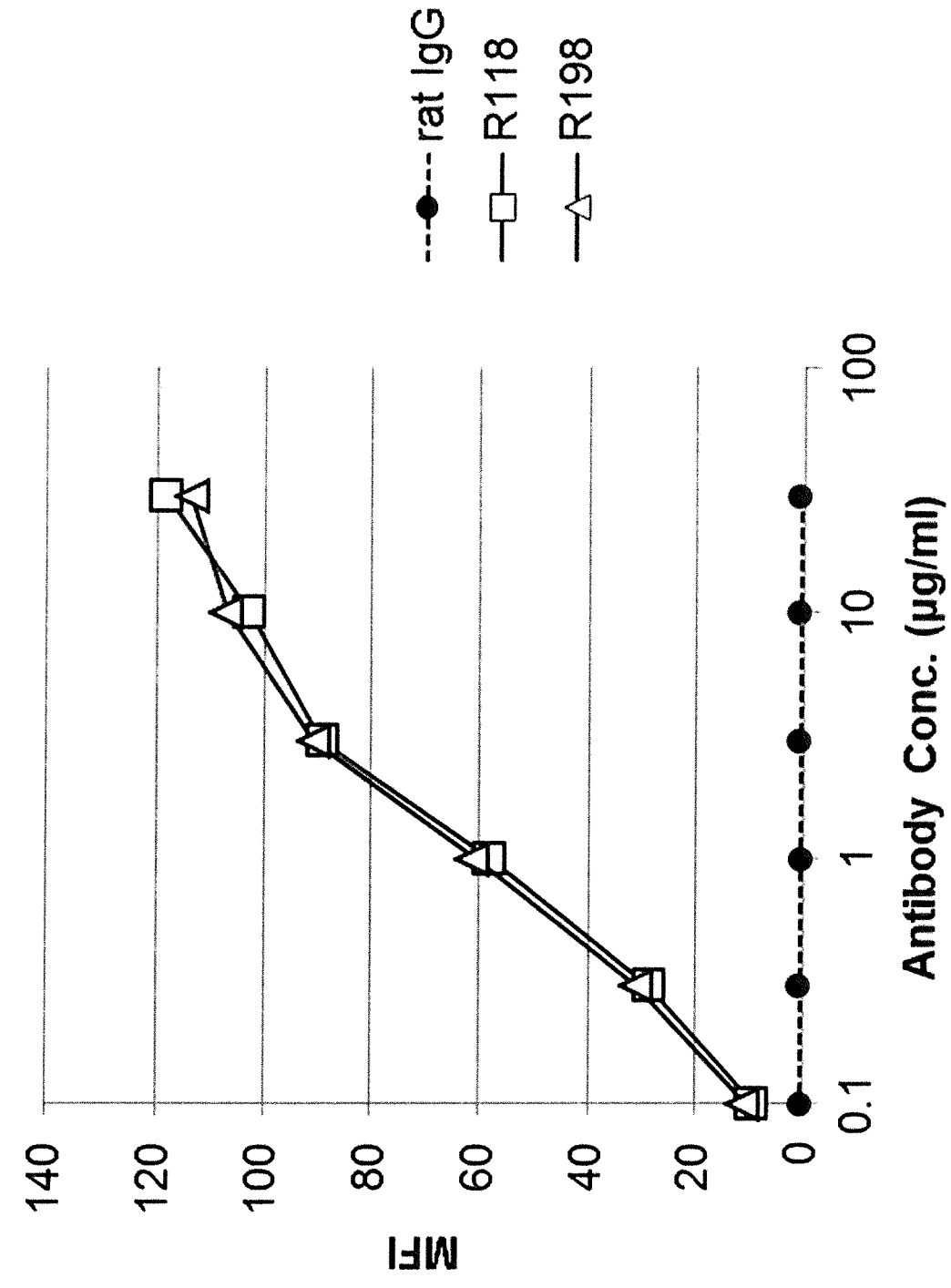

rat IgG
R118
R198
MFI
140
120
100
80
60
40
20
0
0.1
1
10
100
Antibody Conc. (µg/ml)

Figure 1

Figure 2

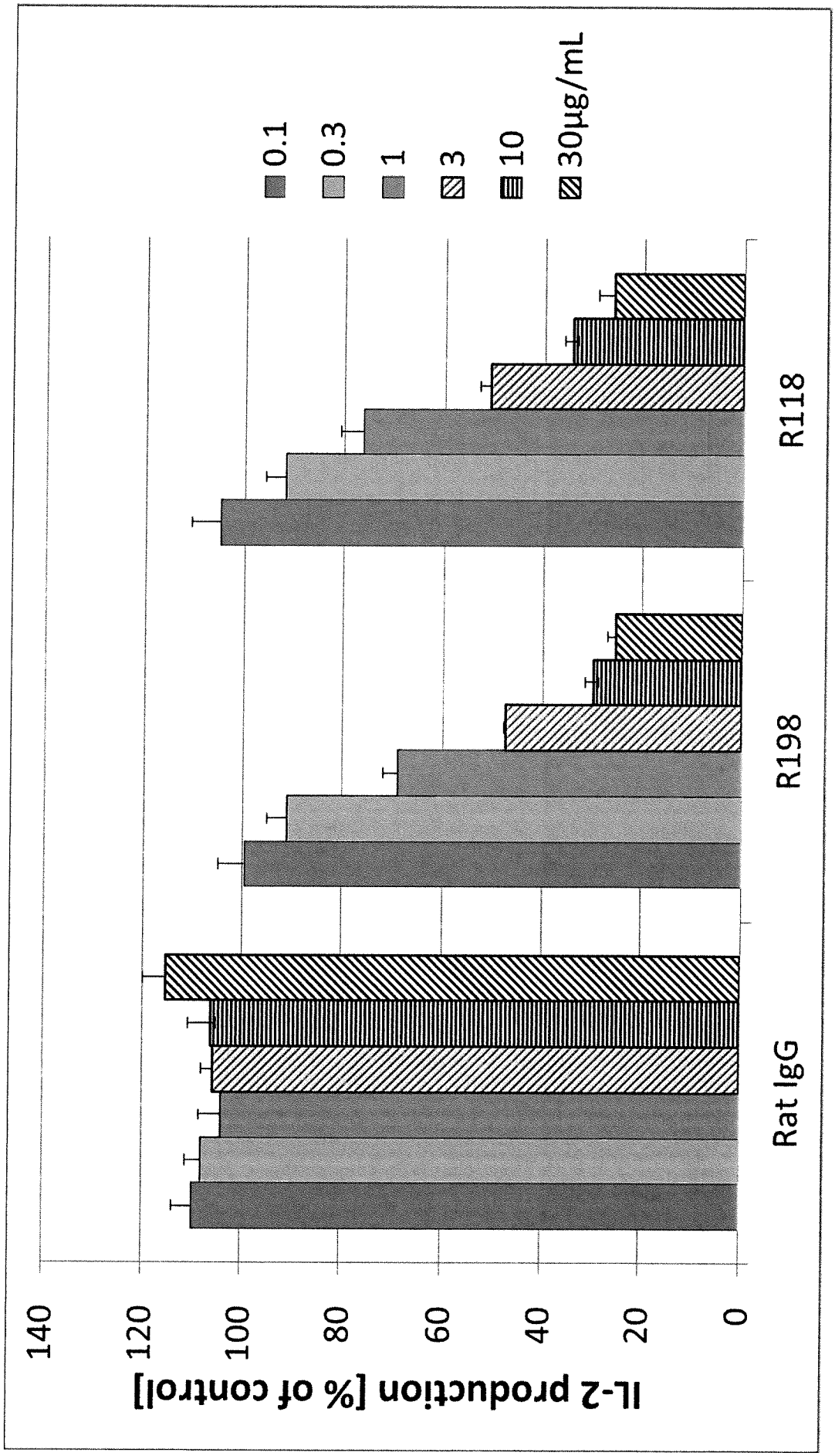

IL-2 production [% of control]
0
20
40
60
80
100
120
140
0.1
0.3
1
3
10
30µg/mL
Rat IgG
R198
R118

Figure 3

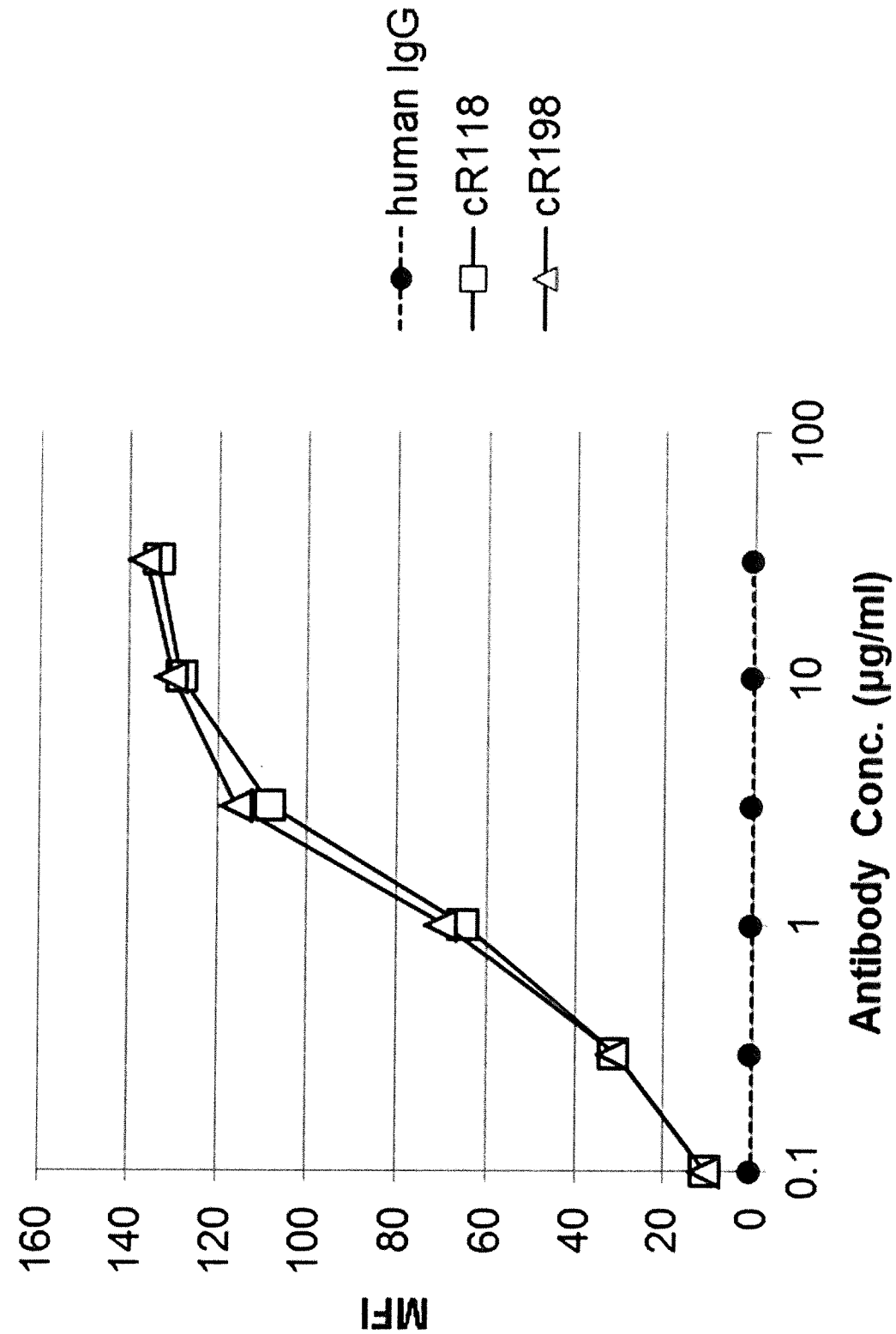

human IgG
cR118
cR198
MFI
160
140
120
100
80
60
40
20
0
0.1
1
10
100
Antibody Conc. (µg/ml)

Figure 4

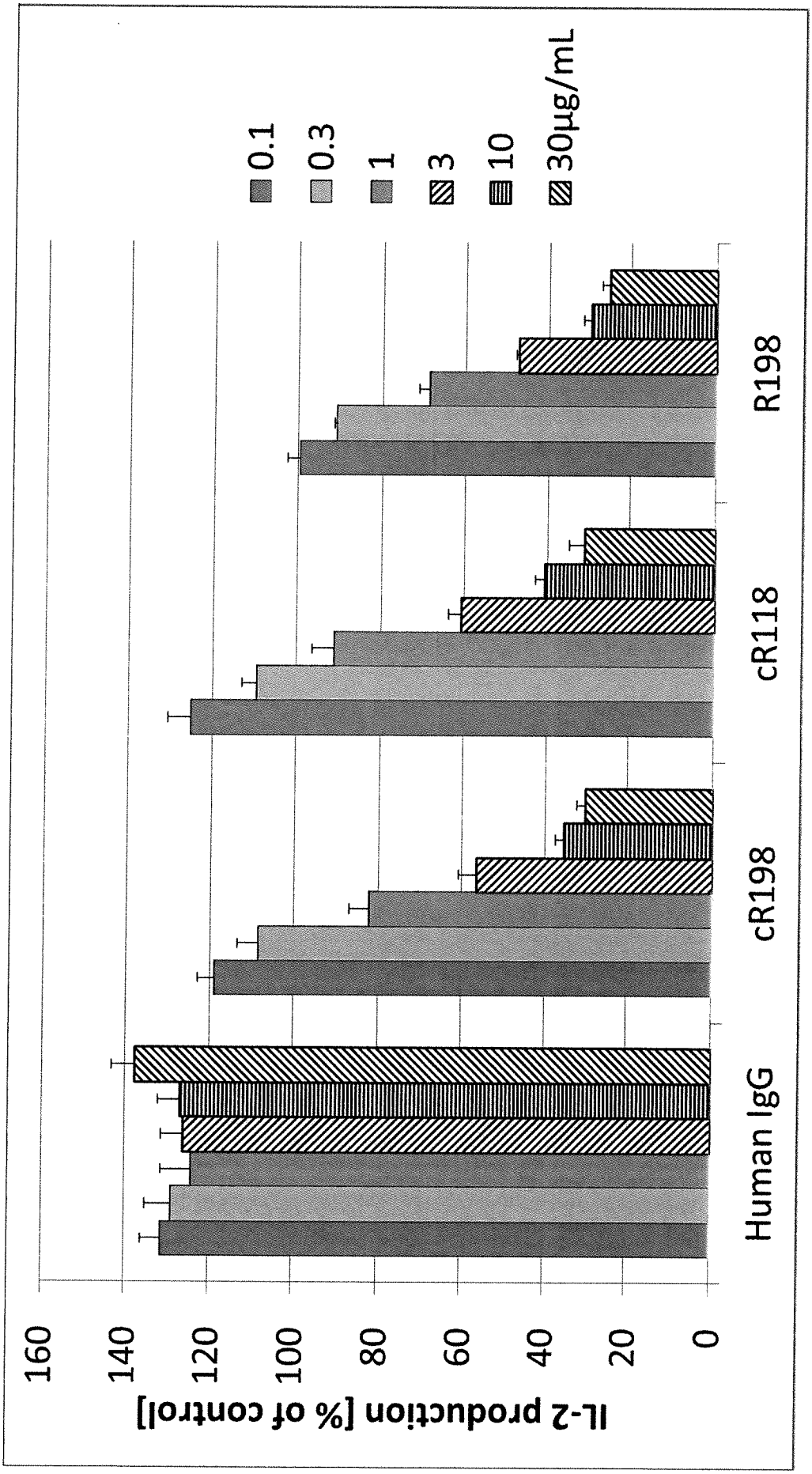

IL-2 production [% of control]
160
140
120
100
80
60
40
20
0
0.1
0.3
1
3
10
30µg/mL
Human IgG
cR198
cR118
R198

Figure 5

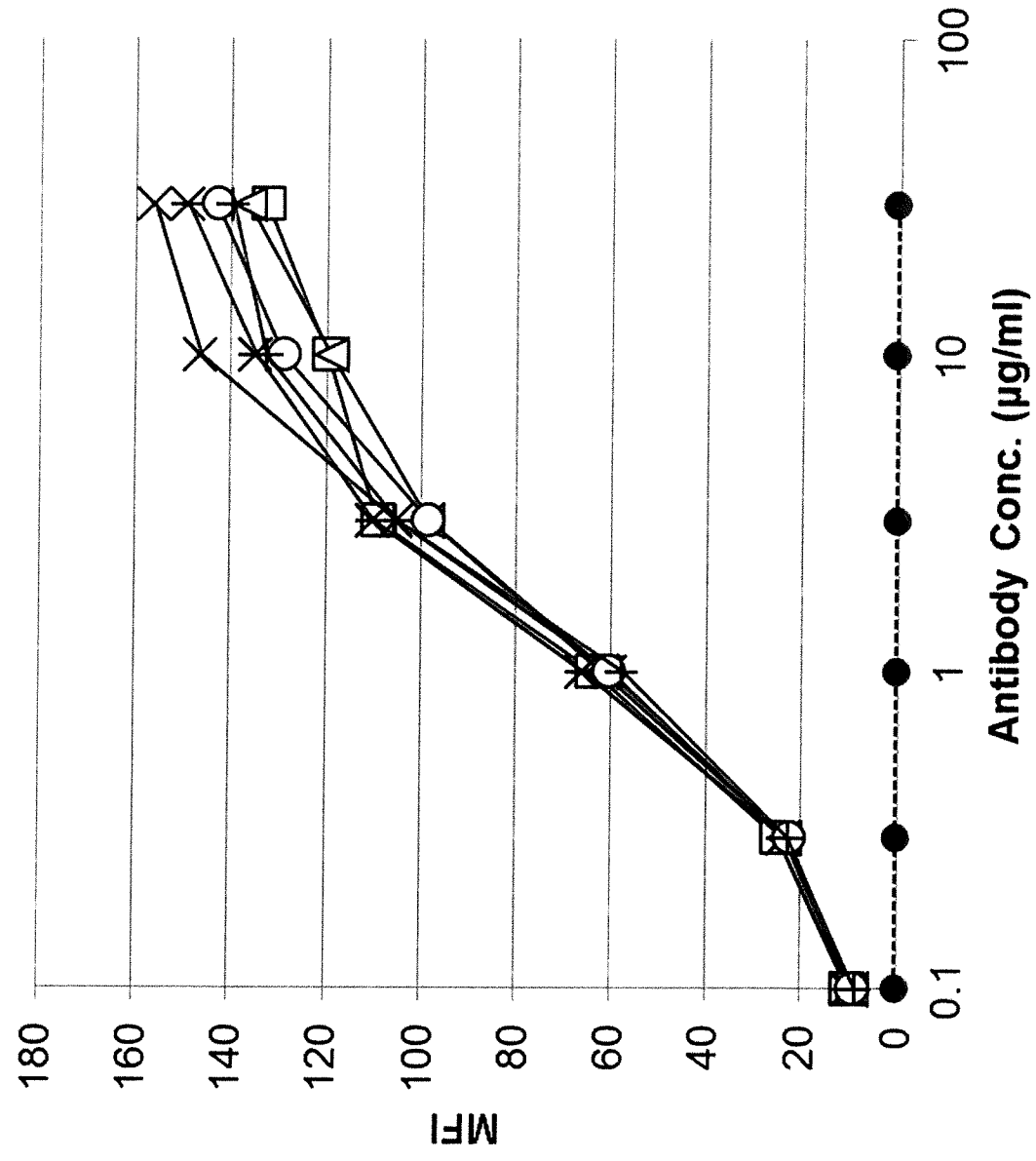

hIgG
hH1/L1
hH2/L2
hH3/L3
hH4/L4
cR118
cR198
MFI
180
160
140
120
100
80
60
40
20
0
0.1
1
10
100
Antibody Conc. (µg/ml)

Figure 6

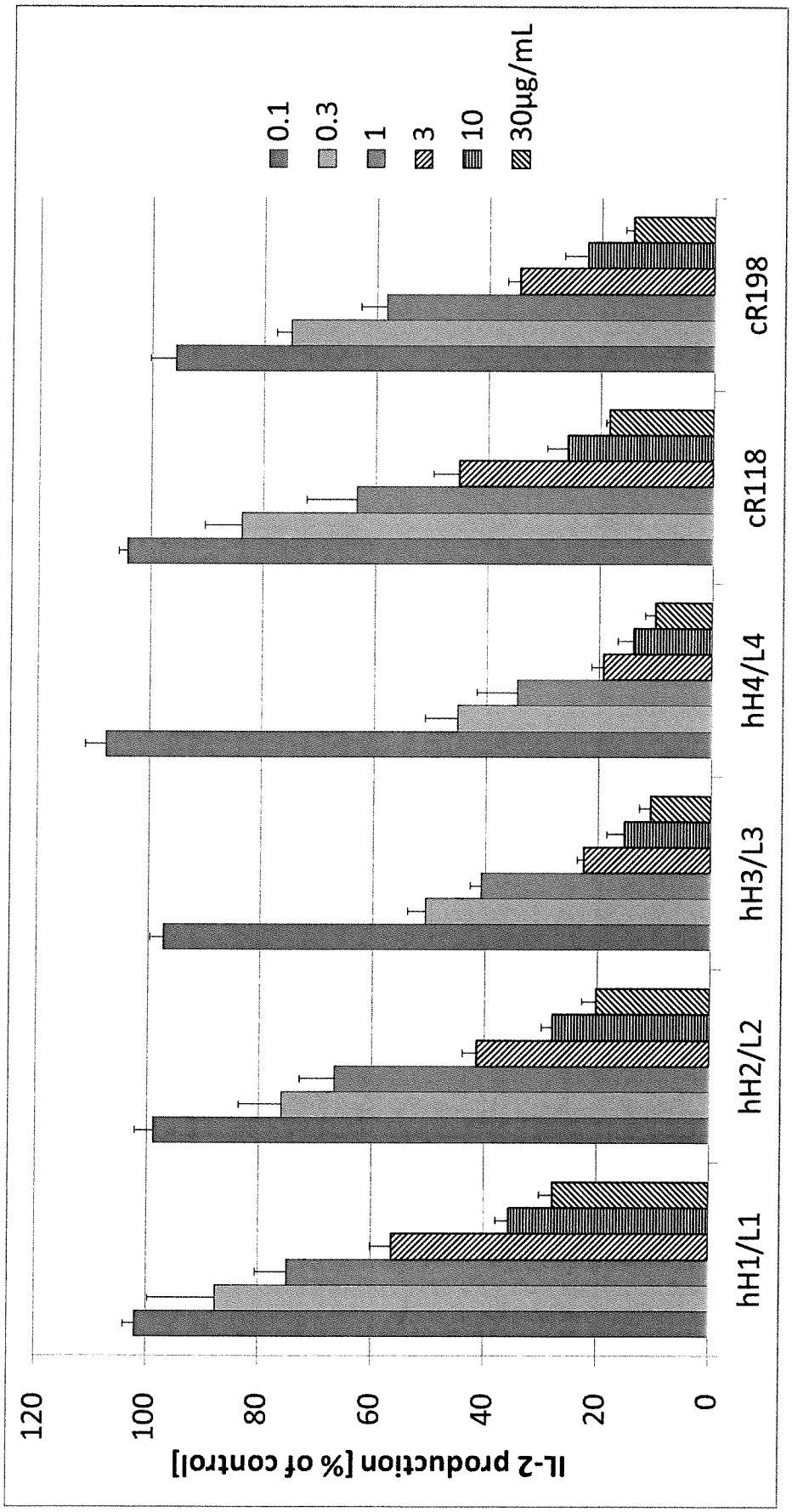
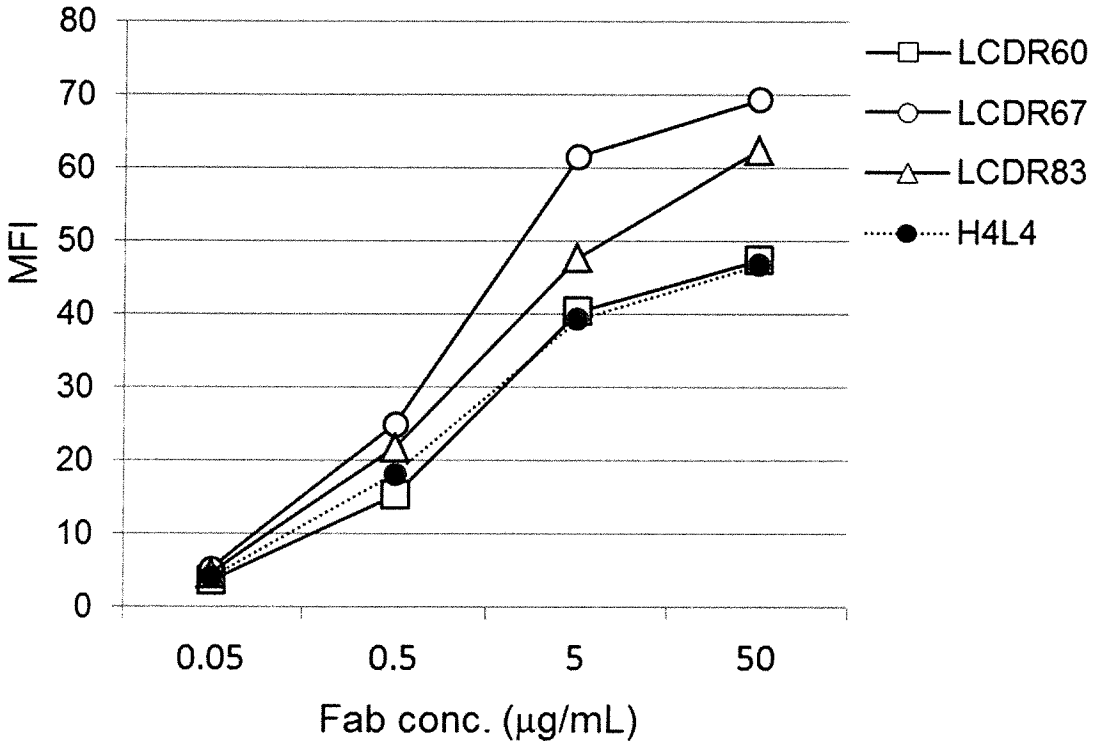
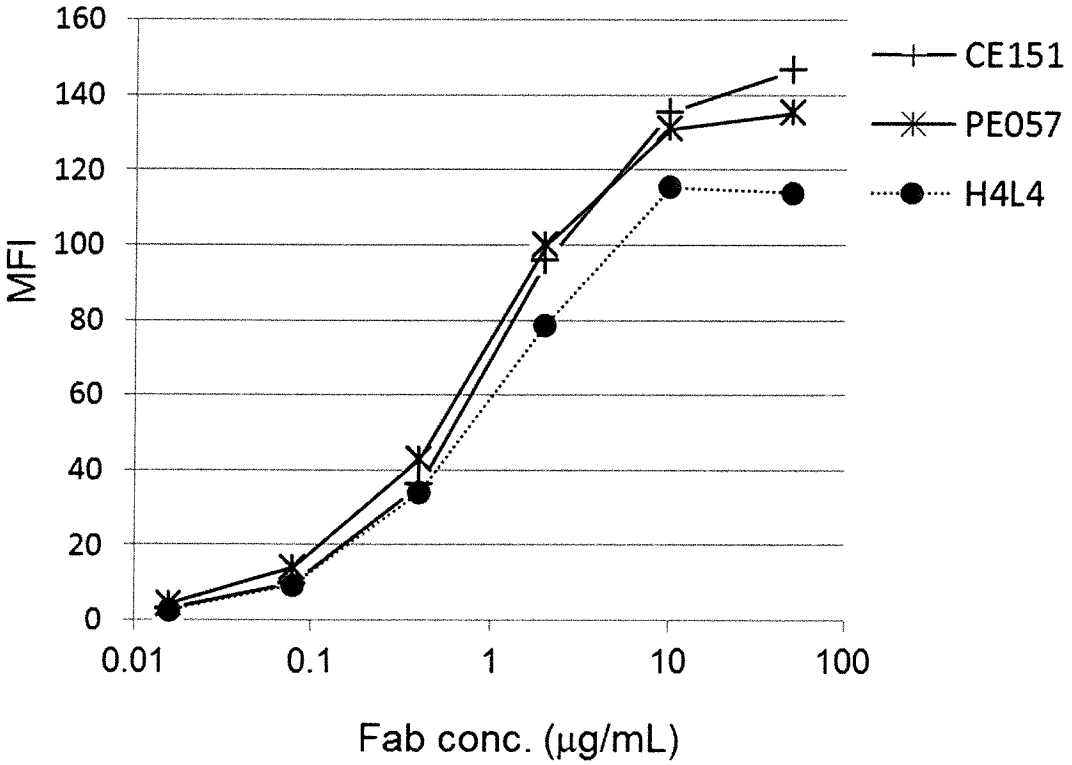

IL-2 production [% of control]
120
100
80
60
40
20
0
0.1
0.3
1
3
10
30µg/mL
hH1/L1
hH2/L2
hH3/L3
hH4/L4
cR118
cR198

Figure 7

(A)


80
70
60
50
40
30
20
10
0
MFI
0.05
0.5
5
50
Fab conc. (μg/mL)
LCDR60
LCDR67
LCDR83
H4L4

(B)


160
140
120
100
80
60
40
20
0
MFI
0.01
0.1
1
10
100
Fab conc. (μg/mL)
CE151
PE057
H4L4

(C)

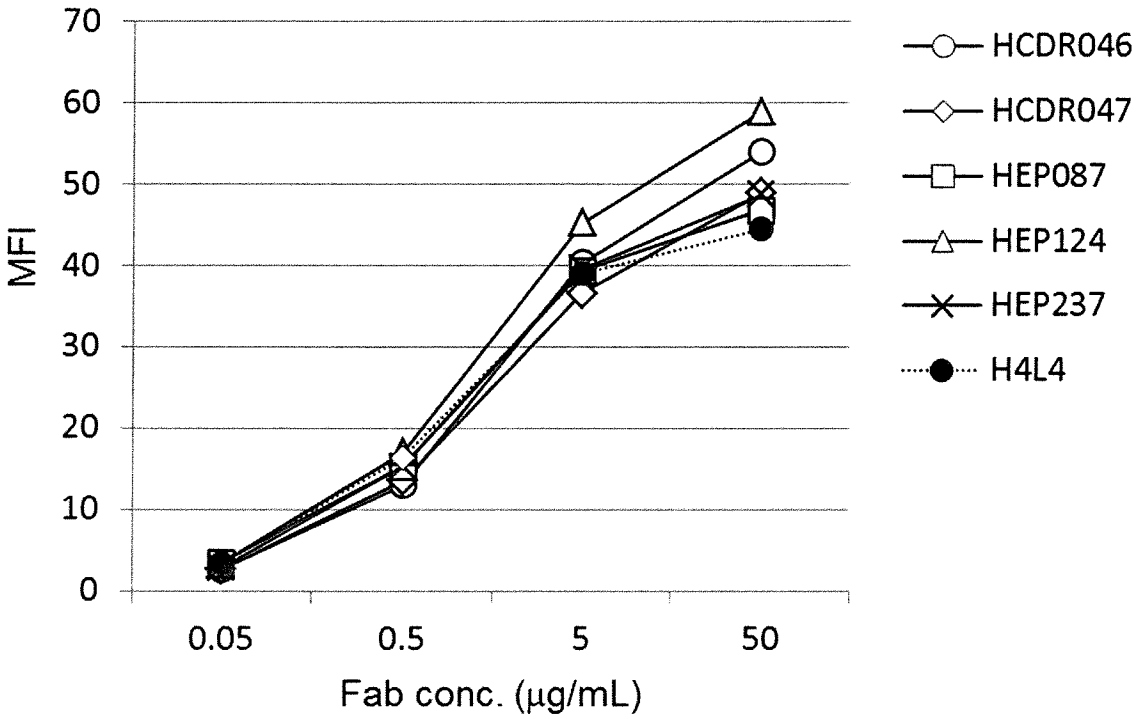

70
60
50
40
30
20
10
0
MFI
0.05
0.5
5
50
Fab conc. (μg/mL)
HCDR046
HCDR047
HEP087
HEP124
HEP237
H4L4

Figure 8

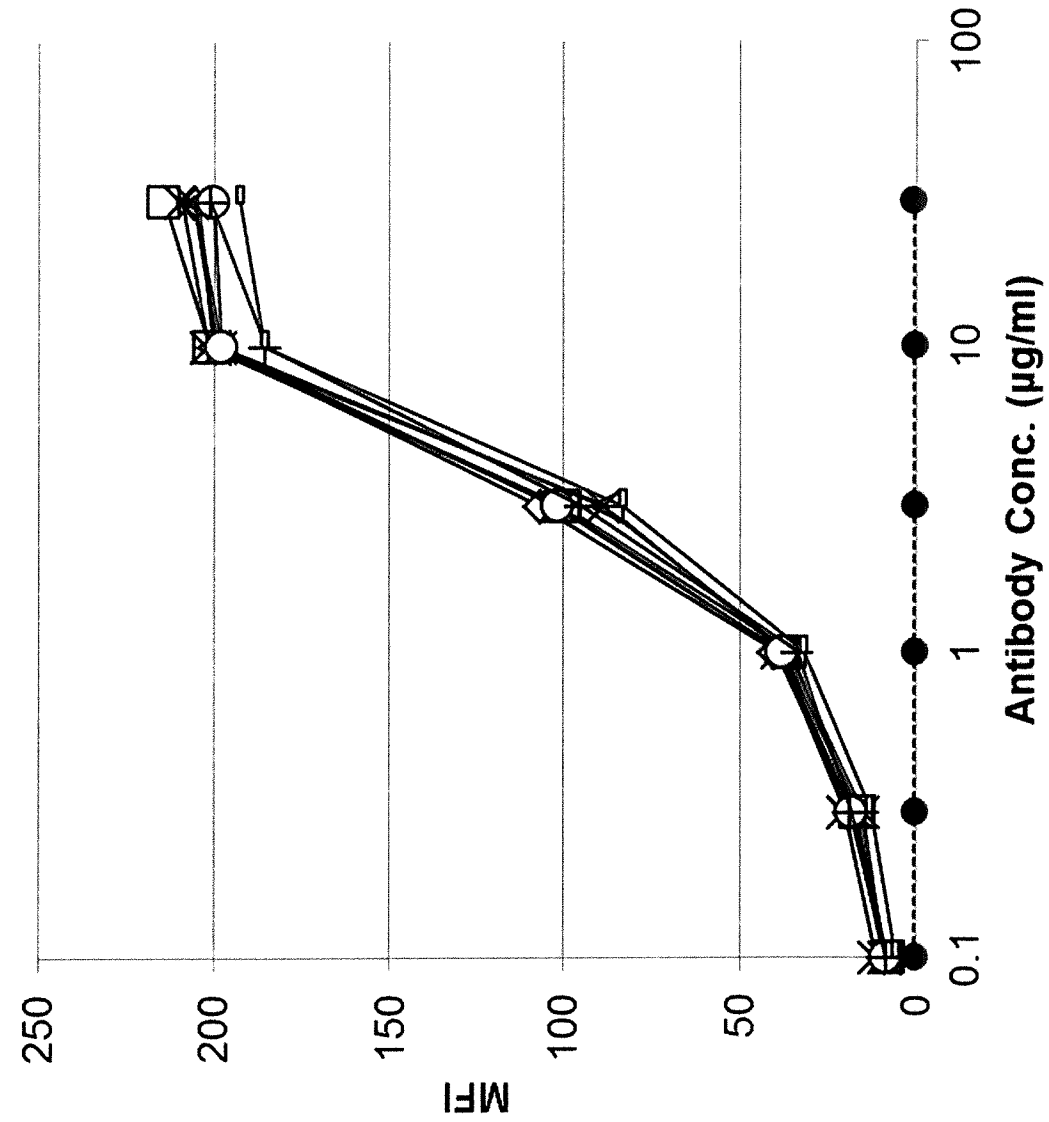

hH3/LG1
hHG1/LG1
hHG1/LG2
hHG1/LG3
hHG2/LG1
hHG3/LG1
hH3/L3
hH4/L4
hIgG
MFI
250
200
150
100
50
0
0.1
1
10
100
Antibody Conc. (µg/ml)

Figure 9

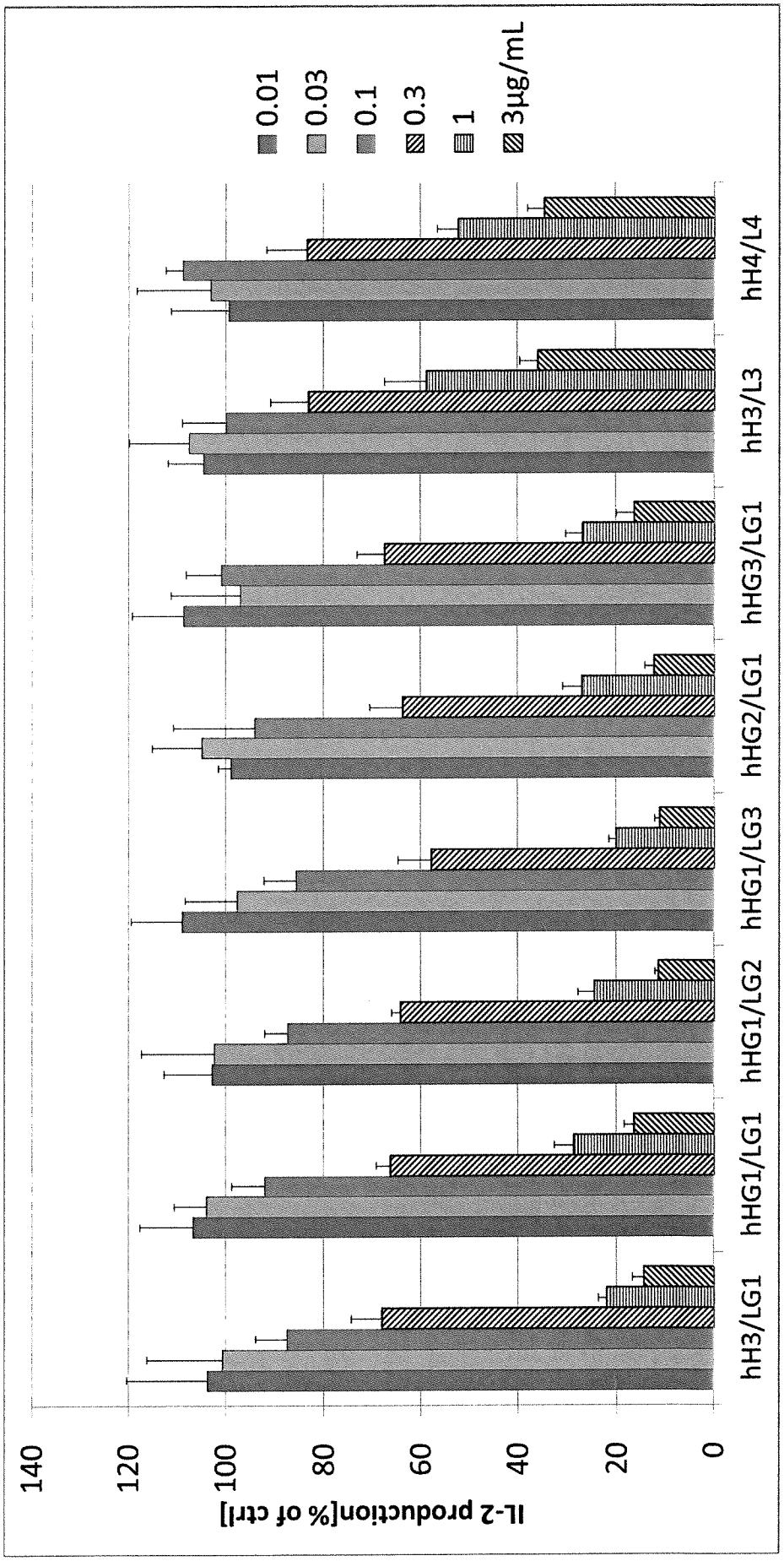

IL-2 production[% of ctrl]
140
120
100
80
60
40
20
0
0.01
0.03
0.1
0.3
1
3µg/mL
hH3/LG1
hHG1/LG1
hHG1/LG2
hHG1/LG3
hHG2/LG1
hHG3/LG1
hH3/L3
hH4/L4

Figure 10

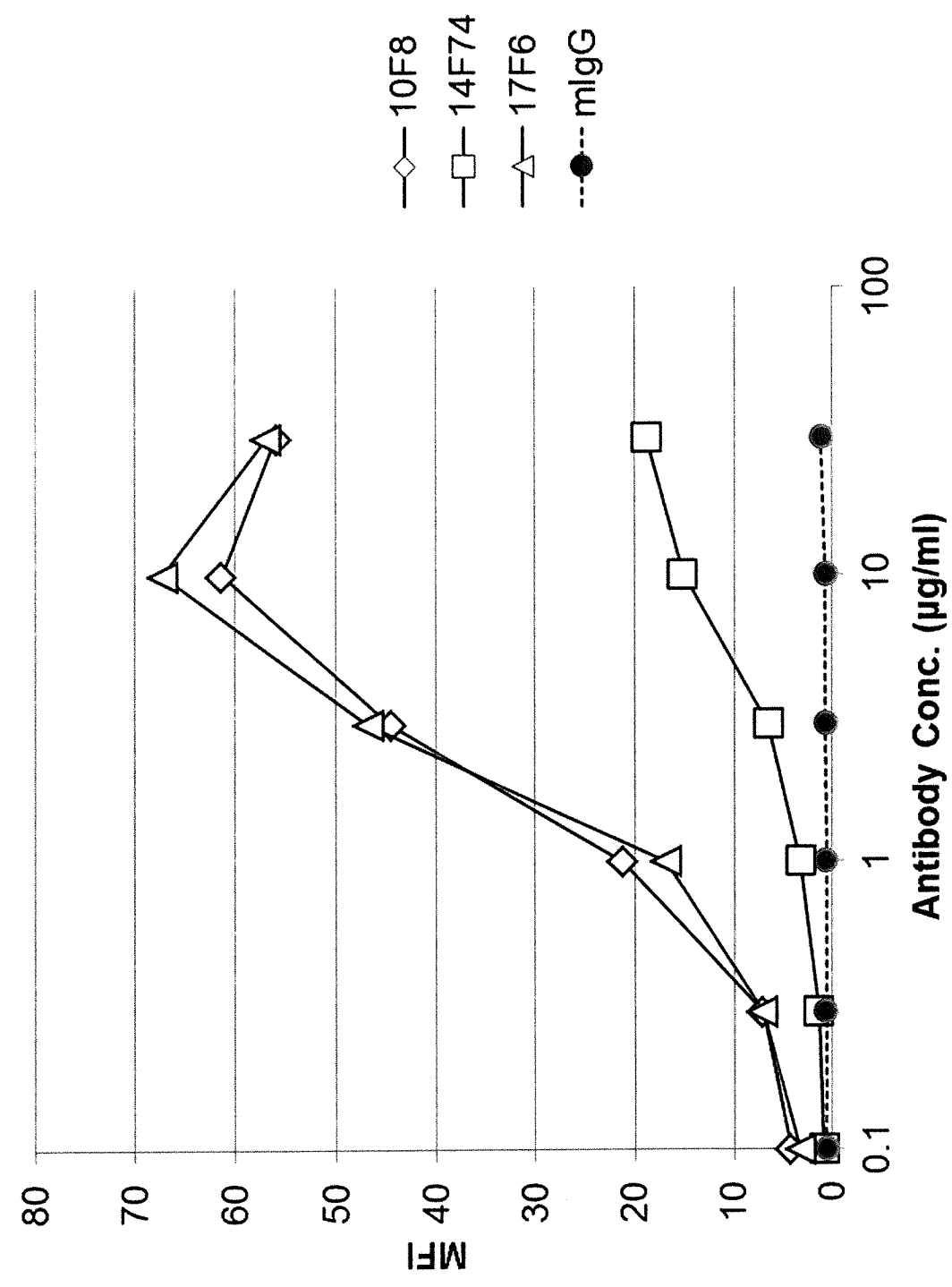

10F8
14F74
17F6
mIgG
MFI
0
10
20
30
40
50
60
70
80
0.1
1
10
100
Antibody Conc. (µg/ml)

Figure 11

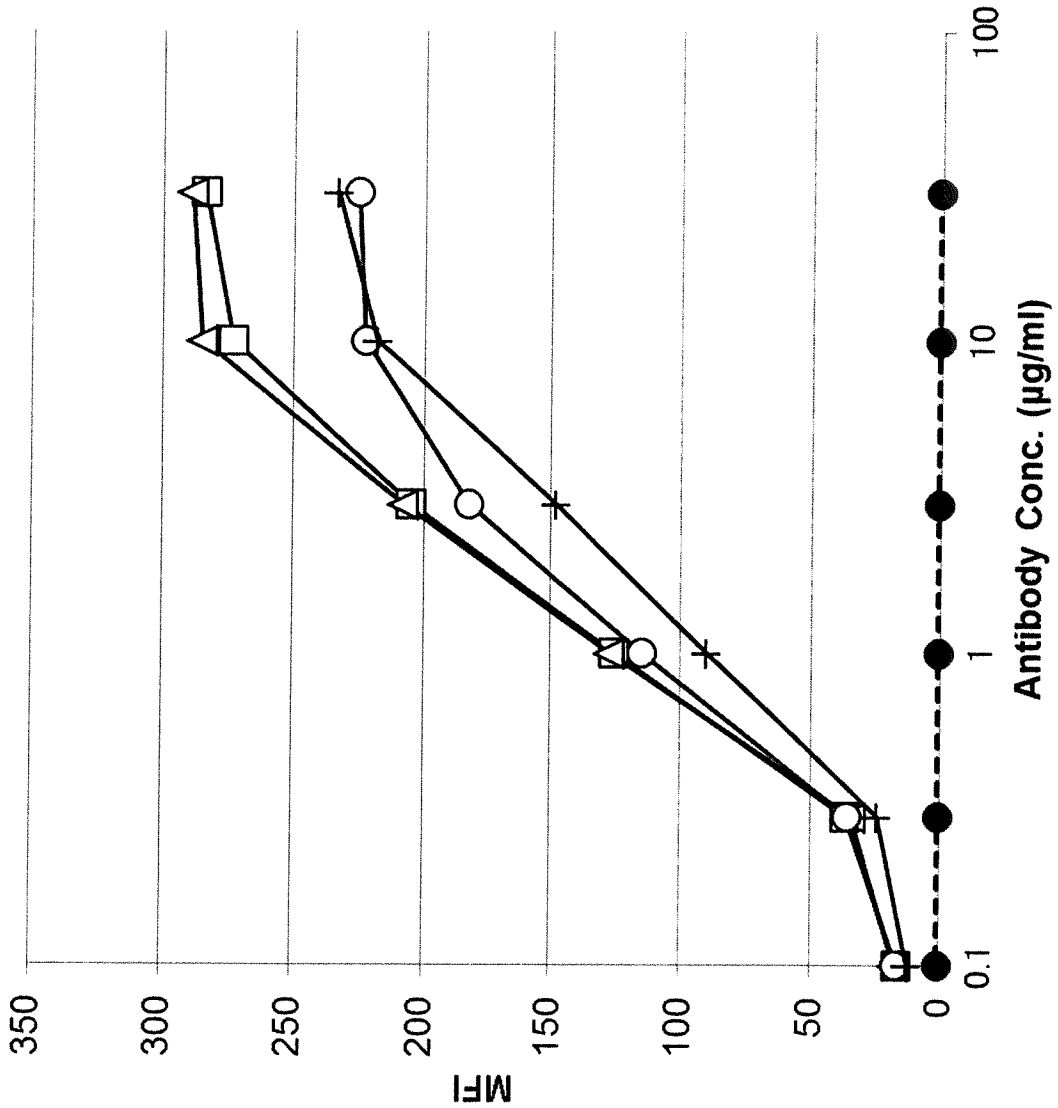

hIgG
hHG1/LG1
hHG1-LALA/LG1
2C1.1
5H3.1
MFI
350
300
250
200
150
100
50
0
0.1
1
10
100
Antibody Conc. (µg/ml)

Figure 12

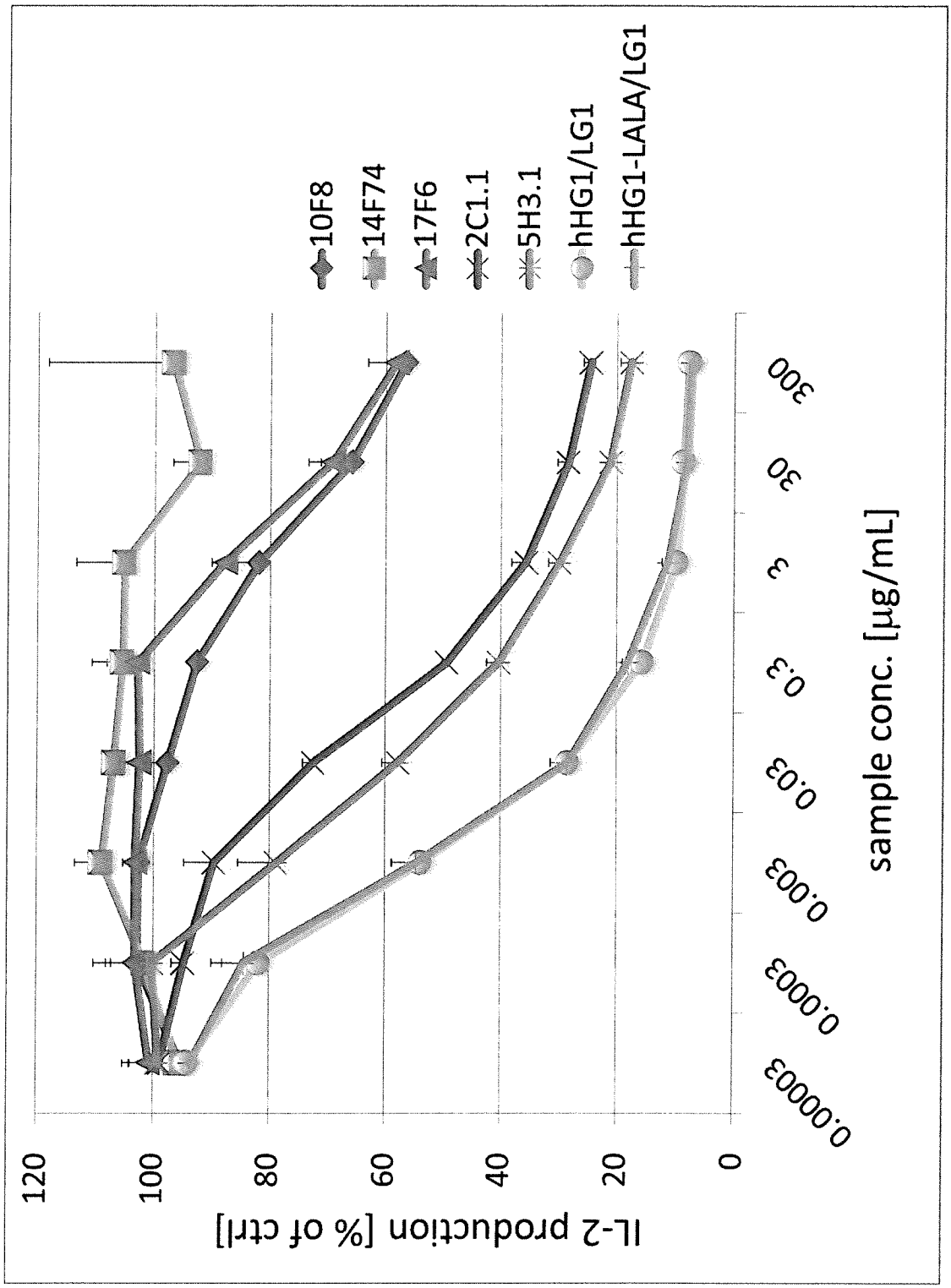

IL-2 production [% of ctrl]
120
100
80
60
40
20
0
0.00003
0.0003
0.003
0.03
0.3
3
30
300
sample conc. [µg/mL]
10F8
14F74
17F6
2C1.1
5H3.1
hHG1/LG1
hHG1-LALA/LG1

Figure 13

	IC50 [ng/mL]	IC80 [ng/mL]
10F8	>300000	>300000
14F74	>300000	>300000
17F6	>300000	>300000
2C1.1	279	>300000
5H3.1	83	60621
hHG1/LG1	4	137
hHG1-LALA/LG1	4	195

Figure 14

SEQ ID NO: 10: Nucleotide sequence encoding R118 light chain

ATGAAAATGACGACACCTGCTCAGTTCCTTGGGCTTCTGTTGCTCTGGTTTCCAGGTGCCAGGTGTGACATCCA
GTTGACCCAGTCTCCATCCACATTGCCTGCATCCCTGGGAGAGAGAGTCACCATCAGTTGCAGAGCAAGTCAGA
GTATTAGCAATAGTTTAAGCTGGTTTCAACAGAAACCAGATGGAACTGTTAAACGCCTGATCTATTCTACATCC
ACTTTAGAATCTGGTGTCCCATCAAGGTTCAGTGGCAGTGGGTCTGGGACAGATTATTCTCTCTCCATCACCAG
TCTTGAGTCTGAAGATTTTGCAATGTATTACTGTCTACAGTTTGCTACTTTTCCGGACACGTTTGGAACTGGGA
CCAAACTGGAANTGAGACGGGCTGATGCTGCANCA

Signal sequence (1-66), Variable region (67-384)

SEQ ID NO: 11: Amino acid sequence of R118 light chain

MKMTTPAQFLGLLLLWFPGARCDIQLTQSPSTLPASLGERVTISCRASQSISNSLSWFQQKPDGTVKRLIYSTS
TLESGVPSRFSGSGSGTDYSLSITSLESEDFAMYYCLQFATFPDTFGTGTKLEXRRADAAX

Signal sequence (1-22), Variable region (23-128)

Figure 15

SEQ ID NO: 12: Nucleotide sequence encoding R118 heavy chain

ATGGAATGGAACTGGGTCTTTCTCCTCCTCCTGTCAGTAACTGCAGAAGTCCAGTCCCAGGTCCAGCTGCAGCA
GTCTGGAGCGGAGCTGGCAAAGCCTGGCTCCTCAGTGAAGATTTCCTGCAAGGCTTCCGGCTACACCGTCACCG
CCTATTATATAAGTTGGATAAGGCAGACGATTGGACAGGGCCTTGAGTATGTTGGATATATTGACATGGGAAAT
GGAAGGACTAACTACAATGCGAGGTTCAAGGGCAAGGCCACATTGACTGTGGACAAATCCTCCAGCACAGCCTT
CATGCAACTCAGCAGCCTGACACCTGACGACTCTGCGGTCTATTACTGTGCAAGGGACTCCAACTGGGGGGTTG
ATTACTGGGGCCAAGGAGTCATGGTCACAGTCTCCTCAGCTGAAACAACAGCCCCATCTGTCTATCCACTGGCT
CCTGGAACTGCTTCTCAAAAGTNA

Signal sequence (1-57), Variable region (58-408)

SEQ ID NO: 13: Amino acid sequence of R118 heavy chain

MEWNWVFLLLLSVTAEVQSQVQLQQSGAELAKPGSSVKISCKASGYTVTAYYISWIRQTIGQGLEYVGYIDMGN
GRTNYNARFKGKATLTVDKSSSTAFMQLSSLTPDDSAVYYCARDSNWGVDYWGQGVMVTVSSAETTAPSVYPLA
PGTASQKX

Signal sequence (1-19), Variable region (20-136)

Figure 16

SEQ ID NO: 14: Nucleotide sequence encoding R198 light chain

ATGAAAATGACGACACCTGCTCAGTTCCTTGGGCTTCTGTTGCTCTGGTTTCCAGGTGCCAGGTGTGACATCCA
GTTGACCCAGTCTCCATCCACATTGCCTGCATCTCTGGGAGAGAGAGTCACCATCAGTTGCAGAGCAAGTCAGA
GTATTGGCAATAGTTTAAGCTGGTTTCAGCAGAAACCAGATGGATCTGTTAAACGCCTGATCTACTCTACATCC
ACTTTAGAATCTGGTGTCCCATCAAGGTTCAGTGGCAGTGGGTCTGGGACAGATTATTCTCTCTCCATCACCAG
TCTTGAGTCTGAAGATTTTGCAATGTATTACTGTCTACAGTTTGCTACTTATCCGGACACGTTTGGAACTGGGA
CCAAACTGGAACTGAGACGGGCTGATGCTGCANCAACT

Signal sequence (1-66), Variable region (67-384)

SEQ ID NO: 15: Amino acid sequence of R198 light chain

MKMTTPAQFLGLLLLWFPGARCDIQLTQSPSTLPASLGERVTISCRASQSIGNSLSWFQQKPDGSVKRLIYSTS
TLESGVPSRFSGSGSGTDYSLSITSLESEDFAMYYCLQFATYPDTFGTGTKLELRRADAAXT

Signal sequence (1-22), Variable region (23-128)

Figure 17

SEQ ID NO: 16: Nucleotide sequence encoding R198 heavy chain

ATGGAATGGAACTGGGTCTTTCTCTTCCTCCTGTCAGTAACTGCAGAAGTCCAGTCCCAGGTCCAGCTGCAGCA
GTCTGGAGCGGAGCTGGCAAAGCCTGGCTCCTCAATGAAGATTTCCTGCAAGGCTTCCGGCTACCCCGTCACCA
GCTATTATATAAGTTGGATAAAGCAGACGACTGGACAGGGCCTTGAGTATATTGGATATGTTGACATGGGAAAT
GGACGGACTAACTACAATGAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAATCCTCCAGCACAGCCTT
CATGCAACTCAGCAGCCTGACACCTGACGACTCTGCGGTCTATTACTGTGCAAGGGACTCCAACTGGGGGGTTG
ATTACTGGGGCCAAGGAGTCATGGTCACAGTCTCCTCAGCTGAAACAACAGCCCCATCTGTCTATCCACTGGCT
CCTGGAACTGCTCTCAAAAGTAACNCC

Signal sequence (1-57), Variable region (58-408)

SEQ ID NO: 17: Amino acid sequence of R198 heavy chain

MEWNWVFLFLLSVTAEVQSQVQLQQSGAELAKPGSSMKISCKASGYPVTSYYISWIKQTTGQGLEYIGYVDMGN
GRTNYNEKFKGKATLTVDKSSSTAFMQLSSLTPDDSAVYYCARDSNWGVDYWGQGVMVTVSSAETTAPSVYPLA
PGTALKSNX

Signal sequence (1-19), Variable region (20-136)

Figure 18

SEQ ID NO: 22: Nucleotide sequence encoding human chimerized cR118 light chain

ATGGTGCTGCAGACCCAGGTGTTCATCTCCCTGCTGCTGTGGATCTCCGGCGCGTACGGCGACATCCAGTTGAC
CCAGTCTCCATCCACATTGCCTGCATCCCTGGGAGAGAGAGTCACCATCAGTTGCAGAGCAAGTCAGAGTATTA
GCAATAGTTTAAGCTGGTTTCAACAGAAACCAGATGGAACTGTTAAACGCCTGATCTATTCTACATCCACTTTA
GAATCTGGTGTCCCATCAAGGTTCAGTGGCAGTGGGTCTGGGACAGATTATTCTCTCTCCATCACCAGTCTTGA
GTCTGAAGATTTTGCAATGTATTACTGTCTACAGTTTGCTACTTTTCCGGACACGTTTGGAACTGGGACCAAAC
TGGAACTGAGACGGGCTGTGGCCGCCCCCTCCGTGTTCATCTTCCCCCCCTCCGACGAGCAGCTGAAGTCCGGC
ACCGCCTCCGTGGTGTGCCTGCTGAATAACTTCTACCCCAGAGAGGCCAAGGTGCAGTGGAAGGTGGACAACGC
CCTGCAGTCCGGGAACTCCCAGGAGAGCGTGACCGAGCAGGACAGCAAGGACAGCACCTACAGCCTGAGCAGCA
CCCTGACCCTGAGCAAAGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCTGAGC
TCCCCCGTCACCAAGAGCTTCAACAGGGGGGAGTGTTAG

Signal sequence (1-60), Variable region (61-378), Constant region (379-702)

SEQ ID NO: 23: Amino acid sequence of human chimerized cR118 light chain

MVLQTQVFISLLLWISGAYGDIQLTQSPSTLPASLGERVTISCRASQSISNSLSWFQQKPDGTVKRLIYSTSTL
ESGVPSRFSGSGSGTDYSLSITSLESEDFAMYYCLQFATFPDTFGTGTKLELRRAVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS
SPVTKSFNRGEC

Signal sequence (1-20), Variable region (21-126), Constant region (127-234)

Figure 19

SEQ ID NO: 24: Nucleotide sequence encoding human chimerized cR198 light chain

ATGGTGCTGCAGACCCAGGTGTTCATCTCCCTGCTGCTGTGGATCTCCGGCGCGTACGGCGACATCCAGTTGAC
CCAGTCTCCATCCACATTGCCTGCATCTCTGGGAGAGAGAGTCACCATCAGTTGCAGAGCAAGTCAGAGTATTG
GCAATAGTTTAAGCTGGTTTCAGCAGAAACCAGATGGATCTGTTAAACGCCTGATCTACTCTACATCCACTTTA
GAATCTGGTGTCCCATCAAGGTTCAGTGGCAGTGGGTCTGGGACAGATTATTCTCTCTCCATCACCAGTCTTGA
GTCTGAAGATTTTGCAATGTATTACTGTCTACAGTTTGCTACTTATCCGGACACGTTTGGAACTGGGACCAAAC
TGGAACTGAGACGGGCTGTGGCCGCCCCCTCCGTGTTCATCTTCCCCCCCTCCGACGAGCAGCTGAAGTCCGGC
ACCGCCTCCGTGGTGTGCCTGCTGAATAACTTCTACCCCAGAGAGGCCAAGGTGCAGTGGAAGGTGGACAACGC
CCTGCAGTCCGGGAACTCCCAGGAGAGCGTGACCGAGCAGGACAGCAAGGACAGCACCTACAGCCTGAGCAGCA
CCCTGACCCTGAGCAAAGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCTGAGC
TCCCCCGTCACCAAGAGCTTCAACAGGGGGGAGTGTTAG

Signal sequence (1-60), Variable region (61-378), Constant region (379-702)

SEQ ID NO: 25: Amino acid sequence of human chimerized cR198 light chain

MVLQTQVFISLLLWISGAYGDIQLTQSPSTLPASLGERVTISCRASQSIGNSLSWFQQKPDGSVKRLIYSTSTL
ESGVPSRFSGSGSGTDYSLSITSLESEDFAMYYCLQFATYPDTFGTGTKLELRRAVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS
SPVTKSFNRGEC

Signal sequence (1-20), Variable region (21-126), Constant region (127-234)

Figure 20

SEQ ID NO: 26: Nucleotide sequence encoding human chimerized cR118 heavy chain

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAGCCAGGTCCAGCTGCAGCA
GTCTGGAGCGGAGCTGGCAAAGCCTGGCTCCTCAGTGAAGATTTCCTGCAAGGCTTCCGGCTACACCGTCACCG
CCTATTATATAAGTTGGATAAGGCAGACGATTGGACAGGGCCTTGAGTATGTTGGATATATTGACATGGGAAAT
GGAAGGACTAACTACAATGCGAGGTTCAAGGGCAAGGCCACATTGACTGTGGACAAATCCTCCAGCACAGCCTT
CATGCAACTCAGCAGCCTGACACCTGACGACTCTGCGGTCTATTACTGTGCAAGGGACTCCAACTGGGGGGTTG
ATTACTGGGGCCAAGGAGTCATGGTCACAGTCAGCTCAGCCTCCACCAAGGGCCCAAGCGTCTTCCCCCTGGCA
CCCTCCTCCAAGAGCACCTCTGGCGGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGT
GACCGTGAGCTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCCGCTGTCCTGCAGTCCTCAGGAC
TCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACC
CTGCCCAGCACCTGAACTCCTGGGGGGACCCTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA
TCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG
TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGTACCGGGT
GGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACACCCTG
CCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGA
CATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACTACAAGACCACCCCTCCCGTGCTGGACTCCG
ACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGC
TCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAATGA

Signal sequence (1-57), Variable region (58-408), Constant region (409-1398)

SEQ ID NO: 27: Amino acid sequence of human chimerized cR118 heavy chain

MKHLWFFLLLVAAPRWVLSQVQLQQSGAELAKPGSSVKISCKASGYTVTAYYISWIRQTIGQGLEYVGYIDMGN
GRTNYNARFKGKATLTVDKSSSTAFMQLSSLTPDDSAVYYCARDSNWGVDYWGQGVMVTVSSASTKGPSVFPLA
PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC
SVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-136), Constant region (137-466)

Figure 21

SEQ ID NO: 28: Nucleotide sequence encoding human chimerized cR198 heavy chain

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAGCCAGGTCCAGCTGCAGCA
GTCTGGAGCGGAGCTGGCAAAGCCTGGCTCCTCAATGAAGATTTCCTGCAAGGCTTCCGGCTACCCCGTCACCA
GCTATTATATAAGTTGGATAAAGCAGACGACTGGACAGGGCCTTGAGTATATTGGATATGTTGACATGGGAAAT
GGACGGACTAACTACAATGAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAATCCTCCAGCACAGCCTT
CATGCAACTCAGCAGCCTGACACCTGACGACTCTGCGGTCTATTACTGTGCAAGGGACTCCAACTGGGGGGTTG
ATTACTGGGGCCAAGGAGTCATGGTCACAGTCAGCTCAGCCTCCACCAAGGGCCCAAGCGTCTTCCCCCTGGCA
CCCTCCTCCAAGAGCACCTCTGGCGGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGT
GACCGTGAGCTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCCGCTGTCCTGCAGTCCTCAGGAC
TCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACC
CTGCCCAGCACCTGAACTCCTGGGGGGACCCTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA
TCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG
TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGTACCGGGT
GGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACACCCTG
CCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGA
CATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACTACAAGACCACCCCTCCCGTGCTGGACTCCG
ACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGC
TCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAATGA

Signal sequence (1-57), Variable region (58-408), Constant region (409-1398)

SEQ ID NO: 29: Amino acid sequence of human chimerized cR198 heavy chain

MKHLWFFLLLVAAPRWVLSQVQLQQSGAELAKPGSSMKISCKASGYPVTSYYISWIKQTTGQGLEYIGYVDMGN
GRTNYNEKFKGKATLTVDKSSSTAFMQLSSLTPDDSAVYYCARDSNWGVDYWGQGVMVTVSSASTKGPSVFPLA
PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC
SVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-136), Constant region (137-466)

Figure 22

SEQ ID NO: 30: Nucleotide sequence encoding hR198_L1 type light chain

ATGGTGCTGCAGACCCAGGTGTTCATCTCCCTGCTGCTGTGGATCTCCGGCGCGTACGGCGATATCCAGCTGAC
CCAGAGCCCTAGCAGCCTGTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTAGAGCCAGCCAGAGCATCG
GCAACAGCCTGAGCTGGTTCCAGCAGAAACCCGGCAAGGCCCCCAAGCGGCTGATCTACAGCACCAGCACCCTG
GAAAGCGGCGTGCCCAGCAGATTTTCTGGCAGCGGCTCCGGCACCGACTACACCCTGACAATCAGCAGCCTGCA
GCCCGAGGACTTCGCCATGTACTACTGCCTGCAGTTCGCCACCTACCCCGACACCTTTGGCCAGGGCACCAAGG
TGGAAATCAAGCGTACGGTGGCCGCCCCCTCCGTGTTCATCTTCCCCCCCTCCGACGAGCAGCTGAAGTCCGGC
ACCGCCTCCGTGGTGTGCCTGCTGAATAACTTCTACCCCAGAGAGGCCAAGGTGCAGTGGAAGGTGGACAACGC
CCTGCAGTCCGGGAACTCCCAGGAGAGCGTGACCGAGCAGGACAGCAAGGACAGCACCTACAGCCTGAGCAGCA
CCCTGACCCTGAGCAAAGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCTGAGC
TCCCCCGTCACCAAGAGCTTCAACAGGGGGGAGTGTTAG

Signal sequence (1-60), Variable region (61-378), Constant region (379-702)

SEQ ID NO: 31: Amino acid sequence of hR198_L1 type light chain

MVLQTQVFISLLLWISGAYGDIQLTQSPSSLSASVGDRVTITCRASQSIGNSLSWFQQKPGKAPKRLIYSTSTL
ESGVPSRFSGSGSGTDYTLTISSLQPEDFAMYYCLQFATYPDTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS
SPVTKSFNRGEC

Signal sequence (1-20), Variable region (21-126), Constant region (127-234)

Figure 23

SEQ ID NO: 32: Nucleotide sequence encoding hR198_L2 type light chain

ATGGTGCTGCAGACCCAGGTGTTCATCTCCCTGCTGCTGTGGATCTCCGGCGCGTACGGCGATATCCAGCTGAC
CCAGAGCCCTAGCAGCCTGTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTAGAGCCAGCCAGAGCATCG
GCAACAGCCTGAGCTGGTTCCAGCAGAAACCCGGCAAGGCCGTGAAGCGGCTGATCTACAGCACCAGCACCCTG
GAAAGCGGCGTGCCCAGCAGATTTTCTGGCAGCGGCTCCGGCACCGACTACACCCTGACAATCAGCAGCCTGCA
GCCCGAGGACTTCGCCATGTACTACTGCCTGCAGTTCGCCACCTACCCCGACACCTTTGGCCAGGGCACCAAGG
TGGAAATCAAGCGTACGGTGGCCGCCCCCTCCGTGTTCATCTTCCCCCCCTCCGACGAGCAGCTGAAGTCCGGC
ACCGCCTCCGTGGTGTGCCTGCTGAATAACTTCTACCCCAGAGAGGCCAAGGTGCAGTGGAAGGTGGACAACGC
CCTGCAGTCCGGGAACTCCCAGGAGAGCGTGACCGAGCAGGACAGCAAGGACAGCACCTACAGCCTGAGCAGCA
CCCTGACCCTGAGCAAAGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCTGAGC
TCCCCCGTCACCAAGAGCTTCAACAGGGGGGAGTGTTAG

Signal sequence (1-60), Variable region (61-378), Constant region (379-702)

SEQ ID NO: 33: Amino acid sequence of hR198_L2 type light chain

MVLQTQVFISLLLWISGAYGDIQLTQSPSSLSASVGDRVTITCRASQSIGNSLSWFQQKPGKAVKRLIYSTSTL
ESGVPSRFSGSGSGTDYTLTISSLQPEDFAMYYCLQFATYPDTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS
SPVTKSFNRGEC

Signal sequence (1-20), Variable region (21-126), Constant region (127-234)

Figure 24

SEQ ID NO: 34: Nucleotide sequence encoding hR198_L3 type light chain

ATGGTGCTGCAGACCCAGGTGTTCATCTCCCTGCTGCTGTGGATCTCCGGCGCGTACGGCGATATCCAGCTGAC
CCAGAGCCCTAGCAGCCTGTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTAGAGCCAGCCAGAGCATCG
GCAACAGCCTGAGCTGGTTCCAGCAGAAACCCGGCAAGGCCCCCAAGCGGCTGATCTACAGCACCAGCACCCTG
GAAAGCGGCGTGCCCAGCAGATTTTCTGGCAGCGGCTCCGGCACCGACTACACCCTGACAATCAGCAGCCTGCA
GCCCGAGGACTTCGCCATGTACTACTGCCTGCAGTTCGCCACCTTCCCCGACACCTTTGGCCAGGGCACCAAGG
TGGAAATCAAGCGTACGGTGGCCGCCCCCTCCGTGTTCATCTTCCCCCCCTCCGACGAGCAGCTGAAGTCCGGC
ACCGCCTCCGTGGTGTGCCTGCTGAATAACTTCTACCCCAGAGAGGCCAAGGTGCAGTGGAAGGTGGACAACGC
CCTGCAGTCCGGGAACTCCCAGGAGAGCGTGACCGAGCAGGACAGCAAGGACAGCACCTACAGCCTGAGCAGCA
CCCTGACCCTGAGCAAAGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCTGAGC
TCCCCCGTCACCAAGAGCTTCAACAGGGGGGAGTGTTAG

Signal sequence (1-60), Variable region (61-378), Constant region (379-702)

SEQ ID NO: 35: Amino acid sequence of hR198_L3 type light chain

MVLQTQVFISLLLWISGAYGDIQLTQSPSSLSASVGDRVTITCRASQSIGNSLSWFQQKPGKAPKRLIYSTSTL
ESGVPSRFSGSGSGTDYTLTISSLQPEDFAMYYCLQFATFPDTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS
SPVTKSFNRGEC

Signal sequence (1-20), Variable region (21-126), Constant region (127-234)

Figure 25

SEQ ID NO: 36: Nucleotide sequence encoding hR198_L4 type light chain

ATGGTGCTGCAGACCCAGGTGTTCATCTCCCTGCTGCTGTGGATCTCCGGCGCGTACGGCGATATCCAGCTGAC
CCAGAGCCCTAGCAGCCTGTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTAGAGCCAGCCAGAGCATCG
GCAACAGCCTGAGCTGGTTCCAGCAGAAACCCGGCAAGGCCGTGAAGCGGCTGATCTACAGCACCAGCACCCTG
GAAAGCGGCGTGCCCAGCAGATTTTCTGGCAGCGGCTCCGGCACCGACTACACCCTGACAATCAGCAGCCTGCA
GCCCGAGGACTTCGCCATGTACTACTGCCTGCAGTTCGCCACCTTCCCCGACACCTTTGGCCAGGGCACCAAGG
TGGAAATCAAGCGTACGGTGGCCGCCCCCTCCGTGTTCATCTTCCCCCCCTCCGACGAGCAGCTGAAGTCCGGC
ACCGCCTCCGTGGTGTGCCTGCTGAATAACTTCTACCCCAGAGAGGCCAAGGTGCAGTGGAAGGTGGACAACGC
CCTGCAGTCCGGGAACTCCCAGGAGAGCGTGACCGAGCAGGACAGCAAGGACAGCACCTACAGCCTGAGCAGCA
CCCTGACCCTGAGCAAAGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCTGAGC
TCCCCCGTCACCAAGAGCTTCAACAGGGGGGAGTGTTAG

Signal sequence (1-60), Variable region (61-378), Constant region (379-702)

SEQ ID NO: 37: Amino acid sequence of hR198_L4 type light chain

MVLQTQVFISLLLWISGAYGDIQLTQSPSSLSASVGDRVTITCRASQSIGNSLSWFQQKPGKAVKRLIYSTSTL
ESGVPSRFSGSGSGTDYTLTISSLQPEDFAMYYCLQFATFPDTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS
SPVTKSFNRGEC

Signal sequence (1-20), Variable region (21-126), Constant region (127-234)

Figure 26

SEQ ID NO: 38: Nucleotide sequence encoding hR198_H1 type heavy chain

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAGCCAGGTGCAGCTGGTGCA
GTCTGGCGCCGAAGTGAAGAAACCAGGCGCCAGCGTGAAGGTGTCCTGCAAGGCCTCTGGCTACCCCGTGACCA
GCTACTACATCAGCTGGGTCAGACAGGCCCCAGGCCAGGGCCTGGAATACATCGGCTATGTGGACATGGGCAAC
GGCCGGACCAACTACAACGAGAAGTTCAAGGGCAGAGCCACCCTGACCGTGGACAAGAGCACCAGCACCGCCTA
CATGGAACTGAGCAGCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGACAGCAACTGGGGCGTGG
ACTATTGGGGCCAGGGCACACTCGTGACCGTCAGCTCAGCCTCCACCAAGGGCCCAAGCGTCTTCCCCCTGGCA
CCCTCCTCCAAGAGCACCTCTGGCGGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGT
GACCGTGAGCTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCCGCTGTCCTGCAGTCCTCAGGAC
TCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACC
CTGCCCAGCACCTGAACTCCTGGGGGGACCCTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA
TCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG
TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGTACCGGGT
GGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACACCCTG
CCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGA
CATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACTACAAGACCACCCCTCCCGTGCTGGACTCCG
ACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGC
TCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAATGA

Signal sequence (1-57), Variable region (58-408), Constant region (409-1398)

SEQ ID NO: 39: Amino acid sequence of hR198_H1 type heavy chain

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGYPVTSYYISWVRQAPGQGLEYIGYVDMGN
GRTNYNEKFKGRATLTVDKSTSTAYMELSSLRSEDTAVYYCARDSNWGVDYWGQGTLVTVSSASTKGPSVFPLA
PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC
SVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-136), Constant region (137-466)

Figure 27

SEQ ID NO: 40: Nucleotide sequence encoding hR198_H2 type heavy chain

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAGCCAGGTGCAGCTGGTGCA
GTCTGGCGCCGAAGTGAAGAAACCAGGCGCCAGCGTGAAGGTGTCCTGCAAGGCCTCTGGCTACCCCGTGACCA
GCTACTACATCAGCTGGATCAGACAGGCCCCAGGCCAGGGCCTGGAATACATCGGCTATGTGGACATGGGCAAC
GGCCGGACCAACTACAACGAGAAGTTCAAGGGCAGAGCCACCCTGACCGTGGACAAGAGCACCAGCACCGCCTA
CATGGAACTGAGCAGCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGACAGCAACTGGGGCGTGG
ACTATTGGGGCCAGGGCACACTCGTGACCGTCAGCTCAGCCTCCACCAAGGGCCCAAGCGTCTTCCCCCTGGCA
CCCTCCTCCAAGAGCACCTCTGGCGGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGT
GACCGTGAGCTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCCGCTGTCCTGCAGTCCTCAGGAC
TCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACC
CTGCCCAGCACCTGAACTCCTGGGGGGACCCTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA
TCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG
TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGTACCGGGT
GGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACACCCTG
CCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGA
CATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACTACAAGACCACCCCTCCCGTGCTGGACTCCG
ACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGC
TCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAATGA

Signal sequence (1-57), Variable region (58-408), Constant region (409-1398)

SEQ ID NO: 41: Amino acid sequence of hR198_H2 type heavy chain

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGYPVTSYYISWIRQAPGQGLEYIGYVDMGN
GRTNYNEKFKGRATLTVDKSTSTAYMELSSLRSEDTAVYYCARDSNWGVDYWGQGTLVTVSSASTKGPSVFPLA
PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC
SVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-136), Constant region (137-466)

Figure 28

SEQ ID NO: 42: Nucleotide sequence encoding hR198_H3 type heavy chain

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAGCCAGGTGCAGCTGGTGCA
GTCTGGCGCCGAAGTGAAGAAACCAGGCGCCAGCGTGAAGGTGTCCTGCAAGGCCTCTGGCTACCCCGTGACCG
CCTACTACATCAGCTGGGTCAGACAGGCCCCAGGCCAGGGCCTGGAATACGTGGGCTACATCGACATGGGCAAC
GGCCGGACCAACTACAACGCCCGGTTTAAGGGCAGAGCCACCCTGACCGTGGACAAGAGCACCAGCACCGCCTA
CATGGAACTGAGCAGCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGACAGCAACTGGGGCGTGG
ACTATTGGGGCCAGGGCACACTCGTGACCGTCAGCTCAGCCTCCACCAAGGGCCCAAGCGTCTTCCCCCTGGCA
CCCTCCTCCAAGAGCACCTCTGGCGGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGT
GACCGTGAGCTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCCGCTGTCCTGCAGTCCTCAGGAC
TCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACC
CTGCCCAGCACCTGAACTCCTGGGGGGACCCTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA
TCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG
TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGTACCGGGT
GGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACACCCTG
CCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGA
CATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACTACAAGACCACCCCTCCCGTGCTGGACTCCG
ACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGC
TCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAATGA

Signal sequence (1-57), Variable region (58-408), Constant region (409-1398)

SEQ ID NO: 43: Amino acid sequence of hR198_H3 type heavy chain

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGYPVTAYYISWVRQAPGQGLEYVGYIDMGN
GRTNYNARFKGRATLTVDKSTSTAYMELSSLRSEDTAVYYCARDSNWGVDYWGQGTLVTVSSASTKGPSVFPLA
PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC
SVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-136), Constant region (137-466)

Figure 29

SEQ ID NO: 44: Nucleotide sequence encoding hR198_H4 type heavy chain

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAGCCAGGTGCAGCTGGTGCA
GTCTGGCGCCGAAGTGAAGAAACCAGGCGCCAGCGTGAAGGTGTCCTGCAAGGCCTCTGGCTACCCCGTGACCG
CCTACTACATCAGCTGGATCAGACAGGCCCCAGGCCAGGGCCTGGAATACGTGGGCTACATCGACATGGGCAAC
GGCCGGACCAACTACAACGCCCGGTTTAAGGGCAGAGCCACCCTGACCGTGGACAAGAGCACCAGCACCGCCTA
CATGGAACTGAGCAGCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGACAGCAACTGGGGCGTGG
ACTATTGGGGCCAGGGCACACTCGTGACCGTCAGCTCAGCCTCCACCAAGGGCCCAAGCGTCTTCCCCCTGGCA
CCCTCCTCCAAGAGCACCTCTGGCGGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGT
GACCGTGAGCTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCCGCTGTCCTGCAGTCCTCAGGAC
TCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACC
CTGCCCAGCACCTGAACTCCTGGGGGGACCCTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA
TCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG
TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGTACCGGGT
GGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACACCCTG
CCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGA
CATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACTACAAGACCACCCCTCCCGTGCTGGACTCCG
ACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGC
TCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAATGA

Signal sequence (1-57), Variable region (58-408), Constant region (409-1398)

SEQ ID NO: 45: Amino acid sequence of hR198_H4 type heavy chain

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGYPVTAYYISWIRQAPGQGLEYVGYIDMGN
GRTNYNARFKGRATLTVDKSTSTAYMELSSLRSEDTAVYYCARDSNWGVDYWGQGTLVTVSSASTKGPSVFPLA
PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC
SVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-136), Constant region (137-466)

Figure 30

SEQ ID NO: 55: Nucleotide sequence encoding hR198_LG1 type light chain

ATGGTGCTGCAGACCCAGGTGTTCATCTCCCTGCTGCTGTGGATCTCCGGCGCGTACGGCGATATCCAGCTGAC
CCAGAGCCCTAGCAGCCTGTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTAGAGCCAGCCAGAGCATCG
GCGGCAGCCTGAGCTGGTTCCAGCAGAAACCCGGCAAGGCCCCCAAGCGGCTGATCTACAGCACCAGCACCCTG
GAAAGCGGCGTGCCCAGCAGATTTTCTGGCAGCGGCTCCGGCACCGACTACACCCTGACAATCAGCAGCCTGCA
GCCCGAGGACTTCGCCATGTACTACTGCCTGCAGTTCGCCATCTTCCCCGACAGCTTTGGCCAGGGCACCAAGG
TGGAAATCAAGCGTACGGTGGCCGCCCCCTCCGTGTTCATCTTCCCCCCCTCCGACGAGCAGCTGAAGTCCGGC
ACCGCCTCCGTGGTGTGCCTGCTGAATAACTTCTACCCCAGAGAGGCCAAGGTGCAGTGGAAGGTGGACAACGC
CCTGCAGTCCGGGAACTCCCAGGAGAGCGTGACCGAGCAGGACAGCAAGGACAGCACCTACAGCCTGAGCAGCA
CCCTGACCCTGAGCAAAGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCTGAGC
TCCCCCGTCACCAAGAGCTTCAACAGGGGGGAGTGTTAG

Signal sequence (1-60), Variable region (61-378), Constant region (379-702)

SEQ ID NO: 56: Amino acid sequence of hR198_LG1 type light chain

MVLQTQVFISLLLWISGAYGDIQLTQSPSSLSASVGDRVTITCRASQSIGGSLSWFQQKPGKAPKRLIYSTSTL
ESGVPSRFSGSGSGTDYTLTISSLQPEDFAMYYCLQFAIFPDSFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS
SPVTKSFNRGEC

Signal sequence (1-20), Variable region (21-126), Constant region (127-234)

Figure 31

SEQ ID NO: 57: Nucleotide sequence encoding hR198_LG2 type light chain

ATGGTGCTGCAGACCCAGGTGTTCATCTCCCTGCTGCTGTGGATCTCCGGCGCGTACGGCGATATCCAGCTGAC
CCAGAGCCCTAGCAGCCTGTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTCACGCCAGCCAGAACATCG
GCGGCAGCCTGAGCTGGTTCCAGCAGAAACCCGGCAAGGCCCCCAAGCGGCTGATCTACCTGACCAGCACCCTG
GACTGGGGCGTGCCCAGCAGATTTTCTGGCAGCGGCTCCGGCACCGACTACACCCTGACAATCAGCAGCCTGCA
GCCCGAGGACTTCGCCATGTACTACTGCCTGCAGTTCGCCATCTTCCCCGACAGCTTTGGCCAGGGCACCAAGG
TGGAAATCAAGCGTACGGTGGCCGCCCCCTCCGTGTTCATCTTCCCCCCCTCCGACGAGCAGCTGAAGTCCGGC
ACCGCCTCCGTGGTGTGCCTGCTGAATAACTTCTACCCCAGAGAGGCCAAGGTGCAGTGGAAGGTGGACAACGC
CCTGCAGTCCGGGAACTCCCAGGAGAGCGTGACCGAGCAGGACAGCAAGGACAGCACCTACAGCCTGAGCAGCA
CCCTGACCCTGAGCAAAGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCTGAGC
TCCCCCGTCACCAAGAGCTTCAACAGGGGGGAGTGTTAG

Signal sequence (1-60), Variable region (61-378), Constant region (379-702)

SEQ ID NO: 58: Amino acid sequence of hR198_LG2 type light chain

MVLQTQVFISLLLWISGAYGDIQLTQSPSSLSASVGDRVTITCHASQNIGGSLSWFQQKPGKAPKRLIYLTSTL
DWGVPSRFSGSGSGTDYTLTISSLQPEDFAMYYCLQFAIFPDSFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS
SPVTKSFNRGEC

Signal sequence (1-20), Variable region (21-126), Constant region (127-234)

Figure 32

SEQ ID NO: 59: Nucleotide sequence encoding hR198_LG3 type light chain

ATGGTGCTGCAGACCCAGGTGTTCATCTCCCTGCTGCTGTGGATCTCCGGCGCGTACGGCGATATCCAGCTGAC
CCAGAGCCCTAGCAGCCTGTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTCACGCCAGCCGGAACATCG
GCGGCAGCCTGAGCTGGTTCCAGCAGAAACCCGGCAAGGCCCCCAAGCGGCTGATCTACCTGACCAGCAGCCTG
GACTGGGGCGTGCCCAGCAGATTTTCTGGCAGCGGCTCCGGCACCGACTACACCCTGACAATCAGCAGCCTGCA
GCCCGAGGACTTCGCCATGTACTACTGCCTGCAGTTCGCCATCTTCCCCGACAGCTTTGGCCAGGGCACCAAGG
TGGAAATCAAGCGTACGGTGGCCGCCCCCTCCGTGTTCATCTTCCCCCCCTCCGACGAGCAGCTGAAGTCCGGC
ACCGCCTCCGTGGTGTGCCTGCTGAATAACTTCTACCCCAGAGAGGCCAAGGTGCAGTGGAAGGTGGACAACGC
CCTGCAGTCCGGGAACTCCCAGGAGAGCGTGACCGAGCAGGACAGCAAGGACAGCACCTACAGCCTGAGCAGCA
CCCTGACCCTGAGCAAAGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCTGAGC
TCCCCCGTCACCAAGAGCTTCAACAGGGGGGAGTGTTAG

Signal sequence (1-60), Variable region (61-378), Constant region (379-702)

SEQ ID NO: 60: Amino acid sequence of hR198_LG3 type light chain

MVLQTQVFISLLLWISGAYGDIQLTQSPSSLSASVGDRVTITCHASRNIGGSLSWFQQKPGKAPKRLIYLTSSL
DWGVPSRFSGSGSGTDYTLTISSLQPEDFAMYYCLQFAIFPDSFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS
SPVTKSFNRGEC

Signal sequence (1-20), Variable region (21-126), Constant region (127-234)

Figure 33

SEQ ID NO: 61: Nucleotide sequence encoding hR198_HG1 type heavy chain

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAGCCAGGTGCAGCTGGTGCA
GTCTGGCGCCGAAGTGAAGAAACCAGGCGCCAGCGTGAAGGTGTCCTGCAAGGCCTCTGGCTACCCCGTGACCG
CCTACTACATCAGCTGGGTCAGACAGGCCCCAGGCCAGGGCCTGGAATACGTGGGCTACATCGACATGGGCAAC
GGCCGGACCGACTACAACGCCCGGTTTAAGGGCAGAGCCACCCTGACCGTGGACAAGAGCACCAGCACCGCCTA
CATGGAACTGAGCAGCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGACAGCAACTGGGGCGCCG
ACTATTGGGGCCAGGGCACACTCGTGACCGTCAGCTCAGCCTCCACCAAGGGCCCAAGCGTCTTCCCCCTGGCA
CCCTCCTCCAAGAGCACCTCTGGCGGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGT
GACCGTGAGCTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCCGCTGTCCTGCAGTCCTCAGGAC
TCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACC
CTGCCCAGCACCTGAACTCCTGGGGGGACCCTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA
TCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG
TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGTACCGGGT
GGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACACCCTG
CCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGA
CATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACTACAAGACCACCCCTCCCGTGCTGGACTCCG
ACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGC
TCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAATGA

Signal sequence (1-57), Variable region (58-408), Constant region (409-1398)

SEQ ID NO: 62: Amino acid sequence of hR198_HG1 type heavy chain

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGYPVTAYYISWVRQAPGQGLEYVGYIDMGN
GRTDYNARFKGRATLTVDKSTSTAYMELSSLRSEDTAVYYCARDSNWGADYWGQGTLVTVSSASTKGPSVFPLA
PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC
SVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-136), Constant region (137-466)

Figure 34

SEQ ID NO: 63: Nucleotide sequence encoding hR198_HG2 type heavy chain

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAGCCAGGTGCAGCTGGTGCA
GTCTGGCGCCGAAGTGAAGAAACCAGGCGCCAGCGTGAAGGTGTCCTGCAAGGCCTCTGGCTACCCCATCACCG
CCTACTACATCAGCTGGGTCAGACAGGCCCCAGGCCAGGGCCTGGAATACGTGGGCTACATCGACATGGGCAAC
GGCCGGACCGACTACAACGGCCGGTTTAAGGGCAGAGCCACCCTGACCGTGGACAAGAGCACCAGCACCGCCTA
CATGGAACTGAGCAGCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGACAGCAACTGGGGCGCCG
ACTATTGGGGCCAGGGCACACTCGTGACCGTCAGCTCAGCCTCCACCAAGGGCCCAAGCGTCTTCCCCCTGGCA
CCCTCCTCCAAGAGCACCTCTGGCGGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGT
GACCGTGAGCTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCCGCTGTCCTGCAGTCCTCAGGAC
TCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACC
CTGCCCAGCACCTGAACTCCTGGGGGGACCCTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA
TCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG
TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGTACCGGGT
GGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACACCCTG
CCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGA
CATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACTACAAGACCACCCCTCCCGTGCTGGACTCCG
ACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGC
TCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAATGA

Signal sequence (1-57), Variable region (58-408), Constant region (409-1398)

SEQ ID NO: 64: Amino acid sequence of hR198_HG2 type heavy chain

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGYPITAYYISWVRQAPGQGLEYVGYIDMGN
GRTDYNGRFKGRATLTVDKSTSTAYMELSSLRSEDTAVYYCARDSNWGADYWGQGTLVTVSSASTKGPSVFPLA
PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC
SVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-136), Constant region (137-466)

Figure 35

SEQ ID NO: 65: Nucleotide sequence encoding hR198_HG3 type heavy chain

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAGCCAGGTGCAGCTGGTGCA
GTCTGGCGCCGAAGTGAAGAAACCAGGCGCCAGCGTGAAGGTGTCCTGCAAGGCCTCTGGCTACCCCATCACCG
CCTACTACATCAGCTGGGTCAGACAGGCCCCAGGCCAGGGCCTGGAATACGTGGGCTACATCGACATGGGCAAC
GGCCGGACCGACTACAACATGCGGTTTAAGGGCAGAGCCACCCTGACCGTGGACAAGAGCACCAGCACCGCCTA
CATGGAACTGAGCAGCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGACAGCAACTGGGGCGCCG
ACTATTGGGGCCAGGGCACACTCGTGACCGTCAGCTCAGCCTCCACCAAGGGCCCAAGCGTCTTCCCCCTGGCA
CCCTCCTCCAAGAGCACCTCTGGCGGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGT
GACCGTGAGCTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCCGCTGTCCTGCAGTCCTCAGGAC
TCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACC
CTGCCCAGCACCTGAACTCCTGGGGGGACCCTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA
TCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG
TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGTACCGGGT
GGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACACCCTG
CCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGA
CATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACTACAAGACCACCCCTCCCGTGCTGGACTCCG
ACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGC
TCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAATGA

Signal sequence (1-57), Variable region (58-408), Constant region (409-1398)

SEQ ID NO: 66: Amino acid sequence of hR198_HG3 type heavy chain

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGYPITAYYISWVRQAPGQGLEYVGYIDMGN
GRTDYNMRFKGRATLTVDKSTSTAYMELSSLRSEDTAVYYCARDSNWGADYWGQGTLVTVSSASTKGPSVFPLA
PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC
SVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-136), Constant region (137-466)

Figure 36

SEQ ID NO: 67: Nucleotide sequence encoding hR198_H4-LALA type heavy chain

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAGCCAGGTGCAGCTGGTGCA
GTCTGGCGCCGAAGTGAAGAAACCAGGCGCCAGCGTGAAGGTGTCCTGCAAGGCCTCTGGCTACCCCGTGACCG
CCTACTACATCAGCTGGATCAGACAGGCCCCAGGCCAGGGCCTGGAATACGTGGGCTACATCGACATGGGCAAC
GGCCGGACCAACTACAACGCCCGGTTTAAGGGCAGAGCCACCCTGACCGTGGACAAGAGCACCAGCACCGCCTA
CATGGAACTGAGCAGCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGACAGCAACTGGGGCGTGG
ACTATTGGGGCCAGGGCACACTCGTGACCGTCAGCTCAGCCTCCACCAAGGGCCCAAGCGTCTTCCCCCTGGCA
CCCTCCTCCAAGAGCACCTCTGGCGGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGT
GACCGTGAGCTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCCGCTGTCCTGCAGTCCTCAGGAC
TCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACC
CTGCCCAGCACCTGAAGCCGCGGGGGGACCCTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA
TCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG
TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGTACCGGGT
GGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACACCCTG
CCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGA
CATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACTACAAGACCACCCCTCCCGTGCTGGACTCCG
ACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGC
TCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAATGA

Signal sequence (1-57), Variable region (58-408), Constant region (409-1398)

SEQ ID NO: 68: Amino acid sequence of hR198_H4-LALA type heavy chain

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGYPVTAYYISWIRQAPGQGLEYVGYIDMGN
GRTNYNARFKGRATLTVDKSTSTAYMELSSLRSEDTAVYYCARDSNWGVDYWGQGTLVTVSSASTKGPSVFPLA
PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC
SVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-136), Constant region (137-466)

Figure 37

SEQ ID NO: 69: Nucleotide sequence encoding hR198_HG1-LALA type heavy chain

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAGCCAGGTGCAGCTGGTGCA
GTCTGGCGCCGAAGTGAAGAAACCAGGCGCCAGCGTGAAGGTGTCCTGCAAGGCCTCTGGCTACCCCGTGACCG
CCTACTACATCAGCTGGGTCAGACAGGCCCCAGGCCAGGGCCTGGAATACGTGGGCTACATCGACATGGGCAAC
GGCCGGACCGACTACAACGCCCGGTTTAAGGGCAGAGCCACCCTGACCGTGGACAAGAGCACCAGCACCGCCTA
CATGGAACTGAGCAGCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGACAGCAACTGGGGCGCCG
ACTATTGGGGCCAGGGCACACTCGTGACCGTCAGCTCAGCCTCCACCAAGGGCCCAAGCGTCTTCCCCCTGGCA
CCCTCCTCCAAGAGCACCTCTGGCGGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGT
GACCGTGAGCTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCCGCTGTCCTGCAGTCCTCAGGAC
TCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACC
CTGCCCAGCACCTGAAGCCGCGGGGGGACCCTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA
TCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG
TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGTACCGGGT
GGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACACCCTG
CCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGA
CATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACTACAAGACCACCCCTCCCGTGCTGGACTCCG
ACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGC
TCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAATGA

Signal sequence (1-57), Variable region (58-408), Constant region (409-1398)

SEQ ID NO: 70: Amino acid sequence of hR198_HG1-LALA type heavy chain

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGYPVTAYYISWVRQAPGQGLEYVGYIDMGN
GRTDYNARFKGRATLTVDKSTSTAYMELSSLRSEDTAVYYCARDSNWGADYWGQGTLVTVSSASTKGPSVFPLA
PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC
SVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-136), Constant region (137-466)

Figure 38

L chain	SEQ ID	CDRL1	SEQ ID	CDRL2	SEQ ID	CDRL3	SEQ ID
cR118_L	NO: 23	RASQSISNSLS	NO: 116	STSTLES	NO: 96	LQFATFPDT	NO: 99
cR198_L	NO: 25	RASQSIGNSLS	NO: 92	STSTLES	NO: 96	LQFATYPDT	NO: 100
hR198_L1	NO: 31	RASQSIGNSLS	NO: 92	STSTLES	NO: 96	LQFATYPDT	NO: 100
hR198_L2	NO: 33	RASQSIGNSLS	NO: 92	STSTLES	NO: 96	LQFATYPDT	NO: 100
hR198_L3	NO: 35	RASQSIGNSLS	NO: 92	STSTLES	NO: 96	LQFATFPDT	NO: 99
hR198_L4	NO: 37	RASQSIGNSLS	NO: 92	STSTLES	NO: 96	LQFATFPDT	NO: 99
hR198_LG1	NO: 56	RASQSIGGSLS	NO: 93	STSTLES	NO: 96	LQFAIFPDS	NO: 101
hR198_LG2	NO: 58	HASQNIGGSLS	NO: 94	LTSTLDW	NO: 97	LQFAIFPDS	NO: 101
hR198_LG3	NO: 60	HASRNIGGSLS	NO: 95	LTSSLDW	NO: 98	LQFAIFPDS	NO: 101

H chain	SEQ ID	CDRH1	SEQ ID	CDRH2	SEQ ID	CDRH3	SEQ ID
cR118_H	NO: 27	AYYIS	NO: 102	YIDMGNGRTNYNARFKG	NO: 104	DSNWGVDY	NO: 109
cR198_H	NO: 29	SYYIS	NO: 103	YVDMGNGRTNYNEKFKG	NO: 105	DSNWGVDY	NO: 109
hR198_H1	NO: 39	SYYIS	NO: 103	YVDMGNGRTNYNEKFKG	NO: 105	DSNWGVDY	NO: 109
hR198_H2	NO: 41	SYYIS	NO: 103	YVDMGNGRTNYNEKFKG	NO: 105	DSNWGVDY	NO: 109
hR198_H3	NO: 43	AYYIS	NO: 102	YIDMGNGRTNYNARFKG	NO: 104	DSNWGVDY	NO: 109
hR198_H4	NO: 45	AYYIS	NO: 102	YIDMGNGRTNYNARFKG	NO: 104	DSNWGVDY	NO: 109
hR198_HG1	NO: 62	AYYIS	NO: 102	YIDMGNGRTDYNARFKG	NO: 106	DSNWGADY	NO: 110
hR198_HG2	NO: 64	AYYIS	NO: 102	YIDMGNGRTDYNGRFKG	NO: 107	DSNWGADY	NO: 110
hR198_HG3	NO: 66	AYYIS	NO: 102	YIDMGNGRTDYNMRFKG	NO: 108	DSNWGADY	NO: 110
hR198_H4-LALA	NO: 68	AYYIS	NO: 102	YIDMGNGRTNYNARFKG	NO: 104	DSNWGVDY	NO: 109
hR198_HG1-LALA	NO: 70	AYYIS	NO: 102	YIDMGNGRTDYNARFKG	NO: 106	DSNWGADY	NO: 110

Figure 39

SEQ ID NO: 72: Nucleotide sequence encoding 2C1.1 antibody heavy chain

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAGCCAGGTGCAGCTGCAGCA
GTGGGGAGCCGGCCTGCTGAAGCCCAGCGAGACACTGAGCCTGACCTGCGCTGTGTACGGAGGCAGCTTCAGCG
GCTACTACTGGTCCTGGATCCGGCAGCCCCCTGGCAAGGGCCTGGAATGGATCGGCGAGATCGACCACAGCGGC
AGCACCAACTACAACCCCGCCCTGAAGTCCCGGCTGACCATCAGCGTGGACACCAGCAAGAACCAGTTCAGCCT
GAAGCTGAGCAGCGTGACAGCCGCCGACACCGCCGTGTACTACTGTGCCAGAGCCGGCAGCGGCGGCTACGAGG
ATTGGTTCGATCCTTGGGGCCAGGGCACCCTGGTGACCGTCAGCTCAGCCAGCACCAAGGGCCCTTCCGTGTTC
CCTCTGGCCCCTTGTAGCCGTTCCACCAGCGAGTCCACCGCCGCCCTTGGCTGTCTGGTGAAGGACTACTTCCC
TGAGCCTGTGACCGTGAGCTGGAACTCCGGAGCCCTTACCAGCGGCGTGCACACCTTCCCTGCCGTGCTGCAGT
CCAGCGGCCTTTACTCCCTGAGCTCCGTGGTGACCGTGCCTAGCTCCAACTTCGGCACCCAAACCTACACCTGT
AACGTGGACCACAAGCCTAGCAACACCAAGGTGGACAAGACCGTGGAGCGTAAGTGTTGTGTGGAGTGTCCTCC
TTGTCCTGCCCCTCCTGTGGCCGGACCTTCCGTGTTCCTTTTCCCTCCTAAGCCTAAGGACACCCTGATGATCA
GCCGTACCCCTGAGGTGACCTGTGTGGTGGTGGACGTGTCCCACGAGGACCCTGAGGTGCAGTTCAACTGGTAC
GTGGACGGCGTGGAGGTGCACAACGCCAAGACCAAGCCTCGTGAGGAGCAATTCAACAGCACCTTCCGTGTGGT
GTCCGTGCTTACCGTGGTGCACCAAGACTGGCTGAACGGCAAGGAGTACAAGTGTAAGGTGAGCAACAAGGGAC
TTCCTGCCCCTATCGAGAAGACCATCTCCAAGACCAAGGGCCAACCTCGTGAGCCTCAAGTGTACACCCTTCCT
CCTAGCCGTGAGGAGATGACCAAGAACCAAGTGTCCCTTACCTGTCTGGTGAAGGGCTTCTACCCTAGCGACAT
CGCCGTGGAGTGGGAGTCCAACGGACAACCTGAGAACAACTACAAGACCACCCCTCCTATGCTTGACAGCGACG
GCTCCTTCTTCCTGTACAGCAAGCTGACCGTGGACAAGTCCCGTTGGCAACAAGGCAACGTGTTCAGCTGTTCC
GTGATGCACGAGGCCCTGCACAACCACTACACCCAAAAGAGCCTTTCCCTGAGCCCTGGAAAG

Signal sequence (1-57), Variable region (58-417), Constant region (418-1395)

SEQ ID NO: 73: Amino acid sequence of 2C1.1 antibody heavy chain

MKHLWFFLLLVAAPRWVLSQVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEIDHSG
STNYNPALKSRLTISVDTSKNQFSLKLSSVTAADTAVYYCARAGSGGYEDWFDPWGQGTLVTVSSASTKGPSVF
PLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTC
NVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWY
VDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLP
PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
VMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-139), Constant region (140-465)

Figure 40

SEQ ID NO: 74: Nucleotide sequence encoding 2C1.1 antibody light chain

ATGGTGCTGCAGACCCAGGTGTTCATCTCCCTGCTGCTGTGGATCTCCGGCGCGTACGGCCAGTCCGTGCTGAC
CCAGCCTCCTTCCGTGTCTGGCGCCCCTGGCCAGAGAGTGACCATCAGCTGTACCGGCAGCAGCAGCAACATCG
GAGCCGGCTACAACGTGCACTGGTATCAGCAGTTCCCCCGGACCGACCCCAAGCTGCTGATCTACGTGTACAAC
ATCCGGCCCAGCGGCGTGCCCGACCGGTTTTCTGGCAGCAGAAGCGGCACAAGCGCCAGCCTGGCCATCACCGG
CCTGCAGACCGAGGACGAGGCCGACTACTACTGCCAGAGCTACGACAGCAGCCTGAGCGGCGTGGTGTTCGGCG
GAGGCACCAAGCTGACAGTGCTGGGCCAGCCCAAGGCCAACCCCACCGTGACCCTGTTCCCCCCAAGCAGCGAG
GAACTGCAGGCCAACAAGGCCACCCTGGTGTGCCTGATCAGCGACTTCTACCCTGGCGCCGTGACAGTGGCCTG
GAAGGCCGATGGATCTCCCGTGAAGGCCGGCGTGGAAACCACCAAGCCCAGCAAGCAGAGCAACAACAAATACG
CCGCCAGCAGCTACCTGAGCCTGACCCCCGAGCAGTGGAAGTCCCACCGGTCCTACAGCTGCCAGGTGACACAC
GAGGGCAGCACCGTGGAAAAGACCGTGGCCCCCACCGAGTGCAGCtaggggcccgtttaaacgggggaggcta

Signal sequence (1-60), Variable region (61-393), Constant region (394-711)

SEQ ID NO: 75: Amino acid sequence of 2C1.1 antibody light chain

MVLQTQVFISLLLWISGAYGQSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYNVHWYQQFPRTDPKLLIYVYN
IRPSGVPDRFSGSRSGTSASLAITGLQTEDEADYYCQSYDSSLSGVVFGGGTKLTVLGQPKANPTVTLFPPSSE
ELQANKATLVCLISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTH
EGSTVEKTVAPTECS

Signal sequence (1-20), Variable region (21-131), Constant region (132-237)

Figure 41

SEQ ID NO: 76: Nucleotide sequence encoding 5H3.1 antibody heavy chain

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAGCCAGGTGCAGCTGGTGCA
GTCTGGCGCCGAAGTGAAGAAACCTGGCGCTAGCGTGAAGGTGTCCTGCAAGGCCAGCGGCTACACCTTCACCG
ACTACTACATGAACTGGGTGCGCCAGGCTCCAGGACAGGGCCTGGAATGGATGGGCTGGATCAACCCCAACAGC
GGCGGCACCAAATACGCCCAGAAATTCCAGGGCAGAGTGACCATGACCCGGGACACCAGCATCCGGACCGCCTA
CATGGAACTGAGCCGGCTGAGAAGCGACGACACCGCCGTGTACTACTGCGCCAGAGAGTACGGCGGCAACAGCG
ATTGGTTCGACCCCTGGGGCCAGGGCACCCTGGTGACCGTCAGCTCAGCCAGCACCAAGGGCCCTTCCGTGTTC
CCTCTGGCCCCTTGTAGCCGTTCCACCAGCGAGTCCACCGCCGCCCTTGGCTGTCTGGTGAAGGACTACTTCCC
TGAGCCTGTGACCGTGAGCTGGAACTCCGGAGCCCTTACCAGCGGCGTGCACACCTTCCCTGCCGTGCTGCAGT
CCAGCGGCCTTTACTCCCTGAGCTCCGTGGTGACCGTGCCTAGCTCCAACTTCGGCACCCAAACCTACACCTGT
AACGTGGACCACAAGCCTAGCAACACCAAGGTGGACAAGACCGTGGAGCGTAAGTGTTGTGTGGAGTGTCCTCC
TTGTCCTGCCCCTCCTGTGGCCGGACCTTCCGTGTTCCTTTTCCCTCCTAAGCCTAAGGACACCCTGATGATCA
GCCGTACCCCTGAGGTGACCTGTGTGGTGGTGGACGTGTCCCACGAGGACCCTGAGGTGCAGTTCAACTGGTAC
GTGGACGGCGTGGAGGTGCACAACGCCAAGACCAAGCCTCGTGAGGAGCAATTCAACAGCACCTTCCGTGTGGT
GTCCGTGCTTACCGTGGTGCACCAAGACTGGCTGAACGGCAAGGAGTACAAGTGTAAGGTGAGCAACAAGGGAC
TTCCTGCCCCTATCGAGAAGACCATCTCCAAGACCAAGGGCCAACCTCGTGAGCCTCAAGTGTACACCCTTCCT
CCTAGCCGTGAGGAGATGACCAAGAACCAAGTGTCCCTTACCTGTCTGGTGAAGGGCTTCTACCCTAGCGACAT
CGCCGTGGAGTGGGAGTCCAACGGACAACCTGAGAACAACTACAAGACCACCCCTCCTATGCTTGACAGCGACG
GCTCCTTCTTCCTGTACAGCAAGCTGACCGTGGACAAGTCCCGTTGGCAACAAGGCAACGTGTTCAGCTGTTCC
GTGATGCACGAGGCCCTGCACAACCACTACACCCAAAAGAGCCTTTCCCTGAGCCCTGGAAAG

Signal sequence (1-57), Variable region (58-417), Constant region (418-1395)

SEQ ID NO: 77: Amino acid sequence of 5H3.1 antibody heavy chain

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGYTFTDYYMNWVRQAPGQGLEWMGWINPNS
GGTKYAQKFQGRVTMTRDTSIRTAYMELSRLRSDDTAVYYCAREYGGNSDWFDPWGQGTLVTVSSASTKGPSVF
PLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTC
NVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWY
VDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLP
PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
VMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-139), Constant region (140-465)

Figure 42

SEQ ID NO: 78: Nucleotide sequence encoding 5H3.1 antibody light chain

ATGGTGCTGCAGACCCAGGTGTTCATCTCCCTGCTGCTGTGGATCTCCGGCGCGTACGGCCAGTCCGTGCTGAC
CCAGCCTCCTTCCGTGTCTGGCGCCCCTGGCCAGAGAGTGACCATCAGCTGTACCGGCAGCAGCAGCAACATCG
GAGCTGGATACGACGTGCACTGGTATCAGCAGCTGCCCGGCACCGCCCCCAAGCTGCTGATCTACGGCAACAGC
AACCGGCCCAGCGGCGTGCCCGATAGATTCAGCGGCAGCAAGAGCGGCACCAGCGCCAGCCTGGCCATTACCGG
ACTGCAGGCCGAGGACGAGGCCGACTACTACTGCCAGAGCTACGACAACCGGCTGAGCGACAGCGTGGTGATCG
GCGGAGGCACCAAGCTGGCCGTGCAGGGACAGCCCAAGGCCAACCCCACCGTGACCCTGTTCCCCCCAAGCAGC
GAGGAACTGCAGGCCAACAAGGCCACCCTGGTGTGCCTGATCAGCGACTTCTACCCTGGCGCCGTGACAGTGGC
CTGGAAGGCCGATGGATCTCCCGTGAAGGCCGGCGTGGAAACCACCAAGCCCAGCAAGCAGAGCAACAACAAAT
ACGCCGCCAGCAGCTACCTGAGCCTGACCCCCGAGCAGTGGAAGTCCCACCGGTCCTACAGCTGCCAGGTGACA
CACGAGGGCAGCACCGTGGAAAAGACCGTGGCCCCCACCGAGTGCAGCtaggggcccgtttaaacgggggaggc
ta

Signal sequence (1-60), Variable region (61-396), Constant region (397-714)

SEQ ID NO: 79: Amino acid sequence of 5H3.1 antibody light chain

MVLQTQVFISLLLWISGAYGQSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQLPGTAPKLLIYGNS
NRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDNRLSDSVVIGGGTKLAVQGQPKANPTVTLFPPSS
EELQANKATLVCLISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVT
HEGSTVEKTVAPTECS

Signal sequence (1-20), Variable region (21-132), Constant region (133-238)

Figure 43

SEQ ID NO: 80: Nucleotide sequence encoding 10F8 antibody heavy chain

ccagcctccggactctagagccaccATGAAGCACCTGTGGTTCTTTCTGCTGCTGGTGGCCGCTCCCAGATGGG
TGCTGTCTCAGGTGCAGCTGCAGCAGTCTGGCGCCGAACTCGTGCGGCCTGGAAGCAGCGTGAAGATCAGCTGC
AAGGCCAGCGGCTACGCCTTCCGGTCCTACTGGATGAACTGGGTCAAGCAGAGGCCAGGCCAGGGCCTGGAATG
GATCGGCCACATCTATCCCGGCGACGGCGACACCAACTACAACGGCAAGTTCAAGGGCAAGGCCACCCTGACCG
CCGACAAGAGCAGCAGCACAGCCTACATGCAGCTGTCCAGCCTGACCAGCGAGGACAGCGCCGTGTACCTGTGT
GGCAGAGGCGGCACAACCGTGGTGGTGGATTATTGGGGCCAGGGCACCACACTGACCGTGTCCAGCGCCAAGAC
CACCCCCCCATCTGTGTATCCTCTGGCCCCTGGATCTGCCGCCCAGACCAACAGCATGGTCACCCTGGGCTGCC
TCGTGAAGGGCTACTTCCCTGAGCCTGTGACCGTGACCTGGAACAGCGGCTCTCTGTCTAGCGGCGTGCACACC
TTTCCAGCCGTGCTGCAGAGCGACCTGTACACCCTGAGCAGCTCCGTGACCGTGCCTAGCAGCACCTGGCCTAG
CGAGACAGTGACCTGCAACGTGGCCCACCCTGCCAGCTCTACCAAGGTGGACAAGAAAATCGTGCCCCGGGACT
GCGGCTGCAAGCCCTGTATCTGTACCGTGCCCGAGGTGTCCTCCGTGTTCATCTTCCCACCCAAGCCCAAGGAC
GTGCTGACCATCACCCTGACACCCAAAGTGACATGTGTGGTGGTGGACATCAGCAAGGACGACCCCGAGGTGCA
GTTCAGTTGGTTCGTGGACGACGTGGAAGTGCACACAGCCCAGACCCAGCCCAGAGAGGAACAGTTCAACAGCA
CCTTCAGAAGCGTGTCCGAGCTGCCCATCATGCACCAGGACTGGCTGAACGGCAAAGAATTCAAGTGCAGAGTG
AACAGCGCCGCCTTCCCTGCCCCCATCGAGAAAACCATCTCCAAGACCAAGGGCAGACCCAAGGCCCCCCAGGT
GTACACAATCCCCCCACCCAAAGAACAGATGGCCAAGGACAAGGTGTCCCTGACCTGCATGATCACCGATTTCT
TCCCAGAGGACATCACCGTGGAATGGCAGTGGAACGGCCAGCCCGCCGAGAACTACAAGAACACCCAGCCTATC
ATGGACACCGACGGCAGCTACTTCGTGTACAGCAAGCTGAACGTGCAGAAGTCCAACTGGGAGGCCGGCAACAC
CTTCACCTGTAGCGTGCTGCACGAGGGCCTGCACAATCACCACACCGAGAAGTCCCTGTCCCACAGCCCCGGCA
AAtgagtttaaacgggggaggctaact

Signal sequence (26-82), Variable region (83-436), Constant region (437-1408)

SEQ ID NO: 81: Amino acid sequence of 10F8 antibody heavy chain

MKHLWFFLLLVAAPRWVLSQVQLQQSGAELVRPGSSVKISCKASGYAFRSYWMNWVKQRPGQGLEWIGHIYPGD
GDTNYNGKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYLCGRGGTTVVVDYWGQGTTLTVSSAKTTPPSVYPL
APGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETVTCNVA
HPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDV
EVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKE
QMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNVQKSNWEAGNTFTCSVLHE
GLHNHHTEKSLSHSPGK

Signal sequence (1-19), Variable region (20-137), Constant region (138-461)

Figure 44

SEQ ID NO: 82: Nucleotide sequence encoding 10F8 antibody light chain

ccagcctccggactctagagccaccATGGTGCTGCAGACCCAGGTGTTCATCAGCCTGCTGCTGTGGATCAGCG
GCGCCTACGGCGACATCGTGATGAGCCAGAGCCCTAGCAGCCTGGCCGTGTCTGCCGGCGAGAAAGTGACCATG
AGCTGCAAGAGCAGCCAGTCCCTGCTGAACAGCCGGACCCGGAAGAACTACCTGGCCTGGTATCAGCAGAAGCC
CGGCCAGTCCCCCAAGCTGCTGATCTACTGGGCCAGCACCAGAGAAAGCGGCGTGCCCGATAGATTCACCGGCA
GCGGCTCTGGCACCGACTTCACCCTGACAATCAGCAGCGTGCAGGCCGAGGACCTGGCTGTGTACTACTGCAAG
CAGAGCTACAACCTGCCCTGGACCTTCGGCGGAGGCACCAAGCTGGAAATCAAGAGAGCCGACGCCGCTCCCAC
CGTGTCCATCTTTCCACCTAGCAGCGAGCAGCTGACCAGCGGCGGAGCTAGCGTCGTGTGCTTCCTGAACAACT
TCTACCCCAAGGACATCAACGTGAAGTGGAAGATCGACGGCAGCGAGCGGCAGAACGGCGTGCTGAATAGCTGG
ACCGACCAGGACAGCAAGGACTCCACCTACAGCATGTCCAGCACCCTGACCCTGACCAAGGACGAGTACGAGCG
GCACAACAGCTACACATGCGAGGCCACCCACAAGACCAGCACCTCCCCCATCGTGAAGTCCTTCAACCGGAACG
AGTGCtgagtttaaacgggggaggctaact

Signal sequence (26-85), Variable region (86-430), Constant region (431-745)

SEQ ID NO: 83: Amino acid sequence of 10F8 antibody light chain

MVLQTQVFISLLLWISGAYGDIVMSQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLI
YWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYNLPWTFGGGTKLEIKRADAAPTVSIFPPSS
EQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEA
THKTSTSPIVKSFNRNEC

Signal sequence (1-20), Variable region (21-135), Constant region (136-240)

Figure 45

SEQ ID NO: 84: Nucleotide sequence encoding 14F74 antibody heavy chain

ccagcctccggactctagagccaccATGAAGCACCTGTGGTTCTTTCTGCTGCTGGTGGCCGCTCCCAGATGGG
TGCTGTCTCAGGTGCAGCTGCAGCAGTCTGGCGCCGAACTCGTGCGGCCTGGAAGCAGCGTGAAGATCAGCTGC
AAGGCCAGCGGCTACGCCTTCAGCAGCTACTGGATGAACTGGGTCAAGCAGCGGCCAGGCCAGGGCCTGGAATG
GATCGGCCATATCTATCCCGGCGACGGCGACACCAACTACAACGGCAAGTTCAAGGGCAAGGCCACCCTGACCG
CCGACAAGAGCAGCAGCACAGCCTACATGCAGCTGAGCGGCCTGACCAGCGAGGACAGCGCCGTGTACTTCTGC
GCCAGAAGCGGCAGACTGAGATTCGCCATGGACTACTGGGGCCAGGGCACCAGCGTGACAGTGTCTAGCGCCAA
GACCACCCCCCCCAGCGTGTACCCTCTGGCTCCTGGATCTGCCGCCCAGACCAACAGCATGGTCACCCTGGGCT
GCCTCGTGAAGGGCTACTTCCCTGAGCCTGTGACCGTGACCTGGAACAGCGGCTCTCTGTCTAGCGGCGTGCAC
ACCTTTCCAGCCGTGCTGCAGAGCGACCTGTACACCCTGAGCAGCTCCGTGACCGTGCCTAGCAGCACCTGGCC
TAGCGAGACAGTGACCTGCAACGTGGCCCACCCTGCCAGCTCTACCAAGGTGGACAAGAAAATCGTGCCCCGGG
ACTGCGGCTGCAAGCCCTGTATCTGTACCGTGCCCGAGGTGTCCAGCGTGTTCATCTTCCCACCCAAGCCCAAG
GACGTGCTGACCATCACCCTGACACCCAAAGTGACCTGTGTGGTGGTGGACATCAGCAAGGACGACCCCGAGGT
GCAGTTCAGTTGGTTCGTGGACGACGTGGAAGTGCACACAGCCCAGACCCAGCCCAGAGAGGAACAGTTCAACA
GCACCTTCAGAAGCGTGTCCGAGCTGCCCATCATGCACCAGGACTGGCTGAACGGCAAAGAATTCAAGTGCAGA
GTGAACAGCGCCGCCTTCCCTGCCCCCATCGAGAAAACCATCTCCAAGACCAAGGGCAGACCCAAGGCCCCTCA
GGTGTACACAATCCCCCCACCCAAAGAACAGATGGCCAAGGACAAGGTGTCCCTGACCTGCATGATCACCGATT
TCTTCCCAGAGGACATCACCGTGGAATGGCAGTGGAACGGCCAGCCCGCCGAGAACTACAAGAACACCCAGCCT
ATCATGGACACCGACGGCAGCTACTTCGTGTACAGCAAGCTGAACGTGCAGAAGTCCAACTGGGAGGCCGGCAA
CACCTTCACCTGTAGCGTGCTGCACGAGGGCCTGCACAATCACCACACCGAGAAGTCCCTGTCCCACAGCCCCG
GCAAAtgagtttaaacgggggaggctaact

Signal sequence (26-82), Variable region (83-439), Constant region (440-1411)

SEQ ID NO: 85: Amino acid sequence of 14F74 antibody heavy chain

MKHLWFFLLLVAAPRWVLSQVQLQQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGHIYPGD
GDTNYNGKFKGKATLTADKSSSTAYMQLSGLTSEDSAVYFCARSGRLRFAMDYWGQGTSVTVSSAKTTPPSVYP
LAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETVTCNV
AHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDD
VEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPK
EQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNVQKSNWEAGNTFTCSVLH
EGLHNHHTEKSLSHSPGK

Signal sequence (1-19), Variable region (20-138), Constant region (139-462)

Figure 46

SEQ ID NO: 86: Nucleotide sequence encoding 14F74 antibody light chain

ccagcctccggactctagagccaccATGGTGCTGCAGACCCAGGTGTTCATCAGCCTGCTGCTGTGGATCAGCG
GCGCCTACGGCGACATCGTGATGAGCCAGAGCCCTAGCAGCCTGGCCGTGTCTGCCGGCGAGAAAGTGACCATG
AGCTGCAAGAGCAGCCAGTCCCTGCTGAACAGCCGGACCCGGAAGAACTACCTGGCCTGGTATCAGCAGAAGCC
CGGCCAGTCCCCCAAGCTGCTGATCTACTGGGCCAGCACCAGAGAAAGCGGCGTGCCCGATAGATTCACCGGCA
GCGGCTCTGGCACCGACTTCACCCTGACAATCAGCAGCGTGCAGGCCGAGGACCTGGCTGTGTACTACTGCAAG
CAGAGCTACAACCTGCGGACCTTCGGCGGAGGCACCAAGCTGGAAATCCAGAGAGCCGACGCCGCTCCCACCGT
GTCCATCTTTCCACCTAGCAGCGAGCAGCTGACCAGCGGCGGAGCTAGCGTCGTGTGCTTCCTGAACAACTTCT
ACCCCAAGGACATCAACGTGAAGTGGAAGATCGACGGCAGCGAGCGGCAGAACGGCGTGCTGAATAGCTGGACC
GACCAGGACAGCAAGGACTCCACCTACAGCATGTCCAGCACCCTGACCCTGACCAAGGACGAGTACGAGCGGCA
CAACAGCTACACATGCGAGGCCACCCACAAGACCAGCACCTCCCCCATCGTGAAGTCCTTCAACCGGAACGAGT
GCtgagtttaaacgggggaggctaact

Signal sequence (26-85), Variable region (86-427), Constant region (428-742)

SEQ ID NO: 87: Amino acid sequence of 14F74 antibody light chain

MVLQTQVFISLLLWISGAYGDIVMSQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLI
YWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYNLRTFGGGTKLEIQRADAAPTVSIFPPSSE
QLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEAT
HKTSTSPIVKSFNRNEC

Signal sequence (1-20), Variable region (21-134), Constant region (135-239)

Figure 47

SEQ ID NO: 88: Nucleotide sequence encoding 17F6 antibody heavy chain

ccagcctccggactctagagccaccATGAAGCACCTGTGGTTCTTTCTGCTGCTGGTGGCCGCTCCCAGATGGG
TGCTGTCTCAGGTGCAGCTGCAGCAGTCTGGCGCCGAACTCGTGCGGCCTGGAAGCAGCGTGAAGATCAGCTGC
AAGGCCAGCGGCTACGCCTTCAGCAGCTACTGGATGAACTGGGTCAAGCAGCGGCCAGGCCAGGGCCTGGAATG
GATCGGCCATATCTATCCCGGCGACGCCGACACCAACTACAACGGCAAGTTCAAGGGCAAGGCCACCCTGACCG
CCGACAAGAGCAGCAGCACAGCCTACATGCACCTGTCCAGCCTGACCAGCGAGGACAGCGCCGTGTACTTCTGC
AGCCGGCAGCTGGGCTTCAGATACGCCATGGACTATTGGGGCCAGGGCACCAGCGTGACCGTGTCTAGCGCCAA
GACCACCCCCCCTAGCGTGTACCCTCTGGCCCCTGGATCTGCCGCCCAGACCAACAGCATGGTCACCCTGGGCT
GCCTCGTGAAGGGCTACTTCCCTGAGCCTGTGACCGTGACCTGGAACAGCGGCTCTCTGTCTAGCGGCGTGCAC
ACCTTTCCAGCCGTGCTGCAGAGCGACCTGTACACCCTGAGCAGCTCCGTGACAGTGCCCAGCTCTACCTGGCC
CAGCGAGACAGTGACCTGCAACGTGGCCCACCCTGCCAGCAGCACCAAGGTGGACAAGAAAATCGTGCCCCGGG
ACTGCGGCTGCAAGCCCTGTATCTGTACCGTGCCCGAGGTGTCCAGCGTGTTCATCTTCCCACCCAAGCCCAAG
GACGTGCTGACCATCACCCTGACACCCAAAGTGACCTGTGTGGTGGTGGACATCAGCAAGGACGACCCCGAGGT
GCAGTTCAGTTGGTTCGTGGACGACGTGGAAGTGCACACAGCCCAGACCCAGCCCAGAGAGGAACAGTTCAACA
GCACCTTCAGAAGCGTGTCCGAGCTGCCCATCATGCACCAGGACTGGCTGAACGGCAAAGAATTCAAGTGCAGA
GTGAACAGCGCCGCCTTCCCTGCCCCCATCGAGAAAACCATCTCCAAGACCAAGGGCAGACCCAAGGCCCCCCA
GGTGTACACAATCCCCCCACCCAAAGAACAGATGGCCAAGGACAAGGTGTCCCTGACCTGCATGATCACCGATT
TCTTCCCAGAGGACATCACCGTGGAATGGCAGTGGAACGGCCAGCCCGCCGAGAACTACAAGAACACCCAGCCT
ATCATGGACACCGACGGCAGCTACTTCGTGTACAGCAAGCTGAACGTGCAGAAGTCCAACTGGGAGGCCGGCAA
CACCTTCACCTGTAGCGTGCTGCACGAGGGCCTGCACAATCACCACACCGAGAAGTCCCTGTCCCACAGCCCCG
GCAAAtgagtttaaacgggggaggctaact

Signal sequence (26-82), Variable region (83-439), Constant region (440-1411)

SEQ ID NO: 89: Amino acid sequence of 17F6 antibody heavy chain

MKHLWFFLLLVAAPRWVLSQVQLQQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGHIYPGD
ADTNYNGKFKGKATLTADKSSSTAYMHLSSLTSEDSAVYFCSRQLGFRYAMDYWGQGTSVTVSSAKTTPPSVYP
LAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETVTCNV
AHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDD
VEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPK
EQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNVQKSNWEAGNTFTCSVLH
EGLHNHHTEKSLSHSPGK

Signal sequence (1-19), Variable region (20-138), Constant region (139-462)

Figure 48

SEQ ID NO: 90: Nucleotide sequence encoding 17F6 antibody light chain

ccagcctccggactctagagccaccATGGTGCTGCAGACCCAGGTGTTCATCAGCCTGCTGCTGTGGATCAGCG
GCGCCTACGGCGACATCGTGATGAGCCAGAGCCCTAGCAGCCTGGCCGTGTCTGCCGGCGAGAAAGTGACCATG
AGCTGCAAGAGCAGCCAGTCCCTGCTGAACAGCCGGACCCGGAAGAACTACCTGGCCTGGTATCAGCAGAAGCC
CGGCCAGTCCCCCAAGCTGCTGATCTACTGGGCCAGCACCAGAGAAAGCGGCGTGCCCGATAGATTCACCGGCA
GCGGCTCTGGCACCGACTTCACCCTGACAATCAGCAGCGTGCAGGCCGAGGACCTGGCTGTGTACTACTGCAAG
CAGAGCTACAACCTGCGGACCTTCGGCGGAGGCACCAAGCTGGAAATCAAGAGAGCCGACGCCGCTCCCACCGT
GTCCATCTTTCCACCTAGCAGCGAGCAGCTGACCAGCGGCGGAGCTAGCGTCGTGTGCTTCCTGAACAACTTCT
ACCCCAAGGACATCAACGTGAAGTGGAAGATCGACGGCAGCGAGCGGCAGAACGGCGTGCTGAATAGCTGGACC
GACCAGGACAGCAAGGACTCCACCTACAGCATGTCCAGCACCCTGACCCTGACCAAGGACGAGTACGAGCGGCA
CAACAGCTACACATGCGAGGCCACCCACAAGACCAGCACCTCCCCCATCGTGAAGTCCTTCAACCGGAACGAGT
GCtgagtttaaacgggggaggctaact

Signal sequence (26-85), Variable region (86-427), Constant region (428-742)

SEQ ID NO: 91: Amino acid sequence of 17F6 antibody light chain

MVLQTQVFISLLLWISGAYGDIVMSQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLI
YWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYNLRTFGGGTKLEIKRADAAPTVSIFPPSSE
QLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEAT
HKTSTSPIVKSFNRNEC

Signal sequence (1-20), Variable region (21-134), Constant region (135-239)

Figure 49

SEQ ID NO: 111: Nucleotide sequence encoding hR198_H0

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAGCCAGGTGCAGCTGGTGCA
GTCTGGCGCCGAAGTGAAGAAACCAGGCGCCAGCGTGAAGGTGTCCTGCAAGGCCTCTGGCTACCCCGTGACCA
GCTACTACATCAGCTGGATCAGACAGGCCCCAGGCCAGGGCCTGGAATGGATCGGCTATGTGGACATGGGCAAC
GGCCGGACCAACTACAACGAGAAGTTCAAGGGCAGAGCCACCCTGACCGTGGACAAGAGCACCAGCACCGCCTA
CATGGAACTGAGCAGCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGACAGCAACTGGGGCGTGG
ACTATTGGGGCCAGGGCACACTCGTGACCGTCAGCTCAGCCTCCACCAAGGGCCCAAGCGTCTTCCCCCTGGCA
CCCTCCTCCAAGAGCACCTCTGGCGGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGT
GACCGTGAGCTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCCGCTGTCCTGCAGTCCTCAGGAC
TCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACC
CTGCCCAGCACCTGAACTCCTGGGGGGACCCTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA
TCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG
TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGTACCGGGT
GGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACACCCTG
CCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGA
CATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACTACAAGACCACCCCTCCCGTGCTGGACTCCG
ACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGC
TCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAATGA

Signal sequence (1-57), Variable region (58-408), Constant region (409-1398)

SEQ ID NO: 112: Amino acid sequence of hR198_H0

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGYPVTSYYISWIRQAPGQGLEWIGYVDMGN
GRTNYNEKFKGRATLTVDKSTSTAYMELSSLRSEDTAVYYCARDSNWGVDYWGQGTLVTVSSASTKGPSVFPLA
PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC
SVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-136), Constant region (137-466)

Figure 50

SEQ ID NO: 113: Nucleotide sequence encoding hR198_H5

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAGCCAGGTGCAGCTGGTGCA
GTCTGGCGCCGAAGTGAAGAAACCAGGCGCCAGCGTGAAGGTGTCCTGCAAGGCCTCTGGCTACCCCGTGACCG
CCTACTACATCAGCTGGATCAGACAGGCCCCAGGCCAGGGCCTGGAATGGATCGGCTACATCGACATGGGCAAC
GGCCGGACCAACTACAACGCCCGGTTTAAGGGCAGAGCCACCCTGACCGTGGACAAGAGCACCAGCACCGCCTA
CATGGAACTGAGCAGCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGACAGCAACTGGGGCGTGG
ACTATTGGGGCCAGGGCACACTCGTGACCGTCAGCTCAGCCTCCACCAAGGGCCCAAGCGTCTTCCCCCTGGCA
CCCTCCTCCAAGAGCACCTCTGGCGGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGT
GACCGTGAGCTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCCGCTGTCCTGCAGTCCTCAGGAC
TCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACC
CTGCCCAGCACCTGAACTCCTGGGGGGACCCTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA
TCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG
TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGTACCGGGT
GGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACACCCTG
CCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGA
CATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACTACAAGACCACCCCTCCCGTGCTGGACTCCG
ACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGC
TCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAATGA

Signal sequence (1-57), Variable region (58-408), Constant region (409-1398)

SEQ ID NO: 114: Amino acid sequence of hR198_H5

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGYPVTAYYISWIRQAPGQGLEWIGYIDMGN
GRTNYNARFKGRATLTVDKSTSTAYMELSSLRSEDTAVYYCARDSNWGVDYWGQGTLVTVSSASTKGPSVFPLA
PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC
SVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-136), Constant region (137-466)

Figure 51

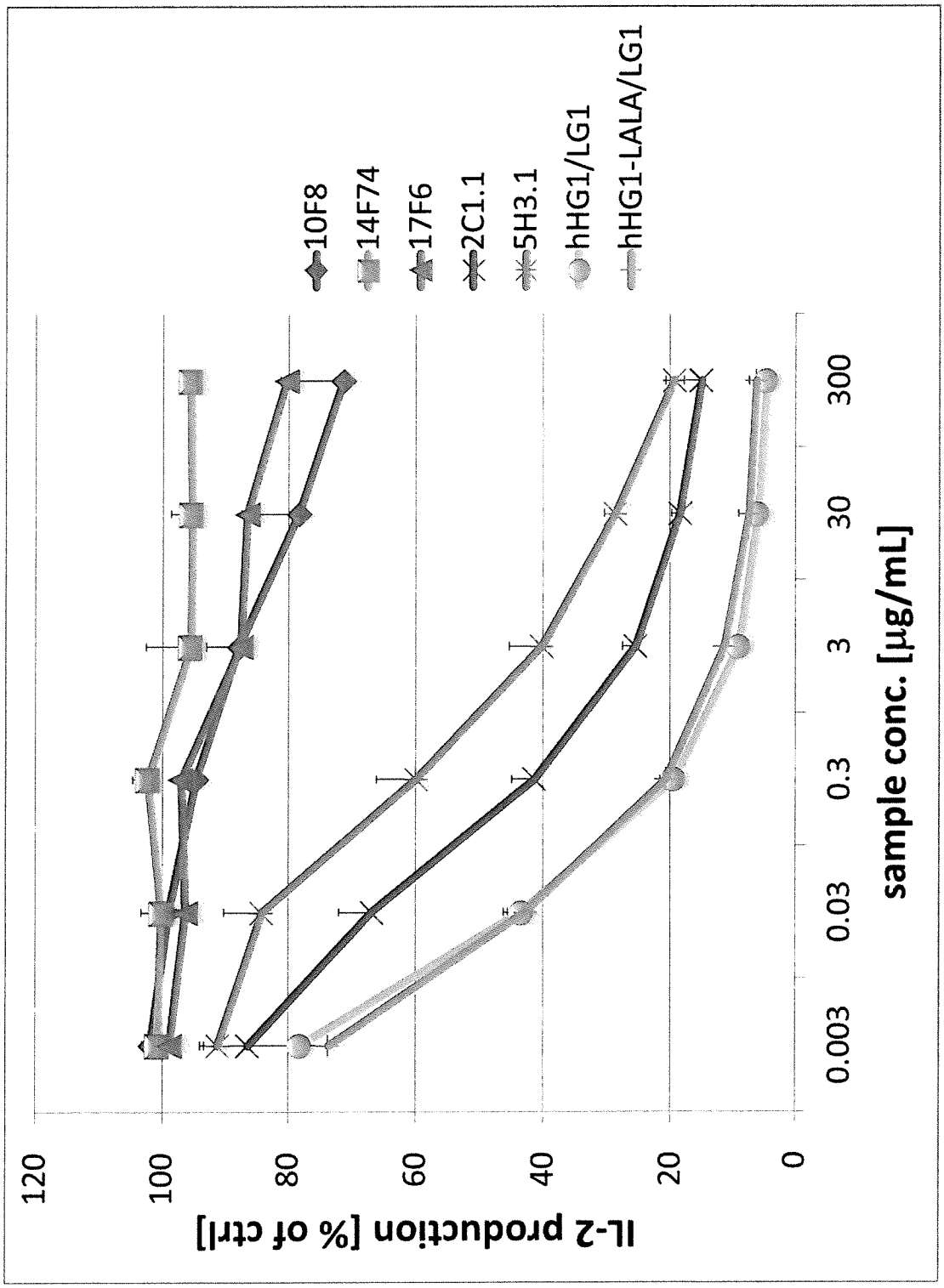

IL-2 production [% of ctrl]
120
100
80
60
40
20
0
0.003
0.03
0.3
3
30
300
sample conc. [µg/mL]
10F8
14F74
17F6
2C1.1
5H3.1
hHG1/LG1
hHG1-LALA/LG1

Figure 52

	IC50 [ng/mL]	IC80 [ng/mL]
10F8	>300000	>300000
14F74	>300000	>300000
17F6	>300000	>300000
2C1.1	137	17572
5H3.1	950	250617
hHG1/LG1	19	282
hHG1-LALA/LG1	17	347

Figure 53

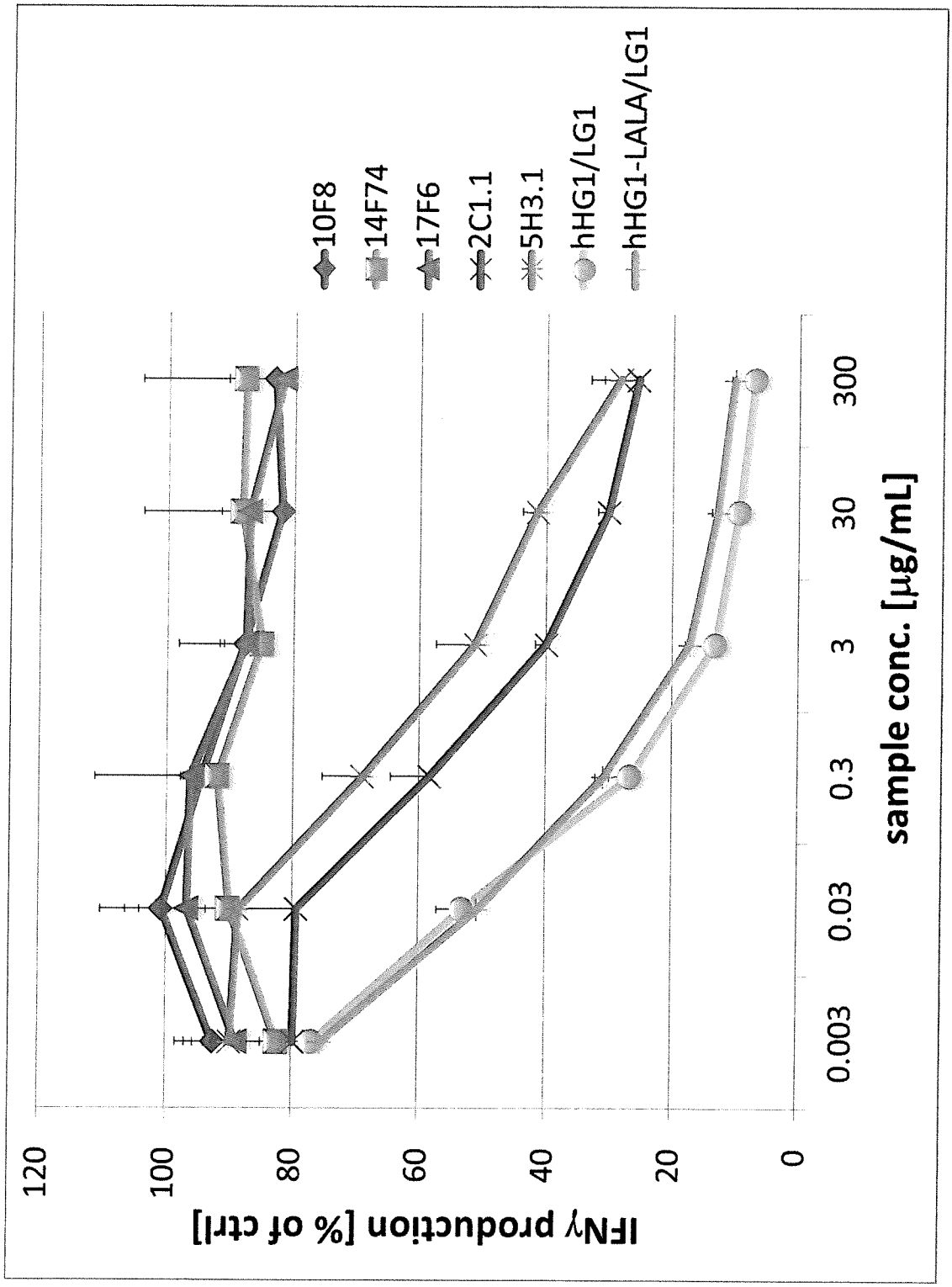

IFNγ production [% of ctrl]
120
100
80
60
40
20
0
0.003
0.03
0.3
3
30
300
sample conc. [µg/mL]
10F8
14F74
17F6
2C1.1
5H3.1
hHG1/LG1
hHG1-LALA/LG1

Figure 54

	IC50 [ng/mL]	IC80 [ng/mL]
10F8	>300000	>300000
14F74	>300000	>300000
17F6	>300000	>300000
2C1.1	852	>300000
5H3.1	3917	>300000
hHG1/LG1	39	915
hHG1-LALA/LG1	33	1840

Figure 55

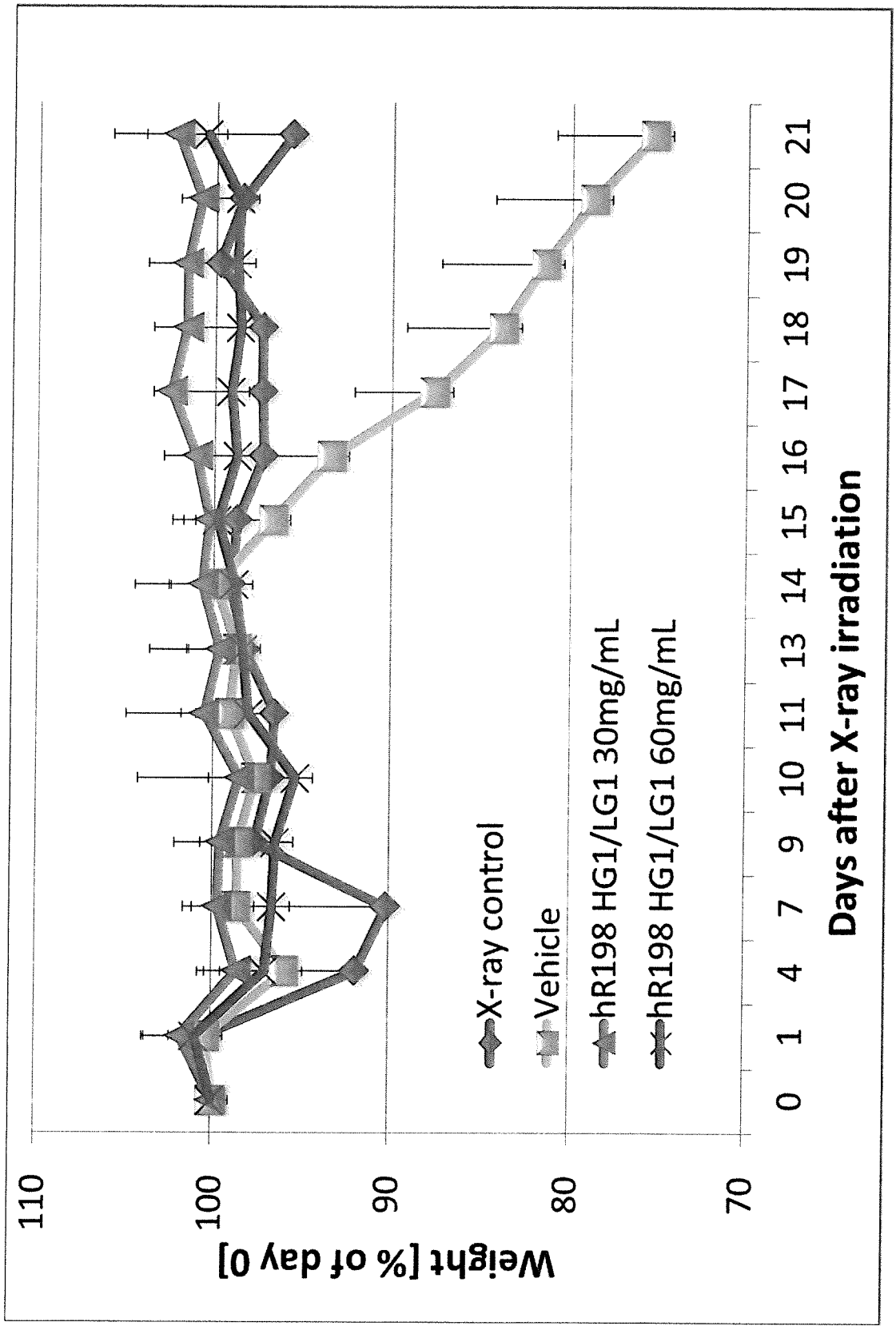

Weight [% of day 0]
110
100
90
80
70
0 1 4 7 9 10 11 13 14 15 16 17 18 19 20 21
Days after X-ray irradiation
X-ray control
Vehicle
hR198 HG1/LG1 30mg/mL
hR198 HG1/LG1 60mg/mL

Figure 56

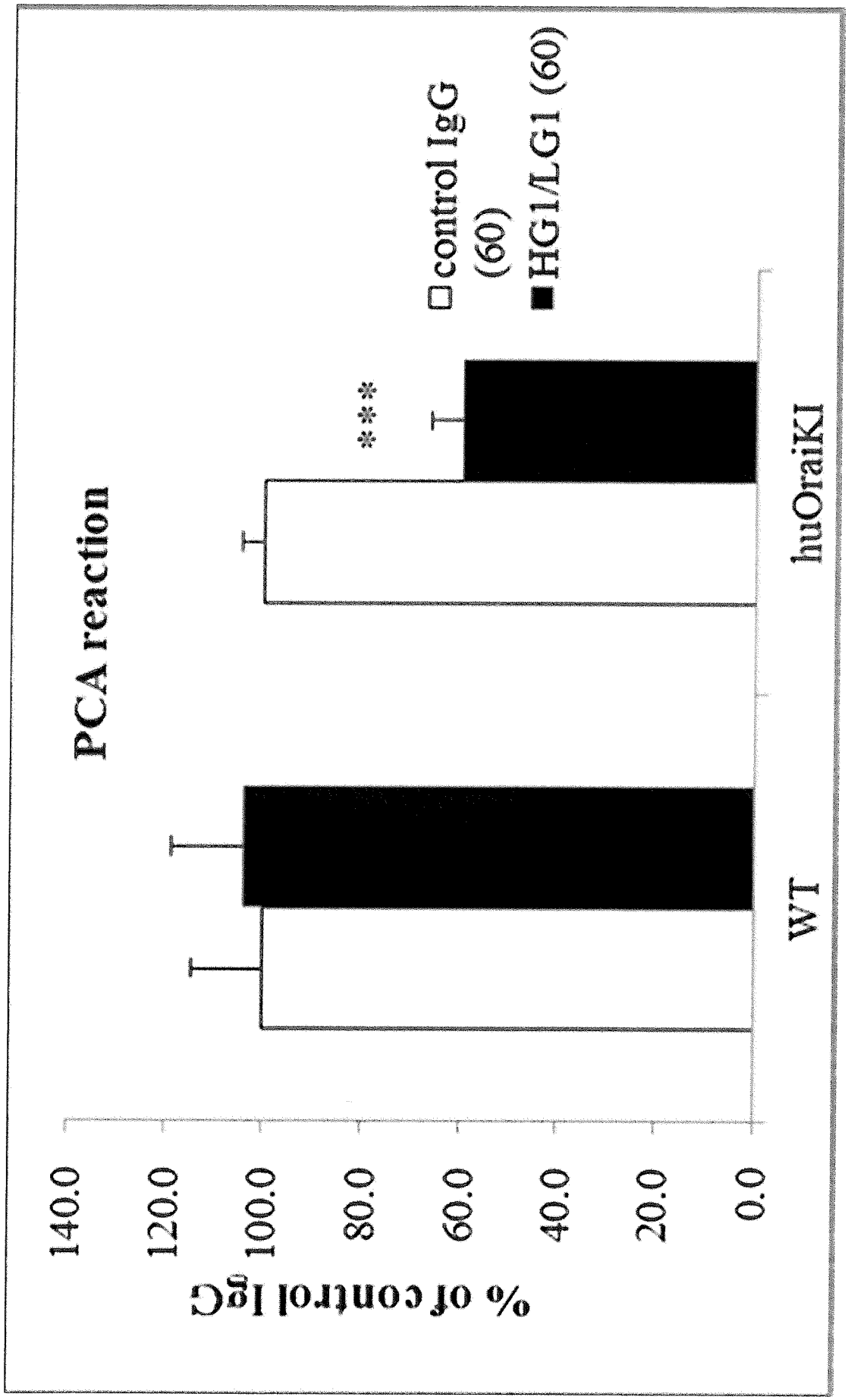
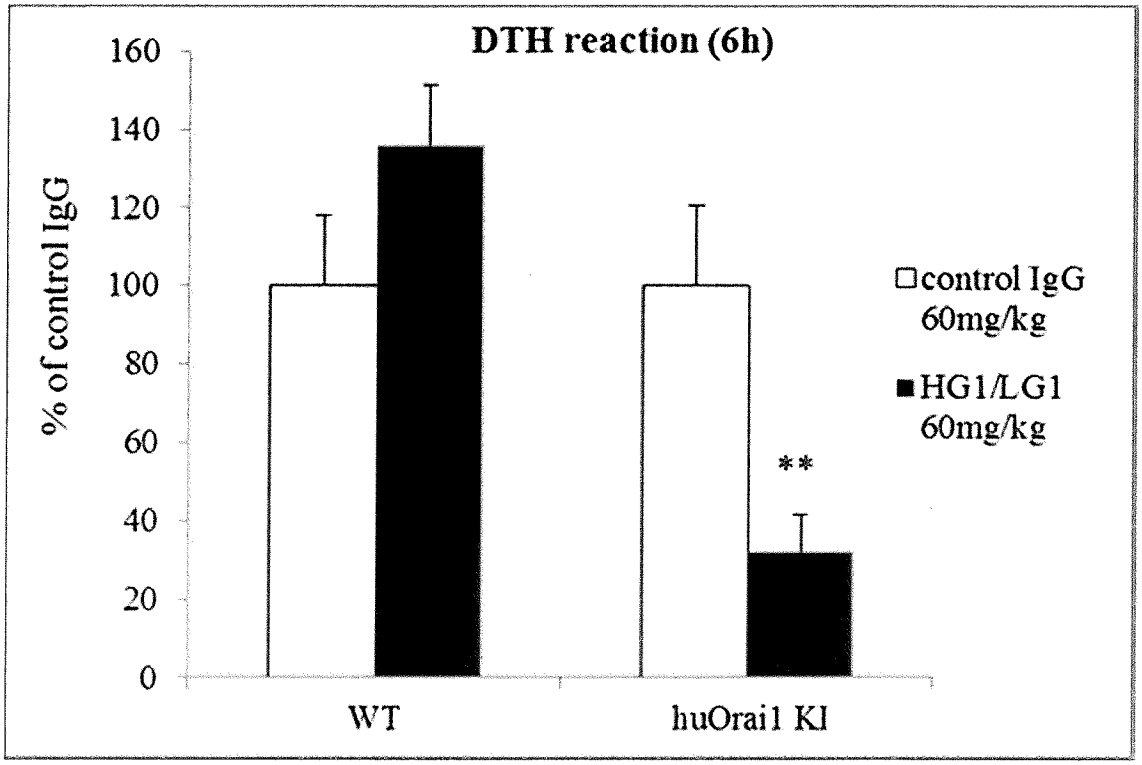
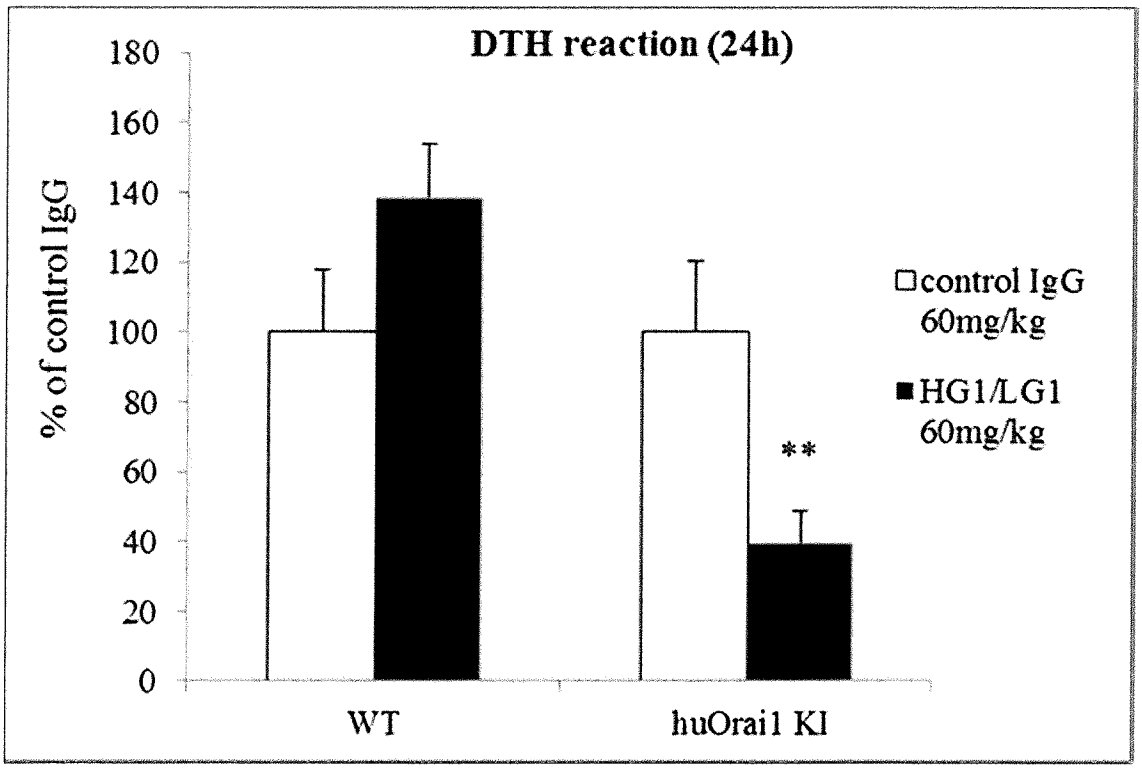

PCA reaction
% of control IgG
140.0
120.0
100.0
80.0
60.0
40.0
20.0
0.0
WT
huOraiKI
****
control IgG (60)
HG1/LG1 (60)

Figure 57

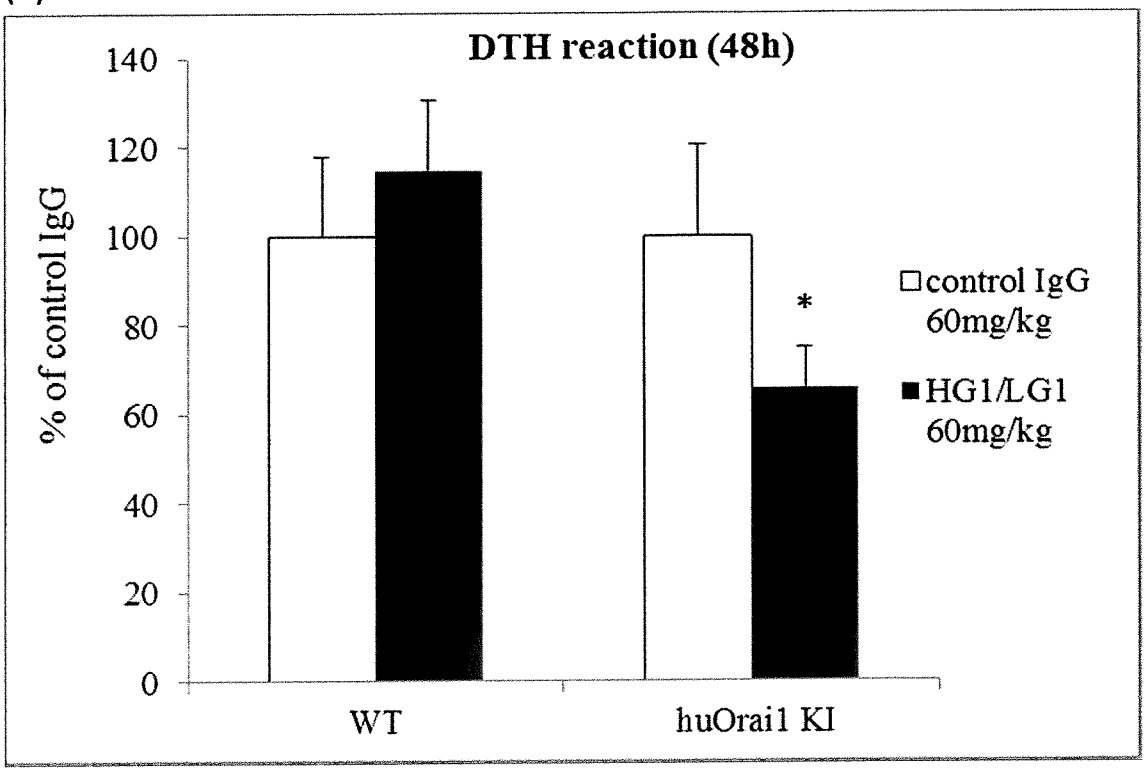
(A)


DTH reaction (6h)
% of control IgG
160
140
120
100
80
60
40
20
0
**
WT
huOrai1 KI
control IgG 60mg/kg
HG1/LG1 60mg/kg

(B)


DTH reaction (24h)
% of control IgG
180
160
140
120
100
80
60
40
20
0
**
WT
huOrai1 KI
control IgG 60mg/kg
HG1/LG1 60mg/kg

(C)


DTH reaction (48h)
% of control IgG
140
120
100
80
60
40
20
0
*
WT
huOrai1 KI
control IgG 60mg/kg
HG1/LG1 60mg/kg

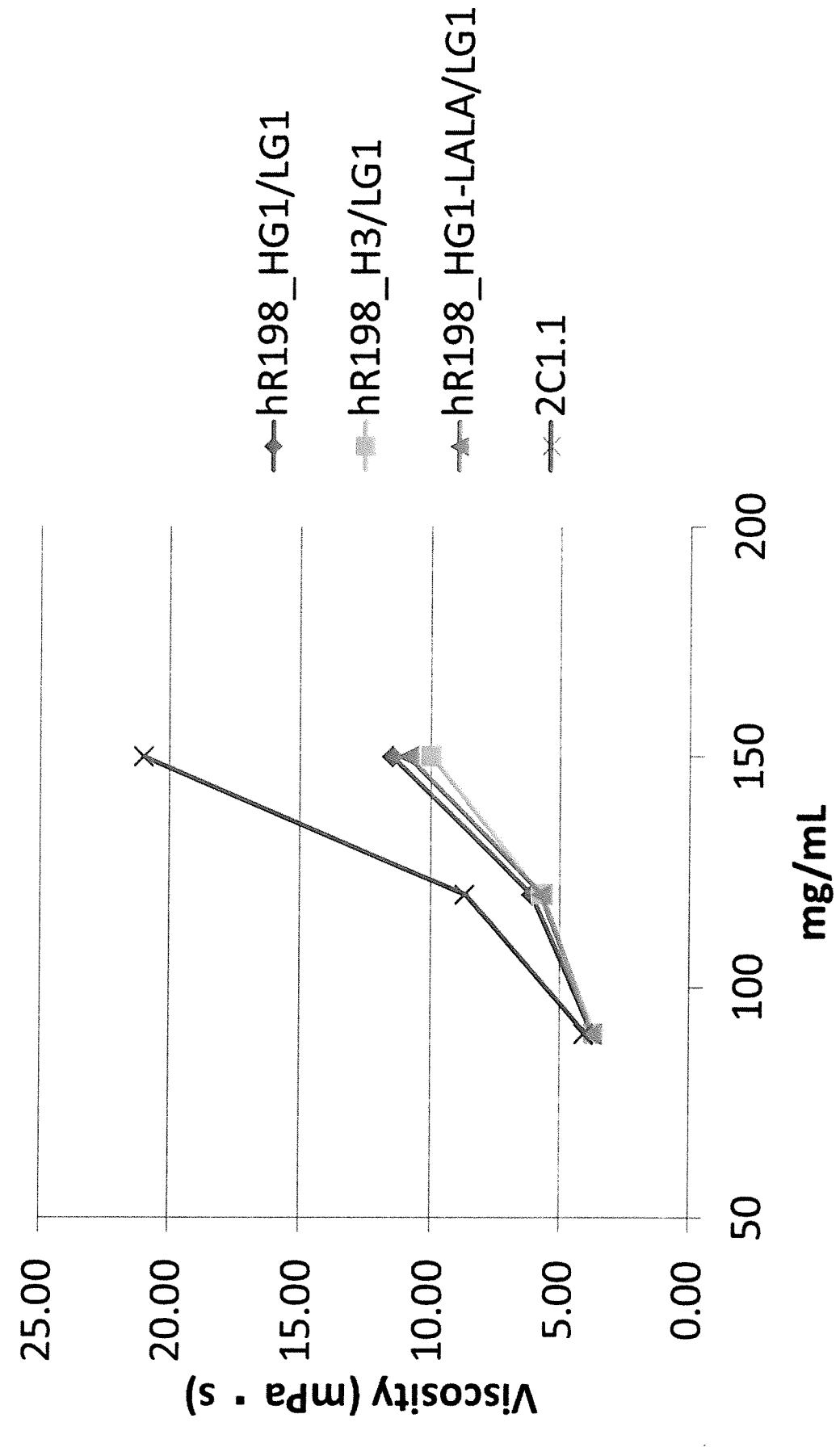

hR198_HG1/LG1
hR198_H3/LG1
hR198_HG1-LALA/LG1
2C1.1
Viscosity (mPa · s)
25.00
20.00
15.00
10.00
5.00
0.00
50
100
150
200
mg/mL

Figure 58

SEQUENCE LISTING

<110> Daiichi Sankyo Co., Ltd.

<120> Anti Orai1 antibodies

<130> FP1522

<160> 116

<170> PatentIn version 3.5

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<211> 906
<212> DNA
<213> Homo sapiens

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ggcagcacca ccagcggcag ccgccggagc cgccgccgca gcggggacgg ggagcccccg 120

ggggccccgc caccgccgcc gtccgccgtc acctacccgg actggatcgg ccagagttac 180

tccgaggtga tgagcctcaa cgagcactcc atgcaggcgc tgtcctggcg caagctctac 240

ttgagccgcg ccaagcttaa agcctccagc cggacctcgg ctctgctctc cggcttcgcc 300

atggtggcaa tggtggaggt gcagctggac gctgaccacg actacccacc ggggctgctc 360

atcgccttca gtgcctgcac cacagtgctg gtggctgtgc acctgtttgc gctcatgatc 420

agcacctgca tcctgcccaa catcgaggcg gtgagcaacg tgcacaatct caactcggtc 480

aaggagtccc cccatgagcg catgcaccgc cacatcgagc tggcctgggc cttctccacc 540

gtcattggca cgctgctctt cctagctgag gtggtgctgc tctgctgggt caagttcttg 600

cccctcaaga agcagccagg ccagccaagg cccaccagca agccccccgc cagtggcgca 660

gcagccaacg tcagcaccag cggcatcacc ccgggccagg cagctgccat cgcctcgacc 720

accatcatgg tgcccttcgg cctgatcttt atcgtcttcg ccgtccactt ctaccgctca 780

ctggttagcc ataagaccga ccgacagttc caggagctca acgagctggc ggagtttgcc 840

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gcctag 906

<210> 2
<211> 301
<212> PRT
<213> Homo sapiens

<400> 2

Met His Pro Glu Pro Ala Pro Pro Pro Ser Arg Ser Ser Pro Glu Leu
1 5 10 15

Pro Pro Ser Gly Gly Ser Thr Thr Ser Gly Ser Arg Arg Ser Arg Arg
20 25 30

Arg Ser Gly Asp Gly Glu Pro Pro Gly Ala Pro Pro Pro Pro Pro Ser
35 40 45

```
Ala Val Thr Tyr Pro Asp Trp Ile Gly Gln Ser Tyr Ser Glu Val Met
    50                  55                  60

Ser Leu Asn Glu His Ser Met Gln Ala Leu Ser Trp Arg Lys Leu Tyr
65                  70                  75                  80

Leu Ser Arg Ala Lys Leu Lys Ala Ser Ser Arg Thr Ser Ala Leu Leu
                85                  90                  95

Ser Gly Phe Ala Met Val Ala Met Val Glu Val Gln Leu Asp Ala Asp
            100                 105                 110

His Asp Tyr Pro Pro Gly Leu Leu Ile Ala Phe Ser Ala Cys Thr Thr
        115                 120                 125

Val Leu Val Ala Val His Leu Phe Ala Leu Met Ile Ser Thr Cys Ile
    130                 135                 140

Leu Pro Asn Ile Glu Ala Val Ser Asn Val His Asn Leu Asn Ser Val
145                 150                 155                 160

Lys Glu Ser Pro His Glu Arg Met His Arg His Ile Glu Leu Ala Trp
                165                 170                 175

Ala Phe Ser Thr Val Ile Gly Thr Leu Leu Phe Leu Ala Glu Val Val
            180                 185                 190

Leu Leu Cys Trp Val Lys Phe Leu Pro Leu Lys Lys Gln Pro Gly Gln
        195                 200                 205

Pro Arg Pro Thr Ser Lys Pro Pro Ala Ser Gly Ala Ala Ala Asn Val
    210                 215                 220

Ser Thr Ser Gly Ile Thr Pro Gly Gln Ala Ala Ala Ile Ala Ser Thr
225                 230                 235                 240

Thr Ile Met Val Pro Phe Gly Leu Ile Phe Ile Val Phe Ala Val His
                245                 250                 255

Phe Tyr Arg Ser Leu Val Ser His Lys Thr Asp Arg Gln Phe Gln Glu
            260                 265                 270

Leu Asn Glu Leu Ala Glu Phe Ala Arg Leu Gln Asp Gln Leu Asp His
        275                 280                 285

Arg Gly Asp His Pro Leu Thr Pro Gly Ser His Tyr Ala
    290                 295                 300
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<211> 37

<212> DNA
<213> artificial

<220>
<223> PCR Primer Nhe-polyC-S

<220>
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<223> n is a, c, g, or t

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<212> DNA
<213> artificial

<220>
<223> PCR Primer rIg gamma-AS1

<400> 4
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<210> 5
<211> 28
<212> DNA
<213> artificial

<220>
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<220>
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<220>
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<223> n is a, c, g, or t

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<211> 28
<212> DNA
<213> artificial

<220>
<223> rIg kappa-AS

<400> 7
tcagtaacac tgtccaggac accatctc 28

<210> 8
<211> 19
<212> DNA
<213> artificial

<220>
<223> rIG gamma-seq

<400> 8
ctggctcagg gaaatagcc 19

<210> 9
<211> 19
<212> DNA
<213> artificial

<220>
<223> rIG kappa-seq

<400> 9
tccagttgct aactgttcc 19

<210> 10
<211> 405
<212> DNA
<213> Rattus rattus

<220>
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<222> (382)..(382)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (403)..(403)
<223> n is a, c, g, or t

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aggtgtgaca tccagttgac ccagtctcca tccacattgc ctgcatccct gggagagaga 120

gtcaccatca gttgcagagc aagtcagagt attagcaata gtttaagctg gtttcaacag 180

aaaccagatg gaactgttaa acgcctgatc tattctacat ccactttaga atctggtgtc 240

ccatcaaggt tcagtggcag tgggtctggg acagattatt ctctctccat caccagtctt 300

gagtctgaag attttgcaat gtattactgt ctacagtttg ctacttttcc ggacacgttt 360

ggaactggga ccaaactgga antgagacgg gctgatgctg canca 405

<210> 11
<211> 135
<212> PRT
<213> Rattus rattus

<220>
<221> misc_feature
<222> (128)..(128)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (135)..(135)
<223> Xaa can be any naturally occurring amino acid

<400> 11

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

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

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

Gln Ser Ile Ser Asn Ser Leu Ser Trp Phe Gln Gln Lys Pro Asp Gly
50 55 60

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

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

Ile Thr Ser Leu Glu Ser Glu Asp Phe Ala Met Tyr Tyr Cys Leu Gln
100 105 110

Phe Ala Thr Phe Pro Asp Thr Phe Gly Thr Gly Thr Lys Leu Glu Xaa
115 120 125

Arg Arg Ala Asp Ala Ala Xaa
130 135

<210> 12
<211> 468
<212> DNA
<213> Rattus rattus

<220>
<221> misc_feature
<222> (467)..(467)
<223> n is a, c, g, or t

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gtccagctgc agcagtctgg agcggagctg gcaaagcctg gctcctcagt gaagatttcc 120

tgcaaggctt ccggctacac cgtcaccgcc tattatataa gttggataag gcagacgatt 180

ggacagggcc ttgagtatgt tggatatatt gacatgggaa atggaaggac taactacaat 240

gcgaggttca agggcaaggc cacattgact gtggacaaat cctccagcac agccttcatg 300

caactcagca gcctgacacc tgacgactct gcggtctatt actgtgcaag ggactccaac 360

tgggggttg attactgggg ccaaggagtc atggtcacag tctcctcagc tgaaacaaca 420

gccccatctg tctatccact ggctcctgga actgcttctc aaaagtna 468

<210> 13
<211> 156
<212> PRT
<213> Rattus rattus

<220>
<221> misc_feature
<222> (156)..(156)
<223> Xaa can be any naturally occurring amino acid

<400> 13

Met Glu Trp Asn Trp Val Phe Leu Leu Leu Leu Ser Val Thr Ala Glu
1 5 10 15

Val Gln Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Lys
20 25 30

Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Val
35 40 45

Thr Ala Tyr Tyr Ile Ser Trp Ile Arg Gln Thr Ile Gly Gln Gly Leu
50 55 60

Glu Tyr Val Gly Tyr Ile Asp Met Gly Asn Gly Arg Thr Asn Tyr Asn
65 70 75 80

Ala Arg Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
85 90 95

Thr Ala Phe Met Gln Leu Ser Ser Leu Thr Pro Asp Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Gly Val Asp Tyr Trp Gly Gln
115 120 125

Gly Val Met Val Thr Val Ser Ser Ala Glu Thr Thr Ala Pro Ser Val
130 135 140

Tyr Pro Leu Ala Pro Gly Thr Ala Ser Gln Lys Xaa
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<210> 14
<211> 408
<212> DNA
<213> Rattus rattus

<220>
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aggtgtgaca tccagttgac ccagtctcca tccacattgc ctgcatctct gggagagaga 120

gtcaccatca gttgcagagc aagtcagagt attggcaata gtttaagctg gtttcagcag 180

aaaccagatg gatctgttaa acgcctgatc tactctacat ccactttaga atctggtgtc 240

ccatcaaggt tcagtggcag tgggtctggg acagattatt ctctctccat caccagtctt 300

gagtctgaag attttgcaat gtattactgt ctacagtttg ctacttatcc ggacacgttt 360

ggaactggga ccaaactgga actgagacgg gctgatgctg cancaact 408

<210> 15
<211> 136
<212> PRT
<213> Rattus rattus

<220>
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<222> (135)..(135)
<223> Xaa can be any naturally occurring amino acid

<400> 15

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

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

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

Gln Ser Ile Gly Asn Ser Leu Ser Trp Phe Gln Gln Lys Pro Asp Gly
50 55 60

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

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

Ile Thr Ser Leu Glu Ser Glu Asp Phe Ala Met Tyr Tyr Cys Leu Gln
100 105 110

Phe Ala Thr Tyr Pro Asp Thr Phe Gly Thr Gly Thr Lys Leu Glu Leu
115 120 125

Arg Arg Ala Asp Ala Ala Xaa Thr
130 135

<210> 16
<211> 471

<212> DNA
<213> Rattus rattus

<220>
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<223> n is a, c, g, or t

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gtccagctgc agcagtctgg agcggagctg gcaaagcctg gctcctcaat gaagatttcc 120

tgcaaggctt ccggctaccc cgtcaccagc tattatataa gttggataaa gcagacgact 180

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gagaagttca agggcaaggc cacattgact gtagacaaat cctccagcac agccttcatg 300

caactcagca gcctgacacc tgacgactct gcggtctatt actgtgcaag ggactccaac 360

tgggggggttg attactgggg ccaaggagtc atggtcacag tctcctcagc tgaaacaaca 420

gccccatctg tctatccact ggctcctgga actgctctca aaagtaacnc c 471

<210> 17
<211> 157
<212> PRT
<213> Rattus rattus

<220>
<221> misc_feature
<222> (157)..(157)
<223> Xaa can be any naturally occurring amino acid

<400> 17

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1 5 10 15

Val Gln Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Lys
20 25 30

Pro Gly Ser Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Pro Val
35 40 45

Thr Ser Tyr Tyr Ile Ser Trp Ile Lys Gln Thr Thr Gly Gln Gly Leu
50 55 60

Glu Tyr Ile Gly Tyr Val Asp Met Gly Asn Gly Arg Thr Asn Tyr Asn
65 70 75 80

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

Thr Ala Phe Met Gln Leu Ser Ser Leu Thr Pro Asp Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Gly Val Asp Tyr Trp Gly Gln
115 120 125

Gly Val Met Val Thr Val Ser Ser Ala Glu Thr Thr Ala Pro Ser Val
130 135 140

Tyr Pro Leu Ala Pro Gly Thr Ala Leu Lys Ser Asn Xaa
145 150 155

<210> 18
<211> 449
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding Human Light Chain Secretory Signal and Human Kappa Constant Region

<400> 18
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gtggatctcc ggcgcgtacg gcgatatcgt gatgattaaa cgtacggtgg ccgccccctc 120

cgtgttcatc ttcccccccct ccgacgagca gctgaagtcc ggcaccgcct ccgtggtgtg 180

cctgctgaat aacttctacc ccagagaggc caaggtgcag tggaaggtgg acaacgccct 240

gcagtccggg aactcccagg agagcgtgac cgagcaggac agcaaggaca gcacctacag 300

cctgagcagc accctgaccc tgagcaaagc cgactacgag aagcacaagg tgtacgcctg 360

cgaggtgacc caccagggcc tgagctcccc cgtcaccaag agcttcaaca gggggggagtg 420

ttaggggccc gtttaaacgg gggaggcta 449

<210> 19
<211> 30
<212> DNA
<213> artificial

<220>
<223> PCR Primer 3.3-F1

<400> 19
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<210> 20
<211> 30
<212> DNA
<213> artificial

<220>
<223> PCR Primer 3.3-R1

<400> 20
gctatggcag ggcctgccgc cccgacgttg 30

<210> 21
<211> 1132
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding Human Heavy Chain Secretory Signal and Human IgG1 Constant Region

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tcccagatgg gtgctgagcc aggtgcaatt gtgcaggcgg ttagctcagc ctccaccaag 120

ggcccaagcg tcttcccccct ggcaccctcc tccaagagca cctctggcgg cacagccgcc 180

ctgggctgcc tggtcaagga ctacttcccc gaacccgtga ccgtgagctg gaactcaggc 240

gccctgacca gcggcgtgca caccttcccc gctgtcctgc agtcctcagg actctactcc 300

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 360

gtgaatcaca agcccagcaa caccaaggtg gacaagagag ttgagcccaa atcttgtgac 420

aaaactcaca catgcccacc ctgcccagca cctgaactcc tgggggggacc ctcagtcttc 480

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggaccccctga ggtcacatgc 540

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 600

gtggaggtgc ataatgccaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg 660

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 720

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggc 780

cagccccggg aaccacaggt gtacaccctg cccccatccc gggaggagat gaccaagaac 840

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 900

gagagcaatg gccagcccga gaacaactac aagaccaccc ctcccgtgct ggactccgac 960

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac 1020

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacaccca gaagagcctc 1080

tccctgtctc ccggcaaatg agatatcggg cccgtttaaa cgggggaggc ta 1132

<210> 22
<211> 705
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding cR118_L

<400> 22
atggtgctgc agacccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc 60

gacatccagt tgacccagtc tccatccaca ttgcctgcat ccctgggaga gagagtcacc 120

atcagttgca gagcaagtca gagtattagc aatagtttaa gctggtttca acagaaacca 180

gatggaactg ttaaacgcct gatctattct acatccactt tagaatctgg tgtcccatca 240

aggttcagtg gcagtgggtc tgggacagat tattctctct ccatcaccag tcttgagtct 300

gaagattttg caatgtatta ctgtctacag tttgctactt ttccggacac gtttggaact 360

gggaccaaac tggaactgag acgggctgtg gccgcccccct ccgtgttcat cttccccccc 420

tccgacgagc agctgaagtc cggcaccgcc tccgtggtgt gcctgctgaa taacttctac 480

cccagagagg ccaaggtgca gtggaaggtg gacaacgccc tgcagtccgg gaactcccag 540

gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc 600

ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 660

ctgagctccc ccgtcaccaa gagcttcaac aggggggagt gttag 705

<210> 23
<211> 234
<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of cR118_L

<400> 23

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

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

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

Ile Ser Asn Ser Leu Ser Trp Phe Gln Gln Lys Pro Asp Gly Thr Val
50 55 60

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

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Ser Ile Thr
85 90 95

Ser Leu Glu Ser Glu Asp Phe Ala Met Tyr Tyr Cys Leu Gln Phe Ala
100 105 110

Thr Phe Pro Asp Thr Phe Gly Thr Gly Thr Lys Leu Glu Leu Arg Arg
115 120 125

Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
180 185 190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
195 200 205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 24
<211> 705
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding cR198_L

<400> 24
atggtgctgc agacccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc 60

gacatccagt tgacccagtc tccatccaca ttgcctgcat ctctgggaga gagagtcacc 120

atcagttgca gagcaagtca gagtattggc aatagtttaa gctggtttca gcagaaacca 180

gatggatctg ttaaacgcct gatctactct acatccactt tagaatctgg tgtcccatca 240

aggttcagtg gcagtgggtc tgggacagat tattctctct ccatcaccag tcttgagtct 300

gaagattttg caatgtatta ctgtctacag tttgctactt atccggacac gtttggaact 360

gggaccaaac tggaactgag acgggctgtg gccgcccccc ccgtgttcat cttcccccc 420

tccgacgagc agctgaagtc cggcaccgcc tccgtggtgt gcctgctgaa taacttctac 480

cccagagagg ccaaggtgca gtggaaggtg gacaacgccc tgcagtccgg gaactcccag 540

gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc 600

ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 660

ctgagctccc ccgtcaccaa gagcttcaac aggggggagt gttag 705

<210> 25
<211> 234
<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of cR198_L

<400> 25

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

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

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

Ile Gly Asn Ser Leu Ser Trp Phe Gln Gln Lys Pro Asp Gly Ser Val
50 55 60

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

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Ser Ile Thr
85 90 95

Ser Leu Glu Ser Glu Asp Phe Ala Met Tyr Tyr Cys Leu Gln Phe Ala
100 105 110

Thr Tyr Pro Asp Thr Phe Gly Thr Gly Thr Lys Leu Glu Leu Arg Arg
115 120 125

Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
180 185 190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
195 200 205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 26
<211> 1401
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding cR118_H

<400> 26
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gtccagctgc agcagtctgg agcggagctg gcaaagcctg gctcctcagt gaagatttcc 120

tgcaaggctt ccggctacac cgtcaccgcc tattatataa gttggataag gcagacgatt 180

ggacagggcc ttgagtatgt tggatatatt gacatgggaa atggaaggac taactacaat 240

gcgaggttca agggcaaggc cacattgact gtggacaaat cctccagcac agccttcatg 300

caactcagca gcctgacacc tgacgactct gcggtctatt actgtgcaag ggactccaac 360

tgggggttg attactgggg ccaaggagtc atggtcacag tcagctcagc ctccaccaag 420

ggcccaagcg tcttcccccc ggcaccctcc tccaagagca cctctggcgg cacagccgcc 480

ctgggctgcc tggtcaagga ctacttcccc gaacccgtga ccgtgagctg gaactcaggc 540

gccctgacca gcggcgtgca caccttcccc gctgtcctgc agtcctcagg actctactcc 600

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 660

gtgaatcaca agcccagcaa caccaaggtg gacaagagag ttgagcccaa atcttgtgac 720

aaaactcaca catgcccacc ctgcccagca cctgaactcc tgggggggacc ctcagtcttc 780

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 840

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 900

gtggaggtgc ataatgccaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg 960

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1020

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggc 1080

cagccccggg aaccacaggt gtacaccctg cccccatccc gggaggagat gaccaagaac 1140

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1200

gagagcaatg gccagcccga gaacaactac aagaccaccc ctcccgtgct ggactccgac 1260

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac 1320

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacaccca gaagagcctc 1380

tccctgtctc ccggcaaatg a 1401

<210> 27
<211> 466
<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of cR118_H

<400> 27

Met Lys His Leu Trp Phe Phe Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Lys
20 25 30

Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Val
35 40 45

Thr Ala Tyr Tyr Ile Ser Trp Ile Arg Gln Thr Ile Gly Gln Gly Leu
50 55 60

Glu Tyr Val Gly Tyr Ile Asp Met Gly Asn Gly Arg Thr Asn Tyr Asn
65 70 75 80

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Ala Arg Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
                85                  90                  95

Thr Ala Phe Met Gln Leu Ser Ser Leu Thr Pro Asp Asp Ser Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Gly Val Asp Tyr Trp Gly Gln
        115                 120                 125

Gly Val Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
    130                 135                 140

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

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

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

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

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

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

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
                245                 250                 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            260                 265                 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
        275                 280                 285

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

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

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
                325                 330                 335

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
            340                 345                 350
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Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
        355                 360                 365

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

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

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

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
        435                 440                 445

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

Gly Lys
465
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<210> 28
<211> 1401
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding cR198_H

<400> 28

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atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag       60

gtccagctgc agcagtctgg agcggagctg gcaaagcctg gctcctcaat gaagatttcc      120

tgcaaggctt ccggctaccc cgtcaccagc tattatataa gttggataaa gcagacgact      180

ggacagggcc ttgagtatat tggatatgtt gacatgggaa atggacggac taactacaat      240

gagaagttca agggcaaggc cacattgact gtagacaaat cctccagcac agccttcatg      300

caactcagca gcctgacacc tgacgactct gcggtctatt actgtgcaag ggactccaac      360

tgggggggttg attactgggg ccaaggagtc atggtcacag tcagctcagc ctccaccaag      420

ggcccaagcg tcttcccccct ggcaccctcc tccaagagca cctctggcgg cacagccgcc      480

ctgggctgcc tggtcaagga ctacttcccc gaacccgtga ccgtgagctg gaactcaggc      540

gccctgacca gcggcgtgca caccttcccc gctgtcctgc agtcctcagg actctactcc      600

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac      660

gtgaatcaca agcccagcaa caccaaggtg gacaagagag ttgagcccaa atcttgtgac      720

aaaactcaca catgcccacc ctgcccagca cctgaactcc tgggggggacc ctcagtcttc      780

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc      840
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gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 900

gtggaggtgc ataatgccaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg 960

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1020

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggc 1080

cagccccggg aaccacaggt gtacaccctg cccccatccc gggaggagat gaccaagaac 1140

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1200

gagagcaatg gccagcccga gaacaactac aagaccaccc ctcccgtgct ggactccgac 1260

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac 1320

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacaccca gaagagcctc 1380

tccctgtctc ccggcaaatg a 1401

<210> 29
<211> 466
<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of cR198_H

<400> 29

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Lys
20 25 30

Pro Gly Ser Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Pro Val
35 40 45

Thr Ser Tyr Tyr Ile Ser Trp Ile Lys Gln Thr Thr Gly Gln Gly Leu
50 55 60

Glu Tyr Ile Gly Tyr Val Asp Met Gly Asn Gly Arg Thr Asn Tyr Asn
65 70 75 80

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

Thr Ala Phe Met Gln Leu Ser Ser Leu Thr Pro Asp Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Gly Val Asp Tyr Trp Gly Gln
115 120 125

Gly Val Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
130 135 140

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

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

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

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

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

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

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
                245                 250                 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            260                 265                 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
        275                 280                 285

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

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

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
                325                 330                 335

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

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

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

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

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

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
435 440 445

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

Gly Lys
465

<210> 30
<211> 705
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding hR198_L1

<400> 30
atggtgctgc agacccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc 60

gatatccagc tgacccagag ccctagcagc ctgtctgcca gcgtgggcga cagagtgacc 120

atcacctgta gagccagcca gagcatcggc aacagcctga gctggttcca gcagaaaccc 180

ggcaaggccc ccaagcggct gatctacagc accagcaccc tggaaagcgg cgtgcccagc 240

agattttctg gcagcggctc cggcaccgac tacaccctga caatcagcag cctgcagccc 300

gaggacttcg ccatgtacta ctgcctgcag ttcgccacct accccgacac ctttggccag 360

ggcaccaagg tggaaatcaa gcgtacggtg gccgcccccct ccgtgttcat cttcccccccc 420

tccgacgagc agctgaagtc cggcaccgcc tccgtggtgt gcctgctgaa taacttctac 480

cccagagagg ccaaggtgca gtggaaggtg gacaacgccc tgcagtccgg gaactcccag 540

gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc 600

ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 660

ctgagctccc ccgtcaccaa gagcttcaac aggggggagt gttag 705

<210> 31
<211> 234
<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of hR198_L1

<400> 31

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

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

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

Ile Gly Asn Ser Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro
50 55 60

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

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Met Tyr Tyr Cys Leu Gln Phe Ala
100 105 110

Thr Tyr Pro Asp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
115 120 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
180 185 190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
195 200 205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 32
<211> 705
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding hR198_L2

<400> 32
atggtgctgc agacccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc 60

gatatccagc tgacccagag ccctagcagc ctgtctgcca gcgtgggcga cagagtgacc 120

atcacctgta gagccagcca gagcatcggc aacagcctga gctggttcca gcagaaaccc 180

ggcaaggccg tgaagcggct gatctacagc accagcaccc tggaaagcgg cgtgcccagc 240

agattttctg gcagcggctc cggcaccgac tacaccctga caatcagcag cctgcagccc 300

gaggacttcg ccatgtacta ctgcctgcag ttcgccacct accccgacac ctttggccag 360

ggcaccaagg tggaaatcaa gcgtacggtg gccgcccccc ccgtgttcat cttcccccccc 420

tccgacgagc agctgaagtc cggcaccgcc tccgtggtgt gcctgctgaa taacttctac 480

cccagagagg ccaaggtgca gtggaaggtg gacaacgccc tgcagtccgg gaactcccag 540

gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc 600

ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 660

ctgagctccc ccgtcaccaa gagcttcaac aggggggagt gttag 705

<210> 33
<211> 234
<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of hR198_L2

<400> 33

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

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

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

Ile Gly Asn Ser Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ala Val
50 55 60

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

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Met Tyr Tyr Cys Leu Gln Phe Ala
100 105 110

Thr Tyr Pro Asp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
115 120 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
180 185 190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
195 200 205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 34
<211> 705
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding hR198_L3

<400> 34
atggtgctgc agacccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc 60

gatatccagc tgacccagag ccctagcagc ctgtctgcca gcgtgggcga cagagtgacc 120

atcacctgta gagccagcca gagcatcggc aacagcctga gctggttcca gcagaaaccc 180

ggcaaggccc ccaagcggct gatctacagc accagcaccc tggaaagcgg cgtgcccagc 240

agattttctg gcagcggctc cggcaccgac tacaccctga caatcagcag cctgcagccc 300

gaggacttcg ccatgtacta ctgcctgcag ttcgccacct tccccgacac ctttggccag 360

ggcaccaagg tggaaatcaa gcgtacggtg gccgcccccct ccgtgttcat cttcccccccc 420

tccgacgagc agctgaagtc cggcaccgcc tccgtggtgt gcctgctgaa taacttctac 480

cccagagagg ccaaggtgca gtggaaggtg gacaacgccc tgcagtccgg gaactcccag 540

gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc 600

ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 660

ctgagctccc ccgtcaccaa gagcttcaac agggggggagt gttag 705

<210> 35
<211> 234
<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of hR198_L3

<400> 35

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

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

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

Ile Gly Asn Ser Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro
50 55 60

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

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Met Tyr Tyr Cys Leu Gln Phe Ala
100 105 110

Thr Phe Pro Asp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
115 120 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
180 185 190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
195 200 205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 36
<211> 705
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding hR198_L4

<400> 36
atggtgctgc agacccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc 60

gatatccagc tgacccagag ccctagcagc ctgtctgcca gcgtgggcga cagagtgacc 120

atcacctgta gagccagcca gagcatcggc aacagcctga gctggttcca gcagaaaccc 180

ggcaaggccg tgaagcggct gatctacagc accagcaccc tggaaagcgg cgtgcccagc 240

agattttctg gcagcggctc cggcaccgac tacaccctga caatcagcag cctgcagccc 300

gaggacttcg ccatgtacta ctgcctgcag ttcgccacct tccccgacac ctttggccag 360

ggcaccaagg tggaaatcaa gcgtacggtg gccgcccccc ccgtgttcat cttcccccccc 420

tccgacgagc agctgaagtc cggcaccgcc tccgtggtgt gcctgctgaa taacttctac 480

cccagagagg ccaaggtgca gtggaaggtg gacaacgccc tgcagtccgg gaactcccag 540

gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc 600

ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 660

ctgagctccc ccgtcaccaa gagcttcaac agggggggagt gttag 705

<210> 37
<211> 234
<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of hR198_L4

<400> 37

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

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

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

Ile Gly Asn Ser Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ala Val
50 55 60

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

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Met Tyr Tyr Cys Leu Gln Phe Ala
100 105 110

Thr Phe Pro Asp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
115 120 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
180 185 190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
195 200 205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 38
<211> 1401
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding hR198_H1

<400> 38
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag 60

gtgcagctgg tgcagtctgg cgccgaagtg aagaaaccag gcgccagcgt gaaggtgtcc 120

tgcaaggcct ctggctaccc cgtgaccagc tactacatca gctgggtcag acaggcccca 180

ggccagggcc tggaatacat cggctatgtg gacatgggca acggccggac caactacaac 240

gagaagttca agggcagagc caccctgacc gtggacaaga gcaccagcac cgcctacatg 300

gaactgagca gcctgcggag cgaggacacc gccgtgtact actgcgccag agacagcaac 360

tggggcgtgg actattgggg ccagggcaca ctcgtgaccg tcagctcagc ctccaccaag 420

ggcccaagcg tcttccccct ggcaccctcc tccaagagca cctctggcgg cacagccgcc 480

ctgggctgcc tggtcaagga ctacttcccc gaacccgtga ccgtgagctg gaactcaggc 540

gccctgacca gcggcgtgca caccttcccc gctgtcctgc agtcctcagg actctactcc 600

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 660

gtgaatcaca agcccagcaa caccaaggtg gacaagagag ttgagcccaa atcttgtgac 720

aaaactcaca catgcccacc ctgcccagca cctgaactcc tgggggggacc ctcagtcttc 780

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 840

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 900

gtggaggtgc ataatgccaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg 960

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1020

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggc 1080

cagccccggg aaccacaggt gtacaccctg cccccatccc gggaggagat gaccaagaac 1140

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1200

gagagcaatg gccagcccga gaacaactac aagaccaccc ctcccgtgct ggactccgac 1260

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac 1320

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacaccca gaagagcctc 1380

tccctgtctc ccggcaaatg a 1401

<210> 39
<211> 466
<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of hR198_H1

<400> 39

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

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

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

Glu Tyr Ile Gly Tyr Val Asp Met Gly Asn Gly Arg Thr Asn Tyr Asn
65 70 75 80

Glu Lys Phe Lys Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Gly Val Asp Tyr Trp Gly Gln
115 120 125

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

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

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

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

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

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

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

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
                245                 250                 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            260                 265                 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
        275                 280                 285

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

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

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
                325                 330                 335

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

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

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

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

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

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
        435                 440                 445
```

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

Gly Lys
465

<210> 40
<211> 1401
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding hR198_H2

<400> 40
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag 60

gtgcagctgg tgcagtctgg cgccgaagtg aagaaaccag gcgccagcgt gaaggtgtcc 120

tgcaaggcct ctggctaccc cgtgaccagc tactacatca gctggatcag acaggcccca 180

ggccagggcc tggaatacat cggctatgtg gacatgggca acggccggac caactacaac 240

gagaagttca agggcagagc caccctgacc gtggacaaga gcaccagcac cgcctacatg 300

gaactgagca gcctgcggag cgaggacacc gccgtgtact actgcgccag agacagcaac 360

tggggcgtgg actattgggg ccagggcaca ctcgtgaccg tcagctcagc ctccaccaag 420

ggcccaagcg tcttcccccc ggcaccctcc tccaagagca cctctggcgg cacagccgcc 480

ctgggctgcc tggtcaagga ctacttcccc gaacccgtga ccgtgagctg gaactcaggc 540

gccctgacca gcggcgtgca caccttcccc gctgtcctgc agtcctcagg actctactcc 600

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 660

gtgaatcaca agcccagcaa caccaaggtg gacaagagag ttgagcccaa atcttgtgac 720

aaaactcaca catgcccacc ctgcccagca cctgaactcc tgggggggacc ctcagtcttc 780

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 840

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 900

gtggaggtgc ataatgccaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg 960

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1020

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggc 1080

cagccccggg aaccacaggt gtacaccctg cccccatccc gggaggagat gaccaagaac 1140

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1200

gagagcaatg gccagcccga gaacaactac aagaccaccc ctcccgtgct ggactccgac 1260

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac 1320

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacaccca gaagagcctc 1380

tccctgtctc ccggcaaatg a 1401

<210> 41
<211> 466

<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of hR198_H2

<400> 41

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

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

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

Glu Tyr Ile Gly Tyr Val Asp Met Gly Asn Gly Arg Thr Asn Tyr Asn
65                  70                  75                  80

Glu Lys Phe Lys Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

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

Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Gly Val Asp Tyr Trp Gly Gln
        115                 120                 125

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

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

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

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

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

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

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
225                 230                 235                 240
```

```
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
                245                 250                 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            260                 265                 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
        275                 280                 285

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

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

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
                325                 330                 335

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

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

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

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

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

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
        435                 440                 445

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

Gly Lys
465
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<210> 42
<211> 1401
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding hR198_H3

<400> 42
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag 60

gtgcagctgg tgcagtctgg cgccgaagtg aagaaaccag gcgccagcgt gaaggtgtcc 120

tgcaaggcct ctggctaccc cgtgaccgcc tactacatca gctgggtcag acaggcccca 180

ggccagggcc tggaatacgt gggctacatc gacatgggca acggccggac caactacaac 240

gcccggttta agggcagagc caccctgacc gtggacaaga gcaccagcac cgcctacatg 300

gaactgagca gcctgcggag cgaggacacc gccgtgtact actgcgccag agacagcaac 360

tggggcgtgg actattgggg ccagggcaca ctcgtgaccg tcagctcagc ctccaccaag 420

ggcccaagcg tcttcccccc ggcaccctcc tccaagagca cctctggcgg cacagccgcc 480

ctgggctgcc tggtcaagga ctacttcccc gaacccgtga ccgtgagctg gaactcaggc 540

gccctgacca gcggcgtgca caccttcccc gctgtcctgc agtcctcagg actctactcc 600

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 660

gtgaatcaca agcccagcaa caccaaggtg gacaagagag ttgagcccaa atcttgtgac 720

aaaactcaca catgcccacc ctgcccagca cctgaactcc tgggggggacc ctcagtcttc 780

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 840

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 900

gtggaggtgc ataatgccaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg 960

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1020

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggc 1080

cagccccggg aaccacaggt gtacaccctg cccccatccc gggaggagat gaccaagaac 1140

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1200

gagagcaatg gccagcccga gaacaactac aagaccaccc ctcccgtgct ggactccgac 1260

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac 1320

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacaccca gaagagcctc 1380

tccctgtctc ccggcaaatg a 1401

<210> 43
<211> 466
<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of hR198_H3

<400> 43

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

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

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

Glu Tyr Val Gly Tyr Ile Asp Met Gly Asn Gly Arg Thr Asn Tyr Asn
65                  70                  75                  80

Ala Arg Phe Lys Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

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

Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Gly Val Asp Tyr Trp Gly Gln
        115                 120                 125

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

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

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

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

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

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

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

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
                245                 250                 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            260                 265                 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
        275                 280                 285

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

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

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
325 330 335

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

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

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

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

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

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
435 440 445

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

Gly Lys
465

<210> 44
<211> 1401
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding hR198_H4

<400> 44
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag 60

gtgcagctgg tgcagtctgg cgccgaagtg aagaaaccag gcgccagcgt gaaggtgtcc 120

tgcaaggcct ctggctaccc cgtgaccgcc tactacatca gctggatcag acaggcccca 180

ggccagggcc tggaatacgt gggctacatc gacatgggca acggccggac caactacaac 240

gcccggttta agggcagagc caccctgacc gtggacaaga gcaccagcac cgcctacatg 300

gaactgagca gcctgcggag cgaggacacc gccgtgtact actgcgccag agacagcaac 360

tggggcgtgg actattgggg ccagggcaca ctcgtgaccg tcagctcagc ctccaccaag 420

ggcccaagcg tcttcccccc ggcaccctcc tccaagagca cctctggcgg cacagccgcc 480

ctgggctgcc tggtcaagga ctacttcccc gaacccgtga ccgtgagctg gaactcaggc 540

gccctgacca gcggcgtgca caccttcccc gctgtcctgc agtcctcagg actctactcc 600

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 660

gtgaatcaca agcccagcaa caccaaggtg gacaagagag ttgagcccaa atcttgtgac 720

aaaactcaca catgcccacc ctgcccagca cctgaactcc tgggggggacc ctcagtcttc 780

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 840

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 900

gtggaggtgc ataatgccaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg 960

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1020

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggc 1080

cagccccggg aaccacaggt gtacaccctg cccccatccc gggaggagat gaccaagaac 1140

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1200

gagagcaatg gccagcccga gaacaactac aagaccaccc ctcccgtgct ggactccgac 1260

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac 1320

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacaccca gaagagcctc 1380

tccctgtctc ccggcaaatg a 1401

<210> 45
<211> 466
<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of hR198_H4

<400> 45

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

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

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

Glu Tyr Val Gly Tyr Ile Asp Met Gly Asn Gly Arg Thr Asn Tyr Asn
65 70 75 80

Ala Arg Phe Lys Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Gly Val Asp Tyr Trp Gly Gln
        115                 120                 125

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

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

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

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

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

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

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

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
                245                 250                 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            260                 265                 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
        275                 280                 285

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

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

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
                325                 330                 335

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

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

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

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

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

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
435 440 445

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

Gly Lys
465

<210> 46
<211> 23
<212> DNA
<213> artificial

<220>
<223> PCR Primer Orai1 HF

<400> 46
atgcaagtcc aactggttca atc 23

<210> 47
<211> 21
<212> DNA
<213> artificial

<220>
<223> PCR Primer Orai1 CH FR

<400> 47
tgacggagcc agcgggaaga c 21

<210> 48
<211> 21
<212> DNA
<213> artificial

<220>
<223> PCR Primer M13 rev long

<400> 48
caggaaacag ctatgaccat g 21

<210> 49
<211> 31
<212> DNA
<213> artificial

<220>
<223> PCR Primer SecM Stop R

<400> 49
ctcgagttat tcattaggtg aggcgttgag g 31

<210> 50
<211> 24
<212> DNA
<213> artificial

<220>
<223> PCR Primer Orai1 Lc F

<400> 50
atggacattc aactgaccca aagc 24

<210> 51
<211> 24
<212> DNA
<213> artificial

<220>
<223> PCR Primer Orai1 CL-FR

<400> 51
gataaaaaca ctcggggccg ccac 24

<210> 52
<211> 63
<212> DNA
<213> artificial

<220>
<223> PCR Primer Orai1 HR-FLAG R

<400> 52
tcattatttg tcatcgtcat ctttatagtc gaattcttcg ccacgattaa aggatttggt 60

gac 63

<210> 53
<211> 63
<212> DNA
<213> artificial

<220>
<223> PCR Primer Orai1 CL -FLAG R

<400> 53
tcattatttg tcatcgtcat ctttatagtc gaattcttcg ccacgattaa aggatttggt 60

gac 63

<210> 54
<211> 30
<212> DNA
<213> artificial

<220>
<223> PCR Primer Myc-R

<400> 54
cagatcctcc tcagagatca gcttctgctc 30

<210> 55
<211> 705
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding hR198_LG1

<400> 55
atggtgctgc agacccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc 60

gatatccagc tgacccagag ccctagcagc ctgtctgcca gcgtgggcga cagagtgacc 120

atcacctgta gagccagcca gagcatcggc ggcagcctga gctggttcca gcagaaaccc 180

ggcaaggccc ccaagcggct gatctacagc accagcaccc tggaaagcgg cgtgcccagc 240

agattttctg gcagcggctc cggcaccgac tacaccctga caatcagcag cctgcagccc 300

gaggacttcg ccatgtacta ctgcctgcag ttcgccatct tccccgacag ctttggccag 360

ggcaccaagg tggaaatcaa gcgtacggtg gccgcccccct ccgtgttcat cttcccccccc 420

tccgacgagc agctgaagtc cggcaccgcc tccgtggtgt gcctgctgaa taacttctac 480

cccagagagg ccaaggtgca gtggaaggtg gacaacgccc tgcagtccgg gaactcccag 540

gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc 600

ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 660

ctgagctccc ccgtcaccaa gagcttcaac agggggggagt gttag 705

<210> 56
<211> 234
<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of hR198_LG1

<400> 56

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

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

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

Ile Gly Gly Ser Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro
50 55 60

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

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Met Tyr Tyr Cys Leu Gln Phe Ala
100 105 110

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

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
180 185 190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
195 200 205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 57
<211> 705
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding hR198_LG2

<400> 57
atggtgctgc agacccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc 60

gatatccagc tgacccagag ccctagcagc ctgtctgcca gcgtgggcga cagagtgacc 120

atcacctgtc acgccagcca gaacatcggc ggcagcctga gctggttcca gcagaaaccc 180

ggcaaggccc ccaagcggct gatctacctg accagcaccc tggactgggg cgtgcccagc 240

agattttctg gcagcggctc cggcaccgac tacaccctga caatcagcag cctgcagccc 300

gaggacttcg ccatgtacta ctgcctgcag ttcgccatct tccccgacag ctttggccag 360

ggcaccaagg tggaaatcaa gcgtacggtg gccgcccccc ccgtgttcat cttcccccccc 420

tccgacgagc agctgaagtc cggcaccgcc tccgtggtgt gcctgctgaa taacttctac 480

cccagagagg ccaaggtgca gtggaaggtg gacaacgccc tgcagtccgg gaactcccag 540

gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc 600

ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 660

ctgagctccc ccgtcaccaa gagcttcaac aggggggagt gttag 705

<210> 58
<211> 234
<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of hR198_LG2

<400> 58

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

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

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys His Ala Ser Gln Asn
35 40 45

Ile Gly Gly Ser Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro
50 55 60

Lys Arg Leu Ile Tyr Leu Thr Ser Thr Leu Asp Trp Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Met Tyr Tyr Cys Leu Gln Phe Ala
100 105 110

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

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
180 185 190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
195 200 205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 59
<211> 705
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding hR198_LG3

<400> 59
atggtgctgc agacccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc 60

gatatccagc tgacccagag ccctagcagc ctgtctgcca gcgtgggcga cagagtgacc 120

atcacctgtc acgccagccg gaacatcggc ggcagcctga gctggttcca gcagaaaccc 180

ggcaaggccc ccaagcggct gatctacctg accagcagcc tggactgggg cgtgcccagc 240

agattttctg gcagcggctc cggcaccgac tacaccctga caatcagcag cctgcagccc 300

gaggacttcg ccatgtacta ctgcctgcag ttcgccatct tccccgacag ctttggccag 360

ggcaccaagg tggaaatcaa gcgtacggtg gccgcccccct ccgtgttcat cttcccccccc 420

tccgacgagc agctgaagtc cggcaccgcc tccgtggtgt gcctgctgaa taacttctac 480

cccagagagg ccaaggtgca gtggaaggtg gacaacgccc tgcagtccgg gaactcccag 540

gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc 600

ctgagcaaag ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 660

ctgagctccc ccgtcaccaa gagcttcaac aggggggagt gttag 705

<210> 60
<211> 234
<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of hR198_LG3

<400> 60

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

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

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys His Ala Ser Arg Asn
35 40 45

Ile Gly Gly Ser Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro
50 55 60

Lys Arg Leu Ile Tyr Leu Thr Ser Ser Leu Asp Trp Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Met Tyr Tyr Cys Leu Gln Phe Ala
100 105 110

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

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
180 185 190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
195 200 205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 61
<211> 1401
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding hR198_HG1

<400> 61
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag 60

gtgcagctgg tgcagtctgg cgccgaagtg aagaaaccag gcgccagcgt gaaggtgtcc 120

tgcaaggcct ctggctaccc cgtgaccgcc tactacatca gctgggtcag acaggcccca 180

ggccagggcc tggaatacgt gggctacatc gacatgggca acggccggac cgactacaac 240

gcccggttta agggcagagc caccctgacc gtggacaaga gcaccagcac cgcctacatg 300

gaactgagca gcctgcggag cgaggacacc gccgtgtact actgcgccag agacagcaac 360

tggggcgccg actattgggg ccagggcaca ctcgtgaccg tcagctcagc ctccaccaag 420

ggcccaagcg tcttccccct ggcaccctcc tccaagagca cctctggcgg cacagccgcc 480

ctgggctgcc tggtcaagga ctacttcccc gaacccgtga ccgtgagctg gaactcaggc 540

gccctgacca gcggcgtgca caccttcccc gctgtcctgc agtcctcagg actctactcc 600

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 660

gtgaatcaca agcccagcaa caccaaggtg gacaagagag ttgagcccaa atcttgtgac 720

aaaactcaca catgcccacc ctgcccagca cctgaactcc tgggggggacc ctcagtcttc 780

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 840

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 900

gtggaggtgc ataatgccaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg 960

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1020

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggc 1080

cagccccggg aaccacaggt gtacaccctg cccccatccc gggaggagat gaccaagaac 1140

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1200

gagagcaatg gccagcccga gaacaactac aagaccaccc ctcccgtgct ggactccgac 1260

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac 1320

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacaccca gaagagcctc 1380

tccctgtctc ccggcaaatg a 1401

<210> 62
<211> 466
<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of hR198_HG1

<400> 62

Met Lys His Leu Trp Phe Phe Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

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

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

Glu Tyr Val Gly Tyr Ile Asp Met Gly Asn Gly Arg Thr Asp Tyr Asn
65 70 75 80

Ala Arg Phe Lys Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Gly Ala Asp Tyr Trp Gly Gln
        115                 120                 125

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

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

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

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

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

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

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

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
                245                 250                 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            260                 265                 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
        275                 280                 285

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

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

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
                325                 330                 335

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

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

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

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

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

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
435 440 445

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

Gly Lys
465

<210> 63
<211> 1401
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding hR198_HG2

<400> 63
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag 60

gtgcagctgg tgcagtctgg cgccgaagtg aagaaaccag gcgccagcgt gaaggtgtcc 120

tgcaaggcct ctggctaccc catcaccgcc tactacatca gctgggtcag acaggcccca 180

ggccagggcc tggaatacgt gggctacatc gacatgggca acggccggac cgactacaac 240

ggccggttta agggcagagc caccctgacc gtggacaaga gcaccagcac cgcctacatg 300

gaactgagca gcctgcggag cgaggacacc gccgtgtact actgcgccag agacagcaac 360

tggggcgccg actattgggg ccagggcaca ctcgtgaccg tcagctcagc ctccaccaag 420

ggcccaagcg tcttcccccct ggcaccctcc tccaagagca cctctggcgg cacagccgcc 480

ctgggctgcc tggtcaagga ctacttcccc gaacccgtga ccgtgagctg gaactcaggc 540

gccctgacca gcggcgtgca caccttcccc gctgtcctgc agtcctcagg actctactcc 600

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 660

gtgaatcaca agcccagcaa caccaaggtg gacaagagag ttgagcccaa atcttgtgac 720

aaaactcaca catgcccacc ctgcccagca cctgaactcc tgggggggacc ctcagtcttc 780

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 840

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 900

gtggaggtgc ataatgccaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg 960

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1020

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggc 1080

cagccccggg aaccacaggt gtacaccctg cccccatccc gggaggagat gaccaagaac 1140

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1200

gagagcaatg gccagcccga gaacaactac aagaccaccc ctcccgtgct ggactccgac 1260

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac 1320

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacaccca gaagagcctc 1380

tccctgtctc ccggcaaatg a 1401

<210> 64
<211> 466
<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of hR198_HG2

<400> 64

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

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

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

Glu Tyr Val Gly Tyr Ile Asp Met Gly Asn Gly Arg Thr Asp Tyr Asn
65 70 75 80

Gly Arg Phe Lys Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Gly Ala Asp Tyr Trp Gly Gln
115 120 125

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

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

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

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

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

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

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

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
                245                 250                 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            260                 265                 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
        275                 280                 285

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

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

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
                325                 330                 335

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

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

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

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

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

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
            420                 425                 430
```

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
435 440 445

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

Gly Lys
465

<210> 65
<211> 1401
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding hR198_HG3

<400> 65
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag 60

gtgcagctgg tgcagtctgg cgccgaagtg aagaaaccag gcgccagcgt gaaggtgtcc 120

tgcaaggcct ctggctaccc catcaccgcc tactacatca gctgggtcag acaggcccca 180

ggccagggcc tggaatacgt gggctacatc gacatgggca acggccggac cgactacaac 240

atgcggttta agggcagagc caccctgacc gtggacaaga gcaccagcac cgcctacatg 300

gaactgagca gcctgcggag cgaggacacc gccgtgtact actgcgccag agacagcaac 360

tggggcgccg actattgggg ccagggcaca ctcgtgaccg tcagctcagc ctccaccaag 420

ggcccaagcg tcttcccccc ggcaccctcc tccaagagca cctctggcgg cacagccgcc 480

ctgggctgcc tggtcaagga ctacttcccc gaacccgtga ccgtgagctg gaactcaggc 540

gccctgacca gcggcgtgca caccttcccc gctgtcctgc agtcctcagg actctactcc 600

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 660

gtgaatcaca agcccagcaa caccaaggtg gacaagagag ttgagcccaa atcttgtgac 720

aaaactcaca catgcccacc ctgcccagca cctgaactcc tgggggggacc ctcagtcttc 780

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 840

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 900

gtggaggtgc ataatgccaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg 960

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1020

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggc 1080

cagccccggg aaccacaggt gtacaccctg cccccatccc gggaggagat gaccaagaac 1140

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1200

gagagcaatg gccagcccga gaacaactac aagaccaccc ctcccgtgct ggactccgac 1260

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac 1320

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacaccca gaagagcctc 1380

tccctgtctc ccggcaaatg a 1401

<210> 66
<211> 466
<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of hR198_HG3

<400> 66

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

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

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

Glu Tyr Val Gly Tyr Ile Asp Met Gly Asn Gly Arg Thr Asp Tyr Asn
65                  70                  75                  80

Met Arg Phe Lys Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

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

Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Gly Ala Asp Tyr Trp Gly Gln
        115                 120                 125

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

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

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

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

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

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
    210                 215                 220
```

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

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
245 250 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
260 265 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
275 280 285

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

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

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
325 330 335

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

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

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

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

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

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
435 440 445

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

Gly Lys
465

<210> 67
<211> 1401
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding hR198_H4-LALA

<400> 67
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag 60

gtgcagctgg tgcagtctgg cgccgaagtg aagaaaccag gcgccagcgt gaaggtgtcc 120

tgcaaggcct ctggctaccc cgtgaccgcc tactacatca gctggatcag acaggcccca 180

ggccagggcc tggaatacgt gggctacatc gacatgggca acggccggac caactacaac 240

gcccggttta agggcagagc caccctgacc gtggacaaga gcaccagcac cgcctacatg 300

gaactgagca gcctgcggag cgaggacacc gccgtgtact actgcgccag agacagcaac 360

tggggcgtgg actattgggg ccagggcaca ctcgtgaccg tcagctcagc ctccaccaag 420

ggcccaagcg tcttccccct ggcaccctcc tccaagagca cctctggcgg cacagccgcc 480

ctgggctgcc tggtcaagga ctacttcccc gaacccgtga ccgtgagctg gaactcaggc 540

gccctgacca gcggcgtgca caccttcccc gctgtcctgc agtcctcagg actctactcc 600

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 660

gtgaatcaca agcccagcaa caccaaggtg gacaagagag ttgagcccaa atcttgtgac 720

aaaactcaca catgcccacc ctgcccagca cctgaagccg cgggggggacc ctcagtcttc 780

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 840

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 900

gtggaggtgc ataatgccaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg 960

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1020

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggc 1080

cagccccggg aaccacaggt gtacaccctg cccccatccc gggaggagat gaccaagaac 1140

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1200

gagagcaatg gccagcccga gaacaactac aagaccaccc ctcccgtgct ggactccgac 1260

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac 1320

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacaccca gaagagcctc 1380

tccctgtctc ccggcaaatg a 1401

<210> 68
<211> 466
<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of hR198_H4-LALA

<400> 68

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

```
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

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

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

Glu Tyr Val Gly Tyr Ile Asp Met Gly Asn Gly Arg Thr Asn Tyr Asn
65                  70                  75                  80

Ala Arg Phe Lys Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

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

Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Gly Val Asp Tyr Trp Gly Gln
        115                 120                 125

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

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

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

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

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

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

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

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
                245                 250                 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            260                 265                 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
        275                 280                 285
```

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

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

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
325 330 335

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

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

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

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

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

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
435 440 445

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

Gly Lys
465

<210> 69
<211> 1401
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding hR198_HG1-LALA

<400> 69
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag 60

gtgcagctgg tgcagtctgg cgccgaagtg aagaaaccag gcgccagcgt gaaggtgtcc 120

tgcaaggcct ctggctaccc cgtgaccgcc tactacatca gctgggtcag acaggcccca 180

ggccagggcc tggaatacgt gggctacatc gacatgggca acggccggac cgactacaac 240

gcccggttta agggcagagc caccctgacc gtggacaaga gcaccagcac cgcctacatg 300

gaactgagca gcctgcggag cgaggacacc gccgtgtact actgcgccag agacagcaac 360

tggggcgccg actattgggg ccagggcaca ctcgtgaccg tcagctcagc ctccaccaag 420

ggcccaagcg tcttcccccc ggcaccctcc tccaagagca cctctggcgg cacagccgcc 480

ctgggctgcc tggtcaagga ctacttcccc gaacccgtga ccgtgagctg gaactcaggc 540

gccctgacca gcggcgtgca caccttcccc gctgtcctgc agtcctcagg actctactcc 600

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 660

gtgaatcaca agcccagcaa caccaaggtg gacaagagag ttgagcccaa atcttgtgac 720

aaaactcaca catgcccacc ctgcccagca cctgaagccg cgggggggacc ctcagtcttc 780

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 840

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 900

gtggaggtgc ataatgccaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg 960

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1020

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggc 1080

cagccccggg aaccacaggt gtacaccctg cccccatccc gggaggagat gaccaagaac 1140

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1200

gagagcaatg gccagcccga gaacaactac aagaccaccc ctcccgtgct ggactccgac 1260

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac 1320

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacaccca gaagagcctc 1380

tccctgtctc ccggcaaatg a 1401

<210> 70
<211> 466
<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of hR198_HG1-LALA

<400> 70

Met Lys His Leu Trp Phe Phe Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

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

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

Glu Tyr Val Gly Tyr Ile Asp Met Gly Asn Gly Arg Thr Asp Tyr Asn
65 70 75 80

```
Ala Arg Phe Lys Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

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

Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Gly Ala Asp Tyr Trp Gly Gln
        115                 120                 125

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

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

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

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

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

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

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

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
                245                 250                 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            260                 265                 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
        275                 280                 285

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

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

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
                325                 330                 335

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

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

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

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

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

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
435 440 445

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

Gly Lys
465

<210> 71
<211> 1118
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding Human Heavy Chain Secretory Signal and Human IgG2 Constant Region

<400> 71
gcctccggac tctagagcca ccatgaaaca cctgtggttc ttcctcctgc tggtggcagc 60

tcccagatgg gtgctgagcc aggtgcaatt gtgcaggcgg ttagctcagc cagcaccaag 120

ggcccttccg tgttccctct ggccccttgt agccgttcca ccagcgagtc caccgccgcc 180

cttggctgtc tggtgaagga ctacttccct gagcctgtga ccgtgagctg gaactccgga 240

gcccttacca gcggcgtgca caccttccct gccgtgctgc agtccagcgg cctttactcc 300

ctgagctccg tggtgaccgt gcctagctcc aacttcggca cccaaaccta cacctgtaac 360

gtggaccaca agcctagcaa caccaaggtg gacaagaccg tggagcgtaa gtgttgtgtg 420

gagtgtcctc cttgtcctgc ccctcctgtg gccggacctt ccgtgttcct tttccctcct 480

aagcctaagg acaccctgat gatcagccgt acccctgagg tgacctgtgt ggtggtggac 540

gtgtcccacg aggaccctga ggtgcagttc aactggtacg tggacggcgt ggaggtgcac 600

aacgccaaga ccaagcctcg tgaggagcaa ttcaacagca ccttccgtgt ggtgtccgtg 660

cttaccgtgg tgcaccaaga ctggctgaac ggcaaggagt acaagtgtaa ggtgagcaac 720

aagggacttc ctgcccctat cgagaagacc atctccaaga ccaagggcca acctcgtgag 780

cctcaagtgt acacccttcc tcctagccgt gaggagatga ccaagaacca agtgtccctt 840

acctgtctgg tgaagggctt ctaccctagc gacatcgccg tggagtggga gtccaacgga 900

caacctgaga acaactacaa gaccacccct cctatgcttg acagcgacgg ctccttcttc 960

ctgtacagca agctgaccgt ggacaagtcc cgttggcaac aaggcaacgt gttcagctgt 1020

tccgtgatgc acgaggccct gcacaaccac tacacccaaa agagcctttc cctgagccct 1080

ggaaagtgat atcgggcccg tttaaacggg ggaggcta 1118

<210> 72
<211> 1395
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding Heavy Chain of 2C1.1

<400> 72
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag 60

gtgcagctgc agcagtgggg agccggcctg ctgaagccca gcgagacact gagcctgacc 120

tgcgctgtgt acggaggcag cttcagcggc tactactggt cctggatccg gcagcccccc 180

ggcaagggcc tggaatggat cggcgagatc gaccacagcg gcagcaccaa ctacaacccc 240

gccctgaagt cccggctgac catcagcgtg gacaccagca agaaccagtt cagcctgaag 300

ctgagcagcg tgacagccgc cgacaccgcc gtgtactact gtgccagagc cggcagcggc 360

ggctacgagg attggttcga tccttggggc cagggcaccc tggtgaccgt cagctcagcc 420

agcaccaagg gcccttccgt gttccctctg gccccttgta gccgttccac cagcgagtcc 480

accgccgccc ttggctgtct ggtgaaggac tacttccctg agcctgtgac cgtgagctgg 540

aactccggag cccttaccag cggcgtgcac accttccctg ccgtgctgca gtccagcggc 600

ctttactccc tgagctccgt ggtgaccgtg cctagctcca acttcggcac ccaaacctac 660

acctgtaacg tggaccacaa gcctagcaac accaaggtgg acaagaccgt ggagcgtaag 720

tgttgtgtgg agtgtcctcc ttgtcctgcc cctcctgtgg ccggaccttc cgtgttcctt 780

ttccctccta agcctaagga caccctgatg atcagccgta cccctgaggt gacctgtgtg 840

gtggtggacg tgtcccacga ggaccctgag gtgcagttca actggtacgt ggacggcgtg 900

gaggtgcaca acgccaagac caagcctcgt gaggagcaat tcaacagcac cttccgtgtg 960

gtgtccgtgc ttaccgtggt gcaccaagac tggctgaacg gcaaggagta caagtgtaag 1020

gtgagcaaca agggacttcc tgcccctatc gagaagacca tctccaagac caagggccaa 1080

cctcgtgagc ctcaagtgta cacccttcct cctagccgtg aggagatgac caagaaccaa 1140

gtgtccctta cctgtctggt gaagggcttc taccctagcg acatcgccgt ggagtgggag 1200

tccaacggac aacctgagaa caactacaag accacccctc ctatgcttga cagcgacggc 1260

tccttcttcc tgtacagcaa gctgaccgtg gacaagtccc gttggcaaca aggcaacgtg 1320

ttcagctgtt ccgtgatgca cgaggccctg cacaaccact acacccaaaa gagcctttcc 1380

ctgagccctg gaaag 1395

<210> 73
<211> 465
<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of Heavy Chain of 2C1.1

<400> 73

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys
20 25 30

Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe
35 40 45

Ser Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
50 55 60

Glu Trp Ile Gly Glu Ile Asp His Ser Gly Ser Thr Asn Tyr Asn Pro
65 70 75 80

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

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

Tyr Cys Ala Arg Ala Gly Ser Gly Gly Tyr Glu Asp Trp Phe Asp Pro
115 120 125

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

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
145 150 155 160

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

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

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

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

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

Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
                245                 250                 255

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
            260                 265                 270

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
        275                 280                 285

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

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

Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu
                325                 330                 335

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

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

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

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

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu
                405                 410                 415

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

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
        435                 440                 445

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
    450                 455                 460

Lys
465
```

<210> 74
<211> 739
<212> DNA

<213> artificial

<220>
<223> Nucleotide Sequence coding Light Chain of 2C1.1

<400> 74
atggtgctgc agacccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc 60

cagtccgtgc tgacccagcc tccttccgtg tctggcgccc ctggccagag agtgaccatc 120

agctgtaccg gcagcagcag caacatcgga gccggctaca acgtgcactg gtatcagcag 180

ttcccccgga ccgaccccaa gctgctgatc tacgtgtaca acatccggcc cagcggcgtg 240

cccgaccggt tttctggcag cagaagcggc acaagcgcca gcctggccat caccggcctg 300

cagaccgagg acgaggccga ctactactgc cagagctacg acagcagcct gagcggcgtg 360

gtgttcggcg gaggcaccaa gctgacagtg ctgggccagc ccaaggccaa ccccaccgtg 420

accctgttcc ccccaagcag cgaggaactg caggccaaca aggccaccct ggtgtgcctg 480

atcagcgact tctaccctgg cgccgtgaca gtggcctgga aggccgatgg atctcccgtg 540

aaggccggcg tggaaaccac caagcccagc aagcagagca acaacaaata cgccgccagc 600

agctacctga gcctgacccc cgagcagtgg aagtcccacc ggtcctacag ctgccaggtg 660

acacacgagg gcagcaccgt ggaaaagacc gtggccccca ccgagtgcag ctaggggccc 720

gtttaaacgg gggaggcta 739

<210> 75
<211> 237
<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of Light Chain of 2C1.1

<400> 75

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

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

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

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

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

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

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

100 105 110

Tyr Asp Ser Ser Leu Ser Gly Val Val Phe Gly Gly Gly Thr Lys Leu
115 120 125

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

Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu
145 150 155 160

Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp
165 170 175

Gly Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln
180 185 190

Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu
195 200 205

Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly
210 215 220

Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
225 230 235

<210> 76
<211> 1395
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding Heavy Chain of 5H3.1

<400> 76
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag 60

gtgcagctgg tgcagtctgg cgccgaagtg aagaaacctg gcgctagcgt gaaggtgtcc 120

tgcaaggcca gcggctacac cttcaccgac tactacatga actgggtgcg ccaggctcca 180

ggacagggcc tggaatggat gggctggatc aaccccaaca gcggcggcac caaatacgcc 240

cagaaattcc agggcagagt gaccatgacc cgggacacca gcatccggac cgcctacatg 300

gaactgagcc ggctgagaag cgacgacacc gccgtgtact actgcgccag agagtacggc 360

ggcaacagcg attggttcga cccctggggc cagggcaccc tggtgaccgt cagctcagcc 420

agcaccaagg gcccttccgt gttccctctg gcccccttgta gccgttccac cagcgagtcc 480

accgccgccc ttggctgtct ggtgaaggac tacttccctg agcctgtgac cgtgagctgg 540

aactccggag cccttaccag cggcgtgcac accttccctg ccgtgctgca gtccagcggc 600

ctttactccc tgagctccgt ggtgaccgtg cctagctcca acttcggcac ccaaacctac 660

acctgtaacg tggaccacaa gcctagcaac accaaggtgg acaagaccgt ggagcgtaag 720

tgttgtgtgg agtgtcctcc ttgtcctgcc cctcctgtgg ccggaccttc cgtgttcctt 780

ttccctccta agcctaagga caccctgatg atcagccgta cccctgaggt gacctgtgtg 840

gtggtggacg tgtcccacga ggaccctgag gtgcagttca actggtacgt ggacggcgtg 900

gaggtgcaca acgccaagac caagcctcgt gaggagcaat tcaacagcac cttccgtgtg 960

gtgtccgtgc ttaccgtggt gcaccaagac tggctgaacg gcaaggagta caagtgtaag 1020

gtgagcaaca agggacttcc tgcccctatc gagaagacca tctccaagac caagggccaa 1080

cctcgtgagc ctcaagtgta cacccttcct cctagccgtg aggagatgac caagaaccaa 1140

gtgtccctta cctgtctggt gaagggcttc taccctagcg acatcgccgt ggagtgggag 1200

tccaacggac aacctgagaa caactacaag accacccctc ctatgcttga cagcgacggc 1260

tccttcttcc tgtacagcaa gctgaccgtg gacaagtccc gttggcaaca aggcaacgtg 1320

ttcagctgtt ccgtgatgca cgaggccctg cacaaccact acacccaaaa gagcctttcc 1380

ctgagccctg gaaag 1395

<210> 77
<211> 465
<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of Heavy Chain of 5H3.1

<400> 77

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr Asp Tyr Tyr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Lys Tyr Ala
65 70 75 80

Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Arg
85 90 95

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

Tyr Tyr Cys Ala Arg Glu Tyr Gly Gly Asn Ser Asp Trp Phe Asp Pro
115 120 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly

130 135 140

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
145 150 155 160

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

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

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

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

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

Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
245 250 255

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
260 265 270

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
275 280 285

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

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

Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu
325 330 335

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

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

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

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

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu

405 410 415

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

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
435 440 445

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
450 455 460

Lys
465

<210> 78
<211> 742
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding Light Chain of 5H3.1

<400> 78
atggtgctgc agacccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc 60

cagtccgtgc tgacccagcc tccttccgtg tctggcgccc ctggccagag agtgaccatc 120

agctgtaccg gcagcagcag caacatcgga gctggatacg acgtgcactg gtatcagcag 180

ctgcccggca ccgcccccaa gctgctgatc tacggcaaca gcaaccggcc cagcggcgtg 240

cccgatagat tcagcggcag caagagcggc accagcgcca gcctggccat taccggactg 300

caggccgagg acgaggccga ctactactgc cagagctacg acaaccggct gagcgacagc 360

gtggtgatcg gcggaggcac caagctggcc gtgcagggac agcccaaggc caaccccacc 420

gtgaccctgt tccccccaag cagcgaggaa ctgcaggcca acaaggccac cctggtgtgc 480

ctgatcagcg acttctaccc tggcgccgtg acagtggcct ggaaggccga tggatctccc 540

gtgaaggccg gcgtggaaac caccaagccc agcaagcaga gcaacaacaa atacgccgcc 600

agcagctacc tgagcctgac ccccgagcag tggaagtccc accggtccta cagctgccag 660

gtgacacacg agggcagcac cgtggaaaag accgtggccc ccaccgagtg cagctagggg 720

cccgtttaaa cgggggaggc ta 742

<210> 79
<211> 238
<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of Light Chain of 5H3.1

<400> 79

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

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

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

Ile Gly Ala Gly Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr
50 55 60

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

Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala
85 90 95

Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser
100 105 110

Tyr Asp Asn Arg Leu Ser Asp Ser Val Val Ile Gly Gly Gly Thr Lys
115 120 125

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

Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys
145 150 155 160

Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala
165 170 175

Asp Gly Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys
180 185 190

Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro
195 200 205

Glu Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu
210 215 220

Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
225 230 235

<210> 80
<211> 1433
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding Heavy Chain of 10F8

<400> 80
ccagcctccg gactctagag ccaccatgaa gcacctgtgg ttctttctgc tgctggtggc 60

cgctcccaga tgggtgctgt ctcaggtgca gctgcagcag tctggcgccg aactcgtgcg 120

gcctggaagc agcgtgaaga tcagctgcaa ggccagcggc tacgccttcc ggtcctactg 180

gatgaactgg gtcaagcaga ggccaggcca gggcctggaa tggatcggcc acatctatcc 240

cggcgacggc gacaccaact acaacggcaa gttcaagggc aaggccaccc tgaccgccga 300

caagagcagc agcacagcct acatgcagct gtccagcctg accagcgagg acagcgccgt 360

gtacctgtgt ggcagaggcg gcacaaccgt ggtggtggat tattggggcc agggcaccac 420

actgaccgtg tccagcgcca agaccacccc cccatctgtg tatcctctgg cccctggatc 480

tgccgcccag accaacagca tggtcaccct gggctgcctc gtgaagggct acttccctga 540

gcctgtgacc gtgacctgga acagcggctc tctgtctagc ggcgtgcaca cctttccagc 600

cgtgctgcag agcgacctgt acaccctgag cagctccgtg accgtgccta gcagcacctg 660

gcctagcgag acagtgacct gcaacgtggc ccaccctgcc agctctacca aggtggacaa 720

gaaaatcgtg ccccgggact gcggctgcaa gccctgtatc tgtaccgtgc ccgaggtgtc 780

ctccgtgttc atcttcccac ccaagcccaa ggacgtgctg accatcaccc tgacacccaa 840

agtgacatgt gtggtggtgg acatcagcaa ggacgacccc gaggtgcagt tcagttggtt 900

cgtggacgac gtggaagtgc acacagccca gacccagccc agagaggaac agttcaacag 960

caccttcaga agcgtgtccg agctgcccat catgcaccag gactggctga acggcaaaga 1020

attcaagtgc agagtgaaca gcgccgcctt ccctgccccc atcgagaaaa ccatctccaa 1080

gaccaagggc agacccaagg ccccccaggt gtacacaatc cccccaccca aagaacagat 1140

ggccaaggac aaggtgtccc tgacctgcat gatcaccgat ttcttcccag aggacatcac 1200

cgtggaatgg cagtggaacg gccagcccgc cgagaactac aagaacaccc agcctatcat 1260

ggacaccgac ggcagctact tcgtgtacag caagctgaac gtgcagaagt ccaactggga 1320

ggccggcaac accttcacct gtagcgtgct gcacgagggc ctgcacaatc accacaccga 1380

gaagtccctg tcccacagcc ccggcaaatg agtttaaacg ggggaggcta act 1433

<210> 81
<211> 461
<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of Heavy Chain of 10F8

<400> 81

Met Lys His Leu Trp Phe Phe Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe
35 40 45

```
Arg Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
    50                  55                  60

Glu Trp Ile Gly His Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn
65                  70                  75                  80

Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
                85                  90                  95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
            100                 105                 110

Tyr Leu Cys Gly Arg Gly Gly Thr Thr Val Val Val Asp Tyr Trp Gly
        115                 120                 125

Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser
    130                 135                 140

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

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

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

Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro
        195                 200                 205

Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro
    210                 215                 220

Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly
225                 230                 235                 240

Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile
                245                 250                 255

Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys
            260                 265                 270

Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln
        275                 280                 285

Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln
    290                 295                 300

Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu
305                 310                 315                 320
```

Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg
325 330 335

Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
340 345 350

Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro
355 360 365

Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr
370 375 380

Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln
385 390 395 400

Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly
405 410 415

Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu
420 425 430

Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn
435 440 445

His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
450 455 460

<210> 82
<211> 770
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding Light Chain of 10F8

<400> 82
ccagcctccg gactctagag ccaccatggt gctgcagacc caggtgttca tcagcctgct 60

gctgtggatc agcggcgcct acggcgacat cgtgatgagc cagagcccta gcagcctggc 120

cgtgtctgcc ggcgagaaag tgaccatgag ctgcaagagc agccagtccc tgctgaacag 180

ccggacccgg aagaactacc tggcctggta tcagcagaag cccggccagt cccccaagct 240

gctgatctac tgggccagca ccagagaaag cggcgtgccc gatagattca ccggcagcgg 300

ctctggcacc gacttcaccc tgacaatcag cagcgtgcag gccgaggacc tggctgtgta 360

ctactgcaag cagagctaca acctgccctg gaccttcggc ggaggcacca agctggaaat 420

caagagagcc gacgccgctc ccaccgtgtc catctttcca cctagcagcg agcagctgac 480

cagcggcgga gctagcgtcg tgtgcttcct gaacaacttc taccccaagg acatcaacgt 540

gaagtggaag atcgacggca gcgagcggca gaacggcgtg ctgaatagct ggaccgacca 600

ggacagcaag gactccacct acagcatgtc cagcaccctg accctgacca aggacgagta 660

cgagcggcac aacagctaca catgcgaggc cacccacaag accagcacct cccccatcgt 720

gaagtccttc aaccggaacg agtgctgagt ttaaacgggg gaggctaact 770

<210> 83
<211> 240
<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of Light Chain of 10F8

<400> 83

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala
20 25 30

Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
35 40 45

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

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65 70 75 80

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

Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
100 105 110

Tyr Cys Lys Gln Ser Tyr Asn Leu Pro Trp Thr Phe Gly Gly Gly Thr
115 120 125

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

Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys
145 150 155 160

Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile
165 170 175

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

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

Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His

210 215 220

Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
225 230 235 240

<210> 84
<211> 1436
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding Heavy Chain of 14F74

<400> 84
ccagcctccg gactctagag ccaccatgaa gcacctgtgg ttctttctgc tgctggtggc 60

cgctcccaga tgggtgctgt ctcaggtgca gctgcagcag tctggcgccg aactcgtgcg 120

gcctggaagc agcgtgaaga tcagctgcaa ggccagcggc tacgccttca gcagctactg 180

gatgaactgg gtcaagcagc ggccaggcca gggcctggaa tggatcggcc atatctatcc 240

cggcgacggc gacaccaact acaacggcaa gttcaagggc aaggccaccc tgaccgccga 300

caagagcagc agcacagcct acatgcagct gagcggcctg accagcgagg acagcgccgt 360

gtacttctgc gccagaagcg gcagactgag attcgccatg gactactggg gccagggcac 420

cagcgtgaca gtgtctagcg ccaagaccac ccccccccagc gtgtaccctc tggctcctgg 480

atctgccgcc cagaccaaca gcatggtcac cctgggctgc ctcgtgaagg gctacttccc 540

tgagcctgtg accgtgacct ggaacagcgg ctctctgtct agcggcgtgc acacctttcc 600

agccgtgctg cagagcgacc tgtacaccct gagcagctcc gtgaccgtgc ctagcagcac 660

ctggcctagc gagacagtga cctgcaacgt ggcccaccct gccagctcta ccaaggtgga 720

caagaaaatc gtgccccggg actgcggctg caagccctgt atctgtaccg tgcccgaggt 780

gtccagcgtg ttcatcttcc cacccaagcc caaggacgtg ctgaccatca ccctgacacc 840

caaagtgacc tgtgtggtgg tggacatcag caaggacgac cccgaggtgc agttcagttg 900

gttcgtggac gacgtggaag tgcacacagc ccagacccag cccagagagg aacagttcaa 960

cagcaccttc agaagcgtgt ccgagctgcc catcatgcac caggactggc tgaacggcaa 1020

agaattcaag tgcagagtga acagcgccgc cttccctgcc cccatcgaga aaaccatctc 1080

caagaccaag ggcagaccca aggcccctca ggtgtacaca atccccccac ccaaagaaca 1140

gatggccaag gacaaggtgt ccctgacctg catgatcacc gatttcttcc cagaggacat 1200

caccgtggaa tggcagtgga acggccagcc cgccgagaac tacaagaaca cccagcctat 1260

catggacacc gacggcagct acttcgtgta cagcaagctg aacgtgcaga agtccaactg 1320

ggaggccggc aacaccttca cctgtagcgt gctgcacgag ggcctgcaca atcaccacac 1380

cgagaagtcc ctgtcccaca gccccggcaa atgagtttaa acgggggagg ctaact 1436

<210> 85
<211> 462
<212> PRT

<213> artificial

<220>
<223> Amino Acid Sequence of Heavy Chain of 14F74

<400> 85

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

Val Leu Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
            20                  25                  30

Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe
        35                  40                  45

Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
    50                  55                  60

Glu Trp Ile Gly His Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn
65                  70                  75                  80

Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
                85                  90                  95

Thr Ala Tyr Met Gln Leu Ser Gly Leu Thr Ser Glu Asp Ser Ala Val
            100                 105                 110

Tyr Phe Cys Ala Arg Ser Gly Arg Leu Arg Phe Ala Met Asp Tyr Trp
        115                 120                 125

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

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

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

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

Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val
        195                 200                 205

Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His
    210                 215                 220

Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys
225                 230                 235                 240

Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe
```

245 250 255

Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro
260 265 270

Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val
275 280 285

Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr
290 295 300

Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu
305 310 315 320

Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys
325 330 335

Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser
340 345 350

Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro
355 360 365

Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile
370 375 380

Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly
385 390 395 400

Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp
405 410 415

Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp
420 425 430

Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His
435 440 445

Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
450 455 460

<210> 86
<211> 767
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding Light Chain of 14F74

<400> 86
ccagcctccg gactctagag ccaccatggt gctgcagacc caggtgttca tcagcctgct 60

gctgtggatc agcggcgcct acggcgacat cgtgatgagc cagagcccta gcagcctggc 120

cgtgtctgcc ggcgagaaag tgaccatgag ctgcaagagc agccagtccc tgctgaacag 180

ccggacccgg aagaactacc tggcctggta tcagcagaag cccggccagt cccccaagct 240

gctgatctac tgggccagca ccagagaaag cggcgtgccc gatagattca ccggcagcgg 300

ctctggcacc gacttcaccc tgacaatcag cagcgtgcag gccgaggacc tggctgtgta 360

ctactgcaag cagagctaca acctgcggac cttcggcgga ggcaccaagc tggaaatcca 420

gagagccgac gccgctccca ccgtgtccat ctttccacct agcagcgagc agctgaccag 480

cggcggagct agcgtcgtgt gcttcctgaa caacttctac cccaaggaca tcaacgtgaa 540

gtggaagatc gacggcagcg agcggcagaa cggcgtgctg aatagctgga ccgaccagga 600

cagcaaggac tccacctaca gcatgtccag caccctgacc ctgaccaagg acgagtacga 660

gcggcacaac agctacacat gcgaggccac ccacaagacc agcacctccc ccatcgtgaa 720

gtccttcaac cggaacgagt gctgagttta aacgggggag gctaact 767

<210> 87
<211> 239
<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of Light Chain of 14F74

<400> 87

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala
20 25 30

Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
35 40 45

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

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65 70 75 80

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

Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
100 105 110

Tyr Cys Lys Gln Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys
115 120 125

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

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

Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp
165 170 175

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

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

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

Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
225 230 235

<210> 88
<211> 1436
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding Heavy Chain of 17F6

<400> 88
ccagcctccg gactctagag ccaccatgaa gcacctgtgg ttctttctgc tgctggtggc 60

cgctcccaga tgggtgctgt ctcaggtgca gctgcagcag tctggcgccg aactcgtgcg 120

gcctggaagc agcgtgaaga tcagctgcaa ggccagcggc tacgccttca gcagctactg 180

gatgaactgg gtcaagcagc ggccaggcca gggcctggaa tggatcggcc atatctatcc 240

cggcgacgcc gacaccaact acaacggcaa gttcaagggc aaggccaccc tgaccgccga 300

caagagcagc agcacagcct acatgcacct gtccagcctg accagcgagg acagcgccgt 360

gtacttctgc agccggcagc tgggcttcag atacgccatg gactattggg gccagggcac 420

cagcgtgacc gtgtctagcg ccaagaccac ccccccctagc gtgtaccctc tggccccctgg 480

atctgccgcc cagaccaaca gcatggtcac cctgggctgc ctcgtgaagg gctacttccc 540

tgagcctgtg accgtgacct ggaacagcgg ctctctgtct agcggcgtgc acacctttcc 600

agccgtgctg cagagcgacc tgtacaccct gagcagctcc gtgacagtgc ccagctctac 660

ctggcccagc gagacagtga cctgcaacgt ggcccaccct gccagcagca ccaaggtgga 720

caagaaaatc gtgccccggg actgcggctg caagccctgt atctgtaccg tgcccgaggt 780

gtccagcgtg ttcatcttcc cacccaagcc caaggacgtg ctgaccatca ccctgacacc 840

caaagtgacc tgtgtggtgg tggacatcag caaggacgac cccgaggtgc agttcagttg 900

gttcgtggac gacgtggaag tgcacacagc ccagacccag cccagagagg aacagttcaa 960

cagcaccttc agaagcgtgt ccgagctgcc catcatgcac caggactggc tgaacggcaa 1020

agaattcaag tgcagagtga acagcgccgc cttccctgcc cccatcgaga aaaccatctc 1080

caagaccaag ggcagaccca aggccccca ggtgtacaca atcccccac ccaaagaaca 1140

gatggccaag gacaaggtgt ccctgacctg catgatcacc gatttcttcc cagaggacat 1200

caccgtggaa tggcagtgga acggccagcc cgccgagaac tacaagaaca cccagcctat 1260

catggacacc gacggcagct acttcgtgta cagcaagctg aacgtgcaga agtccaactg 1320

ggaggccggc aacaccttca cctgtagcgt gctgcacgag ggcctgcaca atcaccacac 1380

cgagaagtcc ctgtcccaca gccccggcaa atgagtttaa acgggggagg ctaact 1436

<210> 89
<211> 462
<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of Heavy Chain of 17F6

<400> 89

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe
35 40 45

Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
50 55 60

Glu Trp Ile Gly His Ile Tyr Pro Gly Asp Ala Asp Thr Asn Tyr Asn
65 70 75 80

Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Phe Cys Ser Arg Gln Leu Gly Phe Arg Tyr Ala Met Asp Tyr Trp
115 120 125

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

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

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

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

Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val
        195                 200                 205

Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His
    210                 215                 220

Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys
225                 230                 235                 240

Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe
                245                 250                 255

Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro
            260                 265                 270

Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val
        275                 280                 285

Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr
    290                 295                 300

Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu
305                 310                 315                 320

Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys
                325                 330                 335

Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser
            340                 345                 350

Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro
        355                 360                 365

Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile
    370                 375                 380

Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly
385                 390                 395                 400

Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp
                405                 410                 415

Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp
            420                 425                 430

Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His
        435                 440                 445
```

Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
450 455 460

<210> 90
<211> 767
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding Light Chain of 17F6

<400> 90
ccagcctccg gactctagag ccaccatggt gctgcagacc caggtgttca tcagcctgct 60

gctgtggatc agcggcgcct acggcgacat cgtgatgagc cagagcccta gcagcctggc 120

cgtgtctgcc ggcgagaaag tgaccatgag ctgcaagagc agccagtccc tgctgaacag 180

ccggacccgg aagaactacc tggcctggta tcagcagaag cccggccagt cccccaagct 240

gctgatctac tgggccagca ccagagaaag cggcgtgccc gatagattca ccggcagcgg 300

ctctggcacc gacttcaccc tgacaatcag cagcgtgcag gccgaggacc tggctgtgta 360

ctactgcaag cagagctaca acctgcggac cttcggcgga ggcaccaagc tggaaatcaa 420

gagagccgac gccgctccca ccgtgtccat ctttccacct agcagcgagc agctgaccag 480

cggcggagct agcgtcgtgt gcttcctgaa caacttctac cccaaggaca tcaacgtgaa 540

gtggaagatc gacggcagcg agcggcagaa cggcgtgctg aatagctgga ccgaccagga 600

cagcaaggac tccacctaca gcatgtccag caccctgacc ctgaccaagg acgagtacga 660

gcggcacaac agctacacat gcgaggccac ccacaagacc agcacctccc ccatcgtgaa 720

gtccttcaac cggaacgagt gctgagttta aacgggggag gctaact 767

<210> 91
<211> 239
<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of Light Chain of 17F6

<400> 91

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala
20 25 30

Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
35 40 45

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

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg

65 70 75 80

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

Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
100 105 110

Tyr Cys Lys Gln Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys
115 120 125

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

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

Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp
165 170 175

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

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

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

Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
225 230 235

<210> 92
<211> 11
<212> PRT
<213> Rattus rattus

<400> 92

Arg Ala Ser Gln Ser Ile Gly Asn Ser Leu Ser
1 5 10

<210> 93
<211> 11
<212> PRT
<213> artificial

<220>
<223> CDRL1 of hR198_LG1

<400> 93

Arg Ala Ser Gln Ser Ile Gly Gly Ser Leu Ser
1 5 10

<210> 94
<211> 11
<212> PRT
<213> artificial

<220>
<223> CDRL1 of hR198_LG2

<400> 94

His Ala Ser Gln Asn Ile Gly Gly Ser Leu Ser
1 5 10

<210> 95
<211> 11
<212> PRT
<213> artificial

<220>
<223> CDRL1 of hR198_LG3

<400> 95

His Ala Ser Arg Asn Ile Gly Gly Ser Leu Ser
1 5 10

<210> 96
<211> 7
<212> PRT
<213> Rattus rattus

<400> 96

Ser Thr Ser Thr Leu Glu Ser
1 5

<210> 97
<211> 7
<212> PRT
<213> artificial

<220>
<223> CDRL2 of hR198_LG2

<400> 97

Leu Thr Ser Thr Leu Asp Trp
1 5

<210> 98
<211> 7
<212> PRT
<213> artificial

<220>
<223> CDRL2 of hR198_LG3

<400> 98

Leu Thr Ser Ser Leu Asp Trp
1 5

<210> 99

<211> 9
<212> PRT
<213> Rattus rattus

<400> 99

Leu Gln Phe Ala Thr Phe Pro Asp Thr
1 5

<210> 100
<211> 9
<212> PRT
<213> Rattus rattus

<400> 100

Leu Gln Phe Ala Thr Tyr Pro Asp Thr
1 5

<210> 101
<211> 9
<212> PRT
<213> artificial

<220>
<223> CDRL3 of hR198_LG1 to LG3

<400> 101

Leu Gln Phe Ala Ile Phe Pro Asp Ser
1 5

<210> 102
<211> 5
<212> PRT
<213> Rattus rattus

<400> 102

Ala Tyr Tyr Ile Ser
1 5

<210> 103
<211> 5
<212> PRT
<213> Rattus rattus

<400> 103

Ser Tyr Tyr Ile Ser
1 5

<210> 104
<211> 17
<212> PRT
<213> Rattus rattus

<400> 104

Tyr Ile Asp Met Gly Asn Gly Arg Thr Asn Tyr Asn Ala Arg Phe Lys
1 5 10 15

Gly

<210> 105
<211> 17
<212> PRT
<213> Rattus rattus

<400> 105

Tyr Val Asp Met Gly Asn Gly Arg Thr Asn Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 106
<211> 17
<212> PRT
<213> artificial

<220>
<223> CDRH2 of hR198_HG1

<400> 106

Tyr Ile Asp Met Gly Asn Gly Arg Thr Asp Tyr Asn Ala Arg Phe Lys
1 5 10 15

Gly

<210> 107
<211> 17
<212> PRT
<213> artificial

<220>
<223> CDRH2 of hR198_HG2

<400> 107

Tyr Ile Asp Met Gly Asn Gly Arg Thr Asp Tyr Asn Gly Arg Phe Lys
1 5 10 15

Gly

<210> 108
<211> 17
<212> PRT
<213> artificial

<220>
<223> CDRH2 of hR198_HG3

<400> 108

Tyr Ile Asp Met Gly Asn Gly Arg Thr Asp Tyr Asn Met Arg Phe Lys
1 5 10 15

Gly

<210> 109
<211> 8
<212> PRT
<213> Rattus rattus

<400> 109

Asp Ser Asn Trp Gly Val Asp Tyr
1 5

<210> 110
<211> 8
<212> PRT
<213> artificial

<220>
<223> CDRH3 of hR198_HG1 to HG3

<400> 110

Asp Ser Asn Trp Gly Ala Asp Tyr
1 5

<210> 111
<211> 1401
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding hR198_H0

<400> 111
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag 60

gtgcagctgg tgcagtctgg cgccgaagtg aagaaaccag gcgccagcgt gaaggtgtcc 120

tgcaaggcct ctggctaccc cgtgaccagc tactacatca gctggatcag acaggcccca 180

ggccagggcc tggaatggat cggctatgtg gacatgggca acggccggac caactacaac 240

gagaagttca agggcagagc caccctgacc gtggacaaga gcaccagcac cgcctacatg 300

gaactgagca gcctgcggag cgaggacacc gccgtgtact actgcgccag agacagcaac 360

tggggcgtgg actattgggg ccagggcaca ctcgtgaccg tcagctcagc ctccaccaag 420

ggcccaagcg tcttccccct ggcaccctcc tccaagagca cctctggcgg cacagccgcc 480

ctgggctgcc tggtcaagga ctacttcccc gaacccgtga ccgtgagctg gaactcaggc 540

gccctgacca gcggcgtgca caccttcccc gctgtcctgc agtcctcagg actctactcc 600

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 660

gtgaatcaca agcccagcaa caccaaggtg gacaagagag ttgagcccaa atcttgtgac 720

aaaactcaca catgcccacc ctgcccagca cctgaactcc tgggggggacc ctcagtcttc 780

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 840

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 900

gtggaggtgc ataatgccaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg 960

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1020

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggc 1080

cagccccggg aaccacaggt gtacaccctg cccccatccc gggaggagat gaccaagaac 1140

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1200

gagagcaatg gccagcccga gaacaactac aagaccaccc ctcccgtgct ggactccgac 1260

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac 1320

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacaccca gaagagcctc 1380

tccctgtctc ccggcaaatg a 1401

<210> 112
<211> 466
<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of hR198_H0

<400> 112

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

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

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

Glu Trp Ile Gly Tyr Val Asp Met Gly Asn Gly Arg Thr Asn Tyr Asn
65 70 75 80

Glu Lys Phe Lys Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Gly Val Asp Tyr Trp Gly Gln
115 120 125

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

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

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

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

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

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

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

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
                245                 250                 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            260                 265                 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
        275                 280                 285

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

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

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
                325                 330                 335

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

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

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

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

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

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
            420                 425                 430
```

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
435 440 445

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

Gly Lys
465

<210> 113
<211> 1401
<212> DNA
<213> artificial

<220>
<223> Nucleotide Sequence coding hR198_H5

<400> 113
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag 60

gtgcagctgg tgcagtctgg cgccgaagtg aagaaaccag gcgccagcgt gaaggtgtcc 120

tgcaaggcct ctggctaccc cgtgaccgcc tactacatca gctggatcag acaggcccca 180

ggccagggcc tggaatggat cggctacatc gacatgggca acggccggac caactacaac 240

gcccggttta agggcagagc caccctgacc gtggacaaga gcaccagcac cgcctacatg 300

gaactgagca gcctgcggag cgaggacacc gccgtgtact actgcgccag agacagcaac 360

tggggcgtgg actattgggg ccagggcaca ctcgtgaccg tcagctcagc ctccaccaag 420

ggcccaagcg tcttcccccc ggcaccctcc tccaagagca cctctggcgg cacagccgcc 480

ctgggctgcc tggtcaagga ctacttcccc gaacccgtga ccgtgagctg gaactcaggc 540

gccctgacca gcggcgtgca caccttcccc gctgtcctgc agtcctcagg actctactcc 600

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 660

gtgaatcaca agcccagcaa caccaaggtg gacaagagag ttgagcccaa atcttgtgac 720

aaaactcaca catgcccacc ctgcccagca cctgaactcc tgggggggacc ctcagtcttc 780

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 840

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 900

gtggaggtgc ataatgccaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg 960

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1020

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggc 1080

cagccccggg aaccacaggt gtacaccctg cccccatccc gggaggagat gaccaagaac 1140

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1200

gagagcaatg gccagcccga gaacaactac aagaccaccc ctcccgtgct ggactccgac 1260

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac 1320

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacaccca gaagagcctc 1380

tccctgtctc ccggcaaatg a 1401

<210> 114
<211> 466
<212> PRT
<213> artificial

<220>
<223> Amino Acid Sequence of hR198_H5

<400> 114

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

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

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

Glu Trp Ile Gly Tyr Ile Asp Met Gly Asn Gly Arg Thr Asn Tyr Asn
65 70 75 80

Ala Arg Phe Lys Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Gly Val Asp Tyr Trp Gly Gln
115 120 125

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

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

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

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

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

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

```
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
225                 230                 235                 240

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
                245                 250                 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            260                 265                 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
        275                 280                 285

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

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

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
                325                 330                 335

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

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

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

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

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

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
        435                 440                 445

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

Gly Lys
465
```

<210> 115
<211> 48

<212> PRT
<213> Homo sapiens

<400> 115

Ser Gly Ser Gly Phe Leu Pro Leu Lys Lys Gln Pro Gly Gln Pro Arg
1 5 10 15

Pro Thr Ser Lys Pro Pro Ala Ser Gly Ala Ala Ala Asn Val Ser Thr
20 25 30

Ser Gly Ile Thr Pro Gly Gln Ala Ala Ala Ile Ala Ser Thr Thr Ile
35 40 45

<210> 116
<211> 11
<212> PRT
<213> Rattus rattus

<400> 116

Arg Ala Ser Gln Ser Ile Ser Asn Ser Leu Ser
1 5 10