

SEQUENCE LISTING

<110> NGM BIOPHARMACEUTICALS, INC.

<120> GLUCAGON RECEPTOR BINDING PROTEINS AND METHODS OF USE THEREOF

<130> 13370-070-228

<140> To Be Assigned

<141> Herewith

<150> 62/451,603

<151> 2017-01-27

<160> 238

<170> PatentIn version 3.5

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

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

Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr 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
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Ala Arg His Thr Asn Tyr Gly Ser Asp Tyr Trp Gly Gln Gly Thr Thr
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Leu Thr Val Ser Ser
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Tyr Gly Asn Thr Phe Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

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

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys Phe Gln Gly
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Ser His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
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Met Ile His Pro Asn Ser Gly Ser Thr His Tyr Asn Glu Lys Phe Lys
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Gly Ala Thr Ala Asp Tyr Val Met Asp

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Leu Leu Ile Asn Leu Val Ser Asn Arg Phe

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

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

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

Gly Ala Thr Ala Asp Tyr Val Met Asp Tyr Trp Gly Gln Gly Thr Ser
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Val Thr Val Ser Ser
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Asp Gln Ala Ser Ile Ser Cys Lys Ser Thr Lys Ser Leu Leu Asn Ser
20 25 30

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

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

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

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

Asn Phe Leu Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
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Ala Arg Thr Asp Tyr Asp Tyr Asp Gly Asp Tyr
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Gly Asn Thr Phe Thr Ser His
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Asp Tyr Asp Tyr Asp Gly Asp
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Thr Ser His Trp Met His
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Trp Ile Gly Met Ser His Pro Asn Ser Gly Ser Ser Asn
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Ala Arg Thr Asp Tyr Asp Tyr Asp Gly Asp
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Leu Asn Ser Asp Gly Leu Thr Tyr Leu Asp Trp Tyr
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Leu Leu Ile Tyr Leu Val Ser Asn Arg Phe
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Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Asn Thr Phe Thr Ser His
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Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Met Ser His Pro Asn Ser Gly Ser Ser Asn Tyr Ser Gly Lys Phe
50 55 60

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

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

Ala Arg Thr Asp Tyr Asp Tyr Asp Gly Asp Tyr Trp Gly Gln Gly Thr
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Thr Leu Thr Val Ser Ser
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Asp Val Val Leu Thr Gln Thr Pro Leu Ser Leu Pro Val Asn Ile Gly
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Asp Gln Ala Ser Ile Ser Cys Lys Ser Ser Lys Ser Leu Leu Asn Ser
20 25 30

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

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

Asn Phe Leu Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
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Gly Tyr Thr Phe Thr Arg Asn Val Ile His
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Tyr Ile Asn Pro Tyr Asn Asp Gly Ala Lys Tyr Asn Ala Lys Phe Lys
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Gly

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Trp Gly Asn Tyr Glu Asp Phe Ala Met Asp Tyr
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Arg Ala Ser Glu Ser Val Asp Ile Tyr Gly Asn Ser Tyr Met His
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Leu Ala Ser Asn Leu Glu Ser
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Gln Gln Asn Asn Glu Asp Pro Phe Thr
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Gly Tyr Thr Phe Thr Arg Asn Val
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Ile Asn Pro Tyr Asn Asp Gly Ala
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Ala Arg Trp Gly Asn Tyr Glu Asp Phe Ala Met Asp Tyr
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Arg Asn Val Ile His
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Gly Tyr Thr Phe Thr Arg Asn
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Pro Tyr Asn Asp
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Gly Asn Tyr Glu Asp Phe Ala Met Asp
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Ser Glu Ser Val Asp Ile Tyr Gly Asn Ser Tyr
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Asn Asn Glu Asp Pro Phe
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Thr Arg Asn Val Ile His
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Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ala Lys
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Ala Arg Trp Gly Asn Tyr Glu Asp Phe Ala Met Asp
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Asp Ile Tyr Gly Asn Ser Tyr Met His Trp Tyr
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Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu
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Gln Gln Asn Asn Glu Asp Pro Phe
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Tyr Ile Asn Pro Tyr Asn Asp Gly Ala Lys
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Thr Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Asn
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 Ala Lys Tyr Asn Ala Lys Phe
50 55 60

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

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

Ala Arg Trp Gly Asn Tyr Glu Asp Phe Ala Met Asp Tyr Trp Gly Gln
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Gly Thr Ser Val Thr Val Ser Ser
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Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Ile Tyr
20 25 30

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

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

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

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

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

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Gly Tyr Thr Phe Thr Ser Ser Val Met His
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Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Asn Phe Lys
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Gly

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

<210> 102
<211> 15
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<220>
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<400> 102

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

<210> 103
<211> 7
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<220>
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<400> 103

Phe Ala Ser Asn Leu Glu Ser
1 5

<210> 104
<211> 9
<212> PRT
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<220>
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<400> 104

Gln Gln Asn Asn Glu Val Pro Phe Thr
1 5

<210> 105
<211> 8
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<220>
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<400> 105

Gly Tyr Thr Phe Thr Ser Ser Val
1 5

<210> 106
<211> 8
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<220>
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<400> 106

Ile Asn Pro Tyr Asn Asp Gly Thr
1 5

<210> 107
<211> 15
<212> PRT
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<220>
<223> CDR Sequence

<400> 107

Ala Arg Gly Ala Gly Tyr Asp Arg Gly Pro Met Ala Met Asp Tyr
1 5 10 15

<210> 108
<211> 10
<212> PRT
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<220>
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<400> 108

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

<210> 109
<211> 3
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<213> Artificial Sequence

<220>
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<400> 109

Phe Ala Ser
1

<210> 110
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
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<400> 110

Ser Ser Val Met His
1 5

<210> 111
<211> 7
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<220>
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<400> 111

Gly Tyr Thr Phe Thr Ser Ser
1 5

<210> 112

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 112

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

<210> 113

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 113

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

<210> 114

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 114

Asn Asn Glu Val Pro Phe
1 5

<210> 115

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 115

Thr Ser Ser Val Met His
1 5

<210> 116

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 116

Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys
1 5 10

<210> 117

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

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<400> 117

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

<210> 118

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 118

Asp Ser Tyr Gly Asp Ser Phe Val His Trp Tyr
1 5 10

<210> 119

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 119

Leu Leu Ile Tyr Phe Ala Ser Asn Leu Glu
1 5 10

<210> 120

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 120

Gln Gln Asn Asn Glu Val Pro Phe
1 5

<210> 121

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 121

Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys
1 5 10

<210> 122

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> 1C3 Heavy chain variable region

<400> 122

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 Ser
20 25 30

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

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

Lys Gly Lys Ala Thr Leu Thr Ser Asp Arg Ser Ser Thr 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

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

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

<210> 123

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> 1C3 Light chain variable region

<400> 123

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

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

Gly Asp Ser Phe Val His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro

35

40

45

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

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

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

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

<210> 124
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 124

Gly Tyr Thr Phe Thr Ser Tyr Trp Ile Thr
1 5 10

<210> 125
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 125

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

Ser

<210> 126
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 126

Asp Asp Asn Tyr Val Gly Phe Thr Tyr
1 5

<210> 127
<211> 16
<212> PRT
<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 127

Arg Ser Ser Gln Thr Ile Ile His Ser Asp Gly Asn Thr Tyr Leu Glu
1 5 10 15

<210> 128

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 128

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 129

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 129

Gly Tyr Thr Phe Thr Ser Tyr Trp
1 5

<210> 130

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 130

Ile His Pro Gly Gly Gly Asp Thr
1 5

<210> 131

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 131

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

<210> 132

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 132

Gln Thr Ile Ile His Ser Asp Gly Asn Thr Tyr
1 5 10

<210> 133

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 133

Ser Tyr Trp Ile Thr
1 5

<210> 134

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 134

Gly Tyr Thr Phe Thr Ser Tyr
1 5

<210> 135

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 135

Pro Gly Gly Gly
1

<210> 136

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 136

Asp Asn Tyr Val Gly Phe Thr
1 5

<210> 137

<211> 12

<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 137

Ser Gln Thr Ile Ile His Ser Asp Gly Asn Thr Tyr
1 5 10

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

<220>
<223> CDR Sequence

<400> 138

Thr Ser Tyr Trp Ile Thr
1 5

<210> 139
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 139

Trp Ile Gly Asp Ile His Pro Gly Gly Gly Asp Thr Asn
1 5 10

<210> 140
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 140

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

<210> 141
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 141

Ile His Ser Asp Gly Asn Thr Tyr Leu Glu Trp Tyr
1 5 10

<210> 142

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

<220>
<223> CDR Sequence

<400> 142

Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
1 5 10

<210> 143
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 143

Asp Ile His Pro Gly Gly Gly Asp Thr Asn
1 5 10

<210> 144
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> 1H2 Heavy chain variable region

<400> 144

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

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

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

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

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

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

Thr Ser Asp Asp Asn Tyr Val Gly Phe Thr Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ala
115

<210> 145
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> 1H2 Light chain variable region

<400> 145

Asp Val Leu 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 Thr Ile Ile His Ser
20 25 30

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

Pro Ile 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 Tyr Cys Phe Gln Gly
85 90 95

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

<210> 146
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 146

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

<210> 147
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 147

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

Gly

<210> 148
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 148

Ser Gly Gly Leu Pro Gly Ala Gly Phe Thr Tyr
1 5 10

<210> 149
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 149

Arg Ser Ser Gln His Ile Val Tyr Ser Asp Gly Asn Thr Tyr Leu Glu
1 5 10 15

<210> 150
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 150

Gly Tyr Thr Phe Ser Asn Tyr Trp
1 5

<210> 151
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 151

Ile Tyr Pro Gly Gly Phe Tyr Asp Asn
1 5

<210> 152
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 152

Ala Arg Ser Gly Gly Leu Pro Gly Ala Gly Phe Thr Tyr
1 5 10

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

<220>
<223> CDR Sequence

<400> 153

Gln His Ile Val Tyr Ser Asp Gly Asn Thr Tyr
1 5 10

<210> 154
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 154

Asn Tyr Trp Ile Gly
1 5

<210> 155
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 155

Gly Tyr Thr Phe Ser Asn Tyr
1 5

<210> 156
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 156

Pro Gly Gly Phe
1

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

<220>
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<400> 157

Gly Gly Leu Pro Gly Ala Gly Phe Thr

1 5

<210> 158
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 158

Ser Gln His Ile Val Tyr Ser Asp Gly Asn Thr Tyr
1 5 10

<210> 159
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 159

Ser Asn Tyr Trp Ile Gly
1 5

<210> 160
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 160

Trp Ile Gly Asp Ile Tyr Pro Gly Gly Phe Tyr Asp Asn
1 5 10

<210> 161
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 161

Ala Arg Ser Gly Gly Leu Pro Gly Ala Gly Phe Thr
1 5 10

<210> 162
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 162

Val Tyr Ser Asp Gly Asn Thr Tyr Leu Glu Trp Tyr
1 5 10

<210> 163
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 163

Asp Ile Tyr Pro Gly Gly Phe Tyr Asp Asn
1 5 10

<210> 164
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> 4F8 Heavy chain variable region

<400> 164

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

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

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

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

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

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

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

Gly Thr Leu Val Thr Val Ser Ala
115 120

<210> 165
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> 4F8 Light chain variable region

<400> 165

Asp Val Leu 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 His Ile Val Tyr Ser
20 25 30

Asp Gly Asn Thr Tyr Leu Glu 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 Glu Ile
65 70 75 80

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

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

<210> 166
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 166

Gly Tyr Thr Phe Thr Asn Tyr Trp Leu Gly
1 5 10

<210> 167
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 167

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

Gly

<210> 168
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 168

Ser Asp Asp Gly Tyr Ser
1 5

<210> 169

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 169

Arg Ser Ser Gln Ser Ile Val Asp Ser Tyr Gly Asn Thr Tyr Leu Glu
1 5 10 15

<210> 170

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 170

Lys Val Ser Asn Arg Phe Ala
1 5

<210> 171

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 171

Phe Gln Gly Ser His Ile Pro Trp Thr
1 5

<210> 172

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 172

Gly Tyr Thr Phe Thr Asn Tyr Trp
1 5

<210> 173

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 173

Ile Tyr Pro Gly Gly Asp Tyr Asn
1 5

<210> 174

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 174

Ala Arg Ser Asp Asp Gly Tyr Ser
1 5

<210> 175

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 175

Gln Ser Ile Val Asp Ser Tyr Gly Asn Thr Tyr
1 5 10

<210> 176

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 176

Asn Tyr Trp Leu Gly
1 5

<210> 177

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 177

Gly Tyr Thr Phe Thr Asn Tyr
1 5

<210> 178

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 178

Pro Gly Gly Asp
1

<210> 179

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 179

Asp Asp Gly Tyr
1

<210> 180

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 180

Ser Gln Ser Ile Val Asp Ser Tyr Gly Asn Thr Tyr
1 5 10

<210> 181

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 181

Gly Ser His Ile Pro Trp
1 5

<210> 182

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 182

Thr Asn Tyr Trp Leu Gly
1 5

<210> 183

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 183

Trp Ile Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Asn Asn
1 5 10

<210> 184

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 184

Ala Arg Ser Asp Asp Gly Tyr
1 5

<210> 185

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 185

Val Asp Ser Tyr Gly Asn Thr Tyr Leu Glu Trp Tyr
1 5 10

<210> 186

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 186

Phe Gln Gly Ser His Ile Pro Trp
1 5

<210> 187

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 187

Asp Ile Tyr Pro Gly Gly Asp Tyr Asn Asn
1 5 10

<210> 188

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> 13G9 Heavy chain variable region

<400> 188

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

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

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

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

Lys Gly Lys Ala Thr Leu Thr Ala 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

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

Val Ser Ser
115

<210> 189

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> 13G9 Light chain variable region

<400> 189

Asp Val Leu 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 Ile Val Asp Ser
20 25 30

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

Pro Thr Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ala 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 Tyr Cys Phe Gln Gly

85

90

95

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

<210> 190
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 190

Gly Tyr Thr Phe Thr Asn Tyr Trp Ile Gly
1 5 10

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

<220>
<223> CDR Sequence

<400> 191

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

Gly

<210> 192
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 192

Ile Trp Asp Arg Gly Phe Asp Tyr
1 5

<210> 193
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 193

Phe Gln Gly Ser His Val Pro Tyr Thr
1 5

<210> 194
<211> 8

<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 194

Ile Phe Pro Gly Gly Phe Tyr Ser
1 5

<210> 195
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 195

Ala Arg Ile Trp Asp Arg Gly Phe Asp Tyr
1 5 10

<210> 196
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 196

Trp Asp Arg Gly Phe Asp
1 5

<210> 197
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 197

Gly Ser His Val Pro Tyr
1 5

<210> 198
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 198

Thr Asn Tyr Trp Ile Gly
1 5

<210> 199

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

<220>
<223> CDR Sequence

<400> 199

Trp Ile Gly Asp Ile Phe Pro Gly Gly Phe Tyr Ser Asn
1 5 10

<210> 200
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 200

Ala Arg Ile Trp Asp Arg Gly Phe Asp
1 5

<210> 201
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 201

Phe Gln Gly Ser His Val Pro Tyr
1 5

<210> 202
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 202

Asp Ile Phe Pro Gly Gly Phe Tyr Ser Asn
1 5 10

<210> 203
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 14F4 Heavy chain variable region

<400> 203

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

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

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

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

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

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

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

Leu Thr Val Ser Ser
 115

<210> 204
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 14F4 Light chain variable region

<400> 204

Asp Val Leu Met Thr Gln Ser 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 Ile Val Asp Ser
 20 25 30

Tyr Gly Asn Thr Tyr Leu Glu 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 Arg Gly Leu Tyr Tyr Cys Phe Gln Gly
 85 90 95

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

<210> 205
 <211> 17
 <212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 205

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

Asp

<210> 206

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 206

Tyr Asp Glu Phe Ala Tyr
1 5

<210> 207

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 207

Arg Ser Ser Gln Ser Ile Val His Ser Asp Gly Asn Thr Tyr Leu Glu
1 5 10 15

<210> 208

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 208

Ile Ser Pro Gly Asn Tyr Tyr Thr
1 5

<210> 209

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Sequence

<400> 209

Ala Arg Tyr Asp Glu Phe Ala Tyr
1 5

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

<220>
<223> CDR Sequence

<400> 210

Gln Ser Ile Val His Ser Asp Gly Asn Thr Tyr
1 5 10

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

<220>
<223> CDR Sequence

<400> 211

Pro Gly Asn Tyr
1

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

<220>
<223> CDR Sequence

<400> 212

Asp Glu Phe Ala
1

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

<220>
<223> CDR Sequence

<400> 213

Ser Gln Ser Ile Val His Ser Asp Gly Asn Thr Tyr
1 5 10

<210> 214
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 214

Trp Ile Gly Asp Ile Ser Pro Gly Asn Tyr Tyr Thr Asn

1 5 10

<210> 215
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 215

Ala Arg Tyr Asp Glu Phe Ala
1 5

<210> 216
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 216

Val His Ser Asp Gly Asn Thr Tyr Leu Glu Trp Tyr
1 5 10

<210> 217
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR Sequence

<400> 217

Asp Ile Ser Pro Gly Asn Tyr Tyr Thr Asn
1 5 10

<210> 218
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> 14E9 Heavy chain variable region

<400> 218

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

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

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

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

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

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

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

Val Ser Ala
115

<210> 219
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> 14E9 Light chain variable region

<400> 219

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

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

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

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

<210> 220
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> H26B5 Heavy chain variable region

<400> 220

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

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

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

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

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

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

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

Val Thr Val Ser Ser
115

<210> 221
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> H26B5 Light chain variable region

<400> 221

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val Asp Ser
20 25 30

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

Pro Arg Leu Leu Ile Tyr Lys Val Ser Asn Arg Leu 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 Val Gly Val Tyr Tyr Cys Phe Gln Gly
85 90 95

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

<210> 222
<211> 477

<212> PRT

<213> Homo sapiens

<220>

<223> Human CGCR with predicted signal sequence

<400> 222

Met Pro Pro Cys Gln Pro Gln Arg Pro Leu Leu Leu Leu Leu Leu Leu
1 5 10 15

Leu Ala Cys Gln Pro Gln Val Pro Ser Ala Gln Val Met Asp Phe Leu
20 25 30

Phe Glu Lys Trp Lys Leu Tyr Gly Asp Gln Cys His His Asn Leu Ser
35 40 45

Leu Leu Pro Pro Pro Thr Glu Leu Val Cys Asn Arg Thr Phe Asp Lys
50 55 60

Tyr Ser Cys Trp Pro Asp Thr Pro Ala Asn Thr Thr Ala Asn Ile Ser
65 70 75 80

Cys Pro Trp Tyr Leu Pro Trp His His Lys Val Gln His Arg Phe Val
85 90 95

Phe Lys Arg Cys Gly Pro Asp Gly Gln Trp Val Arg Gly Pro Arg Gly
100 105 110

Gln Pro Trp Arg Asp Ala Ser Gln Cys Gln Met Asp Gly Glu Glu Ile
115 120 125

Glu Val Gln Lys Glu Val Ala Lys Met Tyr Ser Ser Phe Gln Val Met
130 135 140

Tyr Thr Val Gly Tyr Ser Leu Ser Leu Gly Ala Leu Leu Leu Ala Leu
145 150 155 160

Ala Ile Leu Gly Gly Leu Ser Lys Leu His Cys Thr Arg Asn Ala Ile
165 170 175

His Ala Asn Leu Phe Ala Ser Phe Val Leu Lys Ala Ser Ser Val Leu
180 185 190

Val Ile Asp Gly Leu Leu Arg Thr Arg Tyr Ser Gln Lys Ile Gly Asp
195 200 205

Asp Leu Ser Val Ser Thr Trp Leu Ser Asp Gly Ala Val Ala Gly Cys
210 215 220

Arg Val Ala Ala Val Phe Met Gln Tyr Gly Ile Val Ala Asn Tyr Cys
225 230 235 240

Trp Leu Leu Val Glu Gly Leu Tyr Leu His Asn Leu Leu Gly Leu Ala

245

250

255

Thr Leu Pro Glu Arg Ser Phe Phe Ser Leu Tyr Leu Gly Ile Gly Trp
 260 265 270

Gly Ala Pro Met Leu Phe Val Val Pro Trp Ala Val Val Lys Cys Leu
 275 280 285

Phe Glu Asn Val Gln Cys Trp Thr Ser Asn Asp Asn Met Gly Phe Trp
 290 295 300

Trp Ile Leu Arg Phe Pro Val Phe Leu Ala Ile Leu Ile Asn Phe Phe
 305 310 315 320

Ile Phe Val Arg Ile Val Gln Leu Leu Val Ala Lys Leu Arg Ala Arg
 325 330 335

Gln Met His His Thr Asp Tyr Lys Phe Arg Leu Ala Lys Ser Thr Leu
 340 345 350

Thr Leu Ile Pro Leu Leu Gly Val His Glu Val Val Phe Ala Phe Val
 355 360 365

Thr Asp Glu His Ala Gln Gly Thr Leu Arg Ser Ala Lys Leu Phe Phe
 370 375 380

Asp Leu Phe Leu Ser Ser Phe Gln Gly Leu Leu Val Ala Val Leu Tyr
 385 390 395 400

Cys Phe Leu Asn Lys Glu Val Gln Ser Glu Leu Arg Arg Arg Trp His
 405 410 415

Arg Trp Arg Leu Gly Lys Val Leu Trp Glu Glu Arg Asn Thr Ser Asn
 420 425 430

His Arg Ala Ser Ser Ser Pro Gly His Gly Pro Pro Ser Lys Glu Leu
 435 440 445

Gln Phe Gly Arg Gly Gly Gly Ser Gln Asp Ser Ser Ala Glu Thr Pro
 450 455 460

Leu Ala Gly Gly Leu Pro Arg Leu Ala Glu Ser Pro Phe
 465 470 475

<210> 223

<211> 452

<212> PRT

<213> Homo sapiens

<220>

<223> Human CGCR without predicted signal sequence

<400> 223

Ala Gln Val Met Asp Phe Leu Phe Glu Lys Trp Lys Leu Tyr Gly Asp
 1 5 10 15

Gln Cys His His Asn Leu Ser Leu Leu Pro Pro Pro Thr Glu Leu Val
 20 25 30

Cys Asn Arg Thr Phe Asp Lys Tyr Ser Cys Trp Pro Asp Thr Pro Ala
 35 40 45

Asn Thr Thr Ala Asn Ile Ser Cys Pro Trp Tyr Leu Pro Trp His His
 50 55 60

Lys Val Gln His Arg Phe Val Phe Lys Arg Cys Gly Pro Asp Gly Gln
 65 70 75 80

Trp Val Arg Gly Pro Arg Gly Gln Pro Trp Arg Asp Ala Ser Gln Cys
 85 90 95

Gln Met Asp Gly Glu Glu Ile Glu Val Gln Lys Glu Val Ala Lys Met
 100 105 110

Tyr Ser Ser Phe Gln Val Met Tyr Thr Val Gly Tyr Ser Leu Ser Leu
 115 120 125

Gly Ala Leu Leu Leu Ala Leu Ala Ile Leu Gly Gly Leu Ser Lys Leu
 130 135 140

His Cys Thr Arg Asn Ala Ile His Ala Asn Leu Phe Ala Ser Phe Val
 145 150 155 160

Leu Lys Ala Ser Ser Val Leu Val Ile Asp Gly Leu Leu Arg Thr Arg
 165 170 175

Tyr Ser Gln Lys Ile Gly Asp Asp Leu Ser Val Ser Thr Trp Leu Ser
 180 185 190

Asp Gly Ala Val Ala Gly Cys Arg Val Ala Ala Val Phe Met Gln Tyr
 195 200 205

Gly Ile Val Ala Asn Tyr Cys Trp Leu Leu Val Glu Gly Leu Tyr Leu
 210 215 220

His Asn Leu Leu Gly Leu Ala Thr Leu Pro Glu Arg Ser Phe Phe Ser
 225 230 235 240

Leu Tyr Leu Gly Ile Gly Trp Gly Ala Pro Met Leu Phe Val Val Pro
 245 250 255

Trp Ala Val Val Lys Cys Leu Phe Glu Asn Val Gln Cys Trp Thr Ser
 260 265 270

Asn Asp Asn Met Gly Phe Trp Trp Ile Leu Arg Phe Pro Val Phe Leu

275

280

285

Ala Ile Leu Ile Asn Phe Phe Ile Phe Val Arg Ile Val Gln Leu Leu
290 295 300

Val Ala Lys Leu Arg Ala Arg Gln Met His His Thr Asp Tyr Lys Phe
305 310 315 320

Arg Leu Ala Lys Ser Thr Leu Thr Leu Ile Pro Leu Leu Gly Val His
325 330 335

Glu Val Val Phe Ala Phe Val Thr Asp Glu His Ala Gln Gly Thr Leu
340 345 350

Arg Ser Ala Lys Leu Phe Phe Asp Leu Phe Leu Ser Ser Phe Gln Gly
355 360 365

Leu Leu Val Ala Val Leu Tyr Cys Phe Leu Asn Lys Glu Val Gln Ser
370 375 380

Glu Leu Arg Arg Arg Trp His Arg Trp Arg Leu Gly Lys Val Leu Trp
385 390 395 400

Glu Glu Arg Asn Thr Ser Asn His Arg Ala Ser Ser Ser Pro Gly His
405 410 415

Gly Pro Pro Ser Lys Glu Leu Gln Phe Gly Arg Gly Gly Gly Ser Gln
420 425 430

Asp Ser Ser Ala Glu Thr Pro Leu Ala Gly Gly Leu Pro Arg Leu Ala
435 440 445

Glu Ser Pro Phe
450

<210> 224
<211> 111
<212> PRT
<213> Homo sapiens

<220>
<223> Human CGCR extracellular domain (amino acids 26-136)

<400> 224

Ala Gln Val Met Asp Phe Leu Phe Glu Lys Trp Lys Leu Tyr Gly Asp
1 5 10 15

Gln Cys His His Asn Leu Ser Leu Leu Pro Pro Pro Thr Glu Leu Val
20 25 30

Cys Asn Arg Thr Phe Asp Lys Tyr Ser Cys Trp Pro Asp Thr Pro Ala
35 40 45

Asn Thr Thr Ala Asn Ile Ser Cys Pro Trp Tyr Leu Pro Trp His His
 50 55 60

Lys Val Gln His Arg Phe Val Phe Lys Arg Cys Gly Pro Asp Gly Gln
 65 70 75 80

Trp Val Arg Gly Pro Arg Gly Gln Pro Trp Arg Asp Ala Ser Gln Cys
 85 90 95

Gln Met Asp Gly Glu Glu Ile Glu Val Gln Lys Glu Val Ala Lys
 100 105 110

<210> 225

<211> 96

<212> PRT

<213> Homo sapiens

<220>

<223> Human CGCR extracellular domain (amino acids 28-123)

<400> 225

Val Met Asp Phe Leu Phe Glu Lys Trp Lys Leu Tyr Gly Asp Gln Cys
 1 5 10 15

His His Asn Leu Ser Leu Leu Pro Pro Pro Thr Glu Leu Val Cys Asn
 20 25 30

Arg Thr Phe Asp Lys Tyr Ser Cys Trp Pro Asp Thr Pro Ala Asn Thr
 35 40 45

Thr Ala Asn Ile Ser Cys Pro Trp Tyr Leu Pro Trp His His Lys Val
 50 55 60

Gln His Arg Phe Val Phe Lys Arg Cys Gly Pro Asp Gly Gln Trp Val
 65 70 75 80

Arg Gly Pro Arg Gly Gln Pro Trp Arg Asp Ala Ser Gln Cys Gln Met
 85 90 95

<210> 226

<211> 40

<212> PRT

<213> Homo sapiens

<220>

<223> Human CGCR extracellular domain (amino acids 80-119)

<400> 226

Ser Cys Pro Trp Tyr Leu Pro Trp His His Lys Val Gln His Arg Phe
 1 5 10 15

Val Phe Lys Arg Cys Gly Pro Asp Gly Gln Trp Val Arg Gly Pro Arg
 20 25 30

Gly Gln Pro Trp Arg Asp Ala Ser

35

40

<210> 227

<211> 448

<212> PRT

<213> *Macaca fascicularis*

<220>

<223> GCGR - cynomolgus monkey

<400> 227

Met Pro Pro Cys Gln Pro Arg Arg Pro Leu Leu Leu Leu Leu Leu
1 5 10 15

Leu Ala Cys Gln Pro Gln Ala Pro Ser Ala Gln Val Met Asp Phe Leu
20 25 30

Phe Glu Lys Trp Lys Leu Tyr Gly Asp Gln Cys His His Asn Leu Ser
35 40 45

Leu Leu Pro Pro Pro Thr Glu Leu Val Cys Asn Arg Thr Phe Asp Lys
50 55 60

Tyr Ser Cys Trp Pro Asp Thr Pro Ala Asn Thr Thr Ala Asn Ile Ser
65 70 75 80

Cys Pro Trp Tyr Leu Pro Trp His His Lys Val Gln His Arg Phe Val
85 90 95

Phe Lys Arg Cys Gly Pro Asp Gly Gln Trp Val Arg Gly Pro Arg Gly
100 105 110

Gln Pro Trp Arg Asp Ala Ser Gln Cys Gln Met Asp Gly Glu Glu Leu
115 120 125

Glu Val Gln Lys Glu Val Ala Lys Met Tyr Ser Ser Phe Gln Val Met
130 135 140

Tyr Thr Val Gly Tyr Ser Leu Ser Leu Gly Ala Leu Leu Leu Ala Leu
145 150 155 160

Ala Val Leu Gly Gly Ile Ser Lys Leu His Cys Thr Arg Asn Ala Ile
165 170 175

His Ala Asn Leu Phe Val Ser Phe Val Leu Lys Ala Ser Ser Val Leu
180 185 190

Val Ile Asp Gly Leu Leu Arg Thr Arg Tyr Ser Gln Lys Ile Gly Asp
195 200 205

Asp Leu Ser Val Ser Ile Trp Leu Ser Asp Gly Ala Val Ala Gly Cys
210 215 220

Arg Val Ala Ala Val Phe Met Gln Tyr Gly Val Val Ala Asn Tyr Cys
225 230 235 240

Trp Leu Leu Val Glu Gly Leu Tyr Leu His Asn Leu Leu Gly Leu Ala
245 250 255

Thr Leu Pro Glu Arg Ser Phe Phe Ser Leu Tyr Leu Gly Ile Gly Trp
260 265 270

Gly Ala Pro Met Leu Phe Ile Ile Pro Trp Val Val Val Arg Cys Leu
275 280 285

Phe Glu Asn Ile Gln Cys Trp Thr Ser Asn Asp Asn Met Gly Phe Trp
290 295 300

Trp Ile Leu Arg Phe Pro Val Phe Leu Ala Ile Leu Ile Asn Phe Phe
305 310 315 320

Ile Phe Ile Arg Ile Val His Leu Leu Val Ala Lys Leu Arg Ala Arg
325 330 335

Glu Met His His Thr Asp Tyr Lys Phe Arg Ser Phe Gln Gly Leu Leu
340 345 350

Val Ala Val Leu Tyr Cys Phe Leu Asn Lys Glu Val Gln Ser Glu Leu
355 360 365

Arg Arg His Trp His Arg Trp Arg Leu Gly Lys Val Leu Gln Glu Glu
370 375 380

Arg Gly Thr Ser Asn His Lys Ala Pro Ser Ala Pro Gly Gln Gly Leu
385 390 395 400

Pro Gly Lys Lys Leu Gln Ser Gly Arg Asp Gly Gly Ser Gln Asp Ser
405 410 415

Ser Ala Glu Ile Pro Leu Ala Gly Gly Leu Pro Arg Leu Ala Glu Ser
420 425 430

Pro Phe Ser Thr Leu Leu Gly Pro Gln Leu Gly Leu Asp Ser Gly Thr
435 440 445

<210> 228
<211> 485
<212> PRT
<213> Mus musculus

<220>
<223> GCGR - mouse

<400> 228

Met Pro Leu Thr Gln Leu His Cys Pro His Leu Leu Leu Leu Leu
1 5 10 15

Val Leu Ser Cys Leu Pro Glu Ala Pro Ser Ala Gln Val Met Asp Phe
20 25 30

Leu Phe Glu Lys Trp Lys Leu Tyr Ser Asp Gln Cys His His Asn Leu
35 40 45

Ser Leu Leu Pro Pro Pro Thr Glu Leu Val Cys Asn Arg Thr Phe Asp
50 55 60

Asn Tyr Ser Cys Trp Pro Asp Thr Pro Pro Asn Thr Thr Ala Asn Ile
65 70 75 80

Ser Cys Pro Trp Tyr Leu Pro Trp Cys His Lys Val Gln His Arg Leu
85 90 95

Val Phe Lys Arg Cys Gly Pro Asp Gly Gln Trp Val Arg Gly Pro Arg
100 105 110

Gly Gln Pro Trp Arg Asn Ala Ser Gln Cys Gln Leu Asp Asp Glu Glu
115 120 125

Ile Glu Val Gln Lys Gly Val Ala Lys Met Tyr Ser Ser Gln Gln Val
130 135 140

Met Tyr Thr Val Gly Tyr Ser Leu Ser Leu Gly Ala Leu Leu Leu Ala
145 150 155 160

Leu Val Ile Leu Leu Gly Leu Arg Lys Leu His Cys Thr Arg Asn Tyr
165 170 175

Ile His Gly Asn Leu Phe Ala Ser Phe Val Leu Lys Ala Gly Ser Val
180 185 190

Leu Val Ile Asp Trp Leu Leu Lys Thr Arg Tyr Ser Gln Lys Ile Gly
195 200 205

Asp Asp Leu Ser Val Ser Val Trp Leu Ser Asp Gly Ala Met Ala Gly
210 215 220

Cys Arg Val Ala Thr Val Ile Met Gln Tyr Gly Ile Ile Pro Asn Tyr
225 230 235 240

Cys Trp Leu Leu Val Glu Gly Val Tyr Leu Tyr Ser Leu Leu Ser Leu
245 250 255

Ala Thr Phe Ser Glu Arg Ser Phe Phe Ser Leu Tyr Leu Gly Ile Gly
260 265 270

Trp Gly Ala Pro Leu Leu Phe Val Ile Pro Trp Val Val Val Lys Cys
275 280 285

Leu Phe Glu Asn Val Gln Cys Trp Thr Ser Asn Asp Asn Met Gly Phe
 290 295 300

Trp Trp Ile Leu Arg Ile Pro Val Phe Leu Ala Leu Leu Ile Asn Phe
 305 310 315 320

Phe Ile Phe Val His Ile Ile Gln Leu Leu Val Ala Lys Leu Arg Ala
 325 330 335

His Gln Met His Tyr Ala Asp Tyr Lys Phe Arg Leu Ala Arg Ser Thr
 340 345 350

Leu Thr Leu Ile Pro Leu Leu Gly Val His Glu Val Val Phe Ala Phe
 355 360 365

Val Thr Asp Glu His Ala Gln Gly Thr Leu Arg Ser Thr Lys Leu Phe
 370 375 380

Phe Asp Leu Phe Leu Ser Ser Phe Gln Gly Leu Leu Val Ala Val Leu
 385 390 395 400

Tyr Cys Phe Leu Asn Lys Glu Val Gln Ala Glu Leu Met Arg Arg Trp
 405 410 415

Arg Gln Trp Gln Glu Gly Lys Ala Leu Gln Glu Glu Arg Leu Ala Ser
 420 425 430

Ser His Gly Ser His Met Ala Pro Ala Gly Pro Cys His Gly Asp Pro
 435 440 445

Cys Glu Lys Leu Gln Leu Met Ser Ala Gly Ser Ser Ser Gly Thr Gly
 450 455 460

Cys Val Pro Ser Met Glu Thr Ser Leu Ala Ser Ser Leu Pro Arg Leu
 465 470 475 480

Ala Asp Ser Pro Thr
 485

<210> 229
 <211> 485
 <212> PRT
 <213> Rattus norvegicus

<220>
 <223> GCGR - rat

<400> 229

Met Leu Leu Thr Gln Leu His Cys Pro Tyr Leu Leu Leu Leu Val
 1 5 10 15

Val Leu Ser Cys Leu Pro Lys Ala Pro Ser Ala Gln Val Met Asp Phe
 20 25 30

Leu Phe Glu Lys Trp Lys Leu Tyr Ser Asp Gln Cys His His Asn Leu
 35 40 45

Ser Leu Leu Pro Pro Pro Thr Glu Leu Val Cys Asn Arg Thr Phe Asp
 50 55 60

Lys Tyr Ser Cys Trp Pro Asp Thr Pro Pro Asn Thr Thr Ala Asn Ile
 65 70 75 80

Ser Cys Pro Trp Tyr Leu Pro Trp Tyr His Lys Val Gln His Arg Leu
 85 90 95

Val Phe Lys Arg Cys Gly Pro Asp Gly Gln Trp Val Arg Gly Pro Arg
 100 105 110

Gly Gln Ser Trp Arg Asp Ala Ser Gln Cys Gln Met Asp Asp Asp Glu
 115 120 125

Ile Glu Val Gln Lys Gly Val Ala Lys Met Tyr Ser Ser Tyr Gln Val
 130 135 140

Met Tyr Thr Val Gly Tyr Ser Leu Ser Leu Gly Ala Leu Leu Leu Ala
 145 150 155 160

Leu Val Ile Leu Leu Gly Leu Arg Lys Leu His Cys Thr Arg Asn Tyr
 165 170 175

Ile His Gly Asn Leu Phe Ala Ser Phe Val Leu Lys Ala Gly Ser Val
 180 185 190

Leu Val Ile Asp Trp Leu Leu Lys Thr Arg Tyr Ser Gln Lys Ile Gly
 195 200 205

Asp Asp Leu Ser Val Ser Val Trp Leu Ser Asp Gly Ala Val Ala Gly
 210 215 220

Cys Arg Val Ala Thr Val Ile Met Gln Tyr Gly Ile Ile Ala Asn Tyr
 225 230 235 240

Cys Trp Leu Leu Val Glu Gly Val Tyr Leu Tyr Ser Leu Leu Ser Ile
 245 250 255

Thr Thr Phe Ser Glu Lys Ser Phe Phe Ser Leu Tyr Leu Cys Ile Gly
 260 265 270

Trp Gly Ser Pro Leu Leu Phe Val Ile Pro Trp Val Val Val Lys Cys
 275 280 285

Leu Phe Glu Asn Val Gln Cys Trp Thr Ser Asn Asp Asn Met Gly Phe
 290 295 300

Trp Trp Ile Leu Arg Ile Pro Val Leu Leu Ala Ile Leu Ile Asn Phe
 305 310 315 320

Phe Ile Phe Val Arg Ile Ile His Leu Leu Val Ala Lys Leu Arg Ala
 325 330 335

His Gln Met His Tyr Ala Asp Tyr Lys Phe Arg Leu Ala Arg Ser Thr
 340 345 350

Leu Thr Leu Ile Pro Leu Leu Gly Val His Glu Val Val Phe Ala Phe
 355 360 365

Val Thr Asp Glu His Ala Gln Gly Thr Leu Arg Ser Thr Lys Leu Phe
 370 375 380

Phe Asp Leu Phe Phe Ser Ser Phe Gln Gly Leu Leu Val Ala Val Leu
 385 390 395 400

Tyr Cys Phe Leu Asn Lys Glu Val Gln Ala Glu Leu Leu Arg Arg Trp
 405 410 415

Arg Arg Trp Gln Glu Gly Lys Ala Leu Gln Glu Glu Arg Met Ala Ser
 420 425 430

Ser His Gly Ser His Met Ala Pro Ala Gly Thr Cys His Gly Asp Pro
 435 440 445

Cys Glu Lys Leu Gln Leu Met Ser Ala Gly Ser Ser Ser Gly Thr Gly
 450 455 460

Cys Glu Pro Ser Ala Lys Thr Ser Leu Ala Ser Ser Leu Pro Arg Leu
 465 470 475 480

Ala Asp Ser Pro Thr
 485

<210> 230
 <211> 330
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Human IgG1

<400> 230

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

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

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

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

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
225 230 235 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 231
<211> 330
<212> PRT
<213> Homo sapiens

<220>
<223> Human IgG1 E233A/L235A

<400> 231

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

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

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

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

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

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

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
225 230 235 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 232
<211> 330
<212> PRT
<213> Homo sapiens

<220>
<223> Human IgG1 L234A/L235A

<400> 232

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

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

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 130 135 140

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

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 225 230 235 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 325 330

<210> 233
 <211> 469
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Hz6B5 Heavy Chain with signal sequence

<400> 233

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp
 1 5 10 15

Leu Arg Gly Ala Arg Cys Gln Val Gln Leu Val Gln Ser Gly Ala Glu

20

25

30

Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly
35 40 45

Phe Thr Phe Thr Asn His Trp Leu Gly Trp Val Arg Gln Ala Pro Gly
50 55 60

Gln Gly Leu Glu Trp Ile Gly Asp Ile Tyr Pro Gly Gly Tyr Tyr Ile
65 70 75 80

Asn Tyr Asn Glu Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Glu
85 90 95

Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp
100 105 110

Thr Ala Val Tyr Tyr Cys Ala Arg His Thr Asn Tyr Gly Ser Asp Tyr
115 120 125

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
130 135 140

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
145 150 155 160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
165 170 175

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
180 185 190

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
195 200 205

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
210 215 220

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
225 230 235 240

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Ala Leu
245 250 255

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
260 265 270

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
275 280 285

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
290 295 300

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
 305 310 315 320

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 325 330 335

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
 340 345 350

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 355 360 365

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
 370 375 380

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 385 390 395 400

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 405 410 415

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 420 425 430

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 435 440 445

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 450 455 460

Leu Ser Pro Gly Lys
 465

<210> 234

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Hz6B5 Heavy Chain without signal sequence

<400> 234

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

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

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

Gly Asp Ile Tyr Pro Gly Gly Tyr Tyr Ile Asn Tyr Asn Glu Lys Phe

50

55

60

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

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

Ala Arg His Thr Asn Tyr Gly Ser Asp Tyr Trp Gly Gln Gly Thr Thr
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 Ala Leu Ala 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> 235

<211> 241

<212> PRT

<213> Artificial Sequence

<220>

<223> Hz6B5 Light chain with signal sequence

<400> 235

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Arg Gly Ala Arg Cys Asp Val Val Met Thr Gln Ser Pro Leu Ser
20 25 30

Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser
35 40 45

Gln Ser Ile Val Asp Ser Tyr Gly Asn Thr Phe Leu Glu Trp Tyr Gln
50 55 60

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

Arg Leu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
85 90 95

Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val
100 105 110

Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Trp Thr Phe Gly Gln Gly

115

120

125

Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile
 130 135 140

Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
 145 150 155 160

Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
 165 170 175

Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
 180 185 190

Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu
 195 200 205

Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
 210 215 220

His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
 225 230 235 240

Cys

<210> 236

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> H26B5 Light chain without signal sequence

<400> 236

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val Asp Ser
 20 25 30

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

Pro Arg Leu Leu Ile Tyr Lys Val Ser Asn Arg Leu 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 Val Gly Val Tyr Tyr Cys Phe Gln Gly
 85 90 95

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

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

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

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

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

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

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

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

<210> 237

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain CDR2 consensus sequence

<220>

<221> misc_feature

<222> (3)..(3)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature

<222> (7)..(7)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature

<222> (9)..(9)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature

<222> (13)..(13)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature

<222> (17)..(17)

<223> Xaa can be any naturally occurring amino acid

<400> 237

Asp Ile Xaa Pro Gly Gly Xaa Tyr Xaa Asn Tyr Asn Xaa Lys His Lys

1 5 10 15

Xaa

<210> 238
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain CDR1 consensus sequence

<220>
<221> misc_feature
<222> (5)..(5)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (8)..(8)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (10)..(10)
<223> Xaa can be any naturally occurring amino acid

<400> 238

Arg Ser Ser Gln Xaa Ile Val Xaa Ser Xaa Gly Asn Thr Tyr Leu Glu
1 5 10 15