

SEQUENCE LISTING

<110> Astellas Pharma Inc.

<120> A conjugate comprising a ligand, a spacer, a peptide linker and a biomolecule

<130> A20002A00

<150> JP 2019-000530

<151> 2019-01-07

<150> JP 2019-206560

<151> 2019-11-14

<160> 19

<170> PatentIn version 3.5

<210> 1

<211> 678

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA encoding PB009-01 Fab heavy chain

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

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

 <220>
 <223> Synthetic Construct

 <400> 2

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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

Asp
225

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

<220>
<223> DNA encoding PB009-01 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
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 <220>
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Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly		
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		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 catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420
 gcggccctgg gctgcctggc caaggactac ttccccgaac cggtgacggt gtcgtggaac 480
 tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540
 tactccctta gtagcgtggc gaccgtgccc tccagcagct tgggcaccca 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 tgggtgcagtc tggcgccgaa gtgaagaaac caggcgccag cgtgaagggtg 60

tcctgcaagg ccagcggcta caccttcacc aactacggcc tgagctgggt gcgccaggct 120

cctggacagg gactggaatg gatgggcgag aaccaccctg gcagcggcat catctaccac 180

aacgagaagt tccggggcag agtgaccctg accgccgacc ggagcaccag caccgcctac 240

atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgtgc cagaagcagc 300

ggcaccagag gctttgacta ttggggacag ggcaccctcg tgaccgtgtc ctcagcctcc 360

accaagggcc catcgggtctt cccctggca ccctcctcca agagcacctc tgggggcaca 420

gcggccctgg gctgcctggg caaggactac ttccccgaac cggtgacggg gtcgtggaac 480
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc 540
tactccctta gtagcgtggg 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 antibody light chain

<400> 9
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atcagctgca gatccagcca gagcatcgtg cacagcaacg gcaacaccta cctggaatgg 120
tatctgcaga agcccgcca gagccccag ctgctgatct acagggtgtc caaccggttc 180
agcggcgtgc ccgacagatt ttctggcagc ggctccggca ccgacttcac cctgaagatc 240
tcccgggtgg aagccgagga cgtgggcgtg tactactgtt ttcaaggcag ccacggcccc 300
tggacctttg gccaggaac aaagctggaa atcaagcgta cggtggctgc accatctgtc 360
ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420
ctgaataact tctatcccag agaggccaaa gtacagtggga aggtggataa cgccctccaa 480
tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctg 540
agcagcacc tgacgtgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcaccatc agggcctgag ctcgccgtc acaaagagct tcaacagggg agagtgttag

660

<210> 10

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Antibody 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 gcagcctgcg 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 antibody 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 cgcacagatt ttctggcagc ggctccggca ccgacttcac cctgaagatc 240
 tcccgggtgg aagccgagga cgtgggcgtg tactactggt ttcaaggcag ccacggcccc 300
 tggacctttg gccagggaa aaagctggaa atcaagcgt 339

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

<220>
 <223> Antibody 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

<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

<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

