

SEQUENCE LISTING

<110> NATIONAL RESEARCH COUNCIL OF CANADA

<120> ANTI-EGFRVIII ANTIBODIES AND ANTIGEN-BINDING FRAGMENTS THEREOF

<130> 16600-001-PCT

<150> US 62/824,386

<151> 2019-03-27

<160> 171

<170> PatentIn version 3.5

<210> 1

<211> 1210

<212> PRT

<213> Homo sapiens

<400> 1

Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu Leu Ala
1 5 10 15

Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln
20 25 30

Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
35 40 45

Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn
50 55 60

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

Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
85 90 95

Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
100 105 110

Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
115 120 125

Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
130 135 140

His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
145 150 155 160

Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
165 170 175

Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
180 185 190

Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln
195 200 205

Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg
210 215 220

Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
225 230 235 240

Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp
245 250 255

Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro
260 265 270

Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly
275 280 285

Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His
290 295 300

Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu
305 310 315 320

Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val
325 330 335

Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn
340 345 350

Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
355 360 365

Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
370 375 380

Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
385 390 395 400

Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp
405 410 415

Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
420 425 430

His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu
435 440 445

Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser
450 455 460

Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
465 470 475 480

Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu
485 490 495

Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro
500 505 510

Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn
515 520 525

Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly
530 535 540

Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro
545 550 555 560

Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
565 570 575

Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
580 585 590

Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp
595 600 605

Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys
610 615 620

Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly
625 630 635 640

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

Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met Arg Arg Arg His
660 665 670

Ile Val Arg Lys Arg Thr Leu Arg Arg Leu Leu Gln Glu Arg Glu Leu
675 680 685

Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn Gln Ala Leu Leu
690 695 700

Arg Ile Leu Lys Glu Thr Glu Phe Lys Lys Ile Lys Val Leu Gly Ser
705 710 715 720

Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu
725 730 735

Lys Val Lys Ile Pro Val Ala Ile Lys Glu Leu Arg Glu Ala Thr Ser
740 745 750

Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Ser
755 760 765

Val Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser
770 775 780

Thr Val Gln Leu Ile Thr Gln Leu Met Pro Phe Gly Cys Leu Leu Asp
785 790 795 800

Tyr Val Arg Glu His Lys Asp Asn Ile Gly Ser Gln Tyr Leu Leu Asn
805 810 815

Trp Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu Asp Arg Arg
820 825 830

Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Thr Pro
835 840 845

Gln His Val Lys Ile Thr Asp Phe Gly Leu Ala Lys Leu Leu Gly Ala
850 855 860

Glu Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val Pro Ile Lys Trp
865 870 875 880

Met Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr His Gln Ser Asp
885 890 895

Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ser
900 905 910

Lys Pro Tyr Asp Gly Ile Pro Ala Ser Glu Ile Ser Ser Ile Leu Glu
915 920 925

Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr
930 935 940

Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys
945 950 955 960

Phe Arg Glu Leu Ile Ile Glu Phe Ser Lys Met Ala Arg Asp Pro Gln
965 970 975

Arg Tyr Leu Val Ile Gln Gly Asp Glu Arg Met His Leu Pro Ser Pro
980 985 990

Thr Asp Ser Asn Phe Tyr Arg Ala Leu Met Asp Glu Glu Asp Met Asp
995 1000 1005

Asp Val Val Asp Ala Asp Glu Tyr Leu Ile Pro Gln Gln Gly Phe
1010 1015 1020

Phe Ser Ser Pro Ser Thr Ser Arg Thr Pro Leu Leu Ser Ser Leu
1025 1030 1035

Ser Ala Thr Ser Asn Asn Ser Thr Val Ala Cys Ile Asp Arg Asn
1040 1045 1050

Gly Leu Gln Ser Cys Pro Ile Lys Glu Asp Ser Phe Leu Gln Arg
1055 1060 1065

Tyr Ser Ser Asp Pro Thr Gly Ala Leu Thr Glu Asp Ser Ile Asp
1070 1075 1080

Asp Thr Phe Leu Pro Val Pro Glu Tyr Ile Asn Gln Ser Val Pro
1085 1090 1095

Lys Arg Pro Ala Gly Ser Val Gln Asn Pro Val Tyr His Asn Gln
1100 1105 1110

Pro Leu Asn Pro Ala Pro Ser Arg Asp Pro His Tyr Gln Asp Pro
1115 1120 1125

His Ser Thr Ala Val Gly Asn Pro Glu Tyr Leu Asn Thr Val Gln
1130 1135 1140

Pro Thr Cys Val Asn Ser Thr Phe Asp Ser Pro Ala His Trp Ala
1145 1150 1155

Gln Lys Gly Ser His Gln Ile Ser Leu Asp Asn Pro Asp Tyr Gln
1160 1165 1170

Gln Asp Phe Phe Pro Lys Glu Ala Lys Pro Asn Gly Ile Phe Lys
1175 1180 1185

Gly Ser Thr Ala Glu Asn Ala Glu Tyr Leu Arg Val Ala Pro Gln
1190 1195 1200

Ser Ser Glu Phe Ile Gly Ala
1205 1210

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<211> 1869
<212> DNA
<213> Homo sapiens

<400> 2
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ttggaaatta cctatgtgca gaggaattat gatcttttct tcttaaagac catccaggag 180
gtggctggtt atgtcctcat tgccctcaac acagtggagc gaattccttt ggaaaacctg 240
cagatcatca gaggaaatat gtactacgaa aattcctatg ccttagcagt cttatctaac 300
tatgatgcaa ataaaaccgg actgaaggag ctgcccataa gaaatttaca ggaaatcctg 360
catggcgccg tgcggttcag caacaaccct gccctgtgca acgtggagag catccagtgg 420
cgggacatag tcagcagtga ctttctcagc aacatgtcga tggacttcca gaaccacctg 480
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ggcaagtccc ccagtgactg ctgccacaac cagtgtgctg caggctgcac aggcccccg 660
gagagcgact gcctgggtctg ccgcaaattc cgagacgaag ccacgtgcaa ggacacctgc 720
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tacagctttg gtgccacctg cgtgaagaag tgtccccgta attatgtggt gacagatcac 840
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aagtgtgaaga agtgcgaagg gccttgccgc aaagtgtgta acggaatagg tattggtgaa 960
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cctcctctgg atccacagga actggatatt ctgaaaaccg taaaggaaat cacagggttt 1140
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atcatacgcg gcaggaccaa gcaacatggt cagttttctc ttgcagtcgt cagcctgaac 1260

ataacatcct tgggattacg ctccctcaag gagataagtg atggagatgt gataatttca	1320
ggaaacaaaa atttgtgcta tgcaaataca ataaactgga aaaaactgtt tgggacctcc	1380
ggtcagaaaa ccaaaattat aagcaacaga ggtgaaaaca gctgcaaggc cacaggccag	1440
gtctgccatg ccttgtgctc ccccgagggc tgctggggcc cggagcccag ggactgcgtc	1500
tcttgccgga atgtcagccg aggcagggaa tgcgtggaca agtgcaacct tctggagggt	1560
gagccaaggg agtttgtgga gaactctgag tgcatacagt gccaccaga gtgcctgcct	1620
caggccatga acatcacctg cacaggacgg ggaccagaca actgtatcca gtgtgcccac	1680
tacattgacg gccccactg cgtcaagacc tgcccggcag gagtcatggg agaaaacaac	1740
accctgggtct ggaagtacgc agacgccggc catgtgtgcc acctgtgcca tccaaactgc	1800
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<210> 3
 <211> 621
 <212> PRT
 <213> Homo sapiens

<400> 3

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Leu	Gly	Thr	Phe	Glu	Asp	His	Phe	Leu	Ser	Leu	Gln	Arg	Met	Phe	Asn
			20					25					30		

Asn	Cys	Glu	Val	Val	Leu	Gly	Asn	Leu	Glu	Ile	Thr	Tyr	Val	Gln	Arg
		35					40					45			

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

Val	Leu	Ile	Ala	Leu	Asn	Thr	Val	Glu	Arg	Ile	Pro	Leu	Glu	Asn	Leu
65					70					75				80	

Gln	Ile	Ile	Arg	Gly	Asn	Met	Tyr	Tyr	Glu	Asn	Ser	Tyr	Ala	Leu	Ala
				85					90					95	

Val Leu Ser Asn Tyr Asp Ala Asn Lys Thr Gly Leu Lys Glu Leu Pro
100 105 110

Met Arg Asn Leu Gln Glu Ile Leu His Gly Ala Val Arg Phe Ser Asn
115 120 125

Asn Pro Ala Leu Cys Asn Val Glu Ser Ile Gln Trp Arg Asp Ile Val
130 135 140

Ser Ser Asp Phe Leu Ser Asn Met Ser Met Asp Phe Gln Asn His Leu
145 150 155 160

Gly Ser Cys Gln Lys Cys Asp Pro Ser Cys Pro Asn Gly Ser Cys Trp
165 170 175

Gly Ala Gly Glu Glu Asn Cys Gln Lys Leu Thr Lys Ile Ile Cys Ala
180 185 190

Gln Gln Cys Ser Gly Arg Cys Arg Gly Lys Ser Pro Ser Asp Cys Cys
195 200 205

His Asn Gln Cys Ala Ala Gly Cys Thr Gly Pro Arg Glu Ser Asp Cys
210 215 220

Leu Val Cys Arg Lys Phe Arg Asp Glu Ala Thr Cys Lys Asp Thr Cys
225 230 235 240

Pro Pro Leu Met Leu Tyr Asn Pro Thr Thr Tyr Gln Met Asp Val Asn
245 250 255

Pro Glu Gly Lys Tyr Ser Phe Gly Ala Thr Cys Val Lys Lys Cys Pro
260 265 270

Arg Asn Tyr Val Val Thr Asp His Gly Ser Cys Val Arg Ala Cys Gly
275 280 285

Ala Asp Ser Tyr Glu Met Glu Glu Asp Gly Val Arg Lys Cys Lys Lys
290 295 300

Cys Glu Gly Pro Cys Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu
305 310 315 320

Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys
325 330 335

Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe
340 345 350

Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu
355 360 365

Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln
370 375 380

Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu
385 390 395 400

Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val
405 410 415

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

Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala
435 440 445

Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr
450 455 460

Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln
465 470 475 480

Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro
485 490 495

Arg Asp Cys Val Ser Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val
500 505 510

Asp Lys Cys Asn Leu Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn
515 520 525

Ser Glu Cys Ile Gln Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn
530 535 540

Ile Thr Cys Thr Gly Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His
545 550 555 560

Tyr Ile Asp Gly Pro His Cys Val Lys Thr Cys Pro Ala Gly Val Met
565 570 575

Gly Glu Asn Asn Thr Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val
580 585 590

Cys His Leu Cys His Pro Asn Cys Thr Tyr Gly Cys Thr Gly Pro Gly
595 600 605

Leu Glu Gly Cys Pro Thr Asn Gly Pro Lys Ile Pro Ser
610 615 620

<210> 4
<211> 996
<212> DNA
<213> Artificial Sequence

<220>
<223> Human EGFRVIII ectodomain cDNA sequence (nucleotides 1-996)

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ccctgccgga aagtgtgcaa cggcatcggc atcggagagt tcaaggacag cctgagcatc 180
aacgccacca acatcaagca cttcaagaac tgcaccagca tcagcggcga cctgcacatc 240
ctgcccgtgg ctttagagg cgacagcttc acccacaccc cccactgga ccccaggaa 300
ctggacatcc tgaaaaccgt gaaagagatc accggctttc tgctgattca ggcctggccc 360
gagaaccgga cagacctgca cgccttcgag aacctggaaa tcatccgggg caggaccaag 420
cagcacggcc agttttctct ggccgtggtg tccctgaaca tcaccagcct gggcctgcgg 480
agcctgaaag aaatcagcga cggcgacgtg atcatctccg gcaacaagaa cctgtgctac 540
gccaacacca tcaactggaa gaagctgttc ggcacctccg gccagaaaac aaagatcatc 600
agcaaccggg gcgagaacag ctgcaaggcc acaggacaag tgtgccacgc cctgtgtagc 660

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cctgagggct gttggggacc cgagcccaga gattgcgtgt cctgcagaaa cgtgtcccgg      720
ggcagagaat gcgtgggaaa gtgcaacctg ctggaaggcg agccccgcga gttcgtggaa      780
aacagcgagt gcatccagtg ccaccccagag tgtctgcccc aggccatgaa cattacctgc      840
accggcagag gccccgaaaa ctgtatccag tgcgcccact acatcgacgg cccccactgc      900
gtgaaaacct gtcctgctgg cgtgatggga gagaacaaca ccctcgtgtg gaagtacgcc      960
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<210> 5
<211> 332
<212> PRT
<213> Artificial Sequence

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<220>
<223> Human EGFRVIII ectodomain amino acid sequence (amino acids 1-332)

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<400> 5

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Leu Glu Glu Lys Lys Gly Asn Tyr Val Val Thr Asp His Gly Ser Cys
1           5           10           15

```

```

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

```

```

Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val Cys Asn Gly
          35           40           45

```

```

Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn
          50           55           60

```

```

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

```

```

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

```

```

Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly
          100          105          110

```

```

Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala
          115          120          125

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Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln
130 135 140

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

Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys
165 170 175

Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr
180 185 190

Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys
195 200 205

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

Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn Val Ser Arg
225 230 235 240

Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly Glu Pro Arg
245 250 255

Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro Glu Cys Leu
260 265 270

Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro Asp Asn Cys
275 280 285

Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val Lys Thr Cys
290 295 300

Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp Lys Tyr Ala
305 310 315 320

Asp Ala Gly His Val Cys His Leu Cys His Pro Asn
325 330

<210> 6
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Human EGFRVIII amino acid residues 15 to 37

<400> 6

Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu Asp
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Gly Val Arg Lys Cys Lys Lys
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<210> 7
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> 5G6 light chain variable region

<400> 7

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

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

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

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

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

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

<210> 8
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> 5G6 CDRL1

<400> 8

Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn
1 5 10 15

<210> 9
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 5G6 CDRL2

<400> 9

Leu Ala Ser Lys Leu Asp Ser
1 5

<210> 10
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 5G6 CDRL3

<400> 10

Trp Gln Ala Thr His Phe Pro Trp Thr
1 5

<210> 11
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> 5G6 - Light chain variable region cDNA

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<210> 13
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 5G6 CDRH1

<400> 13

Ser Tyr Trp Met His
1 5

<210> 14
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 5G6 CDRH2

<400> 14

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

Gly

<210> 15
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 5G6 CDRH3

<400> 15

Tyr Asp Tyr Asp Pro Asp Tyr
1 5

<210> 16
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<223> 5G6 - Heavy chain variable region cDNA

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cctggacagg gtctggaatg gattggcgct atttatcctg gaaatagtga tattagctac 180
aatcagaagt tcaagggcaa ggccaaactg actgcagtca catccgccac cactgcctac 240
atggagctca gcagcctaac aatgaggac tctgcggtct attactgtac cctctatgat 300
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<210> 17
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A8 light chain variable region

<400> 17

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

Gln Lys Val Thr Met Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

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

Ser Pro Lys Leu Leu Val Tyr Phe Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

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

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

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

Lys

<210> 18
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A8 CDRL1

<400> 18

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

Ala

<210> 19
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A8 CDRL2

<400> 19

Phe Ala Ser Thr Arg Glu Ser
1 5

<210> 20
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A8 CDRL3

<400> 20

Gln Gln His Tyr Ser Thr Pro Leu Thr
1 5

<210> 21
<211> 339
<212> DNA
<213> Artificial Sequence

<220>

<223> 1A8 light chain variable region cDNA

<400> 21

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tggttccagc agaaaccagg acagtctcct aaacttctgg tatactttgc ttccactagg      180
gaatctggggg tccctgatcg cttcataggc agtggatctg ggacagattt cactcttacc      240
atcagcagtg tgcaggctga agacctggca gattacttct gtcagcaaca ttatagcact      300
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<210> 22

<211> 114

<212> PRT

<213> Artificial Sequence

<220>

<223> 1A8 heavy chain variable region

<400> 22

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Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
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Leu Val Lys Leu Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20              25              30
```

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

```
Gly Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50              55              60
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```
Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
65              70              75              80
```

```
Leu Gln Leu Ser Ser Leu Ala Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85              90              95
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Ala Arg Gly Trp Leu Leu Leu Trp Gly Gln Gly Thr Thr Leu Thr Val
100             105             110
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Ser Ser

<210> 23
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A8 CDRH1

<400> 23

Asp Tyr Tyr Met His
1 5

<210> 24
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A8 CDRH2

<400> 24

Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 25
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A8 CDRH3

<400> 25

Gly Trp Leu Leu Leu
1 5

<210> 26
<211> 342
<212> DNA
<213> Artificial Sequence

<220>

<223> 1A8 heavy chain variable region cDNA

<400> 26

gaggttcagc tgcagcagtc tggggctgag cttgtgaggc caggggcctt agtcaagttg 60
tcctgcaaag cttctggctt caacattaaa gactactata tgcactgggt gaagcagagg 120
cctgaacagg gcctggagtg gattggatgg attgatacctg agaatggtaa tactatatat 180
gacccgaagt tccagggcaa ggccactata acagcagaca catcctccaa cacagcctac 240
ctgcagctca gcagcctggc atctgaggac actgccgtct attactgtgc tagaggatgg 300
ttactacttt ggggccaagg caccactctc acagtctcct ca 342

<210> 27

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> 4B3 light chain variable region

<400> 27

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

Glu Lys Val Thr Ile Thr Cys Ser Val Ser Ser Ser Ile Ser Ser Ser
20 25 30

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

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

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

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

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

<210> 28
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> 4B3 CDRL1

<400> 28

Ser Val Ser Ser Ser Ile Ser Ser Ser Asn Leu His
1 5 10

<210> 29
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 4B3 CDRL2

<400> 29

Gly Thr Ser Asn Leu Ala Ser
1 5

<210> 30
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 4B3 CDRL3

<400> 30

Gln Gln Trp Ser Ser Tyr Pro Leu Thr
1 5

<210> 31
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 4B3 light chain variable region cDNA

<400> 31
gaaattgtgc tcacccagtc tccagcactc atggctgcat ctccagggga gaaggtcacc

atcacctgca gtgtcagctc aagtataagt tccagcaact tgcactggta ccagcagaag	120
tcagaaacct cccccaacc ctggatttat ggcacatcca acctggcttc tggagtcctt	180
gttcgcttca gtggcagtgg atctgggacc tcttattctc tcacaatcag cagcatggag	240
gctgaagatg ctgccactta ttactgtcaa cagtggagta gttaccact cacgttcggt	300
gctgggacca agctggaact ggaa	324

<210> 32
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 4B3 heavy chain variable region

<400> 32

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

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

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

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

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

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

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

Thr Leu Val Thr Val Ser Ala
115

<210> 33
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 4B3 CDRH1

<400> 33

Asp Tyr Asn Met Asp
1 5

<210> 34
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 4B3 CDRH2

<400> 34

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

Gly

<210> 35
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 4B3 CDRH3

<400> 35

Gly Tyr Asp Tyr Asp Leu Trp Phe Ala Tyr
1 5 10

<210> 36
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> 4B3 heavy chain variable region cDNA

<400> 36
gaggtccagc tgcaacagtc tggacctgag ctggtgaagc ctgggtcttc agtgaagata 60
tcctgcaaag cttctggata cacattcact gactacaaca tggactgggt gaagcagagc 120
catggaaaga gccttgagt gattgggtact attaatccta acaatgggtg tactagctac 180
aaccagaagt tcaagggcaa ggccacattg actgtagaca agtcctcaa cacagcctac 240
atggagctcc gcagcctgac atctgaggac tctgcagtct attactgtgc aagaggctat 300
gattacgact tgtggtttgc ttactggggc caagggactc tggtcactgt ctctgca 357

<210> 37
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 4E11 light chain variable region

<400> 37

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

Asp Thr Val Ser Ile Thr Cys His Ala Ser Gln Gly Ile Asn Ser Asn
20 25 30

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

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

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

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

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

<210> 38
<211> 11

<212> PRT
<213> Artificial Sequence

<220>
<223> 4E11 CDRL1

<400> 38

His Ala Ser Gln Gly Ile Asn Ser Asn Ile Gly
1 5 10

<210> 39
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 4E11 CDRL2

<400> 39

His Gly Thr Asn Leu Glu Asp
1 5

<210> 40
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 4E11 CDRL3

<400> 40

Val Gln Tyr Ala Gln Phe Pro Tyr Thr
1 5

<210> 41
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> 4E11 light chain variable region cDNA

<400> 41

gacatcctga tgaccaatc tccatcctcc atgtctgtat ctctgggaga cacagtcagc 60

atcacttgcc atgcaagtca gggcattaac agtaatatag ggtgggttgct gcagaaacca 120

gggaaatcat ttaagggcct gatctatcat ggaaccaact tggaagatgg agttccatca 180

aggttcagtgcgcagtggatctggaacagattattctctccatcagcagcctggaatct 240
 gaggattttgctgactatta ctgtgtacag tatgctcagt ttccgtacac gttcggaggg 300
 gggaccaaactggaaataaa a 321

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

<220>
 <223> 4E11 heavy chain variable region

<400> 42

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

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

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

Met Gly Tyr Ile Gly Tyr Asn Gly Arg Thr Ser Tyr Asn Pro Ser Leu
 50 55 60

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

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

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

Thr Val Ser Ala
 115

<210> 43
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>

<223> 4E11 CDRH1

<400> 43

Ser Asp Tyr Ala Trp Asn

1 5

<210> 44

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> 4E11 CDRH2

<400> 44

Tyr Ile Gly Tyr Asn Gly Arg Thr Ser Tyr Asn Pro Ser Leu Lys Ser

1 5 10 15

<210> 45

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 4E11 CDRH3

<400> 45

Leu Gly Arg Gly Phe Ala Tyr

1 5

<210> 46

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<223> 4E11 heavy chain variable region cDNA

<400> 46

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acctgcactg tccactggcta ctcaatcacc agtgattatg cctgggaactg gatccggcag 120

tttccaggaa acaaaactgga gtggatgggc tacataggct acaatggtag aactagttac 180

aacccatctc tcaaaagtcg aatctctatc actcgagaca catccaagaa ccagttcttc 240

ctgcagttga attatgtgac tactgaggac acagccacat tttactgtgc aagactgggc 300
cgagggtttg cttactgggg ccaagggact ctggtcactg tctctgca 348

<210> 47
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> 5D8 light chain variable region

<400> 47

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

Glu Lys Val Thr Ile Thr Cys Ser Val Ser Ser Ser Ile Ser Ser Ser
20 25 30

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

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

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

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

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

<210> 48
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> 5D8 CDRL1

<400> 48

Ser Val Ser Ser Ser Ile Ser Ser Ser Asn Leu His
1 5 10

<210> 49
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 5D8 CDRL2

<400> 49

Gly Thr Ser Asn Leu Ala Ser
1 5

<210> 50
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 5D8 CDRL3

<400> 50

Gln Gln Trp Ser Ser Tyr Pro Leu Thr
1 5

<210> 51
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 5D8 light chain variable region cDNA

<400> 51
gaaattgtgc tcacccagtc tccagtattc atggctgcat ctccagggga gaaggtcacc 60
atcacctgca gtgtcagctc aagtataagt tccagcaact tgcactggta ccagcagaag 120
tcagaaacct cccccaaacc ctggatttat ggcacatcca acctggcttc tggagtcctt 180
gttcgcttca gtggcagtgg atctgggacc tcttattctc tcacaatcag cagcatggag 240
gctgaagatg ctgccactta ttactgtcaa cagtggagta gttaccact cacgttcggt 300
gctgggacca agctggagct gaaa 324

<210> 52
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 5D8 heavy chain variable region

<400> 52

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

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

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

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

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

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

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

Thr Leu Val Thr Val Ser Ala
115

<210> 53
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 5D8 CDRH1

<400> 53

Asp Tyr Asn Ile Asp
1 5

<210> 54
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 5D8 CDRH2

<400> 54

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

Gly

<210> 55
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 5D8 CDRH3

<400> 55

Gly	Tyr	Asp	Tyr	Asp	Leu	Trp	Phe	Ala	Tyr
1				5				10	

<210> 56
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> 5D8 heavy chain variable region cDNA

<400> 56
gaggtccagc tgcaacagtc tggacctgac ctggtgaagc ctgggtcttc agtgaagatt 60
tcctgcaaag cttctggata cacattcact gactacaaca ttgactgggt gaagcagagc 120
catggaaaga gccttgagt gattggaact attaatccta actatggtgg tacttcctac 180
aaccagaagt tcaagggcaa ggccacattg actgtagaca agtcctccag cacagcctac 240
atggagctcc gcagcctgac atctgaggac tctgcagtct attactgtgc aagaggctat 300
gattacgact tgtggtttgc ttactggggc caagggactc tggtcactgt ctctgca 357

<210> 57
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> 9C9 light chain variable region

<400> 57

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

Glu Lys Val Thr Ile Thr Cys Ser Val Ser Ser Ser Ile Ser Ser Ser
20 25 30

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

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

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

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

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

<210> 58
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> 9C9 CDRL1

<400> 58

Ser Val Ser Ser Ser Ile Ser Ser Ser Asn Leu His
1 5 10

<210> 59
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 9C9 CDRL2

<400> 59

Asp Thr Ser Asn Leu Ala Ser
1 5

<210> 60
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 9C9 CDRL3

<400> 60

Gln Gln Trp Ser Ser Tyr Pro Leu Thr
1 5

<210> 61
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 9C9 light chain variable region cDNA

<400> 61
gaaattgtgc tcaccagtc tccaacactc atggctgcat ctccagggga gaaggtcacc 60
atcacctgca gtgtcagctc aagtataagt tccagcaact tgcactggta ccagcagaag 120
tcagaaacct cccccaacc ctggatttat gacacatcca acctggcttc tggagtcctt 180
attcgcttca gtggcagtgg atctgggacc tcttattctc tcacaatcag cagcgtggag 240
gctgaagatg ctgccactta ttactgtcaa cagtggagta gttaccact caggttcggc 300
tcggggacaa agttggaaat aaaa 324

<210> 62
<211> 114
<212> PRT
<213> Artificial Sequence

<220>

<223> 9C9 heavy chain variable region

<400> 62

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

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

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

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

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

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

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

Ser Ala

<210> 63

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> 9C9 CDRH1

<400> 63

Ser Tyr Trp Met His
1 5

<210> 64

<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> 9C9 CDRH2

<400> 64

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

Gly

<210> 65
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 9C9 CDRH3

<400> 65

Phe Asp Phe Ala Tyr
1 5

<210> 66
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<223> 9C9 heavy chain variable region cDNA

<400> 66
caggtccaac tgcagcagcc tggggctgag cttgtgaagc ctggggcttc agtgaagctg 60
tcctgcaagg cttctggcta caccttcacc agctactgga tgcactgggt gaaacagagg 120
cctggacaag accttgagtg gatcggagag attgatacct ctgatagtta tactaactac 180
aatcaaaaagt tcaagggcaa ggccacattg actgtagaca aatcctccag cacagcctac 240
attcagctca gcagcctgac atctgaggac tctgcgctct attactgtgc aagattcgat 300
tttgcttact ggggcccaagg gactctgggtc actgtctctg ca 342

<210> 67
<211> 112

<212> PRT
<213> Artificial Sequence

<220>
<223> 11B1 light chain 1 (L1) variable region (dominant)

<400> 67

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

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

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

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

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

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

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

<210> 68
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> 11B1 L1 CDRL1

<400> 68

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

<210> 69
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> 11B1 L1 CDRL2

<400> 69

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 70

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> 11B1 L1 CDRL3

<400> 70

Ser Gln Ser Thr His Val Pro Phe Thr
1 5

<210> 71

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> 11B1 light chain 1 (L1) variable region cDNA (dominant)

<400> 71

gatgttgtga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60

atctcttgca gatctagtca gaggcttgta tatagtaatg gaaacaccta ttacattgg 120

tacctgcaga agccaggcca gtctccaaag ctctgatct acaaagtttc caaccgattt 180

tctgggggtcc cagacagggt cagtggcagt ggatcaggga cagatttcac actcaagatc 240

agcagagtgg aggctgagga tctgggagtt tatttctgct ctcaaagtac acatgttcca 300

ttcacgttcg gctcggggac aaagttggaa ataaaa 336

<210> 72

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> 11B1 light chain 2 (L2) variable region

<400> 72

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

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

Tyr Trp Cys Gln Gln Lys Ser Asp Ala Ser Pro Lys Leu Trp Ile Tyr
35 40 45

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

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

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

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

<210> 73

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> 11B1 L2 CDRL1

<400> 73

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

<210> 74

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 11B1 L2 CDRL2

<400> 74

Tyr Thr Ser Asn Leu Ala Pro
1 5

<210> 75
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 11B1 L2 CDRL3

<400> 75

Gln Gln Phe Thr Ser Ser Pro Ser Met His Thr
1 5 10

<210> 76
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 11B1 light chain 2 (L2) variable region cDNA

<400> 76
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atgagctgca gggccagctc aagtgtaaat tacatgtact ggtgccagca gaagtcagat 120
gcctccccc aactatggat ttattacaca tccaacctgg ctcttgagat cccagctcgc 180
ttcagtggca gtgggtctgg gaactcttat tctctcacia tcagcagcat ggagggtgaa 240
gatgttgcca cttattactg ccagcagttt actagttccc catccatgca cacgttcgga 300
ggggggacca agctggaaat aaaa 324

<210> 77
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> 11B1 heavy chain variable region

<400> 77

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

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

Gly Met Gln Trp Val Lys Lys Met Pro Gly Lys Gly Phe Lys Trp Ile
35 40 45

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

Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Tyr Ala Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Thr His Ile Tyr Asp Gly Tyr Asn Tyr Ala Met Asp Tyr Trp
100 105 110

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

<210> 78
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 11B1 CDRH1

<400> 78

Thr Ala Gly Met Gln
1 5

<210> 79
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 11B1 CDRH2

<400> 79

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

Gly

<210> 80
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 11B1 CDRH3

<400> 80

Thr His Ile Tyr Asp Gly Tyr Asn Tyr Ala Met Asp Tyr
1 5 10

<210> 81
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> 11B1 heavy chain variable region cDNA

<400> 81
cagatccagt tggatgcagtc tggacctgag ctgaagaagc ctggagagac agtcaagatc 60
tcctgcaagg cttctgggta taccttcaca actgctggaa tgcagtgggt aaaaaagatg 120
ccaggaaagg gttttaagtg gattggctgg ataaacaccc actctggaga tccaaaatat 180
gcagaagact tcaagggacg gtttgccttc tctttgaaa cctacgccag tactgcatat 240
ttgcagataa gcaacctcaa aaacgaggac actgcttcgt atttctgtgc gaggaccac 300
atctatgatg gttataacta tgctatggac tactggggtc aaggacctc agtcaccgtc 360
tcctca 366

<210> 82
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> 11C8 light chain 1 (L1) variable region (dominant)

<400> 82

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

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

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

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

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

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

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

<210> 83
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> 11C8 L1 CDRL1

<400> 83

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

<210> 84
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 11C8 L1 CDRL2

<400> 84

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 85
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 11C8 L1 CDRL3

<400> 85

Ser Gln Ser Thr His Val Pro Phe Thr
1 5

<210> 86
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> 11C8 light chain 1 (L1) variable region cDNA (dominant)

<400> 86
gatgttgatga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60
atctcttgca gatctagtca gaggccttgta tatagtaatg gaaacaccta ttacattgg 120
tacctgcaga agccaggcca gtctccaaag ctctgatct acaaagtttc caaccgattt 180
tctgggggtcc cagacagggt cagtggcagt ggatcaggga cagatttcac actcaagatc 240
agcagagtgg aggctgagga tctggggagt tatttctgct ctcaaagtac acatgttcca 300
ttcacgttcg gctcggggac aaagttggaa ataaaa 336

<210> 87
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> 11C8 light chain 2 (L2) variable region

<400> 87

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

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

Tyr Trp Cys Gln Gln Lys Ser Asp Ala Ser Pro Lys Leu Trp Ile Tyr
35 40 45

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

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

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

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

<210> 88
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 11C8 L2 CDRL1

<400> 88

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

<210> 89
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 11C8 L2 CDRL2

<400> 89

Tyr Thr Ser Asn Leu Ala Pro
1 5

<210> 90
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> 11C8 L2 CDRL3

<400> 90

Gln Gln Phe Thr Ser Ser Pro Ser Met His Thr
1 5 10

<210> 91

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> 11C8 light chain 2 (L2) variable region cDNA

<400> 91

gaaaatgtgc tcaccagtc tccagcaatc atgtctgcat ctctagggga gaaggtcacc 60
atgagctgca gggccagctc aagtgtaaat tacatgtact ggtgccagca gaagtcagat 120
gcctcccca aactatggat ttattacaca tccaacctgg ctcttgaggt cccagctcgc 180
ttcagtggca gtgggtctgg gaactcttat tctctcaca tcagcagcat ggagggtgaa 240
gatgttgcca cttattactg ccagcagttt actagttccc catccatgca cacgttcgga 300
ggggggacca agctggaaat aaaa 324

<210> 92

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> 11C8 heavy chain variable region

<400> 92

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

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

Gly Met Gln Trp Val Gln Lys Met Pro Gly Lys Gly Phe Lys Trp Ile
35 40 45

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

Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Tyr Ala Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Thr His Ile Tyr Asp Gly Tyr Asn Tyr Ala Met Asp Tyr Trp
100 105 110

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

<210> 93
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 11C8 CDRH1

<400> 93

Thr Ala Gly Met Gln
1 5

<210> 94
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 11C8 CDRH2

<400> 94

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

Gly

<210> 95
<211> 13

<212> PRT
<213> Artificial Sequence

<220>
<223> 11C8 CDRH3

<400> 95

Thr His Ile Tyr Asp Gly Tyr Asn Tyr Ala Met Asp Tyr
1 5 10

<210> 96
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> 11C8 heavy chain variable region cDNA

<400> 96
cagatccagt tggatgcagtc tggacctgag ctgaagaagc ctggagagac agtcaagatc 60
tcctgcaagg cttctgggta taccttcaca actgctggaa tgcagtgggt acaaaagatg 120
ccaggaaagg gttttaagtg gattggctgg ataaacaccc actctggaga tccaaaatat 180
gcagaagact tcaagggacg gtttgccttc tctttggaaa cctacgccag tactgcatat 240
ttgcagataa gcaacctcaa aaacaggagc actgcttcgt atttctgtgc gaggaccac 300
atctatgatg gttacaacta tgctatggac tactgggggtc aaggacctc agtcaccgtc 360
tcctca 366

<210> 97
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> 11H3 light chain variable region

<400> 97

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

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

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

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

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

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

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

<210> 98
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> 11H3 CDRL1

<400> 98

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

<210> 99
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 11H3 CDRL2

<400> 99

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 100
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> 11H3 CDRL3

<400> 100

Ser Gln Ser Thr His Val Pro Phe Thr
1 5

<210> 101

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> 11H3 light chain variable region cDNA

<400> 101

gatgttgtga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60
atctcttgca gatctagtca gagccttgta tatagtaatg gaaacaccta ttacattgg 120
tacctgcaga agccaggcca gtctccaaag ctctgatct acaaagtttc caaccgattt 180
tctgggggtcc cagacagggt cagtggcagt ggatcaggga cagatttcac actcaagatc 240
agcagagtgg aggctgagga tctgggagtt tatttctgct ctcaaagtac acatgtttcca 300
ttcacgttcg gctcggggac aaagttggaa ataaaa 336

<210> 102

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> 11H3 heavy chain variable region

<400> 102

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

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

Gly Met Gln Trp Val Gln Lys Met Pro Gly Lys Gly Phe Lys Trp Ile
35 40 45

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

Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Tyr Ala Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Thr His Ile Tyr Asp Gly Tyr Asn Tyr Ala Met Asp Tyr Trp
100 105 110

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

<210> 103
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 11H3 CDRH1

<400> 103

Thr Ala Gly Met Gln
1 5

<210> 104
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 11H3 CDRH2

<400> 104

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

Gly

<210> 105
<211> 13
<212> PRT
<213> Artificial Sequence

<220>

<223> 11H3 CDRH3

<400> 105

Thr His Ile Tyr Asp Gly Tyr Asn Tyr Ala Met Asp Tyr
1 5 10

<210> 106

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> 11H3 heavy chain variable region cDNA

<400> 106

cagatccagt tgggtgcagtc tggacctgag ctgaagaagc ctggagagac agtcaagatc 60
tcctgcaagg cttctgggta taccttcaca actgctggaa tgcagtgggt acaaaagatg 120
ccaggaaagg gttttaagtg gattggctgg ataaacaccc actctggaga tccaaaatat 180
gcagaagact tcaagggacg gtttgccttc tctttggaaa cctacgccag cactgcatat 240
ttgcagataa gcaacctcaa aaacgaggac actgctacgt atttctgtgc gaggacccat 300
atctatgatg gttataatta tgctatggac tactgggggtc aaggaacctc agtcaccgtc 360
tcctca 366

<210> 107

<211> 445

<212> PRT

<213> Artificial Sequence

<220>

<223> 4E11 Heavy chain human IgG1

<400> 107

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

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

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

Met Gly Tyr Ile Gly Tyr Asn Gly Arg Thr Ser Tyr Asn Pro Ser Leu
50 55 60

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 108

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> 4E11 Light chain human Kappa

<400> 108

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

Asp Thr Val Ser Ile Thr Cys His Ala Ser Gln Gly Ile Asn Ser Asn
20 25 30

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

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

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

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

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

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

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

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

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> 109
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> 5G6 Heavy chain human IgG1

<400> 109

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

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

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

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

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

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

Thr Leu Tyr Asp Tyr Asp Pro Asp Tyr Trp Gly Gln Gly Thr Thr Leu
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 110
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> 5G6 Light chain human Kappa

<400> 110

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

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

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

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

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

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

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

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

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

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

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

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

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

<210> 111
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> 13.1.2 Heavy chain human IgG1

<400> 111

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

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Asp Gly Trp Gln Gln Leu Ala Pro Phe Asp Tyr Trp Gly Gln
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly

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

<220>

<223> 13.1.2 Light chain human Kappa

<400> 112

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Asp Gly Asn Thr Tyr Leu Ser Trp Leu His Gln Arg Pro Gly Gln Pro
35 40 45

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

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

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

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

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

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

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

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

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

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

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

<210> 113
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal light chain signal sequence

<400> 113

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

Gly Ala Tyr Gly
20

<210> 114
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal heavy chain signal sequence

<400> 114

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala

<210> 115
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus VLs of 4B3 and 5D8

<220>

<221> MISC_FEATURE
<222> (9)..(9)
<223> X is a conservative amino acid substitution to alanine (A) or valine (V) or is alanine or valine

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> X is a conservative amino acid substitution to leucine (L) or phenylalanine (F) or is leucine or phenylalanine

<220>
<221> MISC_FEATURE
<222> (108)..(108)
<223> X is a conservative amino acid substitution to lysine (K) or glutamic acid (E) or is lysine or glutamic acid

<400> 115

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

Glu Lys Val Thr Ile Thr Cys Ser Val Ser Ser Ser Ile Ser Ser Ser
20 25 30

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

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

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

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

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

<210> 116
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus VHs of 4B3 and 5D8

<220>
 <221> MISC_FEATURE
 <222> (10)..(10)
 <223> X is a conservative amino acid substitution to glutamic acid (E) or aspartic acid (D) or is glutamic acid or aspartic acid

<220>
 <221> MISC_FEATURE
 <222> (34)..(34)
 <223> X is a conservative amino acid substitution to methionine (M) or isoleucine (I) or is methionine or isoleucine

<220>
 <221> MISC_FEATURE
 <222> (55)..(55)
 <223> X is a conservative amino acid substitution to asparagine (N) or tyrosine (Y) or is asparagine or tyrosine

<220>
 <221> MISC_FEATURE
 <222> (77)..(77)
 <223> X is a conservative amino acid substitution to asparagine (N) or serine (S) or is asparagine or serine

<400> 116

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

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

Asn	Xaa	Asp	Trp	Val	Lys	Gln	Ser	His	Gly	Lys	Ser	Leu	Glu	Trp	Ile
		35					40					45			

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

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

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

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

Thr Leu Val Thr Val Ser Ala
115

<210> 117
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus of VHs of 11B1, 11C8 and 11H3

<220>
<221> MISC_FEATURE
<222> (38)..(38)
<223> X is a conservative amino acid substitution to lysine (K) or glutamine (Q) or is lysine or glutamine

<220>
<221> MISC_FEATURE
<222> (93)..(93)
<223> X is conservative amino acid substitution to serine (S) or threonine (T) or is serine or threonine

<400> 117

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

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

Gly Met Gln Trp Val Xaa Lys Met Pro Gly Lys Gly Phe Lys Trp Ile
35 40 45

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

Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Tyr Ala Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Thr His Ile Tyr Asp Gly Tyr Asn Tyr Ala Met Asp Tyr Trp

Gly Gln Gly Thr Ser Val Thr Val
 115 120

<210> 118
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus VLs of 4B3, 5D8 and 9C9

<220>
 <221> MISC_FEATURE
 <222> (9)..(9)
 <223> X is a conservative amino acid substitution to alanine (A),
 threonine (T) or valine (V) or is alanine, threonine or valine

<220>
 <221> MISC_FEATURE
 <222> (10)..(10)
 <223> X is a conservative amino acid substitution to leucine (L) or
 phenylalanine (F) or is leucine or phenylalanine

<220>
 <221> MISC_FEATURE
 <222> (51)..(51)
 <223> X is a conservative amino acid substitution to glycine (G) or
 aspartic acid (D) or is glycine or glutamic acid

<220>
 <221> MISC_FEATURE
 <222> (61)..(61)
 <223> X is a conservative amino acid substitution to isoleucine (I) or
 valine (V) or is isoleucine or valine

<220>
 <221> MISC_FEATURE
 <222> (79)..(79)
 <223> X is a conservative amino acid substitution to methionine (M) or
 valine (V) or is methionine or valine

<220>
 <221> MISC_FEATURE
 <222> (101)..(101)
 <223> X is a conservative amino acid substitution to alanine (A) or
 serine (S) or is alanine or serine

<220>
 <221> MISC_FEATURE

<222> (107)..(107)
<223> X is a conservative amino acid substitution to isoleucine (I) or leucine (L) or is isoleucine or leucine

<220>
<221> MISC_FEATURE
<222> (108)..(108)
<223> X is a conservative amino acid substitution to lysine (K) or glutamic acid (E) or is lysine or glutamic acid

<400> 118

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

Glu Lys Val Thr Ile Thr Cys Ser Val Ser Ser Ser Ile Ser Ser Ser
20 25 30

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

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

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

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

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

<210> 119
<211> 76
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 1 to 76 of EGFRvIII

<400> 119

Leu Glu Glu Lys Lys Gly Asn Tyr Val Val Thr Asp His Gly Ser Cys
1 5 10 15

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

Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val Cys Asn Gly
35 40 45

Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn
50 55 60

Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly
65 70 75

<210> 120
<211> 62
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 1 to 62 of EGFRvIII

<400> 120

Leu Glu Glu Lys Lys Gly Asn Tyr Val Val Thr Asp His Gly Ser Cys
1 5 10 15

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

Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val Cys Asn Gly
35 40 45

Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala
50 55 60

<210> 121
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 1 to 49 of EGFRvIII

<400> 121

Leu Glu Glu Lys Lys Gly Asn Tyr Val Val Thr Asp His Gly Ser Cys
1 5 10 15

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

Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val Cys Asn Gly
35 40 45

Ile

<210> 122
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 1 to 45 of EGFRVIII

<400> 122

Leu Glu Glu Lys Lys Gly Asn Tyr Val Val Thr Asp His Gly Ser Cys
1 5 10 15

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

Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val
35 40 45

<210> 123
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 1 to 37 of EGFRVIII

<400> 123

Leu Glu Glu Lys Lys Gly Asn Tyr Val Val Thr Asp His Gly Ser Cys
1 5 10 15

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

Arg Lys Cys Lys Lys
35

<210> 124
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 1 to 33 of EGFRvIII

<400> 124

Leu Glu Glu Lys Lys Gly Asn Tyr Val Val Thr Asp His Gly Ser Cys
1 5 10 15

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

Arg

<210> 125
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 1 to 18 of EGFRvIII

<400> 125

Leu Glu Glu Lys Lys Gly Asn Tyr Val Val Thr Asp His Gly Ser Cys
1 5 10 15

Val Arg

<210> 126
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 3 to 49 of EGFRvIII

<400> 126

Glu Lys Lys Gly Asn Tyr Val Val Thr Asp His Gly Ser Cys Val Arg
1 5 10 15

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

Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val Cys Asn Gly Ile
35 40 45

<210> 127
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 3 to 45 of EGFRvIII

<400> 127

Glu Lys Lys Gly Asn Tyr Val Val Thr Asp His Gly Ser Cys Val Arg
1 5 10 15

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

Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val
35 40

<210> 128
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 3 to 37 of EGFRvIII

<400> 128

Glu Lys Lys Gly Asn Tyr Val Val Thr Asp His Gly Ser Cys Val Arg
1 5 10 15

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

Cys Lys Lys
35

<210> 129
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 3 to 18 of EGFRvIII

<400> 129

Glu Lys Lys Gly Asn Tyr Val Val Thr Asp His Gly Ser Cys Val Arg
1 5 10 15

<210> 130
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 6 to 49 of EGFRvIII

<400> 130

Gly Asn Tyr Val Val Thr Asp His Gly Ser Cys Val Arg Ala Cys Gly
1 5 10 15

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

Cys Glu Gly Pro Cys Arg Lys Val Cys Asn Gly Ile
35 40

<210> 131
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 6 to 45 of EGFRvIII

<400> 131

Gly Asn Tyr Val Val Thr Asp His Gly Ser Cys Val Arg Ala Cys Gly
1 5 10 15

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

Cys Glu Gly Pro Cys Arg Lys Val
35 40

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

<220>
<223> Amino acid residues 6 to 37 of EGFRvIII

<400> 132

Gly Asn Tyr Val Val Thr Asp His Gly Ser Cys Val Arg Ala Cys Gly
1 5 10 15

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

<210> 133
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 10 to 49 of EGFRvIII

<400> 133

Val Thr Asp His Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr
1 5 10 15

Glu Met Glu Glu Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro
20 25 30

Cys Arg Lys Val Cys Asn Gly Ile
35 40

<210> 134
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 10 to 45 of EGFRvIII

<400> 134

Val Thr Asp His Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr
1 5 10 15

Glu Met Glu Glu Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro
20 25 30

Cys Arg Lys Val
35

<210> 135

<211> 28

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid residues 10 to 37 of EGFRvIII

<400> 135

Val Thr Asp His Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr
1 5 10 15

Glu Met Glu Glu Asp Gly Val Arg Lys Cys Lys Lys
20 25

<210> 136

<211> 35

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid residues 15 to 49 of EGFRvIII

<400> 136

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

Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val Cys
20 25 30

Asn Gly Ile
35

<210> 137
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 15 to 45 of EGFRvIII

<400> 137

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

Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val
20 25 30

<210> 138
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 19 to 76 of EGFRvIII

<400> 138

Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu Asp Gly Val Arg Lys
1 5 10 15

Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val Cys Asn Gly Ile Gly
20 25 30

Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys
35 40 45

His Phe Lys Asn Cys Thr Ser Ile Ser Gly
50 55

<210> 139
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 19 to 62 of EGFRvIII

<400> 139

Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu Asp Gly Val Arg Lys
1 5 10 15

Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val Cys Asn Gly Ile Gly
20 25 30

Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala
35 40

<210> 140
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 19 to 49 of EGFRvIII

<400> 140

Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu Asp Gly Val Arg Lys
1 5 10 15

Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val Cys Asn Gly Ile
20 25 30

<210> 141
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 19 to 45 of EGFRvIII

<400> 141

Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu Asp Gly Val Arg Lys
1 5 10 15

Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val
20 25

<210> 142
<211> 19
<212> PRT
<213> Artificial Sequence

<220>

<223> Amino acid residues 19 to 37 of EGFRvIII

<400> 142

Ala	Cys	Gly	Ala	Asp	Ser	Tyr	Glu	Met	Glu	Glu	Asp	Gly	Val	Arg	Lys
1				5					10					15	

Cys Lys Lys

<210> 143

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid residues 28 to 45 of EGFRvIII

<400> 143

Glu	Glu	Asp	Gly	Val	Arg	Lys	Cys	Lys	Lys	Cys	Glu	Gly	Pro	Cys	Arg
1				5					10					15	

Lys Val

<210> 144

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid residues 28 to 37 of EGFRvIII

<400> 144

Glu	Glu	Asp	Gly	Val	Arg	Lys	Cys	Lys	Lys
1				5					10

<210> 145

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid residues 15 to 37 of EGFRvIII, with Ser15 to Ala mutation

<400> 145

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

Gly Val Arg Lys Cys Lys Lys
20

<210> 146
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 15 to 37 of EGFRvIII, with Cys16 to Ala
mutation

<400> 146

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

Gly Val Arg Lys Cys Lys Lys
20

<210> 147
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 15 to 37 of EGFRvIII, with Val17 to Ala
mutation

<400> 147

Ser Cys Ala Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu Asp
1 5 10 15

Gly Val Arg Lys Cys Lys Lys
20

<210> 148
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 15 to 37 of EGFRvIII, with Arg18 to Ala

mutation

<400> 148

Ser Cys Val Ala Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu Asp
1 5 10 15

Gly Val Arg Lys Cys Lys Lys
20

<210> 149

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid residues 15 to 37 of EGFRvIII, with Cys20 to Ala
mutation

<400> 149

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

Gly Val Arg Lys Cys Lys Lys
20

<210> 150

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid residues 15 to 37 of EGFRvIII, with Gly21 to Ala
mutation

<400> 150

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

Gly Val Arg Lys Cys Lys Lys
20

<210> 151

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid residues 15 to 37 of EGFRvIII, with Asp23 to Ala mutation

<400> 151

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

Gly	Val	Arg	Lys	Cys	Lys	Lys
			20			

<210> 152

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid residues 15 to 37 of EGFRvIII, with Ser24 to Ala mutation

<400> 152

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

Gly	Val	Arg	Lys	Cys	Lys	Lys
			20			

<210> 153

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid residues 15 to 37 of EGFRvIII, with Tyr25 to Ala mutation

<400> 153

Ser	Cys	Val	Arg	Ala	Cys	Gly	Ala	Asp	Ser	Ala	Glu	Met	Glu	Glu	Asp
1				5					10					15	

Gly	Val	Arg	Lys	Cys	Lys	Lys
			20			

<210> 154

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

<220>
<223> Amino acid residues 15 to 37 of EGFRvIII, with Glu26 to Ala mutation

<400> 154

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

Gly Val Arg Lys Cys Lys Lys
20

<210> 155
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 15 to 37 of EGFRvIII, with Met27 to Ala mutation

<400> 155

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

Gly Val Arg Lys Cys Lys Lys
20

<210> 156
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 15 to 37 of EGFRvIII, with Glu28 to Ala mutation

<400> 156

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

Gly Val Arg Lys Cys Lys Lys
20

<210> 157
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 15 to 37 of EGFRvIII, with Glu29 to Ala mutation

<400> 157

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

Gly Val Arg Lys Cys Lys Lys
20

<210> 158
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 15 to 37 of EGFRvIII, with Asp30 to Ala mutation

<400> 158

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

Gly Val Arg Lys Cys Lys Lys
20

<210> 159
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 15 to 37 of EGFRvIII, with Gly31 to Ala mutation

<400> 159

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

Ala Val Arg Lys Cys Lys Lys
20

<210> 160
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 15 to 37 of EGFRvIII, with Val32 to Ala
mutation

<400> 160

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

Gly Ala Arg Lys Cys Lys Lys
20

<210> 161
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 15 to 37 of EGFRvIII, with Arg33 to Ala
mutation

<400> 161

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

Gly Val Ala Lys Cys Lys Lys
20

<210> 162
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid residues 15 to 37 of EGFRvIII, with Lys34 to Ala
mutation

<400> 162

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

Gly Val Arg Ala Cys Lys Lys
20

<210> 163

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid residues 15 to 37 of EGFRvIII, with Cys35 to Ala mutation

<400> 163

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

Gly Val Arg Lys Ala Lys Lys
20

<210> 164

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid residues 15 to 37 of EGFRvIII, with Lys36 to Ala mutation

<400> 164

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

Gly Val Arg Lys Cys Ala Lys
20

<210> 165

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid residues 15 to 37 of EGFRvIII, with Lys37 to Ala mutation

<400> 165

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

Gly Val Arg Lys Cys Lys Ala
20

<210> 166

<211> 244

<212> PRT

<213> Artificial Sequence

<220>

<223> Single-chain variable fragment composed of VH, linker, VL
sequence derived from 5G6 antibody

<400> 166

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

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

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

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

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

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

Thr Leu Tyr Asp Tyr Asp Pro Asp Tyr Trp Gly Gln Gly Thr Thr Leu
100 105 110

Thr Val Ser Ser Gly Thr Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser
130 135 140

Val Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
145 150 155 160

Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg
165 170 175

Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Ala Ser Lys Leu Asp
180 185 190

Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
195 200 205

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr
210 215 220

Cys Trp Gln Ala Thr His Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys
225 230 235 240

Leu Glu Ile Lys

<210> 167
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> Single-chain variable fragment composed of VH, linker, VL
sequence derived from 4E11 antibody

<400> 167

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

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

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

Met Gly Tyr Ile Gly Tyr Asn Gly Arg Thr Ser Tyr Asn Pro Ser Leu
50 55 60

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

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

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

Thr Val Ser Ala Gly Thr Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Asp Val Asp Ile Leu Met Thr Gln Ser Pro Ser Ser
130 135 140

Met Ser Val Ser Leu Gly Asp Thr Val Ser Ile Thr Cys His Ala Ser
145 150 155 160

Gln Gly Ile Asn Ser Asn Ile Gly Trp Leu Leu Gln Lys Pro Gly Lys
165 170 175

Ser Phe Lys Gly Leu Ile Tyr His Gly Thr Asn Leu Glu Asp Gly Val
180 185 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr
195 200 205

Ile Ser Ser Leu Glu Ser Glu Asp Phe Ala Asp Tyr Tyr Cys Val Gln
210 215 220

Tyr Ala Gln Phe Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
225 230 235 240

Lys

<210> 168

<211> 495
<212> PRT
<213> Artificial Sequence

<220>

<223> CAR construct composed of 5G6 scFV, a CD8 hinge, human CD28 transmembrane domain, human CD28-signaling domain, and human CD3-zeta signaling domain

<400> 168

Met Leu Arg Leu Leu Leu Ala Leu Asn Leu Phe Pro Ser Ile Gln Val
1 5 10 15

Thr Gly Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro
20 25 30

Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
35 40 45

Ser Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu
50 55 60

Trp Ile Gly Ala Ile Tyr Pro Gly Asn Ser Asp Ile Ser Tyr Asn Gln
65 70 75 80

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

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

Tyr Cys Thr Leu Tyr Asp Tyr Asp Pro Asp Tyr Trp Gly Gln Gly Thr
115 120 125

Thr Leu Thr Val Ser Ser Gly Thr Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Thr
145 150 155 160

Leu Ser Val Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser
165 170 175

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

Gln Arg Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Ala Ser Lys
195 200 205

Leu Asp Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr
210 215 220

Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val
225 230 235 240

Tyr Tyr Cys Trp Gln Ala Thr His Phe Pro Trp Thr Phe Gly Gly Gly
245 250 255

Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
260 265 270

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
275 280 285

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
290 295 300

Ala Cys Asp Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly
305 310 315 320

Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe
325 330 335

Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn
340 345 350

Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr
355 360 365

Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Ala Ser Leu Arg Val
370 375 380

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn

385 390 395 400

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
 405 410 415

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln
 420 425 430

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
 435 440 445

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
 450 455 460

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
465 470 475 480

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 485 490 495

<210> 169
<211> 492
<212> PRT
<213> Artificial Sequence

<220>
<223> CAR construct composed of 4E11 scFV, a CD8 hinge, human CD28
transmembrane domain, human CD28-signaling domain, and human
CD3-zeta signaling domain

<400> 169

Met Leu Arg Leu Leu Leu Ala Leu Asn Leu Phe Pro Ser Ile Gln Val
1 5 10 15

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

Ser Gln Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr
 35 40 45

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

Glu Trp Met Gly Tyr Ile Gly Tyr Asn Gly Arg Thr Ser Tyr Asn Pro
65 70 75 80

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

Phe Phe Leu Gln Leu Asn Tyr Val Thr Thr Glu Asp Thr Ala Thr Phe
100 105 110

Tyr Cys Ala Arg Leu Gly Arg Gly Phe Ala Tyr Trp Gly Gln Gly Thr
115 120 125

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

Ser Gly Gly Gly Gly Ser Asp Val Asp Ile Leu Met Thr Gln Ser Pro
145 150 155 160

Ser Ser Met Ser Val Ser Leu Gly Asp Thr Val Ser Ile Thr Cys His
165 170 175

Ala Ser Gln Gly Ile Asn Ser Asn Ile Gly Trp Leu Leu Gln Lys Pro
180 185 190

Gly Lys Ser Phe Lys Gly Leu Ile Tyr His Gly Thr Asn Leu Glu Asp
195 200 205

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
210 215 220

Leu Thr Ile Ser Ser Leu Glu Ser Glu Asp Phe Ala Asp Tyr Tyr Cys
225 230 235 240

Val Gln Tyr Ala Gln Phe Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
245 250 255

Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
260 265 270

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro

275

280

285

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
 290 295 300

Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala
 305 310 315 320

Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg
 325 330 335

Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro
 340 345 350

Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
 355 360 365

Arg Asp Phe Ala Ala Tyr Arg Ser Ala Ser Leu Arg Val Lys Phe Ser
 370 375 380

Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr
 385 390 395 400

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
 405 410 415

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys
 420 425 430

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
 435 440 445

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
 450 455 460

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
 465 470 475 480

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 485 490

<210> 170
<211> 527
<212> PRT
<213> Artificial Sequence

<220>
<223> 4E11 bi-specific T cell engager exemplary sequence

<400> 170

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

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

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

Met Gly Tyr Ile Gly Tyr Asn Gly Arg Thr Ser Tyr Asn Pro Ser Leu
50 55 60

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

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

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

Thr Val Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro
115 120 125

Gly Ser Leu Gly Thr Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

Gly Gly Ser Asp Val Asp Ile Leu Met Thr Gln Ser Pro Ser Ser Met
145 150 155 160

Ser Val Ser Leu Gly Asp Thr Val Ser Ile Thr Cys His Ala Ser Gln
165 170 175

Gly Ile Asn Ser Asn Ile Gly Trp Leu Leu Gln Lys Pro Gly Lys Ser
180 185 190

Phe Lys Gly Leu Ile Tyr His Gly Thr Asn Leu Glu Asp Gly Val Pro
195 200 205

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
210 215 220

Ser Ser Leu Glu Ser Glu Asp Phe Ala Asp Tyr Tyr Cys Val Gln Tyr
225 230 235 240

Ala Gln Phe Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
245 250 255

Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Lys
260 265 270

Leu Gly Asp Leu Gly Gly Gly Gly Ser Arg Asp Asp Ile Lys Leu
275 280 285

Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Met
290 295 300

Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp
305 310 315 320

Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
325 330 335

Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala
340 345 350

Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser
355 360 365

Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr
370 375 380

Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr

385 390 395 400

Val Ser Ser Val Glu Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
405 410 415

Ser Gly Gly Val Asp Asp Ile Gln Leu Thr Gln Ser Pro Ala Ile Met
420 425 430

Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser
435 440 445

Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro
450 455 460

Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro Tyr
465 470 475 480

Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser
485 490 495

Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser
500 505 510

Ser Asn Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
515 520 525

<210> 171
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 171

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

Ser Asp Val