

SEQUENCE LISTING

<110> Astellas Pharma Inc.

<120> PHARMACEUTICAL COMPOSITION CONTAINING TAGGED SITE-ANTI HUMAN ANTIBODY FAB FRAGMENT COMPLEX

<130> FA1535-19221

<150> JP 2018-191605

<151> 2018-10-10

<160> 19

<170> PatentIn version 3.5

<210> 1

<211> 678

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA encoding PB009-1 Fab heavy chain fragment

<220>

<221> CDS

<222> (1)..(678)

<400> 1

gaa	gtg	cag	ctg	gtg	gaa	tct	ggc	ggc	gga	ctg	gtg	cag	cct	ggc	gga	48
Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	
1				5					10					15		

tct	ctg	aga	ctg	agc	tgt	gcc	gcc	agc	ggc	ttc	aac	atc	cgg	gac	acc	96
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Asn	Ile	Arg	Asp	Thr	
			20					25					30			

tac	atg	cac	tgg	gtg	cgc	cag	gcc	cct	ggc	aag	gga	ctg	gaa	tgg	gtg	144
Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35					40					45				

gcc	aga	atc	gac	ccc	gcc	aac	ggc	aac	agc	aga	tac	gtg	ccc	aag	ttc	192
Ala	Arg	Ile	Asp	Pro	Ala	Asn	Gly	Asn	Ser	Arg	Tyr	Val	Pro	Lys	Phe	
	50					55					60					

cag	ggc	cgg	ttc	acc	atc	agc	gcc	gac	acc	agc	aga	aac	acc	gcc	tac	240
Gln	Gly	Arg	Phe	Thr	Ile	Ser	Ala	Asp	Thr	Ser	Arg	Asn	Thr	Ala	Tyr	
65					70				75					80		

ctg	cag	atg	aac	agc	ctg	cgg	gcc	gag	gac	acc	gcc	gtg	tac	tac	tgt	288
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
				85					90					95		

gcc ccc ttc ggc tac tac gtg tcc gac tac gcc atg gcc tat tgg ggc Ala Pro Phe Gly Tyr Tyr Val Ser Asp Tyr Ala Met Ala Tyr Trp Gly 100 105 110	336
cag ggc acc ctc gtg aca gtg tcc tca gcc tcc acc aag ggc cca tcg Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser 115 120 125	384
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala 130 135 140	432
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val 145 150 155 160	480
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala 165 170 175	528
gtc cta cag tcc tca gga ctc tac tcc ctt agt agc gtg gtg acc gtg Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val 180 185 190	576
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His 195 200 205	624
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 210 215 220	672
gac tga Asp 225	678

<210> 2
 <211> 225
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PB009-1 Fab heavy chain fragment

<400> 2

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 Asn Ile Arg Asp Thr

20

25

30

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

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

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

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

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

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

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

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

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

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

Asp
 225

<210> 3
 <211> 657
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA encoding PB009-1 Fab light chain

<220>
 <221> CDS
 <222> (1)..(657)

<400> 3
 gac atc cag ctg acc cag agc cct agc agc ctg tct gcc agc gtg ggc 48
 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 gac aga gtg acc atc acc tgt aga gcc ggc gag agc gtg gac atc ttc 96
 Asp Arg Val Thr Ile Thr Cys Arg Ala Gly Glu Ser Val Asp Ile Phe
 20 25 30
 ggc gtg gga ttt ctg cac tgg tat cag cag aag ccc ggc aag gcc ccc 144
 Gly Val Gly Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
 35 40 45
 aag ctg ctg atc tac aga gcc agc aac ctg gaa agc ggc atc ccc agc 192
 Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Ser
 50 55 60
 aga ttc agc ggc agc ggc tcc aga acc gac ttc acc ctg acc atc agc 240
 Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Ser
 65 70 75 80
 agc ctg cag ccc gag gac ttc gcc acc tac tac tgc cag cag acc aac 288
 Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Asn
 85 90 95
 gag gac ccc tac acc ttt ggc cag ggc acc aag gtg gaa atc aag cgt 336
 Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105 110
 acg gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag 384
 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 115 120 125
 ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat 432
 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
 130 135 140
 ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg 480
 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser

145	150	155	160	
ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc				528
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr	165	170	175	
tac agc ctg agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa				576
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys	180	185	190	
cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc				624
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro	195	200	205	
gtc aca aag agc ttc aac agg gga gag tgt tag				657
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys	210	215		

<210> 4
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PB009-1 Fab light chain

<400> 4

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 5
<211> 669
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA encoding P10-1 Fab heavy chain fragment

<400> 5
caggtgcagc tgggtgcagtc tggcgccgaa gtgaagaaac caggcgccag cgtgaaggtg 60
tcctgcaagg ccagcggcta caccttcacc aactacggcc tgagctgggt gcgccaggct 120
cctggacagg gactggaatg gatgggagcag aaccaccctg gcagcggcat catctaccac 180
aacgagaagt tccggggcag agtgaccctg accgccgacc ggagcaccag caccgcctac 240
atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgtgc cagaagcagc 300
ggcaccagag gctttgccta ttggggacag ggcaccctcg tgaccgtgtc ctcagcctcc 360

accaagggcc catcggctctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420
 gcggccctgg gctgcctggg caaggactac ttccccgaac cggtgacggg gtcgtggaac 480
 tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc 540
 tactccctta gtagcgtggg gaccgtgccc tccagcagct tgggcacca gacctacatc 600
 tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttga gcccaaattc 660
 tgtgactga 669

<210> 6
 <211> 222
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> P10-1 Fab heavy chain fragment

<400> 6

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

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

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

Gly Glu Asn His Pro Gly Ser Gly Ile Ile Tyr His Asn Glu Lys Phe
 50 55 60

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

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

Ala Arg Ser Ser Gly Thr Arg Gly 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
 210 215 220

<210> 7
 <211> 669
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA encoding P10-2 Fab heavy chain fragment

<400> 7
 caggtgcagc tggtgcagtc tggcgccgaa gtgaagaaac caggcgccag cgtgaaggtg 60
 tcctgcaagg ccagcggcta caccttcacc aactacggcc tgagctgggt gcgccaggct 120
 cctggacagg gactggaatg gatgggagcag aaccaccctg gcagcggcat catctaccac 180
 aacgagaagt tccggggcag agtgaccctg accgccgacc ggagcaccag caccgcctac 240
 atggaactga gcagcctgag gagcgaggac accgccgtgt actactgtgc cagaagcagc 300
 ggccaccagag gctttgacta ttggggacag ggcaccctcg tgaccgtgtc ctcagcctcc 360
 accaagggcc catcgggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420
 gcggccctgg gctgcctggg caaggactac ttccccgaac cggtgacggg gtcgtggaac 480
 tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc 540

tactccctta gtagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600
 tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttga gcccaaattc 660
 tgtgactga 669

<210> 8
 <211> 222
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> P10-2 Fab heavy chain fragment

<400> 8

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

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

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

Gly Glu Asn His Pro Gly Ser Gly Ile Ile Tyr His Asn Glu Lys Phe
 50 55 60

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

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

Ala Arg Ser Ser Gly Thr Arg Gly Phe Asp 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
 210 215 220

<210> 9
 <211> 660
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA encoding P10-1 and P10-2 Fab light chain

<400> 9
 gacgtcgtga tgaccagac ccctctgagc ctgagcgtga cacctggaca gcctgccagc 60
 atcagctgca gatccagcca gagcatcgtg cacagcaacg gcaacaccta cctggaatgg 120
 tatctgcaga agcccggcca gagccccag ctgctgatct acagggtgtc caaccggttc 180
 agcggcgtgc ccgacagatt ttctggcagc ggctccggca ccgacttcac cctgaagatc 240
 tcccgggtgg aagccgagga cgtgggcgtg tactactgtt ttcaaggcag ccacggcccc 300
 tggacctttg gccagggaa aaagctggaa atcaagcgta cgggtggctgc accatctgtc 360
 ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420
 ctgaataact tctatcccag agaggccaaa gtacagtggga aggtggataa cgccctccaa 480
 tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctg 540
 agcagcacc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600
 gtcacccatc agggcctgag ctgccccgtc acaaagagct tcaacagggg agagtgttag 660

<210> 10

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

<220>

<223> P10-1 and P10-2 Fab light chain

<400> 10

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

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

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

Pro Gln Leu Leu Ile Tyr Arg 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 Val Gly Val Tyr Tyr Cys Phe Gln Gly
85 90 95

Ser His Gly Pro Trp Thr Phe Gly Gln 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> 11
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA encoding P10-1 Fab heavy chain variable region

<400> 11
caggtgcagc tgggtgcagtc tggcgccgaa gtgaagaaac caggcgccag cgtgaaggtg 60
tcctgcaagg ccagcggcta caccttcacc aactacggcc tgagctgggt gcgccaggct 120
cctggacagg gactggaatg gatgggagcag aaccaccctg gcagcggcat catctaccac 180
aacgagaagt tccggggcag agtgaccctg accgccgacc ggagcaccag caccgcctac 240
atggaactga gcagcctgag gagcgaggac accgccgtgt actactgtgc cagaagcagc 300
ggcaccagag gctttgccta ttggggacag ggcaccctcg tgaccgtgtc ctca 354

<210> 12
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> P10-1 Fab heavy chain variable region

<400> 12

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

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

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

35

40

45

Gly Glu Asn His Pro Gly Ser Gly Ile Ile Tyr His Asn Glu Lys Phe
 50 55 60

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

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

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

Leu Val Thr Val Ser Ser
 115

<210> 13
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA encoding P10-2 Fab heavy chain variable region

<400> 13
 caggtgcagc tgggtgcagtc tggcgccgaa gtgaagaaac caggcgccag cgtgaaggtg 60
 tcctgcaagg ccagcggcta caccttcacc aactacggcc tgagctgggt gcgccaggct 120
 cctggacagg gactggaatg gatgggagcag aaccaccctg gcagcggcat catctaccac 180
 aacgagaagt tccggggcag agtgaccctg accgccgacc ggagcaccag caccgcctac 240
 atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgtgc cagaagcagc 300
 ggcaccagag gctttgacta ttggggacag ggcaccctcg tgaccgtgtc ctca 354

<210> 14
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> P10-2 Fab heavy chain variable region

<400> 14

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

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

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

Gly Glu Asn His Pro Gly Ser Gly Ile Ile Tyr His Asn Glu Lys Phe
50 55 60

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

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

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

Leu Val Thr Val Ser Ser
115

<210> 15

<211> 339

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA encoding P10-1 and P10-2 Fab light chain variable region

<400> 15

gacgtcgtga tgaccagac ccctctgagc ctgagcgtga cacctggaca gcctgccagc 60

atcagctgca gatccagcca gagcatcgtg cacagcaacg gcaacaccta cctggaatgg 120

tatctgcaga agcccgcca gagccccag ctgctgatct acagggtgtc caaccggttc 180

agcggcgtgc ccgacagatt ttctggcagc ggctccggca ccgacttcac cctgaagatc 240

tcccggtgg aagccgagga cgtgggcgtg tactactgtt ttcaaggcag ccacggcccc 300

tggacctttg gccaggggaac aaagctggaa atcaagcgt

339

<210> 16
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> P10-1 and P10-2 Fab light chain variable region

<400> 16

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

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

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

Pro Gln Leu Leu Ile Tyr Arg 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 Val Gly Val Tyr Tyr Cys Phe Gln Gly
85 90 95

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

Arg

<210> 17
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain signal sequence for PB009-1, P10-1 and P10-2 Fab

<400> 17

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

Val His Ser

<210> 18

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Light chain signal sequence for PB009-1, P10-1 and P10-2 Fab

<400> 18

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

Asp Ala Arg Cys
20

<210> 19

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Tandem repeat sequence of an extracellular domain of MUC1

<400> 19

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

Ala Pro Pro Ala
20