Val Ser Ser
        115


<210>  161
<211>  111
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  35A9S79 light chain variable region

<400>  161

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


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


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


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


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

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

Asn Ala Pro Pro Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105 110

<210> 162
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 35A9S79 VH CDR1

<400> 162

Gly Phe Thr Phe Ser Asp Tyr Trp Met Asp
1 5 10

<210> 163
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 35A9S79 VH CDR2

<400> 163

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

Gly

<210> 164
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 35A9S79 VH CDR3

<400> 164

Trp Gly Arg Phe Ala Phe Asp Ser
1 5

<210> 165
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 35A9S79 VL CDR1

<400> 165

Lys Ser Ser Gln Ser Leu Leu Ser Gly Ser Phe Asn Tyr Leu Thr
1 5 10 15

<210> 166
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 35A9S79 VL CDR2

<400> 166

Tyr Ala Ser Thr Arg Gln Thr
1 5

<210> 167
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 35A9S79 VL CDR3

<400> 167

His His His Tyr Asn Ala Pro Pro Thr
1 5

<210> 168
<400> 168
000

<210> 169
<400> 169
000

<210> 170
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 35A9S710 heavy chain variable region

<400> 170

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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 Phe Thr Phe Ser Asp Tyr
            20                  25                  30


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


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


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


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


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


Val Thr Val Ser Ser
        115
```

<210> 171
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> 35A9S710 light chain variable region

<400> 171

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

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

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

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

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

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

Asn Ala Pro Pro Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105 110

<210> 172
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 35A9S710 VH CDR1

<400> 172

Gly Phe Thr Phe Ser Asp Tyr Trp Met Asp
1 5 10

<210> 173
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 35A9S710 VH CDR2

<400> 173

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

Gly

<210> 174
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 35A9S710 VH CDR3

<400> 174

Trp Gly Arg Phe Ala Phe Asp Ser
1 5

<210> 175
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 35A9S710 VL CDR1

<400> 175

Lys Ser Ser Gln Ser Leu Leu Ser Gly Ser Phe Asn Tyr Leu Thr
1 5 10 15

<210> 176
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 35A9S710 VL CDR2

<400> 176

Tyr Ala Ser Thr Arg His Thr
1 5

<210> 177
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 35A9S710 VL CDR3

<400> 177

His His His Tyr Asn Ala Pro Pro Thr
1 5

<210> 178
<400> 178
000

<210> 179
<400> 179
000

<210> 180
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 35A9S89 heavy chain variable region

<400> 180

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

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

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

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

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

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

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

Val Thr Val Ser Ser
115

<210> 181
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> 35A9S89 light chain variable region

<400> 181

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

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

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

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

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

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

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

<210> 182
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 35A9S89 VH CDR1

<400> 182

Gly Phe Thr Phe Ser Asp Tyr Trp Met Asp
1   5   10

<210> 183
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 35A9S89 VH CDR2

<400> 183

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

Gly

<210> 184
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 35A9S89 VH CDR3

<400> 184

Trp Gly Arg Phe Ala Phe Asp Ser
1 5

<210> 185
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 35A9S89 VL CDR1

<400> 185

Lys Ser Ser Gln Ser Leu Leu Ser Gly Ser Phe Asn Tyr Leu Thr
1 5 10 15

<210> 186
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 35A9S89 VL CDR2

<400> 186

Tyr Ala Ser Thr Arg Gln Thr
1 5

<210> 187
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 35A9S89 VL CDR3

<400> 187

His His His Tyr Asn Ala Pro Pro Thr
1 5

<210> 188
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> 37A10S713 human IgG1 heavy chain

<400> 188

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

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

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

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

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

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

```
Thr Arg Trp Gly Arg Phe Gly Phe Asp Ser Trp Gly Gln Gly Thr Leu
            100                 105                 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 189
<211> 218
<212> PRT
<213> Artificial Sequence

<220>

<223> 37A10S713 human kappa light chain

<400> 189

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


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


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


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


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


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


Asn Ala Pro Pro Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg
            100                 105                 110


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


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


Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145                 150                 155                 160


Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
                165                 170                 175
```

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

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 190
<211> 200
<212> PRT
<213> Rattus norvegicus

<400> 190

Met Lys Pro Tyr Phe Ser Cys Val Phe Val Phe Cys Phe Leu Ile Lys
1 5 10 15

Leu Leu Thr Gly Glu Leu Asn Asp Leu Ala Asn His Arg Met Phe Ser
20 25 30

Phe His Asp Gly Gly Val Gln Ile Ser Cys Asn Tyr Pro Glu Thr Val
35 40 45

Gln Gln Leu Lys Met Gln Leu Phe Lys Asp Arg Glu Val Leu Cys Asp
50 55 60

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

Met Ser Cys Pro Tyr Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
85 90 95

Asp Asn Ala Asp Ser Ser Gln Gly Ser Tyr Phe Leu Cys Ser Leu Ser
100 105 110

Ile Phe Asp Pro Pro Pro Phe Gln Glu Lys Asn Leu Ser Gly Gly Tyr

115 120 125

Leu Leu Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
130 135 140

Pro Val Gly Cys Ala Ala Phe Val Ala Ala Leu Leu Phe Gly Cys Ile
145 150 155 160

Phe Ile Val Trp Phe Ala Lys Lys Lys Tyr Arg Ser Ser Val His Asp
165 170 175

Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
180 185 190

Ser Arg Leu Ala Gly Met Thr Ser
195 200

<210> 191
<211> 180
<212> PRT
<213> Rattus norvegicus

<400> 191

Glu Leu Asn Asp Leu Ala Asn His Arg Met Phe Ser Phe His Asp Gly
1 5 10 15

Gly Val Gln Ile Ser Cys Asn Tyr Pro Glu Thr Val Gln Gln Leu Lys
20 25 30

Met Gln Leu Phe Lys Asp Arg Glu Val Leu Cys Asp Leu Thr Lys Thr
35 40 45

Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Asn Pro Met Ser Cys Pro
50 55 60

Tyr Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu Asp Asn Ala Asp
65 70 75 80

```
Ser Ser Gln Gly Ser Tyr Phe Leu Cys Ser Leu Ser Ile Phe Asp Pro
                85                  90                  95

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

Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu Pro Val Gly Cys
        115                 120                 125

Ala Ala Phe Val Ala Ala Leu Leu Phe Gly Cys Ile Phe Ile Val Trp
    130                 135                 140

Phe Ala Lys Lys Lys Tyr Arg Ser Ser Val His Asp Pro Asn Ser Glu
145                 150                 155                 160

Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys Ser Arg Leu Ala
                165                 170                 175

Gly Met Thr Ser
            180
```