

CRBI_007_01WO_SeqList_ST25
SEQUENCE LISTING

<110> Crown Bioscience, Inc.
Zha, Jiping
Sun, Ziyong
Qiu, Junzhuan

<120> ANTI PD-L1 ANTIBODIES

<130> CRBI-007/01WO

<150> PCT/CN2014/083715

<151> 2014-08-05

<160> 156

<170> PatentIn version 3.5

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<211> 348

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<213> Mus sp.

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ccagagaaga ggctggagtg ggtcgcattcc attagtagtg gtggtagcac ctactatcca	180
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35 40 45	
Ala Ser Ile Ser Ser Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val Lys	
50 55 60	
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Arg Asn Ile Leu Tyr Leu	
65 70 75 80	
Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Asp Cys Ala	
85 90 95	

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

Thr Val Ser Glu
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caacagaaac caggacagcc acccaaactc ctcatcaagt atgcatccaa cctagaatct 180
ggggtccctg ccaggttcag tggcagtggg tctgggacag acttcaccct caacatccat 240
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<210> 4
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Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
20 25 30

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

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

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

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

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

<210> 5
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<400> 5

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

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

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

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

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

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

Ile Val Ser Ala
 115

<210> 7
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 caacagaaac caggacagcc tcccaaactc ctcatcaagt atgcatccaa cctagaatct 180
 ggggtccctg ccaggttcag tggcagtggg tctgggacag acttcaccct caacatccat 240
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<210> 8
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 <213> Mus sp.

<400> 8

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Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
 20 25 30

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

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

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

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

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

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<400> 9

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ccaggaaagg gtctggaatg gctgggagtg atatggcgtg gtgtaaccac agactataat 180

gcagctttca tgtccagact gaccatcacc aaggacaatt ccaagagcca agttttcttt 240

aaaatgaaca gtctgcaagc taatgacaca gccatatatt actgtgccag actggggtttc 300

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<400> 10

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

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

Gly Val Ile Trp Arg Gly Val Thr Thr Asp Tyr Asn Ala Ala Phe Met
50 55 60

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

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

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

Thr Val Ser Ser
115

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gggcagtctc ctaaactgct gatataattat gcagccaatc gctacactgg agtccttgat 180
cgcttcactg gcagtggata tgggacggat ttcactttca ccatcagcat tgtgcaggct 240
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gggaccaagc tggaaataaa acgg 324

<210> 12
<211> 107
<212> PRT
<213> Mus sp.

<400> 12

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

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

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

CRBI_007_01WO_SeqList_ST25

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

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

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

<210> 13
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<212> DNA
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ccaggaaagg gtctggagtg gctgggagtg atatggagtg gtggagtcac agactataat 180
gcagctttca tatccagact gagcatcagc aaggacaatt ccaagagcca agttttcttt 240
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Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Tyr
20 25 30

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

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

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

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

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

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Thr Val Ser Ser
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cgcttcactg gcagtggata tgggacggat ttcactttca ccatcagcac tgtgcaggct 240
gaagacctgg cagtttattt ctgtcaacaa gattatacct ctccgtacac gttcggaggg 300
gggaccaagc tggaaataaa a 321

<210> 16
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<212> PRT
<213> Mus sp.

<400> 16

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

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

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

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

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

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

<210> 17
<211> 357
<212> DNA
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 ctgcaaatga gcaaagtga atctgaggac actgcccttt attactgtgc aaaacccggg 300
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<210> 18
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 <213> Mus sp.

<400> 18

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

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

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

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

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

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

Ala Lys Pro Gly Asp Tyr Gly Tyr Asp Phe Asp Cys Trp Gly Gln Gly
 100 105 110

Thr Thr Leu Thr Val Ser Ser
 115

<210> 19
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 <212> DNA
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<400> 19

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<210> 20

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<211> 112
<212> PRT
<213> Mus sp.

<400> 20

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

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

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

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

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

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

<210> 21
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<212> DNA
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<400> 21

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ccagggaata aacttgagta catgggggtac ataagctaca gtggtagcac ttactacaat	180
ccatctctca aaagtcgaat ctccatcact cgagacacat ccaagaacca gtactacctg	240
cagttgaatt ctgtgactac tgaggacaca gccacatatt actgtgcaag aagtctacta	300
tggttctcta cgggggtttgc ttactggggc caagggactc tggtcactgt ctctgca	357

<210> 22
<211> 119
<212> PRT
<213> Mus sp.

<400> 22

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

CRBI_007_01WO_SeqList_ST25

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

Gly Tyr Ile Ser Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Lys
50 55 60

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

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

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

Thr Leu Val Thr Val Ser Ala
115

<210> 23
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<212> DNA
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gctcgcttca gtggcagtgg gtctgggacc tcttactctc tcacaatcag cagcatggag 240
gctgaagatg ctgcctctta tttctgccat cagtggagaa gttaccacc cagctcggt 300
gctgggacca agctggagct gaaa 324

<210> 24
<211> 108
<212> PRT
<213> Mus sp.

<400> 24

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

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

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

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

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Ala Glu Asp Ala Ala Ser Tyr Phe Cys His Gln Trp Arg Ser Tyr Pro
85 90 95

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

<210> 25
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<212> DNA
<213> Mus sp.

<400> 25
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ccaggaaagg gtctggagtg gctgggagtg atatggagtg gtggaatcac agactataat 180
gcagctttca aatccagact gagcatcagc aaggacaatt ccaagagcca agttttcttt 240
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tatgctatgg actactgggg tcaaggaacc tcagtcaccg tctcctca 348

<210> 26
<211> 116
<212> PRT
<213> Mus sp.

<400> 26

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

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

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

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

Lys Met Asn Ser Leu Gln Ala Asn Asp Thr Ala Ile Tyr Phe Cys Ala
85 90 95

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

Thr Val Ser Ser
115

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<210> 27
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 <212> DNA
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 acttccccca aaagatggat ttatgacaca tccaaactgg cttctggagt ccctgctcgc 180
 ttcagtggca gtgggtctgg gacctcttac tctctcacia tcagcagcat gggggctgaa 240
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 accaagctgg aaatcaaa 318

<210> 28
 <211> 106
 <212> PRT
 <213> Mus sp.

<400> 28
 Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
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 Glu Lys Val Thr Met Thr Cys Ser Ala Asn Ser Ser Val Ser Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
 35 40 45
 Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Gly Ala Glu
 65 70 75 80
 Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Trp Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 29
 <211> 348
 <212> DNA
 <213> Mus sp.

<400> 29
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 ccagagaaga ggctggagtg ggtcgcaccc attagtagtg gtggaaccac ctactatcta 180
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caaatgagca gtctgaggtc tgaggacacg gccatgtatt attgtgcaag aggctatgat 300
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<210> 30
 <211> 116
 <212> PRT
 <213> Mus sp.

<400> 30

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

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

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

Ala Ser Ile Ser Ser Gly Gly Thr Thr Tyr Tyr Leu Gly Ser Val Gln
 50 55 60

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

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

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

Ser Val Ser Glu
 115

<210> 31
 <211> 333
 <212> DNA
 <213> Mus sp.

<400> 31

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 caacagaaac caggacagcc tcccaaactc ctcataagt atgcatccaa cctagaatct 180
 ggggtccctg ccaggttcag tggcagtggg tctgggacag acttcaccct caacatccat 240
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 acgttcggag gggggaccaa gctggaaata aaa 333

<210> 32
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 <213> Mus sp.

CRBI_007_01WO_SeqList_ST25

<400> 32

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

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
20 25 30

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

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

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

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

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

<210> 33

<211> 351

<212> DNA

<213> Mus sp.

<400> 33

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ccagggaata aacttgaata catgggatac ataagctaca ctggtagcac ttactacaat	180
ccatctctca aaagtcgaat ctccatctct cgagacacat ccaagagcca gtactacctg	240
cagttgaatt ctgtgactac tgaggacaca gccacatatt actgtgcaag acagagggat	300
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<210> 34

<211> 117

<212> PRT

<213> Mus sp.

<400> 34

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

Thr Leu Ser Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly
20 25 30

Tyr Trp Thr Trp Ile Arg Lys Phe Pro Gly Asn Lys Leu Glu Tyr Met
35 40 45

CRBI_007_01WO_SeqList_ST25

Gly Tyr Ile Ser Tyr Thr Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Lys
50 55 60

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

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

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

Val Thr Val Ser Ala
115

<210> 35
<211> 339
<212> DNA
<213> Mus sp.

<400> 35
gatattgtga tgacacagac tccatcctcc ctagctgtgt cacttggaga gaagggttact 60
atgagctgca agtccagtca gaggctttta tatagtagca atcaaaagaa ctccttggcc 120
tggtaccagc agaaaccagg acagtctcct aaactgctga ttactgggc atccaatagg 180
gaatctgggg tccctgatcg cttcacaggc agtagctctg ggacagattt cactctcacc 240
atcagcagtg tgaaggctga agacctggca gtttattact gtcagcaata ttatagctat 300
ccgctcacgt tcggtgctgg gaccaagctg gagctgaaa 339

<210> 36
<211> 113
<212> PRT
<213> Mus sp.

<400> 36

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

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

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

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

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

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

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

Lys

<210> 37
<211> 348
<212> DNA
<213> Mus sp.

<400> 37
gaagagaagc tggtaggagtc tgggggaggc ttagtgaagc ctggaggggc cctgaaactc 60
tcctgtgcag cctctggatt cagtttcagt agttatggca tgtcttgggt tcgtcagact 120
ccagagaaga ggctggagtg ggtcgcaccc atcagtagtg gtggtagtat ctactatcca 180
gacagtgtga agggccgatt caccatctcc agagataatg ccaggaacat cctgtacctg 240
caaatgagca gtctgaggtc tgaggacacg gccatgtatt attgtgcaag aggctatgat 300
gcgggggtttg ctttctgggg ccaagggaca ctgggtcactg cctctgca 348

<210> 38
<211> 116
<212> PRT
<213> Mus sp.

<400> 38
Glu Glu Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
20 25 30
Gly Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45
Ala Ser Ile Ser Ser Gly Gly Ser Ile Tyr Tyr Pro Asp Ser Val Lys
50 55 60
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Arg Asn Ile Leu Tyr Leu
65 70 75 80
Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95
Arg Gly Tyr Asp Ala Gly Phe Ala Phe Trp Gly Gln Gly Thr Leu Val
100 105 110
Thr Ala Ser Ala
115

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<210> 39
 <211> 333
 <212> DNA
 <213> Mus sp.

<400> 39
 gacattgtgc tgacacagtc tcctgcttcc ttagctgtat ctctggggca gagggccacc 60
 atctcatgca gggccagcca aagtgtcagt acatctagtt atagttatgt gacttggtac 120
 caacagaaac caggacagcc acccaaactc ctcatcaagt atgcatccaa cctagaatct 180
 ggggtccctg ccaggttcag tggcagtggg tctgggacag acttcaccct caacatccat 240
 cctgtggagg aggaggatac tgcaacatat tactgtcagc acagttggga gattccgtac 300
 acgttcggag gggggaccaa gctggaaata aaa 333

<210> 40
 <211> 111
 <212> PRT
 <213> Mus sp.

<400> 40
 Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
 20 25 30
 Ser Tyr Ser Tyr Val His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45
 Lys Leu Leu Ile Lys Tyr Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
 50 55 60
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65 70 75 80
 Pro Val Glu Glu Glu Asp Thr Ala Thr Tyr Tyr Cys Gln His Ser Trp
 85 90 95
 Glu Ile Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 41
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Humanized 5G11 antibody heavy chain variable region sequence

<400> 41
 cagatcacac tgaaagaaag cggccctacc ctgggtcaagc caactcagac cctgacactg 60
 acttgaccg tgtctgggtt ctctctgagt acatacggag tccactggat caggcagccc 120
 cctggcaaag ctctggagtg gctgggagtg atttggcggg gcgtcaccac agactataac 180

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gccgctttta tgtcaagact gacaatcact aaggataaca gcaaaaatca ggtggtcctg 240
 accatgaaca atatggaccc cgtggatacc gcaacatact attgtgcccg gctgggggttc 300
 tacgccatgg actattgggg ccaggggact ctggtgaccg tctcgagc 348

<210> 42
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized 5G11 antibody heavy chain variable region sequence

<400> 42

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

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

Gly Val Ile Trp Arg Gly Val Thr Thr Asp Tyr Asn Ala Ala Phe Met
 50 55 60

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

Thr Met Asn Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala
 85 90 95

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

Thr Val Ser Ser
 115

<210> 43
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Humanized 5G11 antibody light chain variable region sequence

<400> 43

gatatccaga tgactcagtc tccaagcagc ctgtctgcat ctgtggggga cagggtcacc 60

atcacatgca aagcatctca gagtgtgtca aacgatgtcg cctggtacca gcagaagccc 120

ggaaaagctc ctaagctgct gatttactat gccgctaatc ggtacactgg cgtgccagac 180

agattcagcg gatccggata tggaaccgat ttcactttta ccatcagctc cctgcagcca 240

gaggacattg ccacatattt ctgtcagcag gattacacaa gccctatac ttttggccag 300

gggaccaaac tggaaatcaa g

321

<210> 44
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized 5G11 antibody light chain variable region sequence
 <400> 44

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 Lys Ala Ser Gln Ser Val Ser Asn Asp
 20 25 30

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

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

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

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

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

<210> 45
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Humanized 13C5 antibody heavy chain variable region sequence

<400> 45
 gaggtgcagc tggctgagtc aggagggggg ctggtcaagc caggagggtc actgcgactg 60
 agctgcgcag cttccgggtt catcttttagg tcttatggca tgagttgggt gcgccaggca 120
 ccaggggaaag gactggagtg ggtcgcttca atcagctccg gaggcagcac ttactatcct 180
 gactccgtga agggccggtt caccatttct agagataacg ccaaaaatag tctgtacctg 240
 cagatgaact ctctgcgagc agaagacaca gccgtctacg attgtgctag aggatatgac 300
 agcggccttg catactgggg ccaggggacc ctggtgacag tctcgagc 348

<210> 46
 <211> 116
 <212> PRT
 <213> Artificial Sequence

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<220>

<223> Humanized 13C5 antibody heavy chain variable region sequence

<400> 46

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 Gly Phe Ile Phe Arg Ser Tyr
20 25 30

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

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

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

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

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

Thr Val Ser Ser
115

<210> 47

<211> 333

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanized 13C5 antibody light chain variable region sequence

<400> 47

gacattgtgc tgactcagag ccccgttca ctggcagtgt ctccagggca gcgggcaacc 60

atcacatgca gaggctcaca gagcgtctcc accagctcct ctagtttcat gacttggtac 120

cagcagaagc ccggacagcc ccctaagctg ctgatcaaat atgctagcaa cctggagtcc 180

ggcgtgccag ccaggttctc tggcagtggg tcaggaaccg actttactct gaccattaat 240

cccgtcgaag ccaacgatac agctaattac tattgtcagc attcctggga gatcccttac 300

acatttggcc aggggactaa gctggagatc aag 333

<210> 48

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized 13C5 antibody light chain variable region sequence

<400> 48

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

Gln Arg Ala Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
 20 25 30

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

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

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

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

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

<210> 49

<211> 1329

<212> DNA

<213> Artificial Sequence

<220>

<223> 8C6-IgG4 (F234A/L235A) chimeric antibody heavy chain full length sequence

<400> 49

caggtgcagc tgaagcagtc aggacctggc ctagtgcagc cctcacagag cctgtccatc 60
 acctgcacag tctctggttt ctcatctact agctatggtg tacactgggt tcgccagtct 120
 ccaggaaagg gtctggagtg gctgggagtg atatggagtg gtggagtcac agactataat 180
 gcagctttca tatccagact gagcatcagc aaggacaatt ccaagagcca agttttcttt 240
 aaaatgaaca gtctgcaagc taatgacaca gccatatatt actgtgccag actcggtttc 300
 tatgctatgg actactgggg tcaaggaacc tcagtcaccg tctcgagcgc ctccaccaag 360
 ggaccagcgc tgtttcccct ggccccctgt tccagatcca cctccgaaag cacagccgct 420
 ctcggctgcc tgggtcaagga ttacttccct gagcccgtga cagtctcctg gaatagcggc 480
 gctctgacct ccggcgtgca taccttccct gctgtgctgc aatcctccgg actgtacagc 540
 ctgagcagcg tggtcaccgt gccttcctcc agcctgggaa ccaaaaccta cacatgcaac 600
 gtggaccaca agcccagcaa caccaaagtg gacaagaggg tggagtcaa gtacggaccc 660
 ccttgtcctc cctgccctgc tcctgaagcc gctggaggac ctacgctgtt cctgtttccc 720
 cccaagcca aggacacct catgatctcc aggacccccg aggtgacctg tgctcggtg 780
 gacgtgagcc aagaggaccc cgaggtgcag ttcaactggt acgtggatgg cgtcgaggtc 840
 cataacgcca agaccaagcc tagggaggag cagttcaaca gcacctacag agtggtgagc 900

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gtcctgaccg tgctccacca agactggctg aacggcaagg aatacaagtg caaggtctcc 960
aacaagggac tcccttcctc catcgagaag accatcagca aggccaaggg ccagcccaga 1020
gaaccccaag tctacacact gccccccagc caagaggaaa tgaccaagaa ccaggtgagc 1080
ctgacctgcc tggtgaaagg cttctacccc agcgacattg ctgtcgaatg ggagagcaac 1140
ggccaacccg agaacaacta caagaccacc ccccctgtgc tcgacagcga cggctccttc 1200
ttcctctaca gcaggctgac agtggacaag tccaggtggc aagagggcaa tgtcttcagc 1260
tgtagcgtca tgcacgaggc cctccacaac cactacaccc agaagagcct gtccctctcc 1320
ctgggctga 1329

<210> 50

<211> 442

<212> PRT

<213> Artificial Sequence

<220>

<223> 8C6-IgG4 (F234A/L235A) chimeric antibody heavy chain full length sequence

<400> 50

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

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

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

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

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

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

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

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

Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu
130 135 140

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

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

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

Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr
195 200 205

Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
210 215 220

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

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

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
260 265 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
275 280 285

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
290 295 300

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

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

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

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
355 360 365

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

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

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

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
420 425 430

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
 435 440

<210> 51
 <211> 645
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 8C6 chimeric antibody light chain full length sequence

<400> 51
 agtattgtga tgaccagac tcccaaattc ctacttgtat cagcaggaga cagggttacc 60
 ataacctgca aggccagtca gagtgtgagt aatgatgtag gttggtacca acagaagcca 120
 gggcagtctc ctaaactact gatatactat gcatccaatc gctactctgg agtccttgat 180
 cgcttcactg gcagtggata tgggacggat ttcactttca ccatcagcac tgtgcaggct 240
 gaagacctgg cagtttattt ctgtcaacaa gattatacct ctccgtacac gttcggaggg 300
 gggaccaagc tggaaataaa acgtacggtg gccgcaccaa gcgtcttcat cttcccgcca 360
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
 ctgagctcgc ccgtcacaaa gagctttaac agaggcgagt gctga 645

<210> 52
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 8C6 chimeric antibody light chain full length sequence

<400> 52

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

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

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

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

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

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

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

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

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

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

Phe Asn Arg Gly Glu Cys
210

<210> 53
<211> 1329
<212> DNA
<213> Artificial Sequence

<220>
<223> 8H4-IgG4 (F234A/L235A) chimeric antibody heavy chain full length sequence

<400> 53
gaagtgaac tgggtggagtc tgggggaggc ttagtgaagc ctggagggtc cctgaaactc 60
tcctgtgcag cctctggatt cactttcagg agctatggca tgtcttgggc tcgccagatt 120
ccagagaaga ggctggagtg ggtcgcattc attagtagtg gtggaaccac ctactatcta 180
gggagtgtgc agggccgatt cacaatctcc agagataatg ccaggaacat cctgtacctg 240
caaatgagca gtctgaggtc tgaggacacg gccatgtatt attgtgcaag aggctatgat 300
gcgggatttg ctactgggg ccaagggact ctggtcagtg tctcgagcgc ctccaccaag 360
ggacccagcg tgtttccctt ggccccctgt tccagatcca cctccgaaag cacagccgct 420
ctcggctgcc tgggtcaagga ttacttcctt gagcccgtga cagtctcctg gaatagcggc 480
gctctgacct ccggcgtgca taccttcctt gctgtgctgc aatcctccgg actgtacagc 540
ctgagcagcg tggtcaccgt gccttcctcc agcctgggaa ccaaaacctt cacatgcaac 600
gtggaccaca agcccagcaa caccaaagtg gacaagaggg tggagtccaa gtacggaccc 660
ccttgcctc cctgccctgc tcctgaagcc gctggaggac ctagcgtgtt cctgtttccc 720
cccaagccca aggacaccct catgatctcc aggacccccg aggtgacctg tgctcgtggtg 780

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gacgtgagcc aagaggaccc cgaggtgcag ttcaactggt acgtggatgg cgtcgaggtc 840
cataacgcca agaccaagcc tagggaggag cagttcaaca gcacctacag agtggtgagc 900
gtcctgaccg tgctccacca agactggctg aacggcaagg aatacaagtg caaggtctcc 960
aacaagggac tcccttcctc catcgagaag accatcagca aggccaaggg ccagcccaga 1020
gaacccaag tctacacact gccccccagc caagaggaaa tgaccaagaa ccaggtgagc 1080
ctgacctgcc tggtgaaagg cttctacccc agcgacattg ctgtcgaatg ggagagcaac 1140
ggccaacccg agaacaacta caagaccacc cccctgtgc tcgacagcga cggctccttc 1200
ttcctctaca gcaggctgac agtggaacaag tccaggtggc aagagggcaa tgtcttcagc 1260
tgtagcgtca tgcacgaggc cctccacaac cactacaccc agaagagcct gtccctctcc 1320
ctgggctga 1329

<210> 54
<211> 442
<212> PRT
<213> Artificial Sequence

<220>
<223> 8H4-IgG4 (F234A/L235A) chimeric antibody heavy chain full length sequence
<400> 54

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

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

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

Ala Ser Ile Ser Ser Gly Gly Thr Thr Tyr Tyr Leu Gly Ser Val Gln
50 55 60

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

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

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

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

Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu
130 135 140

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

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

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

Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr
195 200 205

Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
210 215 220

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

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

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
260 265 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
275 280 285

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
290 295 300

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

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

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

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
355 360 365

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

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

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

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Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
420 425 430

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
435 440

<210> 55
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> 8H4 chimeric antibody light chain full length sequence

<400> 55
gacattgtgc tgacacagtc tcctgcttcc ttagctgtat ctctggggca gagggccacc 60
atctcatgca gggccagcca aagtgtcagt acatctagct atagttatat gacttggtac 120
caacagaaac caggacagcc tcccaaactc ctcatcaagt atgcatccaa cctagaatct 180
ggggtccctg ccaggttcag tggcagtggg tctgggacag acttcaccct caacatccat 240
cctgtggagg aggaggatac tgcaacatat tactgtcaga acagttggga gattccgtac 300
acgttcggag gggggaccaa gctggaaata aaacgtacgg tggccgcacc aagcgtcttc 360
atcttcccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 420
aataacttct atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg 480
ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 540
agcacctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc 600
acccatcagg gcctgagctc gcccgtcaca aagagcttta acagaggcga gtgctga 657

<210> 56
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> 8H4 chimeric antibody light chain full length sequence

<400> 56

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

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
20 25 30

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

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

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

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

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

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

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

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

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

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

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

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

<210> 57

<211> 1341

<212> DNA

<213> Artificial Sequence

<220>

<223> 5G11-IgG1 (D265A) chimeric antibody heavy chain full length sequence

<400> 57

caggtgcagc tgaagcagtc aggacctggc ctagtgcagc cctcacagag cctgtccatc 60

acctgcacag tctctggttt ctcatctaat acctatggtg tacactgggt tcgccagtct 120

ccaggaaagg gtctggaatg gctgggagtg atatggcgtg gtgtaaccac agactataat 180

gcagctttca tgtccagact gaccatcacc aaggacaatt ccaagagcca agttttcttt 240

aaaatgaaca gtctgcaagc taatgacaca gccatatatt actgtgccag actggggtttc 300

tatgctatgg actactgggg tcaaggaacc tcagtcaccg tctcgagcgc ctccactaag 360

ggcccatccg tgttccctct ggcaccctcc agcaagagca caagcggagg caccgccgca 420

ctgggctgcc tcgtgaagga ctacttccca gaaccctga ccgtcagctg gaatagcggc 480

gctctgacca gcggagtcca cactttcccc gcagtgtgtc agtccagcgg cctgtacagc 540

ctgagcagcg tggtcactgt gccaagcagc agcctgggca ctcagaccta catctgcaac 600

gtcaaccaca agcccagcaa cacaaagggtg gacaagaagg tcgagcccaa gtcctgcgat 660

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 gtcgtggtgg ccgtgagcca cgaagatccc gaggtgaagt tcaactggta cgtggacggc 840
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 gtcgtgagcg tcctgaccgt gctgcaccaa gactggctga acggcaagga gtataagtgc 960
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 caggtctccc tgacttgccct ggtgaagggg ttttatccca gcgacatcgc cgtcgagtgg 1140
 gagagcaatg gccagcccga aaacaactac aagaccacac cccctgtgct ggacagcgac 1200
 ggcagcttct ttctgtatag caaactgaca gtggataaga gcagatggca gcagggcaac 1260
 gtgttctcct gtcctgtgat gcacgaggcc ctgcacaatc actacacca gaagtccttg 1320
 agcctgtccc ccggaatatg a 1341

<210> 58

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> 5G11-IgG1 (D265A) chimeric antibody heavy chain full length sequence

<400> 58

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

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

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

Gly Val Ile Trp Arg Gly Val Thr Thr Asp Tyr Asn Ala Ala Phe Met
 50 55 60

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 59

<211> 1329

<212> DNA

<213> Artificial Sequence

<220>

<223> 5G11-IgG4 (F234A/L235A) chimeric antibody heavy chain full length sequence

<400> 59

caggtgcagc tgaagcagtc aggacctggc ctagtgcagc cctcacagag cctgtccatc	60
acctgcacag tctctggttt ctcatctact acctatggtg tacactgggt tcgccagtct	120
ccaggaaagg gtctggaatg gctgggagtg atatggcgtg gtgtaaccac agactataat	180
gcagctttca tgtccagact gacctcacc aaggacaatt ccaagagcca agttttcttt	240
aaaatgaaca gtctgcaagc taatgacaca gccatatatt actgtgccag actgggtttc	300
tatgctatgg actactgggg tcaaggaacc tcagtcaccg tctcgagcgc ctccaccaag	360
ggacctcagc tggttccctt ggccccctgt tccagatcca cctccgaaag cacagccgct	420
ctcggctgcc tgggtcaagga ttacttccct gagccccgtga cagtctcctg gaatagcggc	480
gctctgacct ccggcgtgca taccttccct gctgtgctgc aatcctccgg actgtacagc	540
ctgagcagcg tgggtaccgt gccttccctc agcctgggaa ccaaaacctc cacatgcaac	600
gtggaccaca agcccagcaa caccaaagtg gacaagaggg tggagtccaa gtacggaccc	660
ccttgtcctc cctgccctgc tcctgaagcc gctggaggac ctagcgtgtt cctgtttccc	720
cccaagccca aggacacct catgatctcc aggacccccg aggtgacctg tgtcgtggtg	780
gacgtgagcc aagaggacct cgaggtgcag ttcaactggt acgtggatgg cgtcgaggtc	840
cataacgcca agaccaagcc tagggaggag cagttcaaca gcacctacag agtggtgagc	900
gtcctgacct tgctccacca agactggctg aacggcaagg aatacaagtg caaggtctcc	960
aacaagggac tcccttctc catcgagaag accatcagca aggccaaggg ccagcccaga	1020
gaaccccaag tctacacact gccccccagc caagaggaaa tgaccaagaa ccaggtgagc	1080
ctgacctgcc tgggtgaaagg cttctacccc agcgacattg ctgtcgaatg ggagagcaac	1140
ggccaacccg agaacaacta caagaccacc cccctgtgc tcgacagcga cggctccttc	1200
ttcctctaca gcaggctgac agtggaagc tccaggtggc aagagggcaa tgtcttcagc	1260
tgtagcgtca tgcacgaggc cctccacaac cactacacc agaagagcct gtccctctcc	1320
ctgggctga	1329

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<210> 60
 <211> 442
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> 5G11-IgG4 (F234A/L235A) chimeric antibody heavy chain full length sequence

 <400> 60
 Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1 5 10 15
 Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Thr Tyr
 20 25 30
 Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
 35 40 45
 Gly Val Ile Trp Arg Gly Val Thr Thr Asp Tyr Asn Ala Ala Phe Met
 50 55 60
 Ser Arg Leu Thr Ile Thr Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
 65 70 75 80
 Lys Met Asn Ser Leu Gln Ala Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
 85 90 95
 Arg Leu Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val
 100 105 110
 Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
 115 120 125
 Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu
 130 135 140
 Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
 145 150 155 160
 Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
 165 170 175
 Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
 180 185 190
 Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr
 195 200 205
 Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
 210 215 220

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

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

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
260 265 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
275 280 285

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
290 295 300

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

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

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

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
355 360 365

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

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

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

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
420 425 430

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
435 440

<210> 61

<211> 645

<212> DNA

<213> Artificial sequence

<220>

<223> 5G11 chimeric antibody light chain full length sequence

<400> 61

agtattgtga tgaccagac tcccaaattc ctgcttgat cagcaggaga cagggttacc 60

ataacctgca aggccagtca gagtgtgagt aatgatgtag cttggtacca gcagaagcca 120

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gggcagtctc ctaaactgct gatataattat gcagccaatc gctacactgg agtccctgat 180
cgcttcactg gcagtggata tgggacggat ttacttttca ccatcagcat tgtgcaggct 240
gaagacctgg cagtttattt ctgtcagcag gattataacct ctccgtacac gttcggaggg 300
gggaccaagc tggaaataaa acgtacggtg gccgcaccaa gcgtcttcat cttcccgcc 360
tctgatgagc agttgaaatc tggaactgcc tctgtttgtgt gcctgctgaa taactttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagctttaac agaggcgagt gctga 645

<210> 62
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> 5G11 chimeric antibody light chain full length sequence
<400> 62

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

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

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

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

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

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

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

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

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Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

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

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

Phe Asn Arg Gly Glu Cys
210

<210> 63
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> 13C5-IgG1 (D265A) chimeric antibody heavy chain full length sequence

<400> 63
gaagtgaagc tgggtggagtc tgggggaggc ttagtgaagc ctggagggtc cctgaaactc 60
tcctgtgcag cctctggatt cattttcaga agctatggca tgtcttgggt tcgccagact 120
ccagagaaga ggctggagtg ggtcgcaccc attagtagtg gtggtagcac ctactatcca 180
gacagtgtga agggccgatt caccatctcc agagataatg ccaggaacat cttgtacctg 240
caaatgagca gtctgaggtc tgaggacacg gccatgtatg actgtgcaag aggctatgat 300
tcgggggtttg cttattgggg ccaagggact ctgggtcactg tctcgagcgc ctccactaag 360
ggcccatccg tgttccctct ggcaccctcc agcaagagca caagcggagg caccgccgca 420
ctgggctgcc tcgtgaagga ctacttccca gaaccctga ccgtcagctg gaatagcggc 480
gctctgacca gcggagtcca cactttcccc gcagtgtgtc agtccagcgg cctgtacagc 540
ctgagcagcg tgggtactgt gccaaagcagc agcctgggca ctcagacctc catctgcaac 600
gtcaaccaca agcccagcaa cacaaggtg gacaagaagg tcgagcccaa gtcctgcatg 660
aagaccaca cctgccctcc atgtcccgcc cccgagctgc tgggaggacc cagcgtcttc 720
ctgtttcccc ccaagccaaa ggacaccctg atgatcagca ggacccccga agtgacctgc 780
gtcgtggtgg ccgtgagcca cgaagatccc gaggtgaagt tcaactggta cgtggacggc 840
gtggaagtgc acaacgcaa gacaaaacc agggaggagc agtatgccag cacctacagg 900
gtcgtgagcg tcctgaccgt gctgcaccaa gactggctga acggcaagga gtataagtgc 960
aaggtgagca acaaggcact gcccgcctcc atcgagaaga ccatttccaa ggccaagggg 1020
caacctaggg agccacaggt ctacactctg cccctagca gggacgagct gaccaagaac 1080
caggtctccc tgacttgccct ggtgaagggg ttttatccca gcgacatcgc cgtcgagtgg 1140
gagagcaatg gccagcccga aaacaactac aagaccacac cccctgtgct ggacagcgac 1200
ggcagcttct ttctgtatag caaactgaca gtggataaga gcagatggca gcagggaac 1260

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gtgttctcct gctccgtgat gcacgaggcc ctgcacaatc actacacca gaagtccttg 1320
agcctgtccc ccggaatatg a 1341

<210> 64
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> 13C5-IgG1 (D265A) chimeric antibody heavy chain full length sequence
<400> 64

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

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Arg Ser Tyr
20 25 30

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 65

<211> 1329

<212> DNA

<213> Artificial Sequence

<220>

<223> 13C5-IgG4 (F234A/L235A) chimeric antibody heavy chain full length sequence

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<400> 65
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tcctgtgcag cctctggatt cattttcaga agctatggca tgtcttgggt tcgccagact      120
ccagagaaga ggctggagtg ggtcgcattcc attagtagtg gtggtagcac ctactatcca      180
gacagtgtga agggccgatt caccatctcc agagataatg ccaggaacat cttgtacctg      240
caaatgagca gtctgaggtc tgaggacacg gccatgtatg actgtgcaag aggctatgat      300
tcgggggtttg cttattgggg ccaagggact ctggtcactg tctcgagcgc ctccaccaag      360
ggacccagcg tgtttcccct ggccccctgt tccagatcca cctccgaaag cacagccgct      420
ctcggctgcc tgggtcaagga ttacttcctc gagcccgtga cagtctcctg gaatagcggc      480
gctctgacct ccggcgtgca taccttcctc gctgtgctgc aatcctccgg actgtacagc      540
ctgagcagcg tggtcaccgt gccttcctcc agcctgggaa ccaaaaccta cacatgcaac      600
gtggaccaca agcccagcaa caccaaagtg gacaagaggg tggagtccaa gtacggaccc      660
ccttgcctc cctgccctgc tcctgaagcc gctggaggac ctagcgtgtt cctgtttccc      720
cccaagccca aggacaccct catgatctcc aggacccccg aggtgacctg tgtcgtgggtg      780
gacgtgagcc aagaggaccc cgagggtgag ttcaactggt acgtggatgg cgtcgaggtc      840
cataacgcca agaccaagcc tagggaggag cagttcaaca gcacctacag agtggtgagc      900
gtcctgaccg tgctccacca agactggctg aacggcaagg aatacaagtg caaggtctcc      960
aacaagggac tcccttcctc catcgagaag accatcagca aggccaaggg ccagcccaga     1020
gaacccaag tctacacact gccccccagc caagaggaaa tgaccaagaa ccaggtgagc     1080
ctgacctgcc tgggtgaaagg cttctacccc agcgacattg ctgtcgaatg ggagagcaac     1140
ggccaacccg agaacaacta caagaccacc ccccctgtgc tcgacagcga cggctccttc     1200
ttcctctaca gcaggctgac agtggacaag tccaggtggc aagagggcaa tgtcttcagc     1260
tgtagcgtca tgcacgaggc cctccacaac cactacaccc agaagagcct gtccctctcc     1320
ctgggctga                                     1329

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<210> 66
<211> 442
<212> PRT
<213> Artificial Sequence

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<220>
<223> 13C5-IgG4 (F234A/L235A) chimeric antibody heavy chain full length
sequence

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<400> 66
Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1          5          10          15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Arg Ser Tyr
          20          25          30

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Gly Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
 35 40 45
 Ala Ser Ile Ser Ser Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val Lys
 50 55 60
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Arg Asn Ile Leu Tyr Leu
 65 70 75 80
 Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Asp Cys Ala
 85 90 95
 Arg Gly Tyr Asp Ser Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
 115 120 125
 Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu
 130 135 140
 Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
 145 150 155 160
 Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
 165 170 175
 Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
 180 185 190
 Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr
 195 200 205
 Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
 210 215 220
 Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro
 225 230 235 240
 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 245 250 255
 Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
 260 265 270
 Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 275 280 285
 Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 290 295 300

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

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

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

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
355 360 365

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

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

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

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
420 425 430

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
435 440

<210> 67

<211> 663

<212> DNA

<213> Artificial Sequence

<220>

<223> 13C5 chimeric antibody light chain full length sequence

<400> 67

gacattgtgc tgacacagtc tcctgcttcc ttagctgttt ctctggggca gagggccacc 60

atctcatgca gggccagcca aagtgtcagt acttctagct ctagttttat gcaactggtac 120

caacagaaaac caggacagcc acccaaactc ctcatcaagt atgcatccaa cctagaatct 180

ggggtccctg ccagggtcag tggcagtggg tctgggacag acttcaccct caacatccat 240

cctgtggagg aggaggatac tgcaacatat tactgtcagc acagttggga gattccgtac 300

acgttcggag gggggaccaa gctggaaata aaacgtacgc gtacggtggc cgcaccaagc 360

gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 420

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgcctc 480

caatcgggta actcccagga gagtgtcaca gacgaggaca gcaaggacag cacctacagc 540

ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600

gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gctttaacag aggcgagtgc 660

tga 663

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<210> 68
 <211> 220
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 13C5 chimeric antibody light chain full length sequence
 <400> 68

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

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
 20 25 30

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215 220

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<210> 69
 <211> 1341
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Humanized 5G11-IgG1 (D265A) antibody heavy chain full length sequence

<400> 69
 cagatcacac tgaaagaaag cggccctacc ctggtcaagc caactcagac cctgacactg 60
 acttgcaccg tgtctggggtt ctctctgagt acatacggag tccactggat caggcagccc 120
 cctggcaaag ctctggagtg gctgggagtg atttggcggg gcgtcaccac agactataac 180
 gccgctttta tgtcaagact gacaatcact aaggataaca gcaaaaatca ggtgggtcctg 240
 accatgaaca atatggaccc cgtggatacc gcaacatact attgtgcccc gctgggggttc 300
 tacgccatgg actattgggg ccaggggact ctggtgaccg tctcgagcgc ctccactaag 360
 ggccccatccg tgttccctct ggcaccctcc agcaagagca caagcggagg caccgccgca 420
 ctgggctgcc tcgtgaagga ctacttccca gaaccctga ccgtcagctg gaatagcggc 480
 gctctgacca gcggagtcca cactttcccc gcagtgtgtc agtccagcgg cctgtacagc 540
 ctgagcagcg tggtcactgt gccaagcagc agcctgggca ctcagacctc catctgcaac 600
 gtcaaccaca agcccagcaa cacaaggtg gacaagaagg tcgagcccaa gtcctgcatg 660
 aagaccaca cctgccctcc atgtcccgcc cccgagctgc tgggaggacc cagcgtcttc 720
 ctgtttcccc ccaagccaaa ggacaccctg atgatcagca ggacccccga agtgacctgc 780
 gtcgtggtgg ccgtgagcca cgaagatccc gaggtgaagt tcaactggta cgtggacggc 840
 gtggaagtgc acaacgcaa gacaaaaccc agggaggagc agtataacag cacctacagg 900
 gtcgtgagcg tcctgaccgt gctgcaccaa gactggctga acggcaagga gtataagtgc 960
 aaggtgagca acaaggcact gcccgcctcc atcgagaaga ccatttccaa ggccaagggg 1020
 caacctaggg agccacaggt ctacactctg cccctagca gggacgagct gaccaagaac 1080
 caggctctcc tgacttgctt ggtgaagggg ttttatccca gcgacatcgc cgtcgagtgg 1140
 gagagcaatg gccagcccga aaacaactac aagaccacac cccctgtgct ggacagcgac 1200
 ggcagcttct ttctgtatag caaactgaca gtggataaga gcagatggca gcagggcaac 1260
 gtgtttctct gtcctgtgat gcacgaggcc ctgcacaatc actacacca gaagtccttg 1320
 agcctgtccc ccgaaaaatg a 1341

<210> 70
 <211> 446
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized 5G11-IgG1 (D265A) antibody heavy chain full length sequence

<400> 70

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

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Thr Leu Thr Leu₂₀ Thr Cys Thr Val Ser₂₅ Gly Phe Ser Leu Ser₃₀ Thr Tyr
 Gly Val His₃₅ Trp Ile Arg Gln Pro₄₀ Pro Gly Lys Ala Leu₄₅ Glu Trp Leu
 Gly Val₅₀ Ile Trp Arg Gly Val₅₅ Thr Thr Asp Tyr Asn₆₀ Ala Ala Phe Met
 Ser Arg Leu Thr Ile Thr₇₀ Lys Asp Asn Ser Lys₇₅ Asn Gln Val Val Leu₈₀
 Thr Met Asn Asn₈₅ Met Asp Pro Val Asp Thr₉₀ Ala Thr Tyr Tyr Cys₉₅ Ala
 Arg Leu Gly Phe₁₀₀ Tyr Ala Met Asp Tyr₁₀₅ Trp Gly Gln Gly Thr₁₁₀ Leu Val
 Thr Val Ser₁₁₅ Ser Ala Ser Thr Lys₁₂₀ Gly Pro Ser Val Phe₁₂₅ Pro Leu Ala
 Pro Ser₁₃₀ Ser Lys Ser Thr Ser₁₃₅ Gly Gly Thr Ala Ala Leu Gly Cys Leu
 Val₁₄₅ Lys Asp Tyr Phe Pro₁₅₀ Glu Pro Val Thr Val₁₅₅ Ser Trp Asn Ser Gly₁₆₀
 Ala Leu Thr Ser Gly₁₆₅ Val His Thr Phe Pro₁₇₀ Ala Val Leu Gln Ser₁₇₅ Ser
 Gly Leu Tyr Ser₁₈₀ Leu Ser Ser Val Val₁₈₅ Thr Val Pro Ser Ser₁₉₀ Ser Leu
 Gly Thr Gln₁₉₅ Thr Tyr Ile Cys Asn₂₀₀ Val Asn His Lys Pro₂₀₅ Ser Asn Thr
 Lys Val₂₁₀ Asp Lys Lys Val Glu₂₁₅ Pro Lys Ser Cys Asp₂₂₀ Lys Thr His Thr
 Cys₂₂₅ Pro Pro Cys Pro Ala₂₃₀ Pro Glu Leu Leu Gly₂₃₅ Gly Pro Ser Val Phe₂₄₀
 Leu Phe Pro Pro Lys₂₄₅ Pro Lys Asp Thr Leu₂₅₀ Met Ile Ser Arg Thr₂₅₅ Pro
 Glu Val Thr Cys₂₆₀ Val Val Val Ala Val₂₆₅ Ser His Glu Asp Pro₂₇₀ Glu Val
 Lys Phe Asn₂₇₅ Trp Tyr Val Asp Gly₂₈₀ Val Glu Val His Asn₂₈₅ Ala Lys Thr

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

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

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

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

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

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

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

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

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

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

<210> 71
<211> 1329
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized 5G11-IgG4 (F234A/L235A) antibody heavy chain full length
sequence

<400> 71
cagatcacac tgaagaaaag cggccctacc ctggtcaagc caactcagac cctgacactg 60
acttgaccg tgtctgggtt ctctctgagt acatacggag tccactggat caggcagccc 120
cctggcaaag ctctggagt gctgggagtg atttggcggg gcgtcaccac agactataac 180
gccgctttta tgtcaagact gacaatcact aaggataaca gcaaaaatca ggtggtcctg 240
accatgaaca atatggaccc cgtggatacc gcaacatact attgtgcccg gctggggttc 300
tacgccatgg actattgggg ccaggggact ctggtgaccg tctcgagcgc ctccaccaag 360
ggacccagcg tgtttccctt ggccccctgt tccagatcca cctccgaaag cacagccgct 420
ctcggctgcc tgggtcaagga ttacttcctt gagcccgtga cagtctcctg gaatagcggc 480

CRBI_007_01WO_SeqList_ST25

gctctgacct ccggcgtgca taccttcctt gctgtgctgc aatcctccgg actgtacagc 540
ctgagcagcg tggtcaccgt gccttcctcc agcctgggaa ccaaaaccta cacatgcaac 600
gtggaccaca agcccagcaa caccaaagtg gacaagaggg tggagtccaa gtacggaccc 660
ccttgtcctc cctgccctgc tcctgaagcc gctggaggac ctagcgtgtt cctgtttccc 720
cccaagccca aggacaccct catgatctcc aggacccccg aggtgacctg tgtcgtggtg 780
gacgtgagcc aagaggaccc cgaggtgcag ttcaactggt acgtggatgg cgtcgaggtc 840
cataacgcca agaccaagcc tagggaggag cagttcaaca gcacctacag agtggtgagc 900
gtcctgaccg tgctccacca agactggctg aacggcaagg aatacaagtg caaggtctcc 960
aacaagggac tcccttcctc catcgagaag accatcagca aggccaaggg ccagcccaga 1020
gaaccccaag tctacacact gccccccagc caagaggaaa tgaccaagaa ccaggtgagc 1080
ctgacctgcc tggtgaaagg cttctacccc agcgacattg ctgtcgaatg ggagagcaac 1140
ggccaacccg agaacaacta caagaccacc ccccctgtgc tcgacagcga cggctccttc 1200
ttcctctaca gcaggctgac agtggacaag tccaggtggc aagagggcaa tgtcttcagc 1260
tgtagcgtca tgcacgaggc cctccacaac cactacaccc agaagagcct gtccctctcc 1320
ctgggctga 1329

<210> 72
<211> 442
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized 5G11-IgG4 (F234A/L235A) antibody heavy chain full length sequence

<400> 72

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

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

Gly Val Ile Trp Arg Gly Val Thr Thr Asp Tyr Asn Ala Ala Phe Met
50 55 60

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

Thr Met Asn Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala
85 90 95

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

CRBI_007_01WO_SeqList_ST25

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

Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu
130 135 140

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

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

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

Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr
195 200 205

Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
210 215 220

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

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

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
260 265 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
275 280 285

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
290 295 300

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

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

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

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
355 360 365

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

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

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

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
420 425 430

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
435 440

<210> 73
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized 5G11 antibody light chain full length sequence

<400> 73
gatatccaga tgactcagtc tccaagcagc ctgtctgcat ctgtggggga cagggtcacc 60
atcacatgca aagcatctca gagtgtgtca aacgatgtcg cctggtacca gcagaagccc 120
ggaaaagctc ctaagctgct gatttactat gccgctaadc ggtacactgg cgtgccagac 180
agattcagcg gatccggata tggaaccgat ttacttttta ccatcagctc cctgcagcca 240
gaggacattg ccacatattt ctgtcagcag gattacacaa gcccctatac ttttggccag 300
gggaccaaac tggaaatcaa gcgtacggtg gccgcaccaa gcgtcttcat cttcccgcc 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagctttaac agaggcgagt gctga 645

<210> 74
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized 5G11 antibody light chain full length sequence

<400> 74

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 Lys Ala Ser Gln Ser Val Ser Asn Asp
20 25 30

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

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

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

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

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

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

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

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

Phe Asn Arg Gly Glu Cys
210

<210> 75

<211> 1341

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanized 13C5-IgG1 (D265A) antibody heavy chain full length sequence

<400> 75

gaggtgcagc tggtcgagtc aggagggggg ctggtcaagc caggagggtc actgcgactg 60

agctgcgcag cttccgggtt catcttttagg tcttatggca tgagttgggt gcgccaggca 120

ccaggggaaag gactggagtg ggtcgcttca atcagctccg gaggcagcac ttactatcct 180

gactccgtga agggccggtt caccatttct agagataacg ccaaaaatag tctgtacctg 240

cagatgaact ctctgcgagc agaagacaca gccgtctacg attgtgctag aggatatgac 300

agcggccttg catactgggg ccagggggacc ctggtgacag tctcgagcgc ctccactaag 360

CRBI_007_01WO_SeqList_ST25

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ggcccatccg tgttcctctt ggcaccctcc agcaagagca caagcggagg caccgccgca      420
ctgggctgcc tcgtgaagga ctacttccca gaaccctgta ccgtcagctg gaatagcggc      480
gctctgacca gcggagtcca cactttcccc gcagtgtgtc agtccagcgg cctgtacagc      540
ctgagcagcg tggtcactgt gccaagcagc agcctgggca ctcagacctt catctgcaac      600
gtcaaccaca agcccagcaa cacaaagggt gacaagaagg tcgagcccaa gtcctgcatg      660
aagaccacac cctgccctcc atgtcccgcc cccgagctgc tgggaggacc cagcgtcttc      720
ctgtttcccc ccaagccaaa ggacaccctg atgatcagca ggacccccga agtgacctgc      780
gtcgtggtgg ccgtgagcca cgaagatccc gaggtgaagt tcaactggta cgtggacggc      840
gtggaagtgc acaacgccaa gacaaaaccc agggaggagc agtataacag cacctacagg      900
gtcgtgagcg tcctgaccgt gctgcaccaa gactggctga acggcaagga gtataagtgc      960
aaggtgagca acaaggcact gcccgcctcc atcgagaaga ccatttccaa ggccaagggg     1020
caacctaggg agccacaggt ctacactctg cccctagca gggacgagct gaccaagaac     1080
caggtctccc tgacttgctt ggtgaagggg ttttatccca gcgacatcgc cgtcagtggt     1140
gagagcaatg gccagccgca aaacaactac aagaccacac cccctgtgct ggacagcgac     1200
ggcagcttct ttctgtatag caaactgaca gtggataaga gcagatggca gcagggcaac     1260
gtgttctcct gctccgtgat gcacgaggcc ctgcacaatc actacacca gaagtccttg     1320
agcctgtccc ccggaataatg a                                     1341

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<210> 76
 <211> 446
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized 13C5-IgG1 (D265A) antibody heavy chain full length sequence
 <400> 76

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 Gly Phe Ile Phe Arg Ser Tyr
 20 25 30

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

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

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

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

CRBI_007_01WO_SeqList_ST25

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

CRBI_007_01WO_SeqList_ST25

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

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

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

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

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

<210> 77
<211> 1329
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized 13C5-IgG4 (F234A/L235A) antibody heavy chain full length sequence

<400> 77
gaggtgcagc tggctcagtc aggagggggg ctggtcaagc caggagggtc actgcgactg 60
agctgcgcag cttccgggtt catctttagg tcttatggca tgagttgggt gcgccaggca 120
ccagggaag gactggagtg ggtcgcttca atcagctccg gaggcagcac ttactatcct 180
gactccgtga agggccgggtt caccatttct agagataacg ccaaaaatag tctgtacctg 240
cagatgaact ctctgcgagc agaagacaca gccgtctacg attgtgctag aggatatgac 300
agcggctttg catactgggg ccaggggacc ctggtgacag tctcgagcgc ctccaccaag 360
ggaccagcg tgtttcccct ggccccctgt tccagatcca cctccgaaag cacagccgt 420
ctcggctgcc tggtaagga ttacttcct gagccgtga cagtctcctg gaatagcggc 480
gctctgacct ccggcgtgca taccttcct gctgtgctgc aatcctccg actgtacagc 540
ctgagcagcg tggtcaccgt gccttcctcc agcctgggaa ccaaaccta cacatgcaac 600
gtggaccaca agcccagcaa caccaaagt gacaagaggg tggagtcaa gtacggaccc 660
ccttgcctc cctgccctgc tcctgaagcc gctggaggac ctagcgtgtt cctgtttccc 720
cccaagcca aggacacct catgatctcc aggaccccc aggtgacctg tgctcgtggtg 780
gacgtgagcc aagaggacc cgaggtgcag ttcaactggt acgtggatgg cgtcgaggtc 840
cataacgcca agaccaagcc tagggaggag cagttcaaca gcacctacag agtggtgagc 900
gtcctgaccg tgctccacca agactggctg aacggcaagg aatacaagt caaggtctcc 960
aacaagggac tcccttcct catcgagaag accatcagca agccaaggg ccagcccaga 1020
gaacccaag tctacacact gccccccagc caagaggaaa tgaccaagaa ccaggtgagc 1080

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ctgacctgcc tgggtgaaagg cttctacccc agcgacattg ctgtcgaatg ggagagcaac 1140
 ggccaacccg agaacaacta caagaccacc ccccctgtgc tcgacagcga cggctccttc 1200
 ttctctaca gcaggctgac agtggacaag tccaggtggc aagagggcaa tgtcttcagc 1260
 tgtagcgtca tgcacgaggc cctccacaac cactacaccc agaagagcct gtcctctccc 1320
 ctgggctga 1329

<210> 78
 <211> 442
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized 13C5-IgG4 (F234A/L235A) antibody heavy chain full length sequence

<400> 78

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 Gly Phe Ile Phe Arg Ser Tyr
 20 25 30

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

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

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

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

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

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

Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu
 130 135 140

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

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

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

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Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr
195 200 205

Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
210 215 220

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

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

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
260 265 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
275 280 285

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
290 295 300

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

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

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

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
355 360 365

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

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

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

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
420 425 430

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
435 440

<210> 79
<211> 657

<212> DNA
 <213> Artificial Sequence
 <220>
 <223> Humanized 13C5 antibody light chain full length sequence
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 cagcagaagc ccggacagcc ccctaagctg ctgatcaaat atgctagcaa cctggagtcc 180
 ggcgtgccag ccaggttctc tggcagtggg tcaggaaccg actttactct gaccattaat 240
 cccgtcgaag ccaacgatac agctaattac tattgtcagc attcctggga gatcccttac 300
 acatttggcc aggggactaa gctggagatc aagcgtacgg tggccgcacc aagcgtcttc 360
 atcttcccg catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 420
 aataacttct atcccagaga ggccaaagta cagtgggaagg tggataacgc cctccaatcg 480
 ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 540
 agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc 600
 acccatcagg gcctgagctc gcccgtcaca aagagcttta acagaggcga gtgctga 657

<210> 80
 <211> 218
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Humanized 13C5 antibody light chain full length sequence
 <400> 80
 Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Pro Gly
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 Gln Arg Ala Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
 20 25 30
 Ser Ser Ser Phe Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45
 Lys Leu Leu Ile Lys Tyr Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
 50 55 60
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn
 65 70 75 80
 Pro Val Glu Ala Asn Asp Thr Ala Asn Tyr Tyr Cys Gln His Ser Trp
 85 90 95
 Glu Ile Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
 100 105 110

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

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

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

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

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

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

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

<210> 81
<211> 5
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<213> Mus sp.

<400> 81

Ser Tyr Gly Met Ser
1 5

<210> 82
<211> 16
<212> PRT
<213> Mus sp.

<400> 82

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

<210> 83
<211> 8
<212> PRT
<213> Mus sp.

<400> 83

Gly Tyr Asp Ser Gly Phe Ala Tyr
1 5

<210> 84
<211> 15
<212> PRT
<213> Mus sp.

<400> 84

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Arg Ala Ser Gln Ser Val Ser Thr Ser Ser Ser Ser Phe Met His
1 5 10 15

<210> 85
<211> 7
<212> PRT
<213> Mus sp.

<400> 85

Tyr Ala Ser Asn Leu Glu Ser
1 5

<210> 86
<211> 9
<212> PRT
<213> Mus sp.

<400> 86

Gln His Ser Trp Glu Ile Pro Tyr Thr
1 5

<210> 87
<211> 5
<212> PRT
<213> Mus sp.

<400> 87

Ser Tyr Gly Met Ser
1 5

<210> 88
<211> 16
<212> PRT
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<400> 88

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

<210> 89
<211> 8
<212> PRT
<213> Mus sp.

<400> 89

Gly Tyr Asp Ser Gly Phe Ala Tyr
1 5

<210> 90
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<400> 90

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

<210> 91
 <211> 7
 <212> PRT
 <213> Mus sp.

<400> 91

Tyr Ala Ser Asn Leu Glu Ser
 1 5

<210> 92
 <211> 9
 <212> PRT
 <213> Mus sp.

<400> 92

Gln His Ser Trp Glu Ile Pro Tyr Thr
 1 5

<210> 93
 <211> 5
 <212> PRT
 <213> Mus sp.

<400> 93

Thr Tyr Gly Val His
 1 5

<210> 94
 <211> 16
 <212> PRT
 <213> Mus sp.

<400> 94

Val Ile Trp Arg Gly Val Thr Thr Asp Tyr Asn Ala Ala Phe Met Ser
 1 5 10 15

<210> 95
 <211> 8
 <212> PRT
 <213> Mus sp.

<400> 95

Leu Gly Phe Tyr Ala Met Asp Tyr
 1 5

<210> 96
 <211> 11
 <212> PRT
 <213> Mus sp.

<400> 96

Lys Ala Ser Gln Ser Val Ser Asn Asp Val Ala
 1 5 10

<210> 97
 <211> 7
 <212> PRT
 <213> Mus sp.

<400> 97

Tyr Ala Ala Asn Arg Tyr Thr
 1 5

<210> 98
 <211> 9
 <212> PRT
 <213> Mus sp.

<400> 98

Gln Gln Asp Tyr Thr Ser Pro Tyr Thr
 1 5

<210> 99
 <211> 5
 <212> PRT
 <213> Mus sp.

<400> 99

Ser Tyr Gly Val His
 1 5

<210> 100
 <211> 16
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<400> 100

Val Ile Trp Ser Gly Gly Val Thr Asp Tyr Asn Ala Ala Phe Ile Ser
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 <211> 8
 <212> PRT
 <213> Mus sp.

<400> 101

Leu Gly Phe Tyr Ala Met Asp Tyr
 1 5

<210> 102
 <211> 11
 <212> PRT
 <213> Mus sp.

<400> 102

Lys Ala Ser Gln Ser Val Ser Asn Asp Val Gly
 1 5 10

<210> 103
 <211> 7

<212> PRT
 <213> Mus sp.

<400> 103

Tyr Ala Ser Asn Arg Tyr Ser
 1 5

<210> 104
 <211> 9
 <212> PRT
 <213> Mus sp.

<400> 104

Gln Gln Asp Tyr Thr Ser Pro Tyr Thr
 1 5

<210> 105
 <211> 5
 <212> PRT
 <213> Mus sp.

<400> 105

Thr Tyr Trp Met His
 1 5

<210> 106
 <211> 17
 <212> PRT
 <213> Mus sp.

<400> 106

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

Asp

<210> 107
 <211> 10
 <212> PRT
 <213> Mus sp.

<400> 107

Pro Gly Asp Tyr Gly Tyr Asp Phe Asp Cys
 1 5 10

<210> 108
 <211> 16
 <212> PRT
 <213> Mus sp.

<400> 108

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

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<210> 109
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<400> 109

Lys Val Ser Asn Arg Phe Ser
 1 5

<210> 110
 <211> 9
 <212> PRT
 <213> Mus sp.

<400> 110

Phe Gln Gly Ser His Val Pro Tyr Thr
 1 5

<210> 111
 <211> 5
 <212> PRT
 <213> Mus sp.

<400> 111

Ser Gly Tyr Trp Asn
 1 5

<210> 112
 <211> 16
 <212> PRT
 <213> Mus sp.

<400> 112

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

<210> 113
 <211> 11
 <212> PRT
 <213> Mus sp.

<400> 113

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

<210> 114
 <211> 12
 <212> PRT
 <213> Mus sp.

<400> 114

Ser Ala Ser Ser Ser Val Ser Ser Ser Tyr Leu Tyr
 1 5 10

<210> 115
 <211> 7

<212> PRT
 <213> Mus sp.

<400> 115

Asn Thr Ser Asn Leu Ala Ser
 1 5

<210> 116
 <211> 9
 <212> PRT
 <213> Mus sp.

<400> 116

His Gln Trp Arg Ser Tyr Pro Pro Thr
 1 5

<210> 117
 <211> 5
 <212> PRT
 <213> Mus sp.

<400> 117

Ser Tyr Gly Val His
 1 5

<210> 118
 <211> 16
 <212> PRT
 <213> Mus sp.

<400> 118

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

<210> 119
 <211> 8
 <212> PRT
 <213> Mus sp.

<400> 119

Leu Gly Phe Tyr Ala Met Asp Tyr
 1 5

<210> 120
 <211> 10
 <212> PRT
 <213> Mus sp.

<400> 120

Ser Ala Asn Ser Ser Val Ser Tyr Met His
 1 5 10

<210> 121
 <211> 7
 <212> PRT
 <213> Mus sp.

<400> 121

Asp Thr Ser Lys Leu Ala Ser
 1 5

<210> 122

<211> 9

<212> PRT

<213> Mus sp.

<400> 122

Gln Gln Trp Ser Ser Asn Pro Trp Thr
 1 5

<210> 123

<211> 5

<212> PRT

<213> Mus sp.

<400> 123

Ser Tyr Gly Met Ser
 1 5

<210> 124

<211> 16

<212> PRT

<213> Mus sp.

<400> 124

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

<210> 125

<211> 8

<212> PRT

<213> Mus sp.

<400> 125

Gly Tyr Asp Ala Gly Phe Ala Tyr
 1 5

<210> 126

<211> 15

<212> PRT

<213> Mus sp.

<400> 126

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

<210> 127

<211> 7

<212> PRT

<213> Mus sp.

<400> 127

Tyr Ala Ser Asn Leu Glu Ser
1 5

<210> 128
<211> 9
<212> PRT
<213> Mus sp.

<400> 128

Gln Asn Ser Trp Glu Ile Pro Tyr Thr
1 5

<210> 129
<211> 5
<212> PRT
<213> Mus sp.

<400> 129

Ser Gly Tyr Trp Thr
1 5

<210> 130
<211> 16
<212> PRT
<213> Mus sp.

<400> 130

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

<210> 131
<211> 9
<212> PRT
<213> Mus sp.

<400> 131

Gln Arg Asp Trp Leu Gly Phe Ala Tyr
1 5

<210> 132
<211> 17
<212> PRT
<213> Mus sp.

<400> 132

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

Ala

<210> 133
<211> 7
<212> PRT
<213> Mus sp.

<400> 133

Trp Ala Ser Asn Arg Glu Ser
 1 5

<210> 134

<211> 9

<212> PRT

<213> Mus sp.

<400> 134

Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr
 1 5

<210> 135

<211> 5

<212> PRT

<213> Mus sp.

<400> 135

Ser Tyr Gly Met Ser
 1 5

<210> 136

<211> 16

<212> PRT

<213> Mus sp.

<400> 136

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

<210> 137

<211> 8

<212> PRT

<213> Mus sp.

<400> 137

Gly Tyr Asp Ala Gly Phe Ala Phe
 1 5

<210> 138

<211> 15

<212> PRT

<213> Mus sp.

<400> 138

Arg Ala Ser Gln Ser Val Ser Thr Ser Ser Tyr Ser Tyr Val His
 1 5 10 15

<210> 139

<211> 7

<212> PRT

<213> Mus sp.

<400> 139

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Tyr Ala Ser Asn Leu Glu Ser
1 5

<210> 140
<211> 9
<212> PRT
<213> Mus sp.

<400> 140

Gln His Ser Trp Glu Ile Pro Tyr Thr
1 5

<210> 141
<211> 660
<212> DNA
<213> Homo sapiens

<400> 141
tttactgtca cggttcccaa ggacctatat gtggtagagt atggtagcaa tatgacaatt 60
gaatgcaaat tcccagtaga aaaacaatta gacctggctg cactaattgt ctattgggaa 120
atggaggata agaacattat tcaatttgtg catggagagg aagacctgaa ggttcagcat 180
agtagctaca gacagagggc ccggctgttg aaggaccagc tctccctggg aaatgctgca 240
cttcagatca cagatgtgaa attgcaggat gcaggggtgt accgctgcat gatcagctat 300
ggtggtgccg actacaagcg aattactgtg aaagtcaatg cccatacaa caaatcaac 360
caaagaattt tggttgtgga tccagtcacc tctgaacatg aactgacatg tcaggctgag 420
ggctacccca aggccgaagt catctggaca agcagtgacc atcaagtcct gagtggtaag 480
accaccacca ccaattccaa gagagaggag aagcttttca atgtgaccag cacactgaga 540
atcaacacaa caactaatga gattttctac tgcactttta ggagattaga tcctgaggaa 600
aaccatacag ctgaattggg catcccagaa ctacctctgg cacatcctcc aaatgaaagg 660

<210> 142
<211> 220
<212> PRT
<213> Homo sapiens

<400> 142

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

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

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Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
210 215 220

<210> 143
<211> 681
<212> DNA
<213> Homo sapiens

<400> 143
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gaatgcaaat tcccagtaga aaaacaatta gacctggctg cactaattgt ctattgggaa 120
atggaggata agaacattat tcaattttgtg catggagagg aagacctgaa ggttcagcat 180
agtagctaca gacagagggc ccggctgttg aaggaccagc tctccctggg aaatgctgca 240
cttcagatca cagatgtgaa attgcaggat gcaggggtgt accgctgcat gatcagctat 300
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caaagaattt tggttgtgga tccagtcacc tctgaacatg aactgacatg tcaggctgag 420
ggctacccca aggccgaagt catctggaca agcagtgacc atcaagtcct gagtggttaag 480
accaccacca ccaattccaa gagagaggag aagcttttca atgtgaccag cacactgaga 540
atcaacacaa caactaatga gattttctac tgcactttta ggagattaga tcctgaggaa 600
aaccatacag ctgaattggg catcccagaa ctacctctgg cacatcctcc aaatgaaagg 660

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<210> 144
 <211> 226
 <212> PRT
 <213> Homo sapiens

<400> 144

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

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
 20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
 35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
 50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
 65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
 85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
 100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
 115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
 130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
 145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
 165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
 180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
 195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg His His His His
 210 215 220

His His
 225

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<210> 145
 <211> 1344
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human PD-L1-mFc sequence

<400> 145
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 atggaggata agaacattat tcaattttgtg catggagagg aagacctgaa ggttcagcat 180
 agtagctaca gacagagggc ccggctgttg aaggaccagc tctccctggg aaatgctgca 240
 cttcagatca cagatgtgaa attgcaggat gcaggggtgt accgctgcat gatcagctat 300
 ggtggtgccg actacaagcg aattactgtg aaagtcaatg cccatacaa caaatcaac 360
 caaagaattt tggttgtgga tccagtcacc tctgaacatg aactgacatg tcaggctgag 420
 ggctaccca aggccgaagt catctggaca agcagtgacc atcaagtcct gagtggtaag 480
 accaccacca ccaattccaa gagagaggag aagcttttca atgtgaccag cacttgaga 540
 atcaacacaa caactaatga gattttctac tgcactttta ggagattaga tcctgaggaa 600
 aaccatacag ctgaattggt catcccagaa ctacctctgg cacatcctcc aaatgaaagg 660
 ggtaccagat ctagaggctg caaacctgt atctgcacag tgcccgaggt gagctccgtg 720
 ttcacttttc ccccaagcc caaggacgtg ctgaccatca cactcacacc caaggtcacc 780
 tgcgtggtcg tggacatctc caaggacgac cccgaagtcc agttcagctg gttcgtggac 840
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 aggtccgtgt ccgagctccc catcatgcac caggactggc tgaatggcaa ggagttcaag 960
 tgcaggggtga actccgctgc tttccccgcc cccattgaga agaccatctc caagaccaag 1020
 ggaaggcca aggccccca ggtgtacacc attccccctc ccaaggagca gatggccaag 1080
 gacaagggtg ccctgacctg tatgatcacc gacttctttc ccgaggacat caccgtcgaa 1140
 tggcagtgga acggccagcc cgccgagaac tataagaaca cccaacccat catggacacc 1200
 gacggcagct acttcgtgta tagcaagctc aacgtgcaga agagcaactg ggaagccgga 1260
 aataccttca cctgctccgt cctgcacgag ggcctgcaca accaccatac cgaaaagagc 1320
 ctgagccaca gccccgaaa gtaa 1344

<210> 146
 <211> 447
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human PD-L1-mFc sequence

<400> 146

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Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
 1 5 10 15
 Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
 20 25 30
 Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
 35 40 45
 Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
 50 55 60
 Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
 65 70 75 80
 Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
 85 90 95
 Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
 100 105 110
 Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
 115 120 125
 Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
 130 135 140
 Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
 145 150 155 160
 Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
 165 170 175
 Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
 180 185 190
 Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
 195 200 205
 Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Gly Thr Arg Ser
 210 215 220
 Arg Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val
 225 230 235 240
 Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr
 245 250 255
 Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu
 260 265 270

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Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln
275 280 285

Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser
290 295 300

Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys
305 310 315 320

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

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

Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met
355 360 365

Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn
370 375 380

Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr
385 390 395 400

Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn
405 410 415

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

His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
435 440 445

<210> 147
<211> 1374
<212> DNA
<213> Artificial Sequence

<220>
<223> Human PD-L1-hFc sequence

<400> 147
tttactgtca cggttcccaa ggacctatat gtggtagagt atggtagcaa tatgacaatt 60
gaatgcaaat tcccagtaga aaaacaatta gacctggctg cactaattgt ctattgggaa 120
atggaggata agaacattat tcaatttgtg catggagagg aagacctgaa gggtcagcat 180
agtagctaca gacagagggc ccggctgttg aaggaccagc tctccctggg aaatgctgca 240
cttcagatca cagatgtgaa attgcaggat gcaggggtgt accgctgcat gatcagctat 300
ggtggtgccg actacaagcg aattactgtg aaagtcaatg ccccatacaa caaatcaac 360
caaagaattt tggttgtgga tccagtcacc tctgaacatg aactgacatg tcaggctgag 420
ggctacccca aggccgaagt catctggaca agcagtgacc atcaagtcct gagtggtaag 480

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accaccacca ccaattccaa gagagaggag aagcttttca atgtgaccag cacactgaga 540
atcaacacaa caactaatga gatttttctac tgcactttta ggagattaga tcctgaggaa 600
aaccatacag ctgaattggt catcccagaa ctacctctgg cacatcctcc aaatgaaagg 660
ggtaccagat ctagagagcc caaatcttct gacaaaactc acacatgccc accgtgccc 720
gcacctgaat tcgagggtgc accgtcagtc ttctctttcc ccccaaaacc caaggacacc 780
ctcatgatct cccggactcc tgaggtcaca tgcgtggtgg tggacgtaag ccacgaagac 840
cctgagggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900
ccgcggggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 960
caggactggc tgaatggcaa ggagtacaag tgcaaggctt ccaacaaagc cctcccaacc 1020
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080
ctgcccccat cccgggatga gctgaccaag aaccagggtca gcctgacctg cctggtcaaa 1140
ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200
tacaagacca cgctcccggt gctggactcc gacggctcct tcttctctta cagcaagctc 1260
accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa atga 1374

<210> 148
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> Human PD-L1-hFc sequence

<400> 148

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

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

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Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
 115 120 125
 Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
 130 135 140
 Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
 145 150 155 160
 Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
 165 170 175
 Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
 180 185 190
 Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
 195 200 205
 Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Gly Thr Arg Ser
 210 215 220
 Arg Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 225 230 235 240
 Ala Pro Glu Phe Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
 245 250 255
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 260 265 270
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 275 280 285
 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 290 295 300
 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 305 310 315 320
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 325 330 335
 Ala Leu Pro Thr Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 340 345 350
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
 355 360 365
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 370 375 380

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Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385 390 395 400

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

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
420 425 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
435 440 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455

<210> 149
<211> 681
<212> DNA
<213> Artificial Sequence

<220>
<223> Cyno-PD-L1-HisTag

<400> 149
tttactgtca cggttcccaa ggacctatat gtggtagagt atggcagcaa tatgacaatt 60
gaatgcaaat tcccagtaga aaaacaatta gacctgactt cactaattgt ctattgggaa 120
atggaggata agaacattat tcaatttgtg catggagagg aagacctgaa ggttcagcat 180
agtaactaca gacagagggc ccagctgttg aaggaccagc tctccctggg aaatgctgca 240
cttcggatca cagatgtgaa attgcaggat gcaggggttt accgctgcat gatcagctat 300
ggtggtgccg actacaagcg gattaccgtg aaagtcaatg ctccatacaa caaaatcaac 360
caaagaattt tggttgtcga tccagtcacc tctgaacatg aactaacatg tcaggctgag 420
ggctaccca aggccgaagt catttggaca agcagtgacc atcaagtcct gagtggtaag 480
accaccacca ccaattccaa gagagaggag aagcttttaa atgtgaccag cacactgaga 540
atcaacacaa cagctaata gattttctac tgcattttta ggagattaga tcctgaggaa 600
aaccatacag ctgaattggt catccagaa ctacctctgg cgcttcctcc aaatgaaagg 660
catcatcacc accatcacta a 681

<210> 150
<211> 226
<212> PRT
<213> Artificial Sequence

<220>
<223> Cyno-PD-L1-HisTag

<400> 150

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

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Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Thr Ser Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Asn Tyr Arg
50 55 60

Gln Arg Ala Gln Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Arg Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Leu Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Ala Asn Glu Ile Phe Tyr Cys Ile
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala Leu Pro Pro Asn Glu Arg His His His His
210 215 220

His His
225

<210> 151
<211> 450
<212> DNA
<213> Homo sapiens

<400> 151
ccaggatggg tcttagactc cccagacagg ccctggaacc ccccccacctt ctccccagcc 60
ctgctcgtgg tgaccgaagg ggacaacgcc accttcacct gcagcttctc caacacatcg 120

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gagagcttcg tgctaaactg gtaccgcatg agccccagca accagacgga caagctggcc 180
gccttccccg aggaccgcag ccagcccggc caggactgcc gcttccgtgt cacacaactg 240
cccaacgggc gtgacttcca catgagcgtg gtcagggccc ggcgcaatga cagcggcacc 300
tacctctgtg gggccatctc cctggccccc aaggcgcaga tcaaagagag cctgcgggca 360
gagctcaggg tgacagagag aagggcagaa gtgcccacag cccaccccag cccctcaccc 420
aggccagccg gccagttcca aaccctggtg 450

<210> 152
<211> 150
<212> PRT
<213> Homo sapiens

<400> 152

Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr
1 5 10 15

Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe
20 25 30

Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr
35 40 45

Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu
50 55 60

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

Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn
85 90 95

Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala
100 105 110

Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg
115 120 125

Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly
130 135 140

Gln Phe Gln Thr Leu Val
145 150

<210> 153
<211> 1134
<212> DNA
<213> Artificial Sequence

<220>
<223> Human PD-1-mFc sequence

CRBI_007_01WO_SeqList_ST25

<400> 153
ccaggatggt tcttagactc cccagacagg ccctggaacc cccccacctt ctccccagcc 60
ctgctcgtgg tgaccgaagg ggacaacgcc accttcacct gcagcttctc caacacatcg 120
gagagcttcg tgctaaactg gtaccgcatg agccccagca accagacgga caagctggcc 180
gccttccccg aggaccgcag ccagcccggc caggactgcc gcttccgtgt cacacaactg 240
cccaacgggc gtgacttcca catgagcgtg gtcagggccc ggcgcaatga cagcggcacc 300
tacctctgtg gggccatctc cctggccccc aaggcgcaga tcaaagagag cctgcgggca 360
gagctcaggg tgacagagag aagggcagaa gtgcccacag cccaccccag cccctcacc 420
aggccagccg gccagtcca aaccctggtg ggtaccagat ctagaggctg caaacctgt 480
atctgcacag tgcccagagt gagctccgtg ttcattcttc cccccaagcc caaggacgtg 540
ctgaccatca cactcacacc caaggtcacc tgcgtggtcg tggacatctc caaggacgac 600
cccgaagtcc agttcagctg gttcgtggac gacgtggagg tgacaccgc tcagacccaa 660
cccagagagg agcagtttaa ctccaccttc aggtccgtgt ccgagctccc catcatgcac 720
caggactggc tgaatggcaa ggagttcaag tgcagggatga actccgctgc tttccccgcc 780
cccattgaga agaccatctc caagaccaag ggaaggccca agggccccca ggtgtacacc 840
attccccctc ccaaggagca gatggccaag gacaaggtgt ccctgacctg tatgatcacc 900
gacttctttc ccgaggacat caccgtcgaa tggcagtggc acggccagcc cgccgagaac 960
tataagaaca cccaacccat catggacacc gacggcagct acttcgtgta tagcaagctc 1020
aacgtgcaga agagcaactg ggaagccgga aataccttca cctgctccgt cctgcacgag 1080
ggcctgcaca accaccatac cgaaaagagc ctgagccaca gccccgaaa gtaa 1134

<210> 154
<211> 377
<212> PRT
<213> Artificial Sequence

<220>
<223> Human PD-1-mFc sequence

<400> 154
Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr
1 5 10 15
Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe
20 25 30
Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr
35 40 45
Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu
50 55 60
Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu
65 70 75 80

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Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn
85 90 95

Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala
100 105 110

Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg
115 120 125

Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly
130 135 140

Gln Phe Gln Thr Leu Val Gly Thr Arg Ser Arg Gly Cys Lys Pro Cys
145 150 155 160

Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys
165 170 175

Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val
180 185 190

Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe
195 200 205

Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu
210 215 220

Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met His
225 230 235 240

Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala
245 250 255

Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg
260 265 270

Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met
275 280 285

Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro
290 295 300

Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn
305 310 315 320

Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val
325 330 335

Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr
340 345 350

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Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His Thr Glu
 355 360 365

Lys Ser Leu Ser His Ser Pro Gly Lys
 370 375

<210> 155
 <211> 1164
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human PD-1-hFc sequence

<400> 155
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 ctgctcgtgg tgaccgaagg ggacaacgcc accttcacct gcagcttctc caacacatcg 120
 gagagcttcg tgctaaactg gtaccgcatg agccccagca accagacgga caagctggcc 180
 gccttccccg aggaccgcag ccagcccggc caggactgcc gcttccgtgt cacacaactg 240
 cccaacgggc gtgacttcca catgagcgtg gtcagggccc ggcgcaatga cagcggcacc 300
 tacctctgtg gggccatctc cctggccccc aaggcgcaga tcaaagagag cctgcgggca 360
 gagctcaggg tgacagagag aagggcagaa gtgcccacag cccaccccag cccctcaccc 420
 aggccagccg gccagttcca aaccctggtg ggtaccagat ctagagagcc caaatcttct 480
 gacaaaactc acacatgccc accgtgcccga gcacctgaat tcgaggggtgc accgtcagtc 540
 ttctcttcc ccccaaaacc caaggacacc ctcatgatct cccggactcc tgaggtcaca 600
 tgcgtggtgg tggacgtaag ccacgaagac cctgaggtca agttcaactg gtacgtggac 660
 ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 720
 cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 780
 tgcaaggtct ccaacaaagc cctcccaacc cccatcgaga aaaccatctc caaagccaaa 840
 gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag 900
 aaccaggtca gcctgacctg cctggtcaaa ggcttctatc caagcgacat cgccgtggag 960
 tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1020
 gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1080
 aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 1140
 ctctccctgt ctccgggtaa atga 1164

<210> 156
 <211> 222
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human PD-1-hFc sequence

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<400> 156

Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr
 1 5 10 15
 Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe
 20 25 30
 Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr
 35 40 45
 Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu
 50 55 60
 Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu
 65 70 75 80
 Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn
 85 90 95
 Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala
 100 105 110
 Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg
 115 120 125
 Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly
 130 135 140
 Gln Phe Gln Thr Leu Val Gly Thr Arg Ser Arg Glu Pro Lys Ser Ser
 145 150 155 160
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly
 165 170 175
 Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 180 185 190
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 195 200 205
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 210 215 220