

SEQUENCE LISTING

<110> AKESO PHARMACEUTICALS, INC.
AD Pharmaceuticals Co., Ltd.

<120> USE OF ANTIBODY IN ANTI-TUMOR TREATMENT

<130> IP220140

<160> 72

<170> PatentIn version 3.5

<210> 1

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial Sequence-nucleic acid sequence of heavy chain variable region of 4G10

<400> 1

cagggtcaagc tgcaggagtc tggacctgag ctggtgaagc ctggagcttc aatgaagata 60

tcctgcaagg cttctgggta ctcattcact ggctacacca tgaactgggt gaagcagagc 120

catggaaaga accttgaatg gattggactt attaatcctt acaataatat tactaactac 180

aaccagaagt tcatgggcaa ggccacattt actgtagaca agtcatccag cacagcctac 240

atggaactcc tcagactgac atctgaagac tctggagtct atttctgtgc aagactcgac 300

tataggtctt attggggcca agggactctg gtcactgtct ctgcagccaa aacgacaccc 360

ccatctgtct at 372

<210> 2

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Sequence-amino acid sequence of heavy chain variable region of 4G10

<400> 2

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

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

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

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

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

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

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

Val Ser Ala Ala Lys Thr Thr Pro Pro Ser Val Tyr
115 120

<210> 3
<211> 378
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence-nucleic acid sequence of light chain variable region of 4G10

<400> 3
caggctgttg tgactcagga atctgcactc accacatcac ctggtgaaac agtcacactc 60
acttgtcgct caagtactgg ggctgttaca actagtaact ttgccaactg ggtccaagaa 120
aaaccagatc atttattcac tagtctaata ggtggtacca acaaccgagc tccagggtgtt 180
cctgccagat tctcaggctc cctgattgga gacaaggctg ccctcaccat cacaggggca 240
cagactgagg atgaggcaat atatttctgt gctctatggt acagcaacca ttgggtgttc 300
ggtaggaggaa ccaaactgac tgtcctaggc cagcccaagt cttcgccatc agtcaccctg 360
tttcaagggc aattctgc 378

<210> 4
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence-amino acid sequence of light chain variable region of 4G10

<400> 4

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

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

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

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

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

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

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

Lys Ser Ser Pro Ser Val Thr Leu Phe Gln Gly Gln Phe Cys
115 120 125

<210> 5
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence-nucleic acid sequence of heavy chain variable region of 4G10H1L1

<400> 5

caggtgcagc	tggtggagtc	tggggccgag	ctggtgaagc	ccggcgcctc	catgaagatc	60
tcttgcaagg	ccagcggata	cagtttctact	ggctatacca	tgaactgggt	caaacaggct	120
ccaggacagg	gactggagtg	gatcgggctg	attaatcctt	acaacaacat	caccaactac	180
aaccagaagt	tcatgggaaa	agcaaccttt	acagtggaca	agagcatttc	cacagcctac	240
atggaactga	gccggctgac	ttcagacgat	agcggggctc	atttttgtgc	aaggctggat	300
tatcgctctt	actgggggca	gggaactctg	gtcactgtct	ccgct		345

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

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

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

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

<210> 7
 <211> 327
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Artificial Sequence-nucleic acid sequence of light chain variable region of 4G10H1L1

<400> 7
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 acatgcggaa gctccaccgg agcagtgacc acatccaact tcgccaattg ggtccaggaa 120
 aagccaggcc aggcatctcg atccctgac ggaggcacia acaatcgggc ttcttgggtg 180
 cccgcaagat tctcaggaag cctgctgggg ggaaaagccg ctctgaccat tagtggcgct 240
 cagcctgagg acgaagccga gtacttctgc gctctgtggt atagcaacca ctgggtgttt 300
 ggccgggggaa caaagctgac tgtgctg 327

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

<220>

<223> Artificial Sequence-amino acid sequence of light chain variable region of 4G10H1L1

<400> 8

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

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
 20 25 30

Asn Phe Ala Asn Trp Val Gln Glu Lys Pro Gly Gln Ala Phe Arg Ser
 35 40 45

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

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala
65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Phe Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 9
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence-nucleic acid sequence of heavy chain variable region of 4G10H3L3

<400> 9
caggtgcagc tggctcgagtc tggggccgaa gtgaagaaac ccggcgcctc agtgaaggtc 60
agctgcaagg ccagcgggta cagtttcact ggatatacca tgaactgggt ccgacaggcc 120
cctggccagg ggctggagtg gatcggcctg attaaccctt acaacaacat cactaactac 180
gcacagaagt tccagggggag agtgaccttt acagtggaca ccagcatttc cacagcctac 240
atggaactgt cccggctgag atctgacgat acaggcgtgt acttctgcgc taggctggat 300
taccgcagct attggggaca gggcacactg gtgactgtca gcgca 345

<210> 10
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence-amino acid sequence of heavy chain variable region of 4G10H3L3

<400> 10

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

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

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

Gly Leu Ile Asn Pro Tyr Asn Asn Ile Thr Asn Tyr Ala Gln Lys Phe
 50 55 60

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

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

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

Val Ser Ala
 115

<210> 11
 <211> 327
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial Sequence-nucleic acid sequence of light chain variable region
 of 4G10H3L3

<400> 11
 caggctgtcg tcactcagga accttcactg accgtgtctc ctggcgggac tgtcaccctg 60
 acatgcggca gctccacagg ggccgtgacc acaagtaact tcccaaattg ggtccagcag 120
 aagccaggac aggtctccccg gagtctgata ggaggcacca acaacaaggc cagctggaca 180
 cccgcacggt tcagcggcag cctgctgggc ggcaaggccg ctctgacaat tagcggagcc 240
 cagcctgagg acgaagccga gtactattgc gctctgtggt actccaacca ctgggtgttc 300
 ggccggcggca ccaagctgac tgtgctg 327

<210> 12
 <211> 109
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Artificial Sequence-amino acid sequence of light chain variable region of 4G10H3L3

<400> 12

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

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Phe Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Ser
35 40 45

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

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala
65 70 75 80

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

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 13

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial Sequence-nucleic acid sequence of heavy chain variable region of 14C12

<400> 13

gagggtcaaac tgggtggagag cggcggcgagg ctggtgaagc ccggcggggtc actgaaactg 60

agctgcgccg cttccggctt cgccttttagc tcctacgaca tgtcatgggt gaggcagacc 120

cctgagaagc gcctggaatg ggtcgtact atcagcggag gcgggcgata cacctactat 180

cctgactctg tcaaagggag attcacaatt agtcgggata acgccagaaa tactctgtat 240

ctgcagatgt ctagtctgcg gtccgaggat acagctctgt actattgtgc aaaccgggtac 300

ggcgaagcat ggtttgccta ttggggacag ggcaccctgg tgacagtctc tgcc

354

<210> 14

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Sequence-amino acid sequence of heavy chain variable region of 14C12

<400> 14

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

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

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

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

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

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

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

Leu Val Thr Val Ser Ala
115

<210> 15

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial Sequence-nucleic acid sequence of light chain variable region of 14C12

<400> 15
gacattaaga tgacacagtc cccttcctca atgtacgcta gcctgggcga gcgagtgacc 60
ttcacatgca aagcatccca ggacatcaac acatacctgt cttggtttca gcagaagcca 120
ggcaaaagcc ccaagaccct gatctaccgg gccaatagac tgggtggacgg ggtccccagc 180
agattctccg gatctggcag tgggcaggat tactccctga ccatcagctc cctggagtat 240
gaagacatgg gcatctacta ttgcctgcag tatgatgagt tccctctgac ctttggagca 300
ggcacaaaac tggaactgaa g 321

<210> 16
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence-amino acid sequence of light chain variable region of 14C12

<400> 16

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

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

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

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

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

Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp Glu Phe Pro Leu
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys

100

105

<210> 17
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Artificial Sequence-nucleic acid sequence of heavy chain variable region of 14C12H1L1

<400> 17
 gaagtgcagc tggtcgagtc tgggggaggg ctggtgcagc ccggcgggtc actgcgactg 60
 agctgcgcag cttccggatt cgcctttagc tcctacgaca tgtcctgggt gcgacaggca 120
 ccaggaaagg gactggattg ggtcgctact atctcaggag gcgggagata cacctactat 180
 cctgacagcg tcaagggccg gttcacaatc tctagagata acagtaagaa caatctgtat 240
 ctgcagatga acagcctgag ggctgaggac accgcactgt actattgtgc caaccgctac 300
 ggggaagcat ggtttgccta ttgggggcag ggaaccctgg tgacagtctc tagt 354

<210> 18
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Artificial Sequence-amino acid sequence of heavy chain variable region of 14C12H1L1

<400> 18

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

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

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

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

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

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

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

Leu Val Thr Val Ser Ser
115

<210> 19
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence-nucleic acid sequence of light chain variable region
of 14C12H1L1

<400> 19
gacattcaga tgactcagag cccctcctcc atgtccgcct ctgtgggcga cagggtcacc 60
ttcacatgcc gcgctagtca ggatatcaac acctacctga gctgggtttca gcagaagcca 120
gggaaaagcc ccaagacact gatctaccgg gctaataagac tgggtgtctgg agtcccaagt 180
cggttcagtg gctcagggag cggacaggac tacactctga ccatcagctc cctgcagcct 240
gaggacatgg caacctacta ttgcctgcag tatgatgagt tcccactgac ctttggcgcc 300
gggacaaaac tggagctgaa g 321

<210> 20
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence-amino acid sequence of light chain variable region of
14C12H1L1

<400> 20

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

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

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

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

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

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

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

<210> 21
 <211> 1344
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial Sequence-DNA sequence of 14C12H1L1 heavy chain (14C12H1)

<400> 21
 gaagtgcagc tggtcgagtc tgggggaggg ctggtgcagc ccggcgggtc actgcgactg 60
 agctgcgcag cttccggatt cgcctttagc tcctacgaca tgtcctgggt gcgacaggca 120
 ccaggaaagg gactggattg ggctcgtact atctcaggag gcgggagata cacctactat 180
 cctgacagcg tcaagggccg gttcacaatc tctagagata acagtaagaa caatctgtat 240
 ctgcagatga acagcctgag ggctgaggac accgcactgt actattgtgc caaccgctac 300
 ggggaagcat ggtttgccta ttgggggcag ggaaccctgg tgacagtctc tagtgccagc 360
 accaaaggac ctagcgtgtt tcctctcgcc ccctcctcca aaagcaccag cggaggaacc 420
 gctgctctcg gatgtctggg gaaggactac ttccctgaac ccgtcaccgt gagctggaat 480
 agcggcgctc tgacaagcgg agtccataca ttccctgctg tgctgcaaag cagcggactc 540
 tattccctgt ccagcgtcgt cacagtgcc agcagcagcc tgggcaccca gacctacatc 600

tgtaacgtca accacaagcc ctccaacacc aaggtggaca agaaagtgga gcccaaatcc	660
tgcgacaaga cacacacctg tccccctgt cctgctcccg aactcctcgg aggccttagc	720
gtcttcctct ttcctcccaa acccaaggac accctcatga tcagcagaac ccctgaagtc	780
acctgtgtcg tcgtggatgt cagccatgag gaccccgagg tgaaattcaa ctggtatgtc	840
gatggcgtcg aggtgcacaa cgccaaaacc aagcccaggg aggaacagta caactccacc	900
tacagggtgg tgtccgtgct gacagtcctc caccaggact ggctgaacgg caaggagtac	960
aagtgcaagg tgtccaacaa ggctctccct gccccattg agaagaccat cagcaaggcc	1020
aaaggccaac ccagggagcc ccaggtctat acactgcctc cctccaggga cgaactcacc	1080
aagaaccagg tgtccctgac ctgcctggtc aagggtttt atcccagcga catcgccgtc	1140
gagtgggagt ccaacggaca gcccgagaat aactacaaga ccaccctcc tgcctcgac	1200
tccgacggct cttcttcct gtacagcaag ctgaccgtgg aaaaagcag gtggcagcag	1260
ggaaacgtgt tctcctgcag cgtgatgcac gaagccctcc acaaccacta caccagaaa	1320
agcctgtccc tgagccccgg caaa	1344

<210> 22

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Sequence-encoded amino acid sequence of 14C12H1L1 heavy chain (14C12H1)

<400> 22

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

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

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

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

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

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

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

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

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

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

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

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

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

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

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 23

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial Sequence-DNA sequence of 14C12H1L1 light chain (14C12L1)

<400> 23
gacattcaga tgactcagag cccctcctcc atgtccgcct ctgtgggcga cagggtcacc 60
ttcacatgcc gcgctagtca ggatatcaac acctacctga gctgggtttca gcagaagcca 120
gggaaaagcc ccaagacact gatctaccgg gctaatagac tgggtgtctgg agtcccaagt 180
cggtttcagtg gctcaggag cgacaggac tacactctga ccatcagctc cctgcagcct 240
gaggacatgg caacctacta ttgcctgcag tatgatgagt tcccactgac ctttggcgcc 300
gggacaaaac tggagctgaa gcgaactgtg gccgctccct ccgtcttcat ttttccccct 360
tctgacgaac agctgaaatc aggcacagcc agcgtggtct gtctgctgaa caatttctac 420
cctagagagg caaaagtga gtggaaggtc gataacgccc tgcagtccgg caacagccag 480
gagagtgtga ctgaacagga ctcaaaagat agcacctatt ccctgtctag tacactgact 540
ctgtccaagg ctgattacga gaagcacaaa gtgtatgcat gcgaagtgac acatcaggga 600
ctgtcaagcc ccgtgactaa gtcttttaac cggggcgaat gt 642

<210> 24
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence-encoded amino acid sequence of 14C12H1L1 light chain (14C12L1)

<400> 24

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

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

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

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

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

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

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
210

<210> 25

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Sequence-amino acid sequence of Linker1

<400> 25

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 26

<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence-amino acid sequence of Linker2

<400> 26

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser
20

<210> 27
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence-HCDR1 of 14C12

<400> 27

Gly Phe Ala Phe Ser Ser Tyr Asp
1 5

<210> 28
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence-HCDR2 of 14C12

<400> 28

Ile Ser Gly Gly Gly Arg Tyr Thr
1 5

<210> 29
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence-HCDR2 of 14C12

<400> 29

Ala Asn Arg Tyr Gly Glu Ala Trp Phe Ala Tyr
1 5 10

<210> 30

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Sequence-LCDR1 of 14C12

<400> 30

Gln Asp Ile Asn Thr Tyr
1 5

<210> 31

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Sequence-LCDR2 of 14C12

<400> 31

Arg Ala Asn
1

<210> 32

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Sequence-LCDR3 of 14C12

<400> 32

Leu Gln Tyr Asp Glu Phe Pro Leu Thr
1 5

<210> 33

<211> 8

<212> PRT

<213> Artificial Sequence

<220>
<223> Artificial Sequence-HCDR1 of 4G10

<400> 33

Gly Tyr Ser Phe Thr Gly Tyr Thr
1 5

<210> 34
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence-HCDR2 of 4G10

<400> 34

Ile Asn Pro Tyr Asn Asn Ile Thr
1 5

<210> 35
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence-HCDR3 of 4G10

<400> 35

Ala Arg Leu Asp Tyr Arg Ser Tyr
1 5

<210> 36
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence-LCDR1 of 4G10

<400> 36

Thr Gly Ala Val Thr Thr Ser Asn Phe
1 5

<210> 37
<211> 3

<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence-LCDR2 of 4G10

<400> 37

Gly Thr Asn
1

<210> 38
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence-LCDR3 of 4G10

<400> 38

Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 39
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence-DNA sequence of heavy chain of immunoglobulin moiety of CP004(hG1TM)

<400> 39
gaagtgcagc tggtcgagtc tgggggaggg ctggtgcagc ccggcgggtc actgcgactg 60
agctgcgcag cttccggatt cgccttttagc tcctacgaca tgtcctgggt gcgacaggca 120
ccaggaaagg gactggattg ggtcgctact atctcaggag gcgggagata cacctactat 180
cctgacagcg tcaagggccg gttcacaatc tctagagata acagtaagaa caatctgtat 240
ctgcagatga acagcctgag ggctgaggac accgcactgt actattgtgc caaccgctac 300
ggggaagcat ggtttgccta ttgggggcag ggaaccctgg tgacagtctc tagtgccagc 360
accaaagggc ccagcgtgtt tcctctcgcc ccctcctcca aaagcaccag cggaggaacc 420
gctgctctcg gatgtctggt gaaggactac ttccctgaac ccgtcaccgt gagctggaat 480
agcggcgctc tgacaagcgg agtccataca ttccctgctg tgctgcaaag cagcggactc 540

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

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

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

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

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

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

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

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

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

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

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

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser
225 230 235 240

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

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro

260

265

270

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

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

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

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

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

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

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

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

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

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

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

<210> 41

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Sequence-amino acid sequence of 4G10H1V(M)

<400> 41

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

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

Thr Met Asn Trp Val Lys Gln Ala Pro Gly Gln Cys Leu Glu Trp Ile
35 40 45

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

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

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

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

Val Ser Ala
115

<210> 42

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Sequence-amino acid sequence of 4G10L1V(M)

<400> 42

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

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Phe Ala Asn Trp Val Gln Glu Lys Pro Gly Gln Ala Phe Arg Ser
35 40 45

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

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala
65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Phe Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu Arg
100 105 110

<210> 43
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence-amino acid sequence of 4G10H3V(M)

<400> 43

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

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

Thr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Ile
35 40 45

Gly Leu Ile Asn Pro Tyr Asn Asn Ile Thr Asn Tyr Ala Gln Lys Phe
50 55 60

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

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

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

Val Ser Ala
115

<210> 44
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence-amino acid sequence of 4G10L3V(M)

<400> 44

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

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Phe Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Ser
35 40 45

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

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala
65 70 75 80

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

His Trp Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu Arg
100 105 110

<210> 45
<211> 116
<212> PRT
<213> Artificial Sequence

<220>

<223> Artificial Sequence-sequence of heavy chain variable region of hIgG

<400> 45

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

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

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

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

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

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

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

Thr Val Ser Ser
115

<210> 46

<211> 327

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Sequence-sequence of heavy chain constant region of hIgG

<400> 46

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

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

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

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

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

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

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
 100 105 110

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

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

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
 145 150 155 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
 165 170 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 180 185 190

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

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 210 215 220

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

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

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

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

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

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

Leu Ser Leu Ser Leu Gly Lys
325

<210> 47

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Sequence-sequence of light chain variable region of hIgG

<400> 47

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

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

Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
35 40 45

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

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

Glu Asp Phe Gly Val Tyr Phe Cys Gln Gln Ser Gly Ser Trp Pro Arg
85 90 95

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

<210> 48
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence-sequence of light chain constant region of hIgG

<400> 48

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

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

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

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

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

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

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 49
<211> 348
<212> DNA
<213> Artificial Sequence

<220>

<223> Artificial Sequence-nucleic acid sequence of heavy chain variable region of HpL3

<400> 49

```
gaagtgcagc tgggtgcagag cggcggggga ctggtgaagc ccggcgggtc cctgcgactg      60
tcttgcgccg ctagtggctt caccttcagc tcctactcta tgaactgggt gagacaggcc      120
cctggaaaag gcctggagtg ggtctctagt atctcaagct cctctagtta catctactat      180
gccgacagcg tgaaggggcg gttcaccatc tcaagagata acgctaaaaa tagtctgtat      240
ctgcagatga acagcctgag ggacagaagac actgccgtgt actattgtgc tcgcgtcacc      300
gacgcatttg atatttgggg gcagggaacc atggtgacag tctcaagc                    348
```

<210> 50

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Sequence-amino acid sequence of heavy chain variable region of HpL3

<400> 50

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

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

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

```
Ser Ser Ile Ser Ser Ser Ser Ser Tyr Ile Tyr Tyr Ala Asp Ser Val
          50          55          60
```

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

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

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

Thr Val Ser Ser
115

<210> 51
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence-nucleic acid sequence of light chain variable region of HpL3

<400> 51
gacattcaga tgactcagag cccttcttca gtgtccgcct ctatcggcga ccgggtcacc 60
attacatgca gagcttccca gggcctcgat aactggctgg ggtggtacca gcagaagcct 120
gggaaagccc caaagctgct gatctacgac gcttccaatc tggataccgg agtgccatct 180
cgattcagtg gctcagggag cggaacatac tttactctga ccatcagctc cctgcaggct 240
gaggacttcg cagtgtatctt ttgccagcag gcaaaggcct tccctccac ctttggcggg 300
ggaacaaaag tggacatcaa g 321

<210> 52
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence-amino acid sequence of light chain variable region of HpL3

<400> 52

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

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

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

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

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

Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Ala Lys Ala Phe Pro Pro
85 90 95

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

<210> 53
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence-HCDR1 of heavy chain variable region of HpL3

<400> 53

Gly Phe Thr Phe Ser Ser Tyr Ser
1 5

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

<220>
<223> Artificial Sequence-HCDR2 of heavy chain variable region of HpL3

<400> 54

Ile Ser Ser Ser Ser Ser Tyr Ile
1 5

<210> 55
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence-HCDR3 of heavy chain variable region

<400> 55

Ala Arg Val Thr Asp Ala Phe Asp Ile
1 5

<210> 56

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Sequence-LCDR1 of light chain variable region of HpL3

<400> 56

Gln Gly Leu Asp Asn Trp
1 5

<210> 57

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Sequence-LCDR2 of light chain variable region

<400> 57

Asp Ala Ser
1

<210> 58

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Sequence-LCDR3 of light chain variable region of HpL3

<400> 58

Gln Gln Ala Lys Ala Phe Pro Pro Thr
1 5

<210> 59

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial Sequence-nucleic acid sequence of heavy chain variable region of bevacizumab

<400> 59

```
gaggtgcagc tggtcgagtc cggggggggg ctggtgcagc caggcgggtc tctgaggctg      60
agttgcgccg cttcagggtg caccttcaca aactatggaa tgaattgggt gcgccaggca      120
ccaggaaagg gactggagtg ggtcggctgg atcaacactt acaccgggga acctacctat      180
gcagccgact ttaagcggcg gttcaccttc agcctggata caagcaaadc cactgcctac      240
ctgcagatga acagcctgcg agctgaggac accgcagtct actattgtgc taaatatccc      300
cactactatg ggagcagcca ttggtatattt gacgtgtggg ggcagggggac tctggtgaca      360
gtgagcagc                                     369
```

<210> 60

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Sequence-amino acid sequence of heavy chain variable region of bevacizumab

<400> 60

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

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

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

```
Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Ala Asp Phe
50           55           60
```

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

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

Ala Lys Tyr Pro His Tyr Tyr Gly Ser Ser His Trp Tyr Phe Asp Val
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 61
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence-nucleic acid sequence of light chain variable region of bevacizumab

<400> 61
gatattcaga tgactcagag cccctcctcc ctgtccgcct ctgtgggcga cagggtcacc 60
atcacatgca gtgcttcaca ggatatttcc aactacctga attggtatca gcagaagcca 120
ggaaaagcac ccaaggtgct gatctacttc actagctccc tgcactcagg agtgccaagc 180
cggttcagcg gatccggatc tggaaccgac tttactctga ccatttctag tctgcagcct 240
gaggatttcg ctacatacta ttgccagcag tattctaccg tgccatggac atttggccag 300
gggactaaag tcgagatcaa g 321

<210> 62
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence-amino acid sequence of light chain variable region of bevacizumab

<400> 62

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile

35

40

45

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

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

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

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

<210> 63

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Sequence-HCDR1 of heavy chain variable region of bevacizumab

<400> 63

Gly Tyr Thr Phe Thr Asn Tyr Gly
 1 5

<210> 64

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Sequence-HCDR2 of heavy chain variable region of bevacizumab

<400> 64

Ile Asn Thr Tyr Thr Gly Glu Pro
 1 5

<210> 65

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Sequence-HCDR3 of heavy chain variable region of bevacizumab

<400> 65

Ala	Lys	Tyr	Pro	His	Tyr	Tyr	Gly	Ser	Ser	His	Trp	Tyr	Phe	Asp	Val
1				5				10						15	

<210> 66

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Sequence-LCDR1 of light chain variable region of bevacizumab

<400> 66

Gln	Asp	Ile	Ser	Asn	Tyr
1				5	

<210> 67

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Sequence-LCDR2 of light chain variable region of bevacizumab

<400> 67

Phe	Thr	Ser
1		

<210> 68

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Sequence-LCDR3 of light chain variable region of bevacizumab

<400> 68

Gln	Gln	Tyr	Ser	Thr	Val	Pro	Trp	Thr
1				5				

<210> 69

<211> 2139

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial Sequence-nucleic acid sequence of CP004(hG1TM) heavy chain

<400> 69

gaagtgcagc tggtcgagtc tgggggaggg ctggtgcagc ccggcgggtc actgcgactg	60
agctgcgcag cttccggatt cgcctttagc tcctacgaca tgtcctgggt gcgacaggca	120
ccaggaaagg gactggattg ggtcgctact atctcaggag gcgggagata cacctactat	180
cctgacagcg tcaagggccg gttcacaatc tctagagata acagtaagaa caatctgtat	240
ctgcagatga acagcctgag ggctgaggac accgcactgt actattgtgc caaccgctac	300
ggggaagcat ggtttgccta ttgggggcag ggaaccctgg tgacagtctc tagtgccagc	360
accaaagggc ccagcgtgtt tcctctcgcc ccctcctcca aaagcaccag cggaggaacc	420
gctgctctcg gatgtctggt gaaggactac ttccctgaac ccgtcaccgt gagctggaat	480
agcggcgctc tgacaagcgg agtccataca ttccctgctg tgctgcaaag cagcggactc	540
tattccctgt ccagcgtcgt cacagtgtccc agcagcagcc tgggcaccca gacctacatc	600
tgtaacgtca accacaagcc ctccaacacc aaggtggaca agaaagtgga gcccaaattcc	660
tgcgacaaga cacacacctg tccccctgt cctgctcccg aagctgctgg agcccctagc	720
gtcttcctct ttctcccaa acccaaggac accctcatga tcagcagaac ccctgaagtc	780
acctgtgtcg tcgtggatgt cagccatgag gaccccgagg tgaaattcaa ctggtatgtc	840
gatggcgctc aggtgcacaa cgccaaaacc aagcccaggg aggaacagta caactccacc	900
tacagggtgg tgtccgtgct gacagtcctc caccaggact ggctgaacgg caaggagtac	960
aagtgcagg tgtccaacaa ggctctccct gccccattg agaagaccat cagcaaggcc	1020
aaaggccaac ccagggagcc ccaggtctat acactgcctc cctccaggga cgaactcacc	1080
aagaaccagg tgtccctgac ctgcctggtc aagggtttt atcccagcga catcgccgtc	1140
gagtgggagt ccaacggaca gcccgagaat aactacaaga ccaccctcc tgtcctcgac	1200
tccgacggct cttcttcct gtacagcaaa ctgaccgtgg ataagtccag atggcagcag	1260
ggcaatgtct tttcatgttc cgtgatgcac gaggcactgc acaaccacta taccagaag	1320
tctctgagtc tgtcaccagg aaaaggagga ggaggctctg gaggagcgga aagtggaggc	1380
ggaggatcag gagggggagg atctcaggtg cagctggtcg aatccggagc cgagggtgaag	1440

aaacccggcg cttccgtgaa ggtctcttgc aaagcatcag gctacagctt cacagggtat 1500
 actatgaact ggggtgcggca ggcacctgga cagtgtctgg aatggatcgg cctgattaac 1560
 ccatacaaca acatcactaa ctacgccag aagttccagg gccgggtgac ttttaccgtg 1620
 gacactagca tttccaccgc ttacatggag ctgagtcggc tgagatcaga cgataccggc 1680
 gtgtatTTTT gcgcaaggct ggattacaga agttattggg gacagggaac acttggtaca 1740
 gtctctgctg gaggaggcgg atctggagga ggaggatctg gcggaggagg cagtggagga 1800
 ggaggatcac aggctgtggt tactcaggaa ccaagcctga ccgtgagccc cggaggcaca 1860
 gtcactctga cctgtgggag ctccacagga gctgtgacca catctaactt ccctaattgg 1920
 gtgcagcaga agccaggaca ggcacctcga tccctgatcg ggggaaccaa caacaaggcc 1980
 agctggacac ccgccagatt ttctggcagt ctgctgggcg ggaaagccgc tctgaccatt 2040
 agcggcgctc agcctgagga cgaagcagag tactattgcg ccctgtggta tagtaatcat 2100
 tgggtgttcg ggtgtgggac aaaactgacc gtgctgaga 2139

<210> 70

<211> 713

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Sequence-amino acid sequence of CP004(hG1TM) heavy chain

<400> 70

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

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Asn Leu Tyr

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

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

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

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

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

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

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

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

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

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

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

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
450 455 460

Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys
465 470 475 480

Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser
485 490 495

Phe Thr Gly Tyr Thr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Cys
500 505 510

Leu Glu Trp Ile Gly Leu Ile Asn Pro Tyr Asn Asn Ile Thr Asn Tyr
515 520 525

Ala Gln Lys Phe Gln Gly Arg Val Thr Phe Thr Val Asp Thr Ser Ile
530 535 540

Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Gly
545 550 555 560

Val Tyr Phe Cys Ala Arg Leu Asp Tyr Arg Ser Tyr Trp Gly Gln Gly
565 570 575

Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly
580 585 590

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ala Val Val Thr
595 600 605

Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr
610 615 620

Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Phe Pro Asn Trp
625 630 635 640

Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Ser Leu Ile Gly Gly Thr
645 650 655

Asn Asn Lys Ala Ser Trp Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
660 665 670

Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala Gln Pro Glu Asp Glu
675 680 685

Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn His Trp Val Phe Gly
690 695 700

Cys Gly Thr Lys Leu Thr Val Leu Arg
705 710

<210> 71
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence-nucleic acid sequence of CP004(hG1TM) light chain

<400> 71
gacattcaga tgactcagag cccctcctcc atgtccgcct ctgtgggcga cagggtcacc 60
ttcacatgcc gcgctagtca ggatatcaac acctacctga gctgggtttca gcagaagcca 120
gggaaaagcc ccaagacact gatctaccgg gctaataagac tgggtgtctgg agtcccaagt 180
cggttcagtg gctcagggag cggacaggac tacactctga ccatcagctc cctgcagcct 240
gaggacatgg caacctacta ttgcctgcag tatgatgagt tcccactgac ctttggcgcc 300
gggacaaaac tggagctgaa gcgaactgtg gccgctccct ccgtcttcat ttttccccct 360
tctgacgaac agctgaaatc aggcacagcc agcgtggtct gtctgctgaa caatttctac 420
cctagagagg caaaagtgca gtggaaggtc gataacgccc tgcagtccgg caacagccag 480
gagagtgtga ctgaacagga ctcaaaagat agcacctatt ccctgtctag tacactgact 540
ctgtccaagg ctgattacga gaagcacaaa gtgtatgcat gcgaagtgac acatcagggg 600
ctgtcaagcc ccgtgactaa gtcttttaac cggggcgaat gt 642

<210> 72
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence-amino acid sequence of CP004(hG1TM) light chain

<400> 72

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

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

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

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

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

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

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
210