SEQUENCE LISTING

<110> The President and Fellows of Harvard College
UCB Biopharma SPRL

<120> ANTI-AP2 ANTIBODIES AND ANTIGEN BINDING AGENTS TO TREAT METABOLIC DISORDERS

<130> 15020-001US1

<150> US 62/155,217
<151> 2015-04-30

<150> US 62/232,148
<151> 2015-09-24

<150> US 62/268,257
<151> 2015-12-16

<160> 602

<170> PatentIn version 3.5

<210> 1
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Phe Asp Asp Tyr Met Lys Glu Val Gly Val Gly Phe Ala Thr Arg Lys
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Val Ala Gly Met Ala Lys Pro Asn Met Ile Ile Ser Val Asn Gly Asp
35 40 45

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

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

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

Lys Trp Asp Gly Lys Ser Thr Thr Ile Lys Arg Lys Arg Asp Gly Asp
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Lys Leu Val Val Glu Cys Val Met Lys Gly Val Thr Ser Thr Arg Val
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Tyr Glu Arg Ala
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Arg Val Tyr
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Lys Ala Ser Thr Leu Ala Ser
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Gln Cys Thr Tyr Gly Thr Tyr Ala Gly Ser Phe Phe Tyr Ser
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Gln Ala Thr Tyr Gly Thr Tyr Ala Gly Ser Phe Phe Tyr Ser
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Gln Gln Ala Ser His Tyr Pro Leu Thr
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Gly Phe Ser Leu Ser Thr Tyr Tyr Met Ser
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Gly Tyr Thr Phe Thr Ser Asn Ala Ile Thr
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Ile Ile Tyr Pro Ser Gly Ser Thr Tyr Cys Ala Ser Trp Ala Lys Gly
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Ile Ile Tyr Pro Ser Gly Ser Thr Tyr Ser Ala Ser Trp Ala Lys Gly
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Asp Ile Ser Pro Gly Ser Gly Ser Thr Thr Asn Asn Glu Lys Phe Lys
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Pro Asp Asn Glu Gly Thr Ser Gly Tyr Leu Ser Gly Phe Gly Leu
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Trp Lys Leu Val Ser Ser Glu Asn Phe
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Tyr Met Lys Glu Val Gly Val Gly Phe
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Cys Val Met Lys Gly Val Thr Ser Thr Arg Val Tyr Glu Arg Ala
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<223> O12 FR1

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Asp Arg Val Thr Ile Thr Cys
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<400> 26

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

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

20 25 30

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Asp Arg Val Thr Ile Thr Cys
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Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
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Asp Arg Val Thr Ile Thr Cys
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Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
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Asp Arg Val Thr Ile Thr Cys
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Trp Tyr Gln Gln Lys Pro Ala Lys Ala Pro Lys Leu Phe Ile Tyr
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Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
20 25 30

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Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
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Asp Arg Val Thr Ile Thr Cys
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<210> 77
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Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
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Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
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Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
20 25 30

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Asp Arg Val Thr Ile Thr Cys
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20 25 30

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Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Pro Gly
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Glu Pro Ala Ser Ile Ser Cys
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Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr
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Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Pro Gly
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Glu Pro Ala Ser Ile Ser Cys
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Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr
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Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
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Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys
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<223> A17 FR1

<400> 88

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
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<210> 89

<211> 15
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<220>
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<400> 89

Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
1 5 10 15

<210> 90
<211> 32
<212> PRT
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<220>
<223> A17 FR3

<400> 90

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys
20 25 30

<210> 91
<211> 23
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<400> 91

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
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<210> 92
<211> 15
<212> PRT
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<220>
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<400> 92

Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
1 5 10 15

<210> 93
<211> 32
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<220>
<223> A1 FR3

<400> 93

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys
20 25 30

<210> 94
<211> 23
<212> PRT
<213> Artificial Sequence

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<400> 94

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

Gln Pro Ala Ser Ile Ser Cys

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<210> 95
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<212> PRT
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<220>
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<400> 95

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr
1 5 10 15

<210> 96
<211> 32
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<220>
<223> A18 FR3

<400> 96

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys
20 25 30

<210> 97
<211> 23
<212> PRT
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<220>
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<400> 97

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

Gln Pro Ala Ser Ile Ser Cys
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<210> 98
<211> 15
<212> PRT
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<220>
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<400> 98

Trp Tyr Leu Gln Lys Pro Gly Gln Pro Pro Gln Leu Leu Ile Tyr
1 5 10 15

<210> 99
<211> 32
<212> PRT
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<220>
<223> A2 FR3

<400> 99

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys
20 25 30

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<400> 100

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

1 5 10 15

Glu Pro Ala Ser Ile Ser Cys
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<210> 101
<211> 15
<212> PRT
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<220>
<223> A19 FR2

<400> 101

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr
1 5 10 15

<210> 102
<211> 32
<212> PRT
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<220>
<223> A19 FR3

<400> 102

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys
20 25 30

<210> 103
<211> 23
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<220>
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<400> 103

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

Glu Pro Ala Ser Ile Ser Cys
20

<210> 104
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<220>
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<400> 104

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr
1 5 10 15

<210> 105
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> A3 FR3

<400> 105

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys
20 25 30

<210> 106
<211> 23
<212> PRT
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<220>
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<400> 106

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

Gln Pro Ala Ser Ile Ser Cys
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<210> 107
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> A23 FR2

<400> 107

Trp Leu Gln Gln Arg Pro Gly Gln Pro Pro Arg Leu Leu Ile Tyr
1 5 10 15

<210> 108
<211> 32
<212> PRT
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<220>
<223> A23 FR3

<400> 108

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

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys
20 25 30

<210> 109
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> A27 FR1

<400> 109

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

Glu Arg Ala Thr Leu Ser Cys
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<210> 110
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> A27 FR2

<400> 110

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
1 5 10 15

<210> 111
<211> 32
<212> PRT
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<220>
<223> A27 FR3

<400> 111

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
20 25 30

<210> 112
<211> 23
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<220>
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<400> 112

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

Glu Arg Ala Thr Leu Ser Cys
20

<210> 113
<211> 15
<212> PRT
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<220>
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<400> 113

Trp Tyr Gln Gln Lys Pro Gly Leu Ala Pro Arg Leu Leu Ile Tyr
1 5 10 15

<210> 114
<211> 32
<212> PRT
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<220>
<223> A11 FR3

<400> 114

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
20 25 30

<210> 115

<211> 23
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<220>
<223> L2 FR1

<400> 115

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

Glu Arg Ala Thr Leu Ser Cys
20

<210> 116
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> L2 FR2

<400> 116

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
1 5 10 15

<210> 117
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> L2 FR3

<400> 117

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
1 5 10 15

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

<210> 118
<211> 23
<212> PRT
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<220>
<223> L16 FR1

<400> 118

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

Glu Arg Ala Thr Leu Ser Cys
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<210> 119
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> L16 FR2

<400> 119

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
1 5 10 15

<210> 120
<211> 32
<212> PRT
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<223> L16 FR3

<400> 120

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
1 5 10 15

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

20 25 30

<210> 121
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
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<400> 121

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

Glu Arg Ala Thr Leu Ser Cys
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<210> 122
<211> 15
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<213> Artificial Sequence

<220>
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<400> 122

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
1 5 10 15

<210> 123
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> L6 FR3

<400> 123

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
            20   25   30

<210> 124
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> L20 FR1

<400> 124

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

Glu Arg Ala Thr Leu Ser Cys
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<210> 125
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> L20 FR2

<400> 125

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
1   5   10   15

<210> 126
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> L20 FR3

<400> 126

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Pro Gly Thr Asp Phe Thr

1 5 10 15

Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
20 25 30

<210> 127
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> L25 FR1

<400> 127

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
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<210> 128
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> L25 FR2

<400> 128

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
1 5 10 15

<210> 129
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> L25 FR3

<400> 129

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr Tyr Cys
20 25 30

<210> 130
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> B3 FR1

<400> 130

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

Glu Arg Ala Thr Ile Asn Cys
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<210> 131
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> B3 FR2

<400> 131

Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
1 5 10 15

<210> 132
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> B3 FR3

<400> 132

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

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

<210> 133
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> B2 FR1

<400> 133

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

Asp Lys Val Asn Ile Ser Cys
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<210> 134
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> B2 FR2

<400> 134

Trp Tyr Gln Gln Lys Pro Gly Glu Ala Ala Ile Phe Ile Ile Gln
1 5 10 15

<210> 135
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> B2 FR3

<400> 135

Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Asn Asn Ile Glu Ser Glu Asp Ala Ala Tyr Tyr Phe Cys
20 25 30

<210> 136
<211> 23
<212> PRT
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<220>
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<400> 136

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

Glu Lys Val Thr Ile Thr Cys
20

<210> 137
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> A26 FR2

<400> 137

Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile Lys
1 5 10 15

<210> 138
<211> 32
<212> PRT

<213> Artificial Sequence

<220>
<223> A26 FR3

<400> 138

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
20 25 30

<210> 139
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> A10 FR1

<400> 139

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

Glu Lys Val Thr Ile Thr Cys
20

<210> 140
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> A10 FR2

<400> 140

Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile Lys
1 5 10 15

<210> 141

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

<220>
<223> A10 FR3

<400> 141

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Asn Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
20 25 30

<210> 142
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> A14 FR1

<400> 142

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

Glu Lys Val Thr Ile Thr Cys
20

<210> 143
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> A14 FR2

<400> 143

Trp Tyr Gln Gln Lys Pro Asp Gln Ala Pro Lys Leu Leu Ile Lys
1 5 10 15

<210> 144
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> A14 FR3

<400> 144

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Phe Thr Ile Ser Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
20 25 30

<210> 145
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> JK1 FR4

<400> 145

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
1 5 10

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

<220>
<223> JK2 FR4

<400> 146

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
1 5 10

<210> 147

<211> 10
<212> PRT
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<220>
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<400> 147

Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
1 5 10

<210> 148
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> JK4 FR4

<400> 148

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 149
<211> 10
<212> PRT
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<220>
<223> JK5 FR4

<400> 149

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
1 5 10

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

<220>
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<400> 150

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

Arg Val Thr Ile Ser Cys
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<210> 151
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<400> 151

Trp Tyr Gln Gln Leu Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
1 5 10 15

<210> 152
<211> 32
<212> PRT
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<220>
<223> 1a FR3

<400> 152

Gly Val Ser Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser
1 5 10 15

Leu Ala Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys
20 25 30

<210> 153
<211> 22
<212> PRT
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<220>
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<400> 153

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

Arg Val Thr Ile Ser Cys
20

<210> 154
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 1e FR2

<400> 154

Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr
1 5 10 15

<210> 155
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 1e FR3

<400> 155

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

Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
20 25 30

<210> 156
<211> 22
<212> PRT

<213> Artificial Sequence

<220>
<223> 1c FR1

<400> 156

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

Arg Val Thr Ile Ser Cys
20

<210> 157
<211> 15
<212> PRT
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<220>
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<400> 157

Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr
1 5 10 15

<210> 158
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 1c FR3

<400> 158

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

Leu Ala Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys
20 25 30

<210> 159

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

<220>
<223> 1g FR1

<400> 159

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

Arg Val Thr Ile Ser Cys
20

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

<220>
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<400> 160

Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr
1 5 10 15

<210> 161
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
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<400> 161

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

Leu Ala Ile Ser Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Cys
20 25 30

<210> 162
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
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<400> 162

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

Lys Val Thr Ile Ser Cys
20

<210> 163
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 1b FR2

<400> 163

Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr
1 5 10 15

<210> 164
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 1b FR3

<400> 164

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

Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala Asp Tyr Tyr Cys

20 25 30

<210> 165
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
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<400> 165

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

Ser Val Thr Ile Ser Cys
20

<210> 166
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 2c FR2

<400> 166

Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu Met Ile Tyr
1 5 10 15

<210> 167
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 2c FR3

<400> 167

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

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

<210> 168
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> 2e FR1

<400> 168

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

Ser Val Thr Ile Ser Cys
20

<210> 169
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<400> 169

Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu Met Ile Tyr
1 5 10 15

<210> 170
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 2e FR3

<400> 170

Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser

1 5 10 15

Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
20 25 30

<210> 171
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> 2a2 FR1

<400> 171

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

Ser Ile Thr Ile Ser Cys
20

<210> 172
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 2a2 FR2

<400> 172

Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu Met Ile Tyr
1 5 10 15

<210> 173
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 2a2 FR3

<400> 173

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Gly Val Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser
1               5                   10                  15


Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
            20                  25                  30


<210>  174
<211>  22
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  2d FR1

<400>  174

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


Ser Val Thr Ile Ser Cys
            20


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

<220>
<223>  2d FR2

<400>  175

Trp Tyr Gln Gln Pro Pro Gly Thr Ala Pro Lys Leu Met Ile Tyr
1               5                   10                  15


<210>  176
<211>  32
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<213>  Artificial Sequence

<220>
<223>  2d FR3
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<400> 176

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

Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
20 25 30

<210> 177
<211> 22
<212> PRT
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<220>
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<400> 177

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

Ser Ile Thr Ile Ser Cys
20

<210> 178
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 2b2 FR2

<400> 178

Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu Met Ile Tyr
1 5 10 15

<210> 179
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 2b2 FR3

<400> 179

Gly Val Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser
1 5 10 15

Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
20 25 30

<210> 180
<211> 22
<212> PRT
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<220>
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<400> 180

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

Thr Ala Ser Ile Thr Cys
20

<210> 181
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 3r FR2

<400> 181

Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu Val Ile Tyr
1 5 10 15

<210> 182
<211> 32
<212> PRT

<213> Artificial Sequence

<220>
<223> 3r FR3

<400> 182

Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr
1 5 10 15

Leu Thr Ile Ser Gly Thr Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys
20 25 30

<210> 183
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> 3j FR1

<400> 183

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

Thr Ala Arg Ile Thr Cys
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<210> 184
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 3j FR2

<400> 184

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
1 5 10 15

<210> 185

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

<220>
<223> 3j FR3

<400> 185

Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr
1 5 10 15

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

<210> 186
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> 3p FR1

<400> 186

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

Thr Ala Arg Ile Thr Cys
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<210> 187
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 3p FR2

<400> 187

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

<210> 188
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 3p FR3

<400> 188

Gly Ile Pro Glu Arg Phe Ser Gly Ser Ser Ser Gly Thr Met Ala Thr
1 5 10 15

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

<210> 189
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> 3a FR1

<400> 189

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

Met Ala Arg Ile Thr Cys
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<210> 190
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 3a FR2

<400> 190

Trp Tyr Gln Gln Lys Pro Gly Gln Phe Pro Val Leu Val Ile Tyr

1 5 10 15

<210> 191
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 3a FR3

<400> 191

Gly Ile Pro Glu Arg Phe Ser Gly Ser Ser Ser Gly Thr Ile Val Thr
1 5 10 15

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

<210> 192
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> 3l FR1

<400> 192

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

Thr Val Arg Ile Thr Cys
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<210> 193
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 3l FR2

<400> 193

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
1 5 10 15

<210> 194
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 3l FR3

<400> 194

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

Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
20 25 30

<210> 195
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> 3h FR1

<400> 195

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

Thr Ala Arg Ile Thr Cys
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<210> 196
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 3h FR2

<400> 196

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
1 5 10 15

<210> 197
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 3h FR3

<400> 197

Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr
1 5 10 15

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

<210> 198
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> 3e FR1

<400> 198

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

Thr Ala Arg Ile Thr Cys
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<210> 199
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 3e FR2

<400> 199

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

<210> 200
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 3e FR3

<400> 200

Gly Ile Pro Glu Arg Phe Ser Gly Ser Thr Ser Gly Asn Thr Thr Thr
1 5 10 15

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

<210> 201
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> 3m FR1

<400> 201

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

Thr Ala Arg Ile Thr Cys
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<210> 202
<211> 15
<212> PRT

<213> Artificial Sequence

<220>
<223> 3m FR2

<400> 202

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
1 5 10 15

<210> 203
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 3m FR3

<400> 203

Gly Ile Pro Glu Arg Phe Ser Gly Ser Ser Ser Gly Thr Thr Val Thr
1 5 10 15

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

<210> 204
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> 2-19 FR1

<400> 204

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

Thr Ala Arg Ile Thr Cys
20

<210> 205

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

<220>
<223> 2-19 FR2

<400> 205

Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
1 5 10 15

<210> 206
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 2-19 FR3

<400> 206

Gly Ile Pro Glu Arg Phe Ser Gly Ser Ser Ser Gly Thr Thr Val Thr
1 5 10 15

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

<210> 207
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> 4c FR1

<400> 207

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

Ser Ile Lys Leu Thr Cys
20

<210> 208
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 4c FR2

<400> 208

Trp Tyr Gln Gln Arg Pro Gly Arg Ser Pro Gln Tyr Ile Met Lys
1 5 10 15

<210> 209
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 4c FR3

<400> 209

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

Leu Thr Phe Ser Asn Leu Gln Ser Asp Asp Glu Ala Glu Tyr His Cys
20 25 30

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

<220>
<223> 4a FR1

<400> 210

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

Ser Val Lys Leu Thr Cys

20

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

<220>
<223> 4a FR2

<400> 211

Trp His Gln Gln Gln Pro Gly Lys Ala Pro Arg Tyr Leu Met Lys
1 5 10 15

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

<220>
<223> 4a FR3

<400> 212

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

Leu Thr Ile Ser Asn Leu Gln Leu Glu Asp Glu Ala Asp Tyr Tyr Cys
20 25 30

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

<220>
<223> 4b FR1

<400> 213

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

Ser Val Lys Leu Thr Cys
            20

<210> 214
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 4b FR2

<400> 214

Trp His Gln Gln Gln Pro Glu Lys Gly Pro Arg Tyr Leu Met Lys
1   5   10   15

<210> 215
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 4b FR3

<400> 215

Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Ala Glu Arg Tyr
1   5   10   15

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

<210> 216
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> 5e FR1

<400> 216

Gln Pro Val Leu Thr Gln Pro Pro Ser Ser Ser Ala Ser Pro Gly Glu

1 5 10 15

Ser Ala Arg Leu Thr Cys
20

<210> 217
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 5e FR2

<400> 217

Trp Tyr Gln Gln Lys Pro Gly Ser Pro Pro Arg Tyr Leu Leu Tyr
1 5 10 15

<210> 218
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> 5e FR3

<400> 218

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

Gly Ile Leu Leu Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr
20 25 30

Tyr Cys

<210> 219
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> 5c FR1

<400> 219

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

Ser Ala Ser Leu Thr Cys
20

<210> 220
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 5c FR2

<400> 220

Trp Tyr Gln Gln Lys Pro Gly Ser Pro Pro Gln Tyr Leu Leu Arg
1 5 10 15

<210> 221
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> 5c FR3

<400> 221

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

Gly Ile Leu Leu Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr
20 25 30

Tyr Cys

<210> 222
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> 5b FR1

<400> 222

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

Ser Val Arg Leu Thr Cys
20

<210> 223
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 5b FR2

<400> 223

Trp Tyr Gln Gln Lys Pro Gly Asn Pro Pro Arg Tyr Leu Leu Tyr
1 5 10 15

<210> 224
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> 5b FR3

<400> 224

Gly Val Pro Ser Arg Phe Ser Gly Ser Asn Asp Ala Ser Ala Asn Ala
1 5 10 15

Gly Ile Leu Arg Ile Ser Gly Leu Gln Pro Glu Asp Glu Ala Asp Tyr

20 25 30

Tyr Cys

<210> 225
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> 6a FR1

<400> 225

Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
1 5 10 15

Thr Val Thr Ile Ser Cys
20

<210> 226
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 6a FR2

<400> 226

Trp Tyr Gln Gln Arg Pro Gly Ser Ser Pro Thr Thr Val Ile Tyr
1 5 10 15

<210> 227
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> 6a FR3

<400> 227

Gly Val Pro Asp Arg Phe Ser Gly Ser Ile Asp Ser Ser Ser Asn Ser
1 5 10 15

Ala Ser Leu Thr Ile Ser Gly Leu Lys Thr Glu Asp Glu Ala Asp Tyr
20 25 30

Tyr Cys

<210> 228
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> 7a FR1

<400> 228

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

Thr Val Thr Leu Thr Cys
20

<210> 229
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 7a FR2

<400> 229

Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Ala Leu Ile Tyr
1 5 10 15

<210> 230
<211> 32
<212> PRT

<213> Artificial Sequence

<220>
<223> 7a FR3

<400> 230

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

Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys
20 25 30

<210> 231
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> 7b FR1

<400> 231

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

Thr Val Thr Leu Thr Cys
20

<210> 232
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 7b FR2

<400> 232

Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Thr Leu Ile Tyr
1 5 10 15

<210> 233

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

<220>
<223> 7b FR3

<400> 233

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

Leu Thr Leu Ser Gly Ala Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys
20 25 30

<210> 234
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> 8a FR1

<400> 234

Gln Thr Val Val Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys
20

<210> 235
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 8a FR2

<400> 235

Trp Tyr Gln Gln Thr Pro Gly Gln Ala Pro Arg Thr Leu Ile Tyr
1 5 10 15

<210> 236
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 8a FR3

<400> 236

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

Leu Thr Ile Thr Gly Ala Gln Ala Asp Asp Glu Ser Asp Tyr Tyr Cys
20 25 30

<210> 237
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> 9a FR1

<400> 237

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

Ser Val Thr Leu Thr Cys
20

<210> 238
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 9a FR2

<400> 238

Trp Tyr Gln Gln Arg Pro Gly Lys Gly Pro Arg Phe Val Met Arg

1 5 10 15

<210> 239
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 9a FR3

<400> 239

Gly Ile Pro Asp Arg Phe Ser Val Leu Gly Ser Gly Leu Asn Arg Tyr
1 5 10 15

Leu Thr Ile Lys Asn Ile Gln Glu Glu Asp Glu Ser Asp Tyr His Cys
20 25 30

<210> 240
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> 10a FR1

<400> 240

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

Thr Ala Thr Leu Thr Cys
20

<210> 241
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 10a FR2

<400> 241

Trp Leu Gln Gln His Gln Gly His Pro Pro Lys Leu Leu Ser Tyr
1 5 10 15

<210> 242
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 10a FR3

<400> 242

Gly Ile Ser Glu Arg Leu Ser Ala Ser Arg Ser Gly Asn Thr Ala Ser
1 5 10 15

Leu Thr Ile Thr Gly Leu Gln Pro Glu Asp Glu Ala Asp Tyr Tyr Cys
20 25 30

<210> 243
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> JL1 FR4

<400> 243

Phe Gly Thr Gly Thr Lys Val Thr Val Leu
1 5 10

<210> 244
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> JL2 FR4

<400> 244

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

1 5 10

<210> 245
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> JL3 FR4

<400> 245

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
1 5 10

<210> 246
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> JL7 FR4

<400> 246

Phe Gly Gly Gly Thr Gln Leu Thr Val Leu
1 5 10

<210> 247
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Ig Kappa Constant Region (IGKC)

<400> 247

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15

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

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Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35                  40                  45

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50                  55                  60

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

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
            100                 105
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<210> 248
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Ig Lambda Constant Region (IGLC)

<400> 248

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

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

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
        35                  40                  45

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
    50                  55                  60

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
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65 70 75 80

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
85 90 95

Lys Thr Val Ala Pro Thr Glu Cys Ser
100 105

<210> 249
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 1-02 FR1

<400> 249

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
20 25

<210> 250
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 1-02 FR2

<400> 250

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

<210> 251
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 1-02 FR3

<400> 251

Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 252
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 1-03 FR1

<400> 252

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
20 25

<210> 253
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 1-03 FR2

<400> 253

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

<210> 254
<211> 32
<212> PRT

<213> Artificial Sequence

<220>
<223> 1-03 FR3

<400> 254

Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr Met Glu
1 5 10 15

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

<210> 255
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 1-08 FR1

<400> 255

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
20 25

<210> 256
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 1-08 FR2

<400> 256

Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met Gly
1 5 10

<210> 257

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

<220>
<223> 1-08 FR3

<400> 257

Arg Val Thr Met Thr Arg Asn Thr Ser Ile Ser Thr Ala Tyr Met Glu
1 5 10 15

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

<210> 258
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 1-18 FR1

<400> 258

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
20 25

<210> 259
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 1-18 FR2

<400> 259

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

<210> 260
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 1-18 FR3

<400> 260

Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 261
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 1-24 FR1

<400> 261

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 Val Ser
20 25

<210> 262
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 1-24 FR2

<400> 262

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

1 5 10

<210> 263
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 1-24 FR3

<400> 263

Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp Thr Ala Tyr Met Glu
1 5 10 15

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

<210> 264
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 1-45 FR1

<400> 264

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

Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

<210> 265
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 1-45 FR2

<400> 265

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

<210> 266
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 1-45 FR3

<400> 266

Arg Val Thr Ile Thr Arg Asp Arg Ser Met Ser Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys Ala Arg
20 25 30

<210> 267
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 1-46 FR1

<400> 267

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
20 25

<210> 268
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 1-46 FR2

<400> 268

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

<210> 269
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 1-46 FR3

<400> 269

Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu
1 5 10 15

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

<210> 270
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 1-58 FR1

<400> 270

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

Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

<210> 271
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 1-58 FR2

<400> 271

Trp Val Arg Gln Ala Arg Gly Gln Arg Leu Glu Trp Ile Gly
1 5 10

<210> 272
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 1-58 FR3

<400> 272

Arg Val Thr Ile Thr Arg Asp Met Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

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

<210> 273
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 1-69 FR1

<400> 273

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
20 25

<210> 274
<211> 14
<212> PRT

<213> Artificial Sequence

<220>
<223> 1-69 FR2

<400> 274

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

<210> 275
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 1-69 FR3

<400> 275

Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

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

<210> 276
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 1-e FR1

<400> 276

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
20 25

<210> 277

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

<220>
<223> 1-e FR2

<400> 277

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

<210> 278
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 1-e FR3

<400> 278

Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

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

<210> 279
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 1-f FR1

<400> 279

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

Thr Val Lys Ile Ser Cys Lys Val Ser
20 25

<210> 280
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<220>
<223> 1-f FR2

<400> 280

Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Glu Trp Met Gly
1 5 10

<210> 281
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 1-f FR3`

<400> 281

Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asp Thr Ala Tyr Met Glu
1 5 10 15

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

<210> 282
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 2-05 FR1

<400> 282

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser

20 25

<210> 283
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 2-05 FR2

<400> 283

Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu Ala
1 5 10

<210> 284
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> 2-05 FR3

<400> 284

Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val Val Leu Thr
1 5 10 15

Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala His
20 25 30

Arg

<210> 285
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 2-26 FR1

<400> 285

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

Thr Leu Thr Leu Thr Cys Thr Val Ser
20 25

<210> 286
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 2-26 FR2

<400> 286

Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu Ala
1 5 10

<210> 287
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> 2-26 FR3

<400> 287

Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Ser Gln Val Val Leu Thr
1 5 10 15

Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala Arg
20 25 30

Ile

<210> 288
<211> 25
<212> PRT

<213> Artificial Sequence

<220>
<223> 2-70 FR1

<400> 288

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser
20 25

<210> 289
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 2-70 FR2

<400> 289

Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu Ala
1 5 10

<210> 290
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> 2-70 FR3

<400> 290

Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Val Leu Thr
1 5 10 15

Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala Arg
20 25 30

Ile

<210> 291
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-07 FR1

<400> 291

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 292
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-07 FR2

<400> 292

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
1 5 10

<210> 293
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-07 FR3

<400> 293

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

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

<210> 294
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-09 FR1

<400> 294

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 295
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-09 FR2

<400> 295

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

<210> 296
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-09 FR3

<400> 296

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln

1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Lys
20 25 30

Asp

<210> 297
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-11 FR1

<400> 297

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 298
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-11 FR2

<400> 298

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

<210> 299
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-11 FR3

<400> 299

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

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

<210> 300
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-13 FR1

<400> 300

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 301
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-13 FR2

<400> 301

Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Val Ser
1 5 10

<210> 302
<211> 32
<212> PRT

<213> Artificial Sequence

<220>
<223> 3-13 FR3

<400> 302

Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn Ser Leu Tyr Leu Gln
1 5 10 15

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

<210> 303
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-15 FR1

<400> 303

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 304
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-15 FR2

<400> 304

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly
1 5 10

<210> 305

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

<220>
<223> 3-15 FR3

<400> 305

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Thr Thr
20 25 30

<210> 306
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-20 FR1

<400> 306

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 307
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-20 FR2

<400> 307

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

<210> 308
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-20 FR3

<400> 308

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

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr His Cys Ala Arg
20 25 30

<210> 309
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-21 FR1

<400> 309

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 310
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-21 FR2

<400> 310

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser

1 5 10

<210> 311
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-21 FR3

<400> 311

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

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

<210> 312
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-23 FR1

<400> 312

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 313
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-23 FR2

<400> 313

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

<210> 314
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-23 FR3

<400> 314

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

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

<210> 315
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-30 FR1

<400> 315

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 316
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-30 FR2

<400> 316

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
1 5 10

<210> 317
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-30 FR3

<400> 317

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

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

<210> 318
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-30.3 FR1

<400> 318

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 319
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-30.3 FR2

<400> 319

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
1 5 10

<210> 320
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-30.3 FR3

<400> 320

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

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

<210> 321
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-3 FR1

<400> 321

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 322
<211> 14
<212> PRT

<213> Artificial Sequence

<220>
<223> 3-30.5 FR2

<400> 322

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
1 5 10

<210> 323
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-30.5 FR3

<400> 323

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

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

<210> 324
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-3 FR13

<400> 324

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 325

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

<220>
<223> 3-33 FR2

<400> 325

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
1 5 10

<210> 326
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-33 FR3

<400> 326

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

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

<210> 327
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-43 FR1

<400> 327

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 328
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-43 FR2

<400> 328

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

<210> 329
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-43 FR3

<400> 329

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Ser Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Lys
20 25 30

Asp

<210> 330
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-48 FR1

<400> 330

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 331
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-48 FR2

<400> 331

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

<210> 332
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-48 FR3

<400> 332

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

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

<210> 333
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-49 FR1

<400> 333

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


Ser Leu Arg Leu Ser Cys Thr Ala Ser
            20                  25


<210>  334
<211>  14
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  3-49 FR2

<400>  334

Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly
1               5                   10


<210>  335
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  3-49 FR3

<400>  335

Arg Phe Thr Ile Ser Arg Asp Gly Ser Lys Ser Ile Ala Tyr Leu Gln
1               5                   10                  15


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


<210>  336
<211>  25
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  3-53 FR1
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<400> 336

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 337
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-53 FR2

<400> 337

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

<210> 338
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-53 FR3

<400> 338

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

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

<210> 339
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-64 FR1

<400> 339

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 340
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-64 FR2

<400> 340

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Tyr Val Ser
1 5 10

<210> 341
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-64 FR3

<400> 341

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Gly Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 342
<211> 25
<212> PRT

<213> Artificial Sequence

<220>
<223> 3-66 FR1

<400> 342

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 343
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<400> 343

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

<210> 344
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-66 FR3

<400> 344

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

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

<210> 345

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

<220>
<223> 3-72 FR1

<400> 345

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 346
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-72 FR2

<400> 346

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly
1 5 10

<210> 347
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-72 FR3

<400> 347

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser Leu Tyr Leu Gln
1 5 10 15

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

<210> 348
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-73 FR1

<400> 348

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

Ser Leu Lys Leu Ser Cys Ala Ala Ser
20 25

<210> 349
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-73 FR2

<400> 349

Trp Val Arg Gln Ala Ser Gly Lys Gly Leu Glu Trp Val Gly
1 5 10

<210> 350
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-73 FR3

<400> 350

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

Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Thr Arg

20 25 30

<210> 351
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-74 FR1

<400> 351

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 352
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-74 FR2

<400> 352

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Val Trp Val Ser
1 5 10

<210> 353
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-74 FR3

<400> 353

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

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

<210> 354
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-d FR1

<400> 354

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser
            20   25

<210> 355
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<212> PRT
<213> Artificial Sequence

<220>
<223> 3-d FR2

<400> 355

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

<210> 356
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-d FR3

<400> 356

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu His Leu Gln

1 5 10 15

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

<210> 357
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-04 FR1

<400> 357

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

Thr Leu Ser Leu Thr Cys Ala Val Ser
20 25

<210> 358
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-04 FR2

<400> 358

Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly
1 5 10

<210> 359
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-04 FR3

<400> 359

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Arg Val Thr Ile Ser Val Asp Lys Ser Lys Asn Gln Phe Ser Leu Lys
1               5                   10                  15


Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg
            20                  25                  30


<210>  360
<211>  25
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  4-28 FR1

<400>  360

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


Thr Leu Ser Leu Thr Cys Ala Val Ser
            20                  25


<210>  361
<211>  14
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  4-28 FR2

<400>  361

Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly
1               5                   10


<210>  362
<211>  32
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  4-28 FR3
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<400> 362

Arg Val Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys
1 5 10 15

Leu Ser Ser Val Thr Ala Val Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 363
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-30.1 FR1

<400> 363

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

Thr Leu Ser Leu Thr Cys Thr Val Ser
20 25

<210> 364
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-30.1 FR2

<400> 364

Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu Trp Ile Gly
1 5 10

<210> 365
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-30.1 FR3

<400> 365

Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys
1 5 10 15

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 366
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-3 FR1

<400> 366

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

Thr Leu Ser Leu Thr Cys Ala Val Ser
20 25

<210> 367
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-30.2 FR2

<400> 367

Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly
1 5 10

<210> 368
<211> 32
<212> PRT

<213> Artificial Sequence

<220>
<223> 4-30.2 FR3

<400> 368

Arg Val Thr Ile Ser Val Asp Arg Ser Lys Asn Gln Phe Ser Leu Lys
1 5 10 15

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 369
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-3 FR10.4

<400> 369

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

Thr Leu Ser Leu Thr Cys Thr Val Ser
20 25

<210> 370
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-30.4 FR2

<400> 370

Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly
1 5 10

<210> 371

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

<220>
<223> 4-30.4 FR3

<400> 371

Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys
1 5 10 15

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 372
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-3 FR1

<400> 372

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

Thr Leu Ser Leu Thr Cys Thr Val Ser
20 25

<210> 373
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-31 FR2

<400> 373

Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu Trp Ile Gly
1 5 10

<210> 374
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-31 FR3

<400> 374

Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys
1 5 10 15

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 375
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-34 FR1

<400> 375

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

Thr Leu Ser Leu Thr Cys Ala Val Tyr
20 25

<210> 376
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-34 FR2

<400> 376

Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly

1 5 10

<210> 377
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-34 FR3

<400> 377

Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys
1 5 10 15

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 378
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-39 FR1

<400> 378

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

Thr Leu Ser Leu Thr Cys Thr Val Ser
20 25

<210> 379
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-39 FR2

<400> 379

Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly
1 5 10

<210> 380
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-39 FR3

<400> 380

Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys
1 5 10 15

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 381
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-59 FR1

<400> 381

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

Thr Leu Ser Leu Thr Cys Thr Val Ser
20 25

<210> 382
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-59 FR2

<400> 382

Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly
1 5 10

<210> 383
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-59 FR3

<400> 383

Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys
1 5 10 15

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 384
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-61 FR1

<400> 384

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

Thr Leu Ser Leu Thr Cys Thr Val Ser
20 25

<210> 385
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-61 FR2

<400> 385

Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly
1 5 10

<210> 386
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-61 FR3

<400> 386

Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys
1 5 10 15

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 387
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-b FR1

<400> 387

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

Thr Leu Ser Leu Thr Cys Ala Val Ser
20 25

<210> 388
<211> 14
<212> PRT

<213> Artificial Sequence

<220>
<223> 4-b FR2

<400> 388

Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly
1 5 10

<210> 389
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-b FR3

<400> 389

Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys
1 5 10 15

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 390
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 5-51 FR1

<400> 390

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser
20 25

<210> 391

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

<220>
<223> 5-51 FR2

<400> 391

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

<210> 392
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 5-51 FR3

<400> 392

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

Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg
20 25 30

<210> 393
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 5-a FR1

<400> 393

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

Ser Leu Arg Ile Ser Cys Lys Gly Ser
20 25

<210> 394
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 5-a FR2

<400> 394

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

<210> 395
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 5-a FR3

<400> 395

His Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln
1 5 10 15

Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg
20 25 30

<210> 396
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 6-01 FR1

<400> 396

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

Thr Leu Ser Leu Thr Cys Ala Ile Ser

20 25

<210> 397
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 6-01 FR2

<400> 397

Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu Gly
1 5 10

<210> 398
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 6-01 FR3

<400> 398

Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn Gln Phe Ser Leu Gln
1 5 10 15

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

<210> 399
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 7-4.1 FR1

<400> 399

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

Ser Val Lys Val Ser Cys Lys Ala Ser
            20   25

<210> 400
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 7-4.1 FR2

<400> 400

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

<210> 401
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> 7-4.1 FR3

<400> 401

Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr Leu Gln
1   5   10   15

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

<210> 402
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> JH1 FR4

<400> 402

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

1 5 10

<210> 403
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> JH2 FR4

<400> 403

Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 404
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> JH3 FR4

<400> 404

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
1 5 10

<210> 405
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> JH4 FR4

<400> 405

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 406
<211> 11
<212> PRT

<213> Artificial Sequence

<220>
<223> JH5 FR4

<400> 406

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 407
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> JH6 FR4

<400> 407

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
1 5 10

<210> 408
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> IGAH1 CH1

<400> 408

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

Gln Pro Asp Gly Asn Val Val Ile Ala Cys Leu Val Gln Gly Phe Phe
20 25 30

Pro Gln Glu Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln Gly Val
35 40 45

Thr Ala Arg Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp Leu Tyr

50 55 60

Thr Thr Ser Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Leu Ala Gly
65 70 75 80

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

Val Thr Val Pro Cys Pro
100

<210> 409
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> IGAH1 Hinge

<400> 409

Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser
1 5 10 15

Pro Ser

<210> 410
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> IGAH1 CH2

<400> 410

Cys Cys His Pro Arg Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu
1 5 10 15

Leu Leu Gly Ser Glu Ala Asn Leu Thr Cys Thr Leu Thr Gly Leu Arg

20 25 30

Asp Ala Ser Gly Val Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser
35 40 45

Ala Val Gln Gly Pro Pro Glu Arg Asp Leu Cys Gly Cys Tyr Ser Val
50 55 60

Ser Ser Val Leu Pro Gly Cys Ala Glu Pro Trp Asn His Gly Lys Thr
65 70 75 80

Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser Lys Thr Pro Leu Thr Ala
85 90 95

Thr Leu Ser Lys Ser
100

<210> 411
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> IGAH1 CH3

<400> 411

Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu
1 5 10 15

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

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

Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser
50 55 60

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


Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu
                85                  90                  95


Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala
            100                 105                 110


<210>  412
<211>  102
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  IGAH2 CH1

<400>  412

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


Pro Gln Asp Gly Asn Val Val Val Ala Cys Leu Val Gln Gly Phe Phe
            20                  25                  30


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


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


Thr Thr Ser Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Pro Asp Gly
65                  70                  75                  80


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


Val Thr Val Pro Cys Pro
```

100

<210> 413
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> IGAH2 Hinge

<400> 413

Pro Pro Pro Pro Pro
1 5

<210> 414
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> IGAH2 CH2

<400> 414

Cys Cys His Pro Arg Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu
1 5 10 15

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

Asp Ala Ser Gly Ala Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser
35 40 45

Ala Val Gln Gly Pro Pro Glu Arg Asp Leu Cys Gly Cys Tyr Ser Val
50 55 60

Ser Ser Val Leu Pro Gly Cys Ala Gln Pro Trp Asn His Gly Glu Thr
65 70 75 80

Phe Thr Cys Thr Ala Ala His Pro Glu Leu Lys Thr Pro Leu Thr Ala

85 90 95

Asn Ile Thr Lys Ser
100

<210> 415
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> IGAH2 CH3

<400> 415

Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu
1 5 10 15

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

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

Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser
50 55 60

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

Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu
85 90 95

Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala
100 105 110

<210> 416
<211> 101
<212> PRT

<213> Artificial Sequence

<220>
<223> IGDH CH1

<400> 416

Ala Pro Thr Lys Ala Pro Asp Val Phe Pro Ile Ile Ser Gly Cys Arg
1 5 10 15

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

Tyr His Pro Thr Ser Val Thr Val Thr Trp Tyr Met Gly Thr Gln Ser
35 40 45

Gln Pro Gln Arg Thr Phe Pro Glu Ile Gln Arg Arg Asp Ser Tyr Tyr
50 55 60

Met Thr Ser Ser Gln Leu Ser Thr Pro Leu Gln Gln Trp Arg Gln Gly
65 70 75 80

Glu Tyr Lys Cys Val Val Gln His Thr Ala Ser Lys Ser Lys Lys Glu
85 90 95

Ile Phe Arg Trp Pro
100

<210> 417
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> IGDH Hinge

<400> 417

Glu Ser Pro Lys Ala Gln Ala Ser Ser Val Pro Thr Ala Gln Pro Gln
1 5 10 15

```
Ala Glu Gly Ser Leu Ala Lys Ala Thr Thr Ala Pro Ala Thr Thr Arg
            20                  25                  30


Asn Thr Gly Arg Gly Gly Glu Glu Lys Lys Lys Glu Lys Glu Lys Glu
        35                  40                  45


Glu Gln Glu Glu Arg Glu Thr Lys Thr Pro
    50                  55


<210>  418
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  IGDH CH2

<400>  418

Glu Cys Pro Ser His Thr Gln Pro Leu Gly Val Tyr Leu Leu Thr Pro
1               5                   10                  15


Ala Val Gln Asp Leu Trp Leu Arg Asp Lys Ala Thr Phe Thr Cys Phe
            20                  25                  30


Val Val Gly Ser Asp Leu Lys Asp Ala His Leu Thr Trp Glu Val Ala
        35                  40                  45


Gly Lys Val Pro Thr Gly Gly Val Glu Glu Gly Leu Leu Glu Arg His
    50                  55                  60


Ser Asn Gly Ser Gln Ser Gln His Ser Arg Leu Thr Leu Pro Arg Ser
65                  70                  75                  80


Leu Trp Asn Ala Gly Thr Ser Val Thr Cys Thr Leu Asn His Pro Ser
                85                  90                  95


Leu Pro Pro Gln Arg Leu Met Ala Leu Arg Glu Pro
```

100 105

<210> 419
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> IGDH CH3

<400> 419

Ala Ala Gln Ala Pro Val Lys Leu Ser Leu Asn Leu Leu Ala Ser Ser
1 5 10 15

Asp Pro Pro Glu Ala Ala Ser Trp Leu Leu Cys Glu Val Ser Gly Phe
20 25 30

Ser Pro Pro Asn Ile Leu Leu Met Trp Leu Glu Asp Gln Arg Glu Val
35 40 45

Asn Thr Ser Gly Phe Ala Pro Ala Arg Pro Pro Pro Gln Pro Arg Ser
50 55 60

Thr Thr Phe Trp Ala Trp Ser Val Leu Arg Val Pro Ala Pro Pro Ser
65 70 75 80

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

Thr Leu Leu Asn Ala Ser Arg Ser Leu Glu Val Ser
100 105

<210> 420
<211> 103
<212> PRT
<213> Artificial Sequence

<220>
<223> IGEH CH1

<400> 420

Ala Ser Thr Gln Ser Pro Ser Val Phe Pro Leu Thr Arg Cys Cys Lys
1 5 10 15

Asn Ile Pro Ser Asn Ala Thr Ser Val Thr Leu Gly Cys Leu Ala Thr
20 25 30

Gly Tyr Phe Pro Glu Pro Val Met Val Thr Cys Asp Thr Gly Ser Leu
35 40 45

Asn Gly Thr Thr Met Thr Leu Pro Ala Thr Thr Leu Thr Leu Ser Gly
50 55 60

His Tyr Ala Thr Ile Ser Leu Leu Thr Val Ser Gly Ala Trp Ala Lys
65 70 75 80

Gln Met Phe Thr Cys Arg Val Ala His Thr Pro Ser Ser Thr Asp Trp
85 90 95

Val Asp Asn Lys Thr Phe Ser
100

<210> 421
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> IGEH CH2

<400> 421

Val Cys Ser Arg Asp Phe Thr Pro Pro Thr Val Lys Ile Leu Gln Ser
1 5 10 15

Ser Cys Asp Gly Gly Gly His Phe Pro Pro Thr Ile Gln Leu Leu Cys
20 25 30

```
Leu Val Ser Gly Tyr Thr Pro Gly Thr Ile Asn Ile Thr Trp Leu Glu
        35                  40                  45

Asp Gly Gln Val Met Asp Val Asp Leu Ser Thr Ala Ser Thr Thr Gln
    50                  55                  60

Glu Gly Glu Leu Ala Ser Thr Gln Ser Glu Leu Thr Leu Ser Gln Lys
65                  70                  75                  80

His Trp Leu Ser Asp Arg Thr Tyr Thr Cys Gln Val Thr Tyr Gln Gly
                85                  90                  95

His Thr Phe Glu Asp Ser Thr Lys Lys Cys Ala
            100                 105


<210>  422
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  IGEH CH3

<400>  422

Asp Ser Asn Pro Arg Gly Val Ser Ala Tyr Leu Ser Arg Pro Ser Pro
1               5                   10                  15

Phe Asp Leu Phe Ile Arg Lys Ser Pro Thr Ile Thr Cys Leu Val Val
            20                  25                  30

Asp Leu Ala Pro Ser Lys Gly Thr Val Asn Leu Thr Trp Ser Arg Ala
        35                  40                  45

Ser Gly Lys Pro Val Asn His Ser Thr Arg Lys Glu Glu Lys Gln Arg
    50                  55                  60

Asn Gly Thr Leu Thr Val Thr Ser Thr Leu Pro Val Gly Thr Arg Asp
```

65 70 75 80

Trp Ile Glu Gly Glu Thr Tyr Gln Cys Arg Val Thr His Pro His Leu
85 90 95

Pro Arg Ala Leu Met Arg Ser Thr Thr Lys Thr Ser
100 105

<210> 423
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> IGEH CH4

<400> 423

Gly Pro Arg Ala Ala Pro Glu Val Tyr Ala Phe Ala Thr Pro Glu Trp
1 5 10 15

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

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

Pro Asp Ala Arg His Ser Thr Thr Gln Pro Arg Lys Thr Lys Gly Ser
50 55 60

Gly Phe Phe Val Phe Ser Arg Leu Glu Val Thr Arg Ala Glu Trp Glu
65 70 75 80

Gln Lys Asp Glu Phe Ile Cys Arg Ala Val His Glu Ala Ala Ser Pro
85 90 95

Ser Gln Thr Val Gln Arg Ala Val Ser Val Asn Pro
100 105

<210> 424
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> IGGH1 CH1

<400> 424

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

<210> 425
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> IGGH1 Hinge

<400> 425

```
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1               5                   10                  15


<210>  426
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  IGGH1 CH2

<400>  426

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


Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            20                  25                  30


Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        35                  40                  45


Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    50                  55                  60


Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65                  70                  75                  80


Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                85                  90                  95


Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
            100                 105                 110


<210>  427
<211>  105
<212>  PRT
<213>  Artificial Sequence
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<220>
<223> IGGH1 CH3

<400> 427

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

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

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

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

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

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

Thr Gln Lys Ser Leu Ser Leu Ser Pro
100 105

<210> 428
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> IGGH2 CH1

<400> 428

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

Ser Thr Ser Glu Ser 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 Asn Phe Gly Thr Gln Thr
65 70 75 80

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

Thr Val

<210> 429
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> IGGH2 Hinge

<400> 429

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro
1 5 10

<210> 430
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> IGGH2 CH2

<400> 430

Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

1 5 10 15

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
20 25 30

Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
35 40 45

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
50 55 60

Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln
65 70 75 80

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
85 90 95

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
100 105

<210> 431
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> IGGH2 CH3

<400> 431

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

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe
50 55 60

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

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

Thr Gln Lys Ser Leu Ser Leu Ser Pro
100 105

<210> 432
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> IGGH3 CH1

<400> 432

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
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 Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys

85 90 95

Arg Val

<210> 433
<211> 62
<212> PRT
<213> Artificial Sequence

<220>
<223> IGGH3 Hinge

<400> 433

Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro Arg Cys
1 5 10 15

Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
20 25 30

Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu
35 40 45

Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
50 55 60

<210> 434
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> IGGH3 CH2

<400> 434

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

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

20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
100 105 110

<210> 435
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> IGGH3 CH3

<400> 435

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

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
20 25 30

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

Asn Asn Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe
50 55 60

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


Asn Ile Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe
                85                  90                  95


Thr Gln Lys Ser Leu Ser Leu Ser Pro
            100                 105


<210>  436
<211>  98
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  IGGH4 CH1

<400>  436

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


Ser Thr Ser Glu Ser 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 Lys Thr
65                  70                  75                  80


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


Arg Val
```

<210> 437
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> IGGH4 Hinge

<400> 437

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro
1 5 10

<210> 438
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> IGGH4 CH2

<400> 438

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

85 90 95

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

<210> 439
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> IGGH4 CH3

<400> 439

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

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

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

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

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

Thr Gln Lys Ser Leu Ser Leu Ser Leu
100 105

<210> 440
<211> 104
<212> PRT

<213> Artificial Sequence

<220>
<223> IGMH CH1

<400> 440

Gly Ser Ala Ser Ala Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn
1 5 10 15

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

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

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

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

Gly Thr Asp Glu His Val Val Cys Lys Val Gln His Pro Asn Gly Asn
85 90 95

Lys Glu Lys Asn Val Pro Leu Pro
100

<210> 441
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> IGMH CH2

<400> 441

Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val Pro Pro Arg
1 5 10 15

```
Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile Cys Gln Ala
            20                  25                  30

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

Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln Ala Glu Ala
    50                  55                  60

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

Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys Arg Val Asp
                85                  90                  95

His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met Cys Val Pro
            100                 105                 110
```

<210> 442
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> IGMH CH3

<400> 442

```
Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro Ser Phe Ala
1               5                   10                  15

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

Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg Gln Asn Gly
        35                  40                  45

Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His Pro Asn Ala
```

50 55 60

Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp Asp Trp Asn
65 70 75 80

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

Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys
100 105

<210> 443
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> IGMH CH4

<400> 443

Gly Val Ala Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg
1 5 10 15

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

Gly Phe Ser Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln
35 40 45

Pro Leu Ser Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro
50 55 60

Gln Ala Pro Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu
65 70 75 80

Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val Ala His Glu Ala
85 90 95

Leu Pro Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr
100 105 110

<210> 444
<211> 137
<212> PRT
<213> Artificial Sequence

<220>
<223> Joining Polypeptide

<400> 444

Gln Glu Asp Glu Arg Ile Val Leu Val Asp Asn Lys Cys Lys Cys Ala
1 5 10 15

Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser Glu Asp Pro Asn Glu Asp
20 25 30

Ile Val Glu Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Asn Arg Glu
35 40 45

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

Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro Thr Glu Val Glu Leu Asp
65 70 75 80

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

Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg Asn Lys Cys Tyr Thr Ala
100 105 110

Val Val Pro Leu Val Tyr Gly Gly Glu Thr Lys Met Val Glu Thr Ala
115 120 125

Leu Thr Pro Asp Ala Cys Tyr Pro Asp

130 135

<210> 445
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Rabbit Ab 909 VL-region

<400> 445

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

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

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

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

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

Asp Asp Ala Ala Thr Tyr Tyr Cys Gln Cys Thr Tyr Gly Thr Tyr Ala
85 90 95

Gly Ser Phe Phe Tyr Ser Phe Gly Gly Gly Thr Glu Val Val Val Glu
100 105 110

<210> 446
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> 909 gL1 VL-region

<400> 446

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

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

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

Tyr Lys Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Lys 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 Thr Tyr Tyr Cys Gln Cys Thr Tyr Gly Thr Tyr Ala
85 90 95

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

<210> 447
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> 909 gL1 VL + CL-region

<400> 447

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

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

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

Tyr Lys Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Lys 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 Thr Tyr Tyr Cys Gln Cys Thr Tyr Gly Thr Tyr Ala
                85                  90                  95

Gly Ser Phe Phe Tyr Ser Phe Gly Gly Gly Thr Lys Val 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> 448
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> 909 gL10 VL-region

<400> 448

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

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

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

Tyr Lys Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Lys 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 Thr Tyr Tyr Cys Gln Ala Thr Tyr Gly Thr Tyr Ala
85 90 95

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

<210> 449
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> 909 gL10 VL + CL-region

<400> 449

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

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

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

Tyr Lys Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Lys 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 Thr Tyr Tyr Cys Gln Ala Thr Tyr Gly Thr Tyr Ala
                85                  90                  95

Gly Ser Phe Phe Tyr Ser Phe Gly Gly Gly Thr Lys Val 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> 450
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> 909 gL54 VL-region

<400> 450

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

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

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

Tyr Lys Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Lys 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 Thr Tyr Tyr Cys Gln Gln Thr Tyr Gly Thr Tyr Ala
85 90 95

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

<210> 451

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

<220>
<223> 909 gL54 VL + CL-region

<400> 451

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


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


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


Tyr Lys Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Lys 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 Thr Tyr Tyr Cys Gln Gln Thr Tyr Gly Thr Tyr Ala
                85                  90                  95


Gly Ser Phe Phe Tyr Ser Phe Gly Gly Gly Thr Lys Val 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>  452
<211>  112
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  909 gL55 VL-region

<400>  452

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


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


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


Tyr Lys Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Lys 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 Thr Tyr Tyr Cys Gln His Thr Tyr Gly Thr Tyr Ala
```

85 90 95

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

<210> 453
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> 909 gL55 VL + CL-region

<400> 453

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

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

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

Tyr Lys Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Lys 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 Thr Tyr Tyr Cys Gln His Thr Tyr Gly Thr Tyr Ala
85 90 95

Gly Ser Phe Phe Tyr Ser Phe Gly Gly Gly Thr Lys Val 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> 454
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Rabbit Ab 909 VH region

<400> 454

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

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

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

Ile Ile Tyr Pro Ser Gly Ser Thr Tyr Cys Ala Ser Trp Ala Lys Gly
```

50 55 60

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

Ser Pro Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Pro Asp
85 90 95

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 455
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> 909gH1 VH region

<400> 455

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

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

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

Gly Ile Ile Tyr Pro Ser Gly Ser Thr Tyr Cys Ala Ser Trp Ala Lys
50 55 60

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

Ser Ser Val Thr Ala Ala Asp Thr Ala Thr Tyr Phe Cys Ala Arg Pro
85 90 95

Asp Asn Asp Gly Thr Ser Gly Tyr Leu Ser Gly Phe Gly Leu Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 456
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> 909gH1 IgG4 VH + human ?-4P constant

<400> 456

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

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

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

Gly Ile Ile Tyr Pro Ser Gly Ser Thr Tyr Cys Ala Ser Trp Ala Lys
50 55 60

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

Ser Ser Val Thr Ala Ala Asp Thr Ala Thr Tyr Phe Cys Ala Arg Pro
85 90 95

Asp Asn Asp Gly Thr Ser Gly Tyr Leu Ser Gly Phe Gly Leu Trp Gly

```
            100                 105                 110

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

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

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

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

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

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

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly
    210                 215                 220

Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser
225                 230                 235                 240

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

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

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

Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val
```

290 295 300

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

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

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

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

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

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

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

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

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

<210> 457
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> 909gH14 VH region

<400> 457

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


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


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


Gly Ile Ile Tyr Pro Ser Gly Ser Thr Tyr Cys Ala Ser Trp Ala Lys
    50                  55                  60


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


Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Thr Tyr Phe Cys Ala
                85                  90                  95


Arg Pro Asp Asn Asp Gly Thr Ser Gly Tyr Leu Ser Gly Phe Gly Leu
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  458
<211>  450
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  909gH14 IgG4 VH + human ?-4P constant

<400>  458

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


Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Phe Ser Leu Ser Thr Tyr
```

```
            20                  25                  30

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

Gly Ile Ile Tyr Pro Ser Gly Ser Thr Tyr Cys Ala Ser Trp Ala Lys
    50                  55                  60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Thr Tyr Phe Cys Ala
                85                  90                  95

Arg Pro Asp Asn Asp Gly Thr Ser Gly Tyr Leu Ser Gly Phe Gly Leu
            100                 105                 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

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

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

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

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys
```

210 215 220

Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly
225 230 235 240

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu
260 265 270

Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg
290 295 300

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

Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu
325 330 335

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

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

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

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp

405 410 415

Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu
435 440 445

Gly Lys
450

<210> 459
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> 909 gH15 VH region

<400> 459

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

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

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

Gly Ile Ile Tyr Pro Ser Gly Ser Thr Tyr Ser Ala Ser Trp Ala Lys
50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Thr Tyr Phe Cys Ala
85 90 95

```
Arg Pro Asp Asn Glu Gly Thr Ser Gly Tyr Leu Ser Gly Phe Gly Leu
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  460
<211>  450
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  909gH15 IgG4 VH + human ?-4P constant

<400>  460

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


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


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


Gly Ile Ile Tyr Pro Ser Gly Ser Thr Tyr Ser Ala Ser Trp Ala Lys
    50                  55                  60


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


Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Thr Tyr Phe Cys Ala
                85                  90                  95


Arg Pro Asp Asn Glu Gly Thr Ser Gly Tyr Leu Ser Gly Phe Gly Leu
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
```

```
        115                 120                 125

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

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

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

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys
    210                 215                 220

Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly
225                 230                 235                 240

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu
            260                 265                 270

Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
```

305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu
325 330 335

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

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

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

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

Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu
435 440 445

Gly Lys
450

<210> 461
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> 909 gH61 VH region

<400> 461

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


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


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


Gly Ile Ile Tyr Pro Ser Gly Ser Thr Tyr Cys Ala Ser Trp Ala Lys
    50                  55                  60


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


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


Arg Pro Asp Asn Asp Gly Thr Ser Gly Tyr Leu Ser Gly Phe Gly Leu
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  462
<211>  450
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  909gH61 IgG4 VH + human ?-4P constant

<400>  462

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


Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Phe Ser Leu Ser Thr Tyr
```

```
            20                  25                  30

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

Gly Ile Ile Tyr Pro Ser Gly Ser Thr Tyr Cys Ala Ser Trp Ala Lys
    50                  55                  60

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

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

Arg Pro Asp Asn Asp Gly Thr Ser Gly Tyr Leu Ser Gly Phe Gly Leu
            100                 105                 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

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

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

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

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys
```

```
    210                 215                 220

Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly
225                 230                 235                 240

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu
            260                 265                 270

Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg
    290                 295                 300

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

Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu
                325                 330                 335

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

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

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

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp
```

405 410 415

Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu
435 440 445

Gly Lys
450

<210> 463
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> 909 gH62 VH region

<400> 463

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

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

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

Gly Ile Ile Tyr Pro Ser Gly Ser Thr Tyr Ser Ala Ser Trp Ala Lys
50 55 60

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

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

```
Arg Pro Asp Asn Glu Gly Thr Ser Gly Tyr Leu Ser Gly Phe Gly Leu
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  464
<211>  450
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  909gH62 IgG4 VH + human ?-4P constant

<400>  464

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


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


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


Gly Ile Ile Tyr Pro Ser Gly Ser Thr Tyr Ser Ala Ser Trp Ala Lys
    50                  55                  60


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


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


Arg Pro Asp Asn Glu Gly Thr Ser Gly Tyr Leu Ser Gly Phe Gly Leu
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
```

```
        115                 120                 125

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

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

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

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys
    210                 215                 220

Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly
225                 230                 235                 240

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu
            260                 265                 270

Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
```

305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu
325 330 335

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

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

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

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

Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu
435 440 445

Gly Lys
450

<210> 465
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Rabbit Ab 909 VL region (Seq. ID No. 445) cDNA

<400> 465

gacgtcgtga tgacccagac tccagcctcc gtgtctgaac ctgtgggagg cacagtcacc 60

atcaagtgcc aggccagtga ggatattagt aggtacttag tctggtatca gcagaaacca 120

gggcagcctc ccaagcgcct gatctacaag gcatccactc tggcatctgg ggtcccatcg 180

cggttcaaag gcagtggatc tgggacagat ttcactctca ccatcagcga cctggagtgt 240

gacgatgctg ccacttacta ctgtcaatgc acttatggta cttatgctgg tagttttttt 300

tattctttcg gcggagggac cgaggtggtc gtcgaa 336

<210> 466
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Rabbit Ab 909 VH region (Seq. ID No. 454) cDNA

<400> 466
cagtcggtgg aggagtccgg gggtcgcctg gtcacgcctg ggacacccct gacactcacc 60

tgcacagtct ctggattctc cctcagtacc tactacatga gctgggtccg ccaggctcca 120

gggaaggggc tggaatggat cggaatcatt tatcctagtg gtagcacata ctgcgcgagc 180

tgggcgaaag gccgattcac catctccaaa gcctcaacca cggtggatct gaaaatcacc 240

agtccgacaa ccgaggacac ggccacctat ttctgtgcca gacctgataa tgatggtact 300

tctggttatt tgagtggttt cggcttgtgg ggccaaggca ccctcgtcac cgtctcgagc 360

<210> 467
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> 909 gL1 V-region (Seq. ID No. 446) cDNA

<400> 467
gacgtcgtca tgacccagtc cccttcctcc ctttcagcca gcgtgggcga tagagtgact 60

atcacttgcc aagcgtcgga ggacatctcg cgctacctgg tgtggtatca acagaagcca 120

ggtaaagcgc ccaagcggct gatctacaag gcctcaactt tggcatccgg agtgccgtcg 180

aggttcaagg gcagcggatc gggaaccgac ttcactctca ccattagctc actgcagccg 240

gaagattttg ccacttacta ctgccagtgt acctacggga cctacgctgg gtcgttcttt 300

tacagcttcg gaggcggaac caaagtggaa atcaag 336

<210> 468
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> 909 gL1 light chain (V + constant) (Seq. ID No. 447) cDNA

<400> 468
gacgtcgtca tgacccagtc cccttcctcc ctttcagcca gcgtgggcga tagagtgact 60

atcacttgcc aagcgtcgga ggacatctcg cgctacctgg tgtggtatca acagaagcca 120

ggtaaagcgc ccaagcggct gatctacaag gcctcaactt tggcatccgg agtgccgtcg 180

aggttcaagg gcagcggatc gggaaccgac ttcactctca ccattagctc actgcagccg 240

gaagattttg ccacttacta ctgccagtgt acctacggga cctacgctgg gtcgttcttt 300

tacagcttcg gaggcggaac caaagtggaa atcaagcgta cggtggccgc tccctccgtg 360

ttcatcttcc caccctccga cgagcagctg aagtccggca ccgcctccgt cgtgtgcctg 420

ctgaacaact tctacccccg cgaggccaag gtgcagtgga aggtggacaa cgccctgcag 480

tccggcaact cccaggaatc cgtcaccgag caggactcca aggacagcac ctactccctg 540

tcctccaccc tgaccctgtc caaggccgac tacgagaagc acaaggtgta cgcctgcgaa 600

gtgacccacc agggcctgtc cagccccgtg accaagtcct tcaaccgggg cgagtgc 657

<210> 469
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> 909 gL10 V-region (Seq. ID No. 448) cDNA

<400> 469
gacgtcgtca tgacccagtc cccttcctcc ctttcagcca gcgtgggcga tagagtgact 60

atcacttgcc aagcgtcgga ggacatctcg cgctacctgg tgtggtatca acagaagcca 120

ggtaaagcgc ccaagcggct gatctacaag gcctcaactt tggcatccgg agtgccgtcg 180

aggttcaagg gcagcggatc gggaaccgac ttcactctca ccattagctc actgcagccg 240

gaagattttg ccacttacta ctgccaggct acctacggga cctacgctgg gtcgttcttt 300

tacagcttcg gaggcggaac caaagtggaa atcaag 336

<210> 470
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> 909 gL10 light chain (V + constant) (Seq. ID No. 449) cDNA

<400> 470
gacgtcgtca tgacccagtc cccttcctcc ctttcagcca gcgtgggcga tagagtgact 60

atcacttgcc aagcgtcgga ggacatctcg cgctacctgg tgtggtatca acagaagcca 120

ggtaaagcgc ccaagcggct gatctacaag gcctcaactt tggcatccgg agtgccgtcg 180

aggttcaagg gcagcggatc gggaaccgac ttcactctca ccattagctc actgcagccg 240

gaagattttg ccacttacta ctgccaggct acctacggga cctacgctgg gtcgttcttt 300

tacagcttcg gaggcggaac caaagtggaa atcaagcgta cggtggccgc tccctccgtg 360

ttcatcttcc caccctccga cgagcagctg aagtccggca ccgcctccgt cgtgtgcctg 420

ctgaacaact tctacccccg cgaggccaag gtgcagtgga aggtggacaa cgccctgcag 480

tccggcaact cccaggaatc cgtcaccgag caggactcca aggacagcac ctactccctg 540

tcctccaccc tgaccctgtc caaggccgac tacgagaagc acaaggtgta cgcctgcgaa 600

gtgacccacc agggcctgtc cagccccgtg accaagtcct tcaaccgggg cgagtgc 657

<210> 471

<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> 909 gL54 V-region (Seq. ID No. 450) cDNA

<400> 471
gacgtcgtca tgacccagtc cccttcctcc ctttcagcca gcgtgggcga tagagtgact 60

atcacttgcc aagcgtcgga ggacatctcg cgctacctgg tgtggtatca acagaagcca 120

ggtaaagcgc ccaagcggct gatctacaag gcctcaactt tggcatccgg agtgccgtcg 180

aggttcaagg gcagcggatc gggaaccgac ttcactctca ccattagctc actgcagccg 240

gaagattttg ccacttacta ctgccagcag acctacggga cctacgctgg gtcgttcttt 300

tacagcttcg gaggcggaac caaagtggaa atcaag 336

<210> 472
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> 909 gL54 light chain (V + constant) (Seq. ID No. 451) cDNA

<400> 472
gacgtcgtca tgacccagtc cccttcctcc ctttcagcca gcgtgggcga tagagtgact 60

atcacttgcc aagcgtcgga ggacatctcg cgctacctgg tgtggtatca acagaagcca 120

ggtaaagcgc ccaagcggct gatctacaag gcctcaactt tggcatccgg agtgccgtcg 180

aggttcaagg gcagcggatc gggaaccgac ttcactctca ccattagctc actgcagccg 240

gaagattttg ccacttacta ctgccagcag acctacggga cctacgctgg gtcgttcttt 300

tacagcttcg gaggcggaac caaagtggaa atcaagcgta cggtggccgc tccctccgtg 360

ttcatcttcc caccctccga cgagcagctg aagtccggca ccgcctccgt cgtgtgcctg 420

ctgaacaact tctacccccg cgaggccaag gtgcagtgga aggtggacaa cgccctgcag 480

tccggcaact cccaggaatc cgtcaccgag caggactcca aggacagcac ctactccctg 540

tcctccaccc tgaccctgtc caaggccgac tacgagaagc acaaggtgta cgcctgcgaa 600

gtgacccacc agggcctgtc cagccccgtg accaagtcct tcaaccgggg cgagtgc 657

<210> 473
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> 909 gL55 V-region (Seq. ID No. 452) cDNA

<400> 473
gacgtcgtca tgacccagtc cccttcctcc ctttcagcca gcgtgggcga tagagtgact 60

atcacttgcc aagcgtcgga ggacatctcg cgctacctgg tgtggtatca acagaagcca 120

ggtaaagcgc ccaagcggct gatctacaag gcctcaactt tggcatccgg agtgccgtcg 180

aggttcaagg gcagcggatc gggaaccgac ttcactctca ccattagctc actgcagccg 240

gaagattttg ccacttacta ctgccagcat acctacggga cctacgctgg gtcgttcttt 300

tacagcttcg gaggcggaac caaagtggaa atcaag 336

<210> 474
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> 909 gL55 light chain (V + constant) (Seq. ID No. 453) cDNA

<400> 474
gacgtcgtca tgacccagtc cccttcctcc ctttcagcca gcgtgggcga tagagtgact 60

atcacttgcc aagcgtcgga ggacatctcg cgctacctgg tgtggtatca acagaagcca 120

ggtaaagcgc ccaagcggct gatctacaag gcctcaactt tggcatccgg agtgccgtcg 180

aggttcaagg gcagcggatc gggaaccgac ttcactctca ccattagctc actgcagccg 240

gaagattttg ccacttacta ctgccagcat acctacggga cctacgctgg gtcgttcttt 300

tacagcttcg gaggcggaac caaagtggaa atcaagcgta cggtggccgc tccctccgtg 360

ttcatcttcc caccctccga cgagcagctg aagtccggca ccgcctccgt cgtgtgcctg 420

ctgaacaact tctacccccg cgaggccaag gtgcagtgga aggtggacaa cgccctgcag 480

tccggcaact cccaggaatc cgtcaccgag caggactcca aggacagcac ctactccctg 540

tcctccaccc tgaccctgtc caaggccgac tacgagaagc acaaggtgta cgcctgcgaa 600

gtgacccacc agggcctgtc cagccccgtg accaagtcct tcaaccgggg cgagtgc 657

<210> 475
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> 909gH1 V-region (Seq. ID No. 455) cDNA

<400> 475
gaagtccagc tgcaagaatc aggtccaggc ctcgtcaaac catcaggaac tttgtcattg 60

acttgcacgg tgagcgggtt ctcgctttcg acctactaca tgtcgtgggt gcgccagccg 120

cctgggaagg gactggagtg gatcggcatc atctacccgt ccggcagcac gtactgcgct 180

agctgggcca aggggcggtt caccatcagc aaggcgtcca ctactgtgga cctcaagctg 240

tcgtcagtta ctgcggccga cactgcaacc tacttttgtg cccgcccgga taacgatgga 300

acctccggct acctgtccgg attcggactg tggggacagg gaaccttgt gactgtctcg 360

agc 363

<210> 476
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> 909 gH1 IgG4 heavy chain (V + human ?-4P constant) Seq. ID No. 456) cDNA

<400> 476
gaagtccagc tgcaagaatc aggtccaggc ctcgtcaaac catcaggaac tttgtcattg 60

acttgcacgg tgagcgggtt ctcgctttcg acctactaca tgtcgtgggt gcgccagccg 120

cctgggaagg gactggagtg gatcggcatc atctacccgt ccggcagcac gtactgcgct 180

agctgggcca aggggcggtt caccatcagc aaggcgtcca ctactgtgga cctcaagctg 240

tcgtcagtta ctgcggccga cactgcaacc tacttttgtg cccgcccgga taacgatgga 300

acctccggct acctgtccgg attcggactg tggggacagg gaaccttgt gactgtctcg 360

agcgcctcca ccaagggccc ctccgtgttc cctctggccc cttgctcccg gtccacctcc 420

gagtctaccg ccgctctggg ctgcctggtc aaggactact tccccgagcc cgtgacagtg 480

tcctggaact ctggcgccct gacctccggc gtgcacacct tccctgccgt gctgcagtcc 540

tccggcctgt actccctgtc ctccgtcgtg accgtgccct cctccagcct gggcaccaag 600

acctacacct gtaacgtgga ccacaagccc tccaacacca aggtggacaa gcgggtggaa 660

tctaagtacg gccctccctg ccccccctgc cctgcccctg aatttctggg cggaccttcc 720

gtgttcctgt tccccccaaa gcccaaggac accctgatga tctcccggac ccccgaagtg 780

acctgcgtgg tggtggacgt gtcccaggaa gatcccgagg tccagttcaa ttggtacgtg 840

gacggcgtgg aagtgcacaa tgccaagacc aagcccagag aggaacagtt caactccacc 900

taccgggtgg tgtccgtgct gaccgtgctg caccaggact ggctgaacgg caaagagtac 960

aagtgcaagg tgtccaacaa gggcctgccc tccagcatcg aaaagaccat ctccaaggcc 1020

aagggccagc cccgcgagcc ccaggtgtac accctgcccc ctagccagga agagatgacc 1080

aagaaccagg tgtccctgac ctgtctggtc aagggcttct acccctccga cattgccgtg 1140

gaatgggagt ccaacggcca gcccgagaac aactacaaga ccacccccc tgtgctggac 1200

agcgacggct ccttcttcct gtactctcgg ctgaccgtgg acaagtcccg gtggcaggaa 1260

ggcaacgtct tctcctgctc cgtgatgcac gaggccctgc acaaccacta cacccagaag 1320

tccctgtccc tgagcctggg caag 1344

<210> 477
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> 909gH15 V-region (Seq. ID. No. 457) cDNA

<400> 477
gaagtccagc tgcaagaatc aggtccaggc ctcgtcaaac catcaggaac tttgtcattg 60

acttgcacgg tgagcgggtt ctcgctttcg acctactaca tgtcgtgggt gcgccagccg 120

cctgggaagg gactggagtg gatcggcatc atctacccgt ccggcagcac gtactccgct 180

agctgggcca aggggcggtt caccatcagc aaggcgtcca ctaaaaatac tgtggacctc 240

aagctgtcgt cagttactgc ggccgacact gcaacctact tttgtgcccg cccggataac 300

gagggaacct ccggctacct gtccggattc ggactgtggg gacagggaac ccttgtgact 360

gtctcgagc 369

<210> 478
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> 909 gH15 IgG4 heavy chain (V + human gamma-4P constant) (Seq. ID No. 458) cDNA

<400> 478
gaagtccagc tgcaagaatc aggtccaggc ctcgtcaaac catcaggaac tttgtcattg 60

acttgcacgg tgagcgggtt ctcgctttcg acctactaca tgtcgtgggt gcgccagccg 120

cctgggaagg gactggagtg gatcggcatc atctacccgt ccggcagcac gtactccgct 180

agctgggcca aggggcggtt caccatcagc aaggcgtcca ctaaaaatac tgtggacctc 240

aagctgtcgt cagttactgc ggccgacact gcaacctact tttgtgcccg cccggataac 300

gagggaacct ccggctacct gtccggattc ggactgtggg gacagggaac ccttgtgact 360

gtctcgagcg cctccaccaa gggcccctcc gtgttccctc tggcccctg ctcccggtcc 420

acctccgagt ctaccgccgc tctgggctgc ctggtcaagg actacttccc cgagcccgtg 480

acagtgtcct ggaactctgg cgccctgacc tccggcgtgc acaccttccc tgccgtgctg 540

cagtcctccg gcctgtactc cctgtcctcc gtcgtgaccg tgccctcctc cagcctgggc 600

accaagacct acacctgtaa cgtggaccac aagccctcca acaccaaggt ggacaagcgg 660

gtggaatcta agtacggccc tccctgcccc ccctgccctg cccctgaatt tctgggcgga 720

ccttccgtgt tcctgttccc cccaaagccc aaggacaccc tgatgatctc ccggaccccc 780

gaagtgacct gcgtggtggt ggacgtgtcc caggaagatc ccgaggtcca gttcaattgg 840

tacgtggacg gcgtggaagt gcacaatgcc aagaccaagc ccagagagga acagttcaac 900

tccacctacc gggtggtgtc cgtgctgacc gtgctgcacc aggactggct gaacggcaaa 960

gagtacaagt gcaaggtgtc caacaagggc ctgccctcca gcatcgaaaa gaccatctcc 1020

aaggccaagg gccagccccg cgagccccag gtgtacaccc tgcccctag ccaggaagag 1080

atgaccaaga accaggtgtc cctgacctgt ctggtcaagg gcttctaccc ctccgacatt 1140

gccgtggaat gggagtccaa cggccagccc gagaacaact acaagaccac ccccctgtg 1200

ctggacagcg acggctcctt cttcctgtac tctcggctga ccgtggacaa gtcccggtgg 1260

caggaaggca acgtcttctc ctgctccgtg atgcacgagg ccctgcacaa ccactacacc 1320

cagaagtccc tgtccctgag cctgggcaag 1350

<210> 479
<211> 320
<212> DNA
<213> Artificial Sequence

<220>
<223> Human IGKV1-17 (A30)-JK4 acceptor framework cDNA

<400> 479
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gggcattaga aatgatttag gctggtatca gcagaaacca 120

gggaaagccc ctaagcgcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtctacag cataatagtt accctctcac tttcggcgga 300

gggaccaagg tggagatcaa 320

<210> 480
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> Human IGHV4-4 JH4 acceptor framework cDNA

<400> 480
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcagggac cctgtccctc 60

acctgcgctg tctctggtgg ctccatcagc agtagtaact ggtggagttg ggtccgccag 120

cccccaggga aggggctgga gtggattggg gaaatctatc atagtgggag caccaactac 180

aacccgtccc tcaagagtcg agtcaccata tcagtagaca agtccaagaa ccagttctcc 240

ctgaagctga gctctgtgac cgccgcggac acggccgtgt attactgtgc gagatacttt 300

gactactggg gccaaggaac cctggtcacc gtctcctca 339

<210> 481
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> IGHV4-4

<400> 481

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

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Ser Ser Ser
20 25 30

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

Ile Gly Glu Ile Tyr His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu

50 55 60

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

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

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

Ser

<210> 482
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> H3 gH1 heavy chain variable region

<400> 482

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 Asn
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 Tyr Pro Gly Ser Gly Ser Thr Thr Asn Asn Glu 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 Tyr Cys
                85                  90                  95


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


Thr Thr Leu Thr Val Ser Ser
        115


<210>  483
<211>  119
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  H3 gH19 heavy chain variable region

<400>  483

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 Asn
            20                  25                  30


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


Gly Asp Ile Ser Pro Gly Ser Gly Ser Thr Thr Asn Asn Glu 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 Tyr Cys
                85                  90                  95


Ala Arg Leu Arg Gly Tyr Tyr Asp Tyr Phe Asp Phe Trp Gly Gln Gly
```

100 105 110

Thr Thr Leu Thr Val Ser Ser
115

<210> 484
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> H3 gH20 heavy chain variable region

<400> 484

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 Asn
20 25 30

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

Gly Asp Ile Ser Pro Gly Ser Gly Ser Thr Thr Asn Asn Glu 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 Tyr Cys
85 90 95

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

Thr Thr Leu Thr Val Ser Ser
115

<210> 485
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> H3 gL1 light chain variable region

<400> 485

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

Glu Lys Val Thr Ile Thr Cys Ser Val Ser Ser Ser Ile Ser Ser Ser
20 25 30

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

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

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

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

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

<210> 486
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> H3 gL11 light chain variable region

<400> 486

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


Glu Lys Val Thr Ile Thr Cys Ser Val Ser Ser Ser Ile Ser Ser Ser
            20                  25                  30


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


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


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


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


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


<210>  487
<211>  112
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  909 gL13 VL-region

<400>  487

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


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


Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
```

35 40 45

Tyr Lys Ala Ser Thr Leu Ala 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 Thr Tyr Tyr Cys Gln Ala Thr Tyr Gly Thr Tyr Ala
85 90 95

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

<210> 488
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> 909 gL50 VL-region

<400> 488

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

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

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

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


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


<210>  489
<211>  219
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  909 gL13 VL + CL-region

<400>  489

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


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


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


Tyr Lys Ala Ser Thr Leu Ala 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 Thr Tyr Tyr Cys Gln Ala Thr Tyr Gly Thr Tyr Ala
                85                  90                  95


Gly Ser Phe Phe Tyr Ser Phe Gly Gly Gly Thr Lys Val 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> 490
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> 909 gL50 VL + CL-region

<400> 490

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

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

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

```
Tyr Lys Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Lys 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 Thr Tyr Tyr Ala Gln Ala Thr Tyr Gly Thr Tyr Ala
                85                  90                  95

Gly Ser Phe Phe Tyr Ser Phe Gly Gly Gly Thr Lys Val 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> 491
<211> 336
<212> DNA

<213> Artificial Sequence

<220>
<223> 909 gL13 V-region (Seq. ID No. 487) cDNA

<400> 491
gacatccaaa tgacccagtc cccttcctcc ctttcagcca gcgtgggcga tagagtgact 60

atcacttgcc aagcgtcgga ggacatctcg cgctacctgg tgtggtatca acagaagcca 120

ggtaaagcgc ccaagcggct gatctacaag gcctcaactt tggcatccgg agtgccgtcg 180

aggttctccg gcagcggatc gggaaccgag ttcactctca ccattagctc actgcagccg 240

gaagattttg ccacttacta ctgccaggct acctacggga cctacgctgg gtcgttcttt 300

tacagcttcg gaggcggaac caaagtggaa atcaag 336

<210> 492
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> 909 gL13 light chain (V + constant) (Seq. ID No. 489) cDNA

<400> 492
gacatccaaa tgacccagtc cccttcctcc ctttcagcca gcgtgggcga tagagtgact 60

atcacttgcc aagcgtcgga ggacatctcg cgctacctgg tgtggtatca acagaagcca 120

ggtaaagcgc ccaagcggct gatctacaag gcctcaactt tggcatccgg agtgccgtcg 180

aggttctccg gcagcggatc gggaaccgag ttcactctca ccattagctc actgcagccg 240

gaagattttg ccacttacta ctgccaggct acctacggga cctacgctgg gtcgttcttt 300

tacagcttcg gaggcggaac caaagtggaa atcaagcgta cggtggccgc tccctccgtg 360

ttcatcttcc caccctccga cgagcagctg aagtccggca ccgcctccgt cgtgtgcctg 420

ctgaacaact tctacccccg cgaggccaag gtgcagtgga aggtggacaa cgccctgcag 480

tccggcaact cccaggaatc cgtcaccgag caggactcca aggacagcac ctactccctg 540

tcctccaccc tgaccctgtc caaggccgac tacgagaagc acaaggtgta cgcctgcgaa 600

gtgacccacc agggcctgtc cagccccgtg accaagtcct tcaaccgggg cgagtgc 657

<210> 493
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> 909 gL50 V-region (Seq. ID No. 488) cDNA

<400> 493
gacgtcgtca tgacccagtc cccttcctcc ctttcagcca gcgtgggcga tagagtgact 60

atcacttgcc aagcgtcgga ggacatctcg cgctacctgg tgtggtatca acagaagcca 120

ggtaaagcgc ccaagcggct gatctacaag gcctcaactt tggcatccgg agtgccgtcg 180

aggttcaagg gcagcggatc gggaaccgac ttcactctca ccattagctc actgcagccg 240

gaagattttg ccacttacta cgcccaggct acctacggga cctacgctgg gtcgttcttt 300

tacagcttcg gaggcggaac caaagtggaa atcaag 336

<210> 494
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> 909 gL50 light chain (V + constant) (Seq. ID No. 490) cDNA

<400> 494
gacgtcgtca tgacccagtc cccttcctcc ctttcagcca gcgtgggcga tagagtgact 60

atcacttgcc aagcgtcgga ggacatctcg cgctacctgg tgtggtatca acagaagcca 120

ggtaaagcgc ccaagcggct gatctacaag gcctcaactt tggcatccgg agtgccgtcg 180

aggttcaagg gcagcggatc gggaaccgac ttcactctca ccattagctc actgcagccg 240

gaagattttg ccacttacta cgcccaggct acctacggga cctacgctgg gtcgttcttt 300

tacagcttcg gaggcggaac caaagtggaa atcaagcgta cggtggccgc tccctccgtg 360

ttcatcttcc caccctccga cgagcagctg aagtccggca ccgcctccgt cgtgtgcctg 420

ctgaacaact tctacccccg cgaggccaag gtgcagtgga aggtggacaa cgccctgcag 480

tccggcaact cccaggaatc cgtcaccgag caggactcca aggacagcac ctactccctg 540

tcctccaccc tgaccctgtc caaggccgac tacgagaagc acaaggtgta cgcctgcgaa 600

gtgacccacc agggcctgtc cagccccgtg accaagtcct tcaaccgggg cgagtgc 657

<210> 495
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> H3 gH20 heavy chain variable region (Seq. ID No. 484) cDNA

<400> 495
caggtccaac tacagcagcc tggggctgaa cttgtgaagc ctggggcttc agtgaagctg 60

tcctgcaagg cttctggcta caccttcacc agcaacgcga taacctgggt gaagcagagg 120

cctggacaag gccttgagtg gattggagat atttctcctg gtagtggtag tactactaac 180

aatgagaagt tcaagagcaa ggccacactg actgtagaca catcctccag cacagcctac 240

atgcagctca gcagcctgac atctgaggac tctgcggtct attactgtgc aaggctaagg 300

ggcttctatg attactttga cttctggggc caaggcacca ctctcacagt ctcgagt 357

<210> 496
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain Fab gamma 1 constant region

<400> 496

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

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

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

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

Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val
65 70 75 80

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

Ile Val Pro Arg Asp Cys
100

<210> 497
<211> 306
<212> DNA
<213> Artificial Sequence

<220>
<223> Heavy chain Fab gamma 1 constant region (Seq. ID No. 496) cDNA

<400> 497
gccaaaacga cacccccatc tgtctatcca ctggcccctg gatctgctgc ccaaactaac 60

tccatggtga ccctgggatg cctggtcaag ggctatttcc ctgagccagt gacagtgacc 120

tggaactctg gatccctgtc cagcggtgtg cacaccttcc cggctgtcct gcaatctgac 180

ctctacactc tgagcagctc agtgactgtc ccctccagca cctggcccag cgagaccgtc 240

acctgcaacg ttgcccaccc ggccagcagc accaaggtgg acaagaaaat tgtgcccagg 300

gattgt 306

<210> 498
<211> 324
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain full length gamma 1 constant region

<400> 498

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


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


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


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


Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val
65                  70                  75                  80


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


Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro
            100                 105                 110


Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu
        115                 120                 125


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


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


Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr
                165                 170                 175
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Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn
            180                 185                 190


Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro
        195                 200                 205


Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln
    210                 215                 220


Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val
225                 230                 235                 240


Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val
                245                 250                 255


Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln
            260                 265                 270


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


Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val
    290                 295                 300


Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His
305                 310                 315                 320


Ser Pro Gly Lys
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<210> 499
<211> 1044
<212> DNA
<213> Artificial Sequence

<220>
<223> Heavy chain full length gamma 1 constant region (Seq. ID No. 498)

cDNA

<400> 499
gccaaaacga cacccccatc tgtctatcca ctggcccctg gatctgctgc ccaaactaac 60

tccatggtga ccctgggatg cctggtcaag ggctatttcc ctgagccagt gacagtgacc 120

tggaactctg gatccctgtc cagcggtgtg cacaccttcc agctgtcct gcagtctgac 180

ctctacactc tgagcagctc agtgactgtc ccctccagca cctggcccag cgagaccgtc 240

acctgcaacg ttgcccaccc ggccagcagc accaaggtgg acaagaaaat tgtgcccagg 300

gattgtggtt gtaagccttg catatgtaca gtcccagaag tatcatctgt cttcatcttc 360

cccccaaagc ccaaggatgt gctcaccatt actctgactc ctaaggtcac gtgtgttgtg 420

gtagacatca gcaaggatga tcccgaggtc agttcagct ggtttgtaga tgatgtggag 480

gtgcacacag ctcagacgca accccgggag gagcagttca acagcacttt ccgctcagtc 540

agtgaacttc ccatcatgca ccaggactgg ctcaatggca aggagttcaa atgcagggtc 600

aacagtgcag ctttccctgc ccccatcgag aaaaccatct ccaaaaccaa aggcagaccg 660

aaggctccac aggtgtacac cattccacct cccaaggagc agatggccaa ggataaagtc 720

agtctgacct gcatgataac agacttcttc cctgaagaca ttactgtgga gtggcagtgg 780

aatgggcagc cagcggagaa ctacaagaac actcagccca tcatggacac agatggctct 840

tacttcgtct acagcaagct caatgtgcag aagagcaact gggaggcagg aaatactttc 900

acctgctctg tgttacatga gggcctgcac aaccaccata ctgagaagag cctctcccac 960

tctcctggta aatgatccca gtgtccttgg agccctctgg tcctacagga ctctgacacc 1020

tacctccacc cctccctgta taaa 1044

<210> 500
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain kappa constant

<400> 500

Arg Thr Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu
1 5 10 15

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

Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
35 40 45

Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
50 55 60

Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
65 70 75 80

Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
85 90 95

Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
100 105

<210> 501
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Light chain kappa constant (Seq. ID No. 500) cDNA

<400> 501
cgtacggatg ctgcaccaac tgtatccatc ttcccaccat ccagtgagca gttaacatct 60

ggaggtgcct cagtcgtgtg cttcttgaac aacttctacc ccaaagacat caatgtcaag 120

tggaagattg atggcagtga acgacaaaat ggcgtcctga acagttggac tgatcaggac 180

agcaaagaca gcacctacag catgagcagc accctcacgt tgaccaagga cgagtatgaa 240

cgacataaca gctatacctg tgaggccact cacaagacat caacttcacc cattgtcaag 300

agcttcaaca ggaatgagtg t 321

<210> 502
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> H3 gL1 light chain variable region (Seq. ID No. 485) cDNA

<400> 502
gaagttgtgc tcacccagtc tccagcactc atggctgcat ctccagggga gaaggtcacc 60

atcacctgca gtgtcagctc aagtataagt tccagcaact tgcactggta ccagcagaag 120

tcagaaacct cccccaaacc ctggatttat ggcacatcca acctggcttc tggagtccct 180

gttcgcttca gtggcagtgg atctgggacc tcttattctc tcacaatcag cagcatggag 240

gctgaagatg ctgccactta ttactgtcaa cagtggagtc attacccgct cacgttcggt 300

gctgggacca agctggagct gaaa 324

<210> 503
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> H3 gL11 light chain variable region (Seq. ID No. 486) cDNA

<400> 503
gaagttgtgc tcacccagtc tccagcactc atggctgcat ctccagggga gaaggtcacc 60

atcacctgca gtgtcagctc aagtataagt tccagcaact tgcactggta ccagcagaag 120

tcagaaacct cccccaaacc ctggatttat ggcacatcca acctggcttc tggagtccct 180

gttcgcttca gtggcagtgg atctgggacc tcttattctc tcacaatcag cagcatggag 240

gctgaagatg ctgccactta ttactgtcaa caggcgagtc attacccgct cacgttcggt 300

gctgggacca agctggagct gaaa 324

<210> 504
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> H3 gH1 heavy chain variable region (Seq. ID No. 482) cDNA

<400> 504
caggtccaac tacagcagcc tggggctgaa cttgtgaagc ctggggcttc agtgaagctg 60

tcctgcaagg cttctggcta caccttcacc agcaactgga taacctgggt gaagcagagg 120

cctggacaag gccttgagtg gattggagat atttatcctg gtagtggtag tactactaac 180

aatgagaagt tcaagagcaa ggccacactg actgtagaca catcctccag cacagcctac 240

atgcagctca gcagcctgac atctgaggac tctgcggtct attactgtgc aaggctaagg 300

ggctactatg attactttga cttctggggc caaggcacca ctctcacagt ctcgagt 357

<210> 505
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> H3 gH19 heavy chain variable region (Seq. ID No. 483) cDNA

<400> 505
caggtccaac tacagcagcc tggggctgaa cttgtgaagc ctggggcttc agtgaagctg 60

tcctgcaagg cttctggcta caccttcacc agcaacgcga taacctgggt gaagcagagg 120

cctggacaag gccttgagtg gattggagat atttctcctg gtagtggtag tactactaac 180

aatgagaagt tcaagagcaa ggccacactg actgtagaca catcctccag cacagcctac 240

atgcagctca gcagcctgac atctgaggac tctgcggtct attactgtgc aaggctaagg 300

ggctactatg attactttga cttctggggc caaggcacca ctctcacagt ctcgagt 357

<210> 506
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> IGKV1-17

<400> 506

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

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

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

Tyr Ala Ala Ser Ser 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 Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Tyr
85 90 95

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

<210> 507
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> 909gH14 V-region (Seq. ID No. 457) cDNA

<400> 507
gaagtccagc tgcaagaatc aggtccaggc ctcgtcaaac catcaggaac tttgtcattg 60

acttgcgccg tgagcgggtt ctcgctttcg acctactaca tgtcgtgggt gcgccagccg 120

cctgggaagg gactggagtg gatcggcatc atctacccgt ccggcagcac gtactgcgct 180

agctgggcca aggggcggtt caccatcagc aaggcgtcca ctaaaaatac tgtggacctc 240

aagctgtcgt cagttactgc ggccgacact gcaacctact tttgtgcccg cccggataac 300

gatggaacct ccggctacct gtccggattc ggactgtggg gacagggaac ccttgtgact 360

gtctcgagc 369

<210> 508
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> 909 gH14 IgG4 heavy chain (V + human gamma-4P constant) (Seq. ID No. 457) cDNA

<400> 508
gaagtccagc tgcaagaatc aggtccaggc ctcgtcaaac catcaggaac tttgtcattg 60

acttgcgccg tgagcgggtt ctcgctttcg acctactaca tgtcgtgggt gcgccagccg 120

cctgggaagg gactggagtg gatcggcatc atctacccgt ccggcagcac gtactgcgct 180

agctgggcca aggggcggtt caccatcagc aaggcgtcca ctaaaaatac tgtggacctc 240

aagctgtcgt cagttactgc ggccgacact gcaacctact tttgtgcccg cccggataac 300

gatggaacct ccggctacct gtccggattc ggactgtggg gacagggaac ccttgtgact 360

gtctcgagcg cctccaccaa gggcccctcc gtgttccctc tggcccctg ctcccggtcc 420

acctccgagt ctaccgccgc tctgggctgc ctggtcaagg actacttccc cgagcccgtg 480

acagtgtcct ggaactctgg cgccctgacc tccggcgtgc acaccttccc tgccgtgctg 540

cagtcctccg gcctgtactc cctgtcctcc gtcgtgaccg tgccctcctc cagcctgggc 600

accaagacct acacctgtaa cgtggaccac aagccctcca acaccaaggt ggacaagcgg 660

gtggaatcta agtacggccc tccctgcccc ccctgccctg cccctgaatt tctgggcgga 720

ccttccgtgt tcctgttccc cccaaagccc aaggacaccc tgatgatctc ccggacccc 780

gaagtgacct gcgtggtggt ggacgtgtcc caggaagatc ccgaggtcca gttcaattgg 840

tacgtggacg gcgtggaagt gcacaatgcc aagaccaagc ccagagagga acagttcaac 900

tccacctacc gggtggtgtc cgtgctgacc gtgctgcacc aggactggct gaacggcaaa 960

gagtacaagt gcaaggtgtc caacaagggc ctgccctcca gcatcgaaaa gaccatctcc 1020

aaggccaagg gccagccccg cgagccccag gtgtacaccc tgcccctag ccaggaagag 1080

atgaccaaga accaggtgtc cctgacctgt ctggtcaagg gcttctaccc ctccgacatt 1140

gccgtggaat gggagtccaa cggccagccc gagaacaact acaagaccac cccccctgtg 1200

ctggacagcg acggctcctt cttcctgtac tctcggctga ccgtggacaa gtcccggtgg 1260

caggaaggca acgtcttctc ctgctccgtg atgcacgagg ccctgcacaa ccactacacc 1320

cagaagtccc tgtccctgag cctgggcaag 1350

<210> 509
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> 909gH61 V-region (Seq. ID. No. 461) cDNA

<400> 509
gaagtccagc tgcaagaatc aggtccaggc ctcgtcaaac catcaggaac tttgtcattg 60

acttgcgccg tgagcgggtt ctcgctttcg acctactaca tgtcgtgggt gcgccagccg 120

cctgggaagg gactggagtg gatcggcatc atctacccgt ccggcagcac gtactgcgct 180

agctgggcca aggggcgggt gaccatcagc aaggactcca gcaaaaatca ggtgagcctc 240

aagctgtcgt cagttactgc ggccgacact gcagtgtact attgtgcccg cccggataac 300

gatggaacct ccggctacct gtccggattc ggactgtggg gacagggaac ccttgtgact 360

gtctcgagc 369

<210> 510
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> 909 gH61 IgG4 heavy chain (V + human gamma-4P constant) (Seq. ID No. 462) cDNA

<400> 510
gaagtccagc tgcaagaatc aggtccaggc ctcgtcaaac catcaggaac tttgtcattg 60

acttgcgccg tgagcgggtt ctcgctttcg acctactaca tgtcgtgggt gcgccagccg 120

cctgggaagg gactggagtg gatcggcatc atctacccgt ccggcagcac gtactgcgct 180

agctgggcca aggggcgggt gaccatcagc aaggactcca gcaaaaatca ggtgagcctc 240

aagctgtcgt cagttactgc ggccgacact gcagtgtact attgtgcccg cccggataac 300

gatggaacct ccggctacct gtccggattc ggactgtggg gacagggaac ccttgtgact 360

gtctcgagcg cctccaccaa gggcccctcc gtgttccctc tggcccctg ctcccggtcc 420

acctccgagt ctaccgccgc tctgggctgc ctggtcaagg actacttccc cgagcccgtg 480

acagtgtcct ggaactctgg cgccctgacc tccggcgtgc acaccttccc tgccgtgctg 540

cagtcctccg gcctgtactc cctgtcctcc gtcgtgaccg tgccctcctc cagcctgggc 600

accaagacct acacctgtaa cgtggaccac aagccctcca acaccaaggt ggacaagcgg 660

gtggaatcta agtacggccc tccctgcccc ccctgccctg cccctgaatt tctgggcgga 720

ccttccgtgt tcctgttccc cccaaagccc aaggacaccc tgatgatctc ccggaccccc 780

gaagtgacct gcgtggtggt ggacgtgtcc caggaagatc ccgaggtcca gttcaattgg 840

tacgtggacg gcgtggaagt gcacaatgcc aagaccaagc ccagagagga acagttcaac 900

tccacctacc gggtggtgtc cgtgctgacc gtgctgcacc aggactggct gaacggcaaa 960

gagtacaagt gcaaggtgtc caacaagggc ctgccctcca gcatcgaaaa gaccatctcc 1020

aaggccaagg gccagccccg cgagccccag gtgtacaccc tgcccctag ccaggaagag 1080

atgaccaaga accaggtgtc cctgacctgt ctggtcaagg gcttctaccc ctccgacatt 1140

gccgtggaat gggagtccaa cggccagccc gagaacaact acaagaccac cccccctgtg 1200

ctggacagcg acggctcctt cttcctgtac tctcggctga ccgtggacaa gtcccggtgg 1260

caggaaggca acgtcttctc ctgctccgtg atgcacgagg ccctgcacaa ccactacacc 1320

cagaagtccc tgtccctgag cctgggcaag 1350

<210> 511
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> 909gH62 V-region (Seq. ID. No. 463) cDNA

<400> 511
gaagtccagc tgcaagaatc aggtccaggc ctcgtcaaac catcaggaac tttgtcattg 60

acttgcgccg tgagcgggtt ctcgctttcg acctactaca tgtcgtgggt gcgccagccg 120

cctgggaagg gactggagtg gatcggcatc atctacccgt ccggcagcac gtactccgct 180

agctgggcca aggggcgggt gaccatcagc aaggactcca gcaaaaatca ggtgagcctc 240

aagctgtcgt cagttactgc ggccgacact gcagtgtact attgtgcccg cccggataac 300

gagggaacct ccggctacct gtccggattc ggactgtggg gacagggaac ccttgtgact 360

gtctcgagc 369

<210> 512
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> 909 gH62 IgG4 heavy chain (V + human gamma-4P constant) (Seq. ID No. 464) cDNA

<400> 512
gaagtccagc tgcaagaatc aggtccaggc ctcgtcaaac catcaggaac tttgtcattg 60

acttgcgccg tgagcgggtt ctcgctttcg acctactaca tgtcgtgggt gcgccagccg 120

cctgggaagg gactggagtg gatcggcatc atctacccgt ccggcagcac gtactccgct 180

agctgggcca aggggcgggt gaccatcagc aaggactcca gcaaaaatca ggtgagcctc 240

aagctgtcgt cagttactgc ggccgacact gcagtgtact attgtgcccg cccggataac 300

gagggaacct ccggctacct gtccggattc ggactgtggg gacagggaac ccttgtgact 360

gtctcgagcg cctccaccaa gggcccctcc gtgttccctc tggccccttg ctcccggtcc 420

acctccgagt ctaccgccgc tctgggctgc ctggtcaagg actacttccc cgagcccgtg 480

acagtgtcct ggaactctgg cgccctgacc tccggcgtgc acaccttccc tgccgtgctg 540

cagtcctccg gcctgtactc cctgtcctcc gtcgtgaccg tgccctcctc cagcctgggc 600

accaagacct acacctgtaa cgtggaccac aagccctcca acaccaaggt ggacaagcgg 660

gtggaatcta agtacggccc tccctgcccc ccctgccctg cccctgaatt tctgggcgga 720

ccttccgtgt tcctgttccc cccaaagccc aaggacaccc tgatgatctc ccggaccccc 780

gaagtgacct gcgtggtggt ggacgtgtcc caggaagatc ccgaggtcca gttcaattgg 840

tacgtggacg gcgtggaagt gcacaatgcc aagaccaagc ccagagagga acagttcaac 900

tccacctacc gggtggtgtc cgtgctgacc gtgctgcacc aggactggct gaacggcaaa 960

gagtacaagt gcaaggtgtc caacaagggc ctgccctcca gcatcgaaaa gaccatctcc 1020

aaggccaagg gccagccccg cgagccccag gtgtacaccc tgcccctag ccaggaagag 1080

atgaccaaga accaggtgtc cctgacctgt ctggtcaagg gcttctaccc ctccgacatt 1140

gccgtggaat gggagtccaa cggccagccc gagaacaact acaagaccac ccccctgtg 1200

ctggacagcg acggctcctt cttcctgtac tctcggctga ccgtggacaa gtcccggtgg 1260

caggaaggca acgtcttctc ctgctccgtg atgcacgagg ccctgcacaa ccactacacc 1320

cagaagtccc tgtccctgag cctgggcaag 1350

<210> 513
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> 36B4 primer 1

<400> 513
cactggtcta ggacccgaga a 21

<210> 514
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> 36B4 primer 2

<400> 514
aggggagat gttcagcatg t 21

<210> 515
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> FAS primer 1

<400> 515
ggaggtggtg atagccggta t 21

<210> 516
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> FAS primer 2

<400> 516
tgggtaatcc atagagccca g 21

<210> 517
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> SCD1 primer 1

<400> 517
ttcttgcgat acactctggt gc 22

<210> 518
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> SCD1 primer 2

<400> 518
cgggattgaa tgttcttgtc gt 22

<210> 519
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Pck1 primer 1

<400> 519
ctgcataacg gtctggactt c 21

<210> 520
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Pck1 primer 2

<400> 520
cagcaactgc ccgtactcc 19

<210> 521
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> G6pc primer 1

<400> 521
cgactcgcta tctccaagtg a 21

<210> 522
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> G6pc primer 2

<400> 522
gttgaaccag tctccgacca 20

<210> 523
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> ACC1 primer 1

<400> 523
atgtctggct tgcacctagt a 21

<210> 524
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> ACC1 primer 2

<400> 524
ccccaaagcg agtaacaaat tct 23

<210> 525
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TNF primer 1

<400> 525
ccctcacact cagatcatct tct 23

<210> 526
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> TNF primer 2

<400> 526
gctacgacgt gggctacag 19

<210> 527
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-1beta primer 1

<400> 527
gcaactgttc ctgaactcaa ct 22

<210> 528
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-1beta primer 2

<400> 528
atcttttggg gtccgtcaac t 21

<210> 529
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-6 primer 1

<400> 529
acaaccacgg ccttccctac tt 22

<210> 530
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-6 primer 2

<400> 530
cacgatttcc cagagaacat gtg 23

<210> 531
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> CCL2 primer 1

<400> 531
catccacgtg ttggctca 18

<210> 532
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> CCL2 primer 2

<400> 532
gatcatcttg ctggtgaatg agt 23

<210> 533
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> CXCL1 primer 1

<400> 533
gactccagcc acactccaac 20

<210> 534
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> CXCL1 primer 2

<400> 534
tgacagcgca gctcattg 18

<210> 535
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> F4/80 primer 1

<400> 535
tgactcacct tgtggtccta a 21

<210> 536
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> F4/80 primer 2

<400> 536
cttcccagaa tccagtcttt cc 22

<210> 537
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> CD68 primer 1

<400> 537
tgtctgatct tgctaggacc g 21

<210> 538
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> CD68 primer 2

<400> 538
gagagtaacg gccttttgt ga 22

<210> 539
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> TBP primer 1

<400> 539
agaacaatcc agactagcag ca 22

<210> 540
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> TBP primer 2

<400> 540
gggaacttca catcacagct c 21

<210> 541
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Control target sequence

<400> 541
gtctccacgc gcagtacatt t 21

<210> 542
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Foxo1 target sequence

<400> 542
gcatgtttat tgagcgcttg g 21

<210> 543
<211> 21
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atgaagtgca ccctaacaag cc 22

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tgagcgactc aaactgccct 20

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

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<400> 602

Leu Arg Gly Tyr Tyr Asp Tyr Phe Asp Phe
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