

SEQUENCE LISTING

<110> Phanes Therapeutics, Inc.
 <120> Anti-CD47 Antibodies and Uses Thereof
 <130> 689204.2WO
 <150> US62/540,118
 <151> 2017-08-02
 <150> US62/657,094
 <151> 2018-04-13
 <160> 207
 <170> PatentIn version 3.5
 <210> 1
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 <223> 9023A Heavy Chain Variable Region
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Gln Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg Pro Gly Ala
 1 5 10 15

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

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

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

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

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

Ala Arg Arg Gly Pro Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr

100

105

110

Val Thr Val Ser Ser
115

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<223> 9023A Light Chain Variable Region

<400> 2

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 Asp 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 Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

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

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

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

<210> 3
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<223> 14P6A Heavy Chain Variable Region

<400> 3

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

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

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

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

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

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

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

Val Thr Val Ser Ser
115

<210> 4

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<220>

<223> 14P6A Light Chain Variable Region

<400> 4

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 Asn Leu Leu Ile

35

40

45

Tyr Gly Ala Ser Asn Arg Tyr 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 Thr Tyr Ser Tyr Pro Leu
 85 90 95

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

<210> 5

<211> 118

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<223> 4M8A Heavy Chain Variable Region

<400> 5

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 Thr Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30

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

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

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

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

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

Thr Leu Thr Val Ser Ser
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<223> 4M8A Light Chain Variable Region

<400> 6

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

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

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

Tyr Ser Gly Ser Thr Leu Gln Ser Gly Ile Pro Ser 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 Met Tyr Tyr Cys Gln Gln His Asn Glu Tyr Pro Trp
85 90 95

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

<210> 7
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<223> 16M17A Heavy Chain Variable Region

<400> 7

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

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

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

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

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

Thr Thr Leu Thr Val Ser Ser
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<211> 107

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<223> 16M17A Light Chain Variable Region

<400> 8

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

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

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

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

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

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

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

<210> 9
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<223> 13C4A Heavy Chain Variable Region

<400> 9

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 Ser Tyr
20 25 30

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

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

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

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

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

Gly Thr Thr Leu Thr Val Ser Ser
115 120

<210> 10
<211> 107
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<220>
<223> 13C4A Light Chain Variable Region

<400> 10

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

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

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

Tyr Ser Gly Ser Ser Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

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

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

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

<210> 11
<211> 120
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<213> Artificial Sequence

<220>

<223> 14018A Heavy Chain Variable Region

<400> 11

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 Ser Tyr
20 25 30

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

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

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

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

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

Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 12

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<223> 14018A Light Chain Variable Region

<400> 12

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

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

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

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

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

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

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

<210> 13
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<220>
<223> 5D24A 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 Ser Ser
20 25 30

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

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

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

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

Ala Arg Trp Gly Tyr Tyr Gly Lys Ser Ala Ile Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Ser Val Thr Val Ser Ser
115 120

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<223> 5D24A Light Chain Variable Region

<400> 14

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

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

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

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

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

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

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

<210> 15
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<223> 11G2A Heavy Chain Variable Region

<400> 15

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 Ser Tyr
20 25 30

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

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

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

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

Ala Arg Trp Gly Tyr Tyr Gly Lys Ser Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 16

<211> 107

<212> PRT

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<223> 11G2A Light Chain Variable Region

<400> 16

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

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

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

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

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

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

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

<210> 17
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<223> 13B18A Heavy Chain Variable Region

<400> 17

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 Ser Tyr
20 25 30

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

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

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

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys

85

90

95

Ser Arg Trp Gly Tyr Tyr Gly Lys Ser Ala Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Ser Val Thr Val Ser Ser
 115 120

<210> 18

<211> 107

<212> PRT

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<223> 13B18A Light Chain Variable Region

<400> 18

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

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

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

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

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

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

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

<210> 19

<211> 117

<212> PRT

<213> Artificial Sequence

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<223> 1J7A Heavy Chain Variable Region

<400> 19

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 Ser Tyr
20 25 30

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

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

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

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

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

Ser Val Thr Val Ser
115

<210> 20

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> 1J7A Light Chain Variable Region

<400> 20

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

Glu Thr Ile Thr Ile Asn Cys Arg Ala Asn Lys Ser Ile Ser Lys Tyr

20

25

30

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

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

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

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

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

<210> 21

<211> 120

<212> PRT

<213> Artificial Sequence

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<223> 14D18A 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 Ser Tyr
 20 25 30

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

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

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

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

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

Gly Thr Thr Leu Thr Val Ser Ser
115 120

<210> 22

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> 14D18A Light Chain Variable Region

<400> 22

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

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

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

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

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

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

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

<210> 23

<211> 115

<212> PRT

<213> Artificial Sequence

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<223> 305A Heavy Chain Variable Region

<400> 23

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

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

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

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

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

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

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

Val Ser Ala
115

<210> 24

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> 305A Light Chain Variable Region

<400> 24

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

Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu His Ser
20 25 30

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

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

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

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

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

<210> 25

<211> 114

<212> PRT

<213> Artificial Sequence

<220>

<223> 17C6A Heavy Chain Variable Region

<400> 25

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 Ser Tyr
20 25 30

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

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

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

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser 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 Ala

<210> 26
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<212> PRT
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<220>
<223> 17C6A Light Chain Variable Region

<400> 26

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

Asp Thr 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 Trp
85 90 95

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

<210> 27
<211> 114

<212> PRT
<213> Artificial Sequence

<220>
<223> 14N13A Heavy Chain Variable Region

<400> 27

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 Ile Phe Thr Ser Tyr
20 25 30

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

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

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

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

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

Ser Ser

<210> 28
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> 14N13A Light Chain Variable Region

<400> 28

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 Val 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 Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
100 105 110

Lys

<210> 29
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<220>
<223> 10I23A Heavy Chain Variable Region

<400> 29

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

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

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

Gly Trp Ile Asp Pro Glu Asp Gly Glu Thr Lys Cys Ala Pro Lys Phe
50 55 60

Gln Asp Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

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

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

Thr Leu Thr Val Ser Ser
115

<210> 30

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<213> Artificial Sequence

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<223> 10I23A Light Chain Variable Region

<400> 30

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

Val Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

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

Thr His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

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<400> 31

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

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

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

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

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

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

Leu Thr Val Ser Ser
 115

<210> 32
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 <212> PRT
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<220>
 <223> 12B18A Light Chain Variable Region

<400> 32

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Arg Pro Gly Gln Ser
35 40 45

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

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

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

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

<210> 33

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<212> PRT

<213> Artificial Sequence

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<223> 17012A Heavy Chain Variable Region

<400> 33

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

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

Gly Arg Ile Asn Pro Tyr Asn Gly Asp Thr Phe Asn Asn Gln Lys Phe

50

55

60

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

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

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

Thr Val Ser Ser
115

<210> 34

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> 17012A Light Chain Variable Region

<400> 34

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

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

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

<210> 35
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 15G23A Heavy Chain Variable Region

<400> 35

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 Asn Tyr
20 25 30

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

Ala Lys Gly Gly Thr Gly Thr Gly Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Ser Ser
115

<210> 36
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> 15G23A Light Chain Variable Region

<400> 36

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

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

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

Lys

<210> 37

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> 17N8A Heavy Chain Variable Region

<400> 37

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

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

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

Ala Gln Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu
50 55 60

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

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

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

Thr Leu Val Thr Val Ser Ala
115

<210> 38
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> 17N8A Light Chain Variable Region

<400> 38

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Thr Gln Ser Leu Val His Ser
20 25 30

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

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

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

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

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

<210> 39
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 18M19A Heavy Chain Variable Region

<400> 39

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

Ala Lys Gly Gly Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
100 105 110

Val Thr Val Ser Ser
115

<210> 40
<211> 112

<212> PRT
<213> Artificial Sequence

<220>
<223> 18M19A Light Chain Variable Region

<400> 40

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

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

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

<210> 41
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> 11F6 Heavy Chain Variable Region

<400> 41

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

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

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

Gly Trp Ile Asp Pro Glu Asp Gly Glu Thr Lys Cys Ala Pro Lys Phe
50 55 60

Gln Asp Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

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

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

Thr Leu Thr Val Ser Ser
115

<210> 42

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> 11F6A Light Chain Variable Region

<400> 42

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

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

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

<210> 43
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 19L14A Heavy Chain Variable Region

<400> 43

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 Ser Tyr
20 25 30

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

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

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

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

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

Val Thr Val Ser Ala
115

<210> 44

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

<220>
<223> 19L14A Light Chain Variable Region

<400> 44

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

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Ser Ser
20 25 30

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

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

Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Val Glu
65 70 75 80

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

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

<210> 45
<211> 8
<212> PRT
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<220>
<223> 9023A HC CDR1

<400> 45

Gly Tyr Thr Phe Thr Asp Tyr Tyr
1 5

<210> 46
<211> 8

<212> PRT
<213> Artificial Sequence

<220>
<223> 9023A HC CDR2

<400> 46

Ile Tyr Pro Gly Ser Gly Asn Thr
1 5

<210> 47
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 9023A HC CDR3

<400> 47

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

<210> 48
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 14P6A HC CDR1

<400> 48

Gly Tyr Thr Phe Thr Ala Tyr Tyr
1 5

<210> 49
<211> 8
<212> PRT
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<220>
<223> 14P6A HC CDR2

<400> 49

Ile Tyr Pro Gly Ser Gly Asn Thr
1 5

<210> 50
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 14P6A HC CDR3

<400> 50

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

<210> 51
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M8A HC CDR1

<400> 51

Gly Tyr Thr Phe Thr Ser Tyr Trp
1 5

<210> 52
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M8A HC CDR2

<400> 52

Ile Asp Pro Ser Asp Ser Glu Thr
1 5

<210> 53
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M8A HC CDR3

<400> 53

Ala Arg Trp Gly Gly Trp Leu Pro Leu Asp Tyr
1 5 10

<210> 54
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 16M17A HC CDR1

<400> 54

Gly Tyr Thr Phe Thr Asn Tyr Trp
1 5

<210> 55
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 16M17A HC CDR2

<400> 55

Ile Asp Pro Ser Asp Ser Glu Thr
1 5

<210> 56
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> 16M17A HC CDR3

<400> 56

Ala Arg Met Ala Phe Ile Thr Thr Val Val Asp Tyr
1 5 10

<210> 57
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 13C4A HC CDR1

<400> 57

Gly Tyr Thr Phe Thr Ser Tyr Trp
1 5

<210> 58

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 13C4A HC CDR2

<400> 58

Ile Asp Pro Ser Asp Ser Glu Thr
1 5

<210> 59

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> 13C4A HC CDR3

<400> 59

Ala Arg Trp Gly Tyr Tyr Gly Arg Ser Pro Leu Asp His
1 5 10

<210> 60

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 14018A HC CDR1

<400> 60

Gly Tyr Thr Phe Thr Ser Tyr Trp
1 5

<210> 61

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 14018A HC CDR2

<400> 61

Ile Asp Pro Ser Asp Ser Glu Thr
1 5

<210> 62

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> 14018A HC CDR3

<400> 62

Ala Arg Trp Tyr Tyr Gly Gly Ser Gly Ala Met Asp Tyr
1 5 10

<210> 63

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 5D24A HC CDR1

<400> 63

Gly Tyr Thr Phe Thr Ser Ser Trp
1 5

<210> 64

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 5D24A HC CDR2

<400> 64

Ile Asp Pro Ser Asp Ser Glu Thr
1 5

<210> 65

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

<220>
<223> 5D24A HC CDR3

<400> 65

Ala Arg Trp Gly Tyr Tyr Gly Lys Ser Ala Ile Asp Tyr
1 5 10

<210> 66
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 11G2A HC CDR1

<400> 66

Gly Tyr Thr Phe Thr Ser Tyr Trp
1 5

<210> 67
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 11G2A HC CDR2

<400> 67

Ile Asp Pro Ser Asp Ser Glu Ala
1 5

<210> 68
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 11G2A HC CDR3

<400> 68

Ala Arg Trp Gly Tyr Tyr Gly Lys Ser Ala Met Asp Tyr
1 5 10

<210> 69
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 13B18A HC CDR1

<400> 69

Gly Tyr Thr Phe Thr Ser Tyr Trp
1 5

<210> 70
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 13B18A HC CDR2

<400> 70

Ile Asp Pro Ser Asp Ser Glu Thr
1 5

<210> 71
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 13B18A HC CDR3

<400> 71

Ser Arg Trp Gly Tyr Tyr Gly Lys Ser Ala Met Asp Tyr
1 5 10

<210> 72
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 1J7A HC CDR1

<400> 72

Gly Tyr Thr Phe Thr Ser Tyr Trp
1 5

<210> 73
<211> 8
<212> PRT
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<220>
<223> 1J7A HC CDR2

<400> 73

Ile Asp Pro Ser Asp Ser Glu Thr
1 5

<210> 74
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 1J7A HC CDR3

<400> 74

Ala Arg Trp Gly Leu Arg Gly Ala Met Asp Tyr
1 5 10

<210> 75
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 14D18A HC CDR1

<400> 75

Gly Tyr Thr Phe Thr Ser Tyr Trp
1 5

<210> 76
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> 14D18A HC CDR2

<400> 76

Ile Asp Pro Ser Asp Ser Glu Thr
1 5

<210> 77

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> 14D18A HC CDR3

<400> 77

Ala Arg Trp Gly Tyr Tyr Gly Arg Ser Pro Leu Asp His
1 5 10

<210> 78

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 305A HC CDR1

<400> 78

Gly Phe Thr Phe Ser Asp Phe Tyr
1 5

<210> 79

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> 305A HC CDR2

<400> 79

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

<210> 80

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> 305A HC CDR3

<400> 80

Ala Arg Asp Thr Ala Tyr
1 5

<210> 81

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 17C6A HC CDR1

<400> 81

Gly Tyr Thr Phe Thr Ser Tyr Trp
1 5

<210> 82

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 17C6A HC CDR2

<400> 82

Ile Asp Pro Ser Asp Ser Glu Thr
1 5

<210> 83

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 17C6A HC CDR3

<400> 83

Ala Gly Thr Asp Leu Ala Tyr
1 5

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

<220>
<223> 14N13A HC CDR1

<400> 84

Gly Tyr Ile Phe Thr Ser Tyr Trp
1 5

<210> 85
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 14N13A HC CDR2

<400> 85

Ile Asp Pro Ser Asp Ser Glu Thr
1 5

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

<220>
<223> 14N13A HC CDR3

<400> 86

Ala Lys Gly Phe Ser Asp Tyr
1 5

<210> 87
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 10I23A HC CDR1

<400> 87

Gly Phe Asn Ile Lys Asp Ser Leu

1 5

<210> 88
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 10I23A HC CDR2

<400> 88

Ile Asp Pro Glu Asp Gly Glu Thr
1 5

<210> 89
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 10I23A HC CDR3

<400> 89

Ala Val Ile Ser Thr Val Val Ala Pro Asp Tyr
1 5 10

<210> 90
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 12B18A HC CDR1

<400> 90

Gly Tyr Ser Phe Thr Gly Tyr Phe
1 5

<210> 91
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 12B18A HC CDR2

<400> 91

Ile Asn Pro Tyr Asn Gly Asp Thr
1 5

<210> 92

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> 12B18A HC CDR3

<400> 92

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

<210> 93

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 17012A HC CDR1

<400> 93

Gly Tyr Ser Phe Thr Gly Tyr Phe
1 5

<210> 94

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 17012A HC CDR2

<400> 94

Ile Asn Pro Tyr Asn Gly Asp Thr
1 5

<210> 95

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> 17012A HC CDR3

<400> 95

Ala Arg Gly Gly Tyr Ala Met Asp Tyr
1 5

<210> 96

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 15G23A HC CDR1

<400> 96

Gly Tyr Thr Phe Thr Asn Tyr Val
1 5

<210> 97

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 15G23A HC CDR2

<400> 97

Ile Asn Pro Tyr Asn Asp Gly Thr
1 5

<210> 98

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> 15G23A HC CDR3

<400> 98

Ala Lys Gly Gly Thr Gly Thr Gly Asp Tyr
1 5 10

<210> 99

<211> 8

<212> PRT
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<220>
<223> 17N8A HC CDR1

<400> 99

Gly Phe Thr Phe Ser Asn Tyr Trp
1 5

<210> 100
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 17N8A HC CDR2

<400> 100

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

<210> 101
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 17N8A HC CDR3

<400> 101

Thr Gly Gly Gly Lys Gly Gly Phe Ala Tyr
1 5 10

<210> 102
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 18M19A HC CDR1

<400> 102

Gly Tyr Thr Phe Thr Ser Tyr Val
1 5

<210> 103
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 18M19A HC CDR2

<400> 103

Ile Asn Pro Tyr Asn Asp Gly Thr
1 5

<210> 104
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 18M19A HC CDR3

<400> 104

Ala Lys Gly Gly Tyr Tyr Ala Met Asp Tyr
1 5 10

<210> 105
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 11F6A HC CDR1

<400> 105

Gly Phe Asn Ile Lys Asp Ser Leu
1 5

<210> 106
<211> 8
<212> PRT
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<220>
<223> 11F6A HC CDR2

<400> 106

Ile Asp Pro Glu Asp Gly Glu Thr
1 5

<210> 107
<211> 11
<212> PRT
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<220>
<223> 11F6A HC CDR3

<400> 107

Ala Arg Ile Thr Thr Val Val Ala Thr Asp Tyr
1 5 10

<210> 108
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 19L14A HC CDR1

<400> 108

Gly Tyr Thr Phe Thr Ser Tyr Trp
1 5

<210> 109
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 19L14A HC CDR2

<400> 109

Ser Asn Pro Gly Ser Ser Ser Thr
1 5

<210> 110
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 19L14A HC CDR3

<400> 110

Ala Arg Glu Gly Leu Arg Arg Phe Ala Tyr
1 5 10

<210> 111

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> 9023A LC CDR1

<400> 111

Asp Asn Val Gly Thr Tyr
1 5

<210> 112

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> 9023A LC CDR2

<400> 112

Gly Ala Ser
1

<210> 113

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> 9023A LC CDR3

<400> 113

Gly Gln Ser Tyr Ser Tyr Pro Leu Thr
1 5

<210> 114

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> 14P6A LC CDR1

<400> 114

Glu Asn Val Gly Thr Tyr
1 5

<210> 115

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> 14P6A LC CDR2

<400> 115

Gly Ala Ser
1

<210> 116

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> 14P6A LC CDR3

<400> 116

Gly Gln Thr Tyr Ser Tyr Pro Leu Thr
1 5

<210> 117

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> 4M8A LC CDR1

<400> 117

Lys Asn Ile Ser Lys Tyr
1 5

<210> 118

<211> 3
<212> PRT
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<220>
<223> 4M8A LC CDR2

<400> 118

Ser Gly Ser
1

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

<220>
<223> 4M8A LC CDR3

<400> 119

Gln Gln His Asn Glu Tyr Pro Trp Thr
1 5

<210> 120
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 16M17A LC CDR1

<400> 120

Lys Ser Ile Ser Lys Tyr
1 5

<210> 121
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> 16M17A LC CDR2

<400> 121

Ser Gly Ser
1

<210> 122
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 16M17A LC CDR3

<400> 122

Gln Gln His Asn Glu Tyr Pro Trp Thr
1 5

<210> 123
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 13C4A LC CDR1

<400> 123

Lys Ser Ile Ser Lys Tyr
1 5

<210> 124
<211> 3
<212> PRT
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<220>
<223> 13C4A LC CDR2

<400> 124

Ser Gly Ser
1

<210> 125
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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<400> 125

Gln Gln His Asn Glu Tyr Pro Trp Thr
1 5

<210> 126
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 14018A LC CDR1

<400> 126

Lys Ser Ile Ser Lys Tyr
1 5

<210> 127
<211> 3
<212> PRT
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<220>
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<400> 127

Ser Gly Ser
1

<210> 128
<211> 9
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<213> Artificial Sequence

<220>
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<400> 128

Gln Gln His Asn Glu Tyr Pro Trp Thr
1 5

<210> 129
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> 5D24A LC CDR1

<400> 129

Lys Ser Ile Ser Lys Tyr
1 5

<210> 130

<211> 3

<212> PRT

<213> Artificial Sequence

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<223> 5D24A LC CDR2

<400> 130

Ser Gly Ser
1

<210> 131

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> 5D24A LC CDR3

<400> 131

Gln Gln His Asn Glu Tyr Pro Trp Thr
1 5

<210> 132

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> 11G2A LC CDR1

<400> 132

Lys Ser Ile Ser Lys Tyr
1 5

<210> 133

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> 11G2A LC CDR2

<400> 133

Ser Gly Ser

1

<210> 134

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> 11G2A LC CDR3

<400> 134

Gln Gln His Asn Glu Tyr Pro Trp Thr

1

5

<210> 135

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> 13B18A LC CDR1

<400> 135

Lys Ser Ile Ser Lys Tyr

1

5

<210> 136

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> 13B18A LC CDR2

<400> 136

Ser Gly Ser

1

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

<220>
<223> 13B18A LC CDR3

<400> 137

Gln Gln His Asn Glu Tyr Pro Trp Thr
1 5

<210> 138
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 1J7A LC CDR1

<400> 138

Lys Ser Ile Ser Lys Tyr
1 5

<210> 139
<211> 3
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<220>
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<400> 139

Ser Gly Ser
1

<210> 140
<211> 9
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<213> Artificial Sequence

<220>
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<400> 140

Gln Gln His Asn Glu Tyr Pro Trp Thr

1 5

<210> 141
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<400> 141

Lys Ser Ile Ser Lys Tyr
1 5

<210> 142
<211> 3
<212> PRT
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<220>
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<400> 142

Ser Gly Ser
1

<210> 143
<211> 9
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<213> Artificial Sequence

<220>
<223> 14D18A LC CDR3

<400> 143

Gln Gln His Asn Glu Tyr Pro Trp Thr
1 5

<210> 144
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 305A LC CDR1

<400> 144

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

<210> 145

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> 305A LC CDR2

<400> 145

Arg Met Ser
1

<210> 146

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> 305A LC CDR3

<400> 146

Met Gln His Leu Glu Tyr Pro Phe Thr
1 5

<210> 147

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> 17C6A LC CDR1

<400> 147

Gln Asn Ile Asn Val Trp
1 5

<210> 148

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> 17C6A LC CDR2

<400> 148

Lys Ala Ser

1

<210> 149

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> 17C6A LC CDR3

<400> 149

Gln Gln Gly Gln Ser Tyr Pro Trp Thr

1

5

<210> 150

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> 14N13A LC CDR1

<400> 150

Gln Ser Leu Leu Tyr Ser Ser Asn Gln Lys Asn Tyr

1

5

10

<210> 151

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> 14N13A LC CDR2

<400> 151

Trp Ala Ser

1

<210> 152

<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> 14N13A LC CDR3

<400> 152

Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr
1 5

<210> 153
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 10I23A LC CDR1

<400> 153

Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr
1 5 10

<210> 154
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> 10I23A LC CDR2

<400> 154

Lys Val Ser
1

<210> 155
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 10I23A LC CDR3

<400> 155

Ser Gln Ser Thr His Val Pro Trp Thr
1 5

<210> 156
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 12B18A LC CDR1

<400> 156

Gln	Ser	Leu	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr
1				5					10	

<210> 157
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> 12B18A LC CDR2

<400> 157

Lys	Val	Ser
1		

<210> 158
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 12B18A LC CDR3

<400> 158

Ser	Gln	Ser	Thr	His	Val	Pro	Phe	Thr
1				5				

<210> 159
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 17012A LC CDR1

<400> 159

Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr
1 5 10

<210> 160
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> 17012A LC CDR2

<400> 160

Arg Val Ser
1

<210> 161
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 17012A LC CDR3

<400> 161

Phe Gln Ser Thr His Val Pro His Thr
1 5

<210> 162
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 15G23A LC CDR1

<400> 162

Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr
1 5 10

<210> 163
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> 15G23A LC CDR2

<400> 163

Lys Val Ser
1

<210> 164

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> 15G23A LC CDR3

<400> 164

Ser Gln Ser Thr His Val Pro Pro Leu Thr
1 5 10

<210> 165

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> 17N8A LC CDR1

<400> 165

Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr
1 5 10

<210> 166

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> 17N8A LC CDR2

<400> 166

Lys Val Ser
1

<210> 167

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> 17N8A LC CDR3

<400> 167

Ser Gln Ser Thr His Val Pro Leu Thr
1 5

<210> 168

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> 18M19A LC CDR1

<400> 168

Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr
1 5 10

<210> 169

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> 18M19A LC CDR2

<400> 169

Lys Val Ser
1

<210> 170

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> 18M19A LC CDR3

<400> 170

Ser Gln Ser Thr His Val Pro Trp Thr
1 5

<210> 171

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

<220>
<223> 11F6A LC CDR1

<400> 171

Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr
1 5 10

<210> 172
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> 11F6A LC CDR2

<400> 172

Lys Val Ser
1

<210> 173
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 11F6A LC CDR3

<400> 173

Ser Gln Ser Thr His Val Pro Leu Thr
1 5

<210> 174
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 19L14A LC CDR1

<400> 174

Ser Ser Val Ser Ser Ser Tyr
1 5

<210> 175
<211> 3
<212> PRT
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<220>
<223> 19L14A LC CDR2

<400> 175

Ser Thr Ser
1

<210> 176
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 19L14A LC CDR3

<400> 176

Gln Gln Tyr Ser Gly Tyr Pro Phe Thr
1 5

<210> 177
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> HC CDR1

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is Asp or Ala

<400> 177

Gly Tyr Thr Phe Thr Xaa Tyr Tyr
1 5

<210> 178
<211> 6
<212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR1

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Xaa is Asp or Glu

<400> 178

Xaa Asn Val Gly Thr Tyr

1 5

<210> 179

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR3

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> Xaa is Ser or Thr

<400> 179

Gly Gln Xaa Tyr Ser Tyr Pro Leu Thr

1 5

<210> 180

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> HC CDR1

<220>

<221> MISC_FEATURE

<222> (7)..(7)

<223> Xaa is Ser or Tyr

<400> 180

Gly Tyr Thr Phe Thr Ser Xaa Trp
1 5

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

<220>
<223> HC CDR2

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Xaa is Thr or Ala

<400> 181

Ile Asp Pro Ser Asp Ser Glu Xaa
1 5

<210> 182
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> HC CDR3

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa is Ala or Ser

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> Xaa is Ile or Met

<400> 182

Xaa Arg Trp Gly Tyr Tyr Gly Lys Ser Ala Xaa Asp Tyr
1 5 10

<210> 183
<211> 120
<212> PRT
<213> Artificial Sequence

<220>

<223> Heavy chain variable region H1

<400> 183

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 Met
35 40 45

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

Lys Asp Arg Val Thr Leu Thr Val Asp Thr 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

Ser Arg Trp Gly Tyr Tyr Gly Lys Ser Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 184

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain variable region H2

<400> 184

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

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

Lys Asp Arg Val Thr Leu Thr Val Asp Thr 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

Ser Arg Trp Gly Tyr Tyr Gly Lys Ser Ala Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 185

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain variable region H3

<400> 185

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys 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 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 Asn Gln Lys Phe
 50 55 60

Lys Asp Arg Ala Thr Leu Thr Val Asp Thr 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

Ser Arg Trp Gly Tyr Tyr Gly Lys Ser Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 186
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain variable region H4

<400> 186

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

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

Lys Asp Arg Ala Thr Leu Thr Val Asp Thr 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

Ser Arg Trp Gly Tyr Tyr Gly Lys Ser Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 187
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain variable region H5

<400> 187

Gln Ile 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 Ala Tyr
20 25 30

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

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

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

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

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

Val Thr Val Ser Ser
115

<210> 188
<211> 117
<212> PRT
<213> Artificial Sequence

<220>

<223> Heavy chain variable region H6

<400> 188

Gln Ile 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 Ala Tyr
20 25 30

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

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

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

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

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

Val Thr Val Ser Ser
115

<210> 189

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain variable region H7

<400> 189

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

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

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

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

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

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

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

Val Thr Val Ser Ser
115

<210> 190

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Light chain variable region L1

<400> 190

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

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

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

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

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

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

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

<210> 191
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain variable region L2

<400> 191

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

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

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

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

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

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

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

<210> 192
<211> 107
<212> PRT
<213> Artificial Sequence

<220>

<223> Light chain variable region L3

<400> 192

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

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

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

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

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

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

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

<210> 193

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Light chain variable region L4

<400> 193

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

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

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

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

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

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

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

<210> 194
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain variable region L5

<400> 194

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys

100

105

<210> 195
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Light chain variable region L6

<400> 195

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

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

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

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

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

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

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

<210> 196
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Light chain variable region L7

<400> 196

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

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

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

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

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

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

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

<210> 197
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain variable region L8

<400> 197

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

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

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

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

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

65		70		75		80									
Glu	Asp	Phe	Ala	Asp	Tyr	His	Cys	Gly	Gln	Thr	Tyr	Ser	Tyr	Pro	Leu
				85					90					95	

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

<210> 198
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Light chain variable region L9

<400> 198

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

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

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

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

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

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

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

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

<220>

<223> H8 Heavy Chain Variable Region

<400> 199

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> 200

<211> 107

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<213> Artificial Sequence

<220>

<223> L10 Light Chain Variable Region

<400> 200

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> 201
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> H8 HC CDR1

<400> 201

Gly Tyr Thr Phe Thr Ser Tyr Trp
 1 5

<210> 202
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 202

Ile Asp Pro Ser Asp Ser Glu Thr
 1 5

<210> 203
 <211> 7

<212> PRT
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<220>
<223> H8 HC CDR3

<400> 203

Ala Gly Thr Asp Leu Ala Tyr
1 5

<210> 204
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> L10 LC CDR1

<400> 204

Gln Asn Ile Asn Val Trp
1 5

<210> 205
<211> 3
<212> PRT
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<400> 205

Lys Ala Ser
1

<210> 206
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> L10 LC CDR3

<400> 206

Gln Gln Gly Gln Ser Tyr Pro Phe Thr
1 5

<210> 207
 <211> 323
 <212> PRT
 <213> Homo sapiens

<400> 207

Met Trp Pro Leu Val Ala Ala Leu Leu Leu Gly Ser Ala Cys Cys Gly
 1 5 10 15

Ser Ala Gln Leu Leu Phe Asn Lys Thr Lys Ser Val Glu Phe Thr Phe
 20 25 30

Cys Asn Asp Thr Val Val Ile Pro Cys Phe Val Thr Asn Met Glu Ala
 35 40 45

Gln Asn Thr Thr Glu Val Tyr Val Lys Trp Lys Phe Lys Gly Arg Asp
 50 55 60

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

Phe Ser Ser Ala Lys Ile Glu Val Ser Gln Leu Leu Lys Gly Asp Ala
 85 90 95

Ser Leu Lys Met Asp Lys Ser Asp Ala Val Ser His Thr Gly Asn Tyr
 100 105 110

Thr Cys Glu Val Thr Glu Leu Thr Arg Glu Gly Glu Thr Ile Ile Glu
 115 120 125

Leu Lys Tyr Arg Val Val Ser Trp Phe Ser Pro Asn Glu Asn Ile Leu
 130 135 140

Ile Val Ile Phe Pro Ile Phe Ala Ile Leu Leu Phe Trp Gly Gln Phe
 145 150 155 160

Gly Ile Lys Thr Leu Lys Tyr Arg Ser Gly Gly Met Asp Glu Lys Thr
 165 170 175

Ile Ala Leu Leu Val Ala Gly Leu Val Ile Thr Val Ile Val Ile Val

180

185

190

Gly Ala Ile Leu Phe Val Pro Gly Glu Tyr Ser Leu Lys Asn Ala Thr
 195 200 205

Gly Leu Gly Leu Ile Val Thr Ser Thr Gly Ile Leu Ile Leu Leu His
 210 215 220

Tyr Tyr Val Phe Ser Thr Ala Ile Gly Leu Thr Ser Phe Val Ile Ala
 225 230 235 240

Ile Leu Val Ile Gln Val Ile Ala Tyr Ile Leu Ala Val Val Gly Leu
 245 250 255

Ser Leu Cys Ile Ala Ala Cys Ile Pro Met His Gly Pro Leu Leu Ile
 260 265 270

Ser Gly Leu Ser Ile Leu Ala Leu Ala Gln Leu Leu Gly Leu Val Tyr
 275 280 285

Met Lys Phe Val Ala Ser Asn Gln Lys Thr Ile Gln Pro Pro Arg Lys
 290 295 300

Ala Val Glu Glu Pro Leu Asn Ala Phe Lys Glu Ser Lys Gly Met Met
 305 310 315 320

Asn Asp Glu