

SEQUENCE LISTING

<110> Astellas Pharma Inc.
 <120> Anti-human Fn14 antibody
 <130> A19011A00
 <150> JP 2018-205995
 <151> 2018-10-31

<160> 9
 <170> PatentIn version 3.5

<210> 1
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> H-chain of 4-1h antibody

<220>
 <221> CDS
 <222> (1).. (1365)

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 acc ctg tcc ctc acc tgc gct gtc tat ggt ggg tcc ttc agt ggt tac 96
 Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
 20 25 30
 tac tgg agc tgg atc cgc cag ccc cca ggg aag ggg ctg gag tgg att 144
 Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 ggg gaa atc aat cat cgt gga agc acc aac tcc aac ccg tcc ctc aag 192
 Gly Glu Ile Asn His Arg Gly Ser Thr Asn Ser Asn Pro Ser Leu Lys
 50 55 60
 agt cga gac acc ata tca gta gac acg tcc aag aac cag ttc tcc ctg 240
 Ser Arg Asp Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80
 agg ctg agg tct gtg acc gcc gcg gac acg gct gtg tat tac tgt gcg 288
 Arg Leu Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 cgc gag ggt ata agt gga agt atg ggg atc tac gac tac agc gga atg 336
 Arg Glu Gly Ile Ser Gly Ser Met Gly Ile Tyr Asp Tyr Ser Gly Met
 100 105 110

gac gtc tgg ggc caa ggg acc acg gtc acc gtc tcc tca gcc tcc acc	384
Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr	
115 120 125	
aag ggc cca tcg gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct	432
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser	
130 135 140	
ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa	480
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu	
145 150 155 160	
ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac	528
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His	
165 170 175	
acc ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc ctt agt agc	576
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser	
180 185 190	
gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc	624
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys	
195 200 205	
aac gtg aat cac aag ccc agc aac acc aag gtg gac aag aaa gtt gag	672
Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu	
210 215 220	
ccc aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct	720
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro	
225 230 235 240	
gaa gcc gct ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag	768
Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys	
245 250 255	
gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg	816
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val	
260 265 270	
gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac	864
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp	
275 280 285	
ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac	912
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr	
290 295 300	
aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac	960
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp	
305 310 315 320	
tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc	1008
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu	
325 330 335	

cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga	1056
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg	
340 345 350	
gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag	1104
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys	
355 360 365	
aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac	1152
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp	
370 375 380	
atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag	1200
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys	
385 390 395 400	
acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc	1248
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser	
405 410 415	
aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca	1296
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser	
420 425 430	
tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc	1344
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser	
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ctc tcc ctg tct ccg ggt aaa	1365
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450 455	

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Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile	
35 40 45	
Gly Glu Ile Asn His Arg Gly Ser Thr Asn Ser Asn Pro Ser Leu Lys	
50 55 60	

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

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

Arg Glu Gly Ile Ser Gly Ser Met Gly Ile Tyr Asp Tyr Ser Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
115 120 125

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

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

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

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

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

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

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
225 230 235 240

Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
260 265 270

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

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
 290 295 300

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
 325 330 335

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

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 385 390 395 400

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

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
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Leu Ser Leu Ser Pro Gly Lys
 450 455

<210> 3
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1 5 10 15																			
gag agg gcc acc atc aac tgc aag tcc agg cag agt att tta tat agt	96																		
Glu Arg Ala Thr Ile Asn Cys Lys Ser Arg Gln Ser Ile Leu Tyr Ser																			
20 25 30																			
tcc aac aat aag aac tac tta act tgg tac cag cag aaa cca gga cag	144																		
Ser Asn Asn Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln																			
35 40 45																			
cct cct aag ttg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc	192																		
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val																			
50 55 60																			
cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc	240																		
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr																			
65 70 75 80																			
atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa	288																		
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln																			
85 90 95																			
tat tat agt act cct tac act ttt ggc cag ggg acc aag ctg gag atc	336																		
Tyr Tyr Ser Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile																			
100 105 110																			
aaa cgg act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat	384																		
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp																			
115 120 125																			
gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac	432																		
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn																			
130 135 140																			
ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc	480																		
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu																			
145 150 155 160																			
caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac	528																		
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp																			
165 170 175																			
agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac	576																		
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr																			
180 185 190																			
gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc	624																		
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser																			
195 200 205																			
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35 40 45

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

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

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

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

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

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

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

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

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
7

180

185

190

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215 220

<210> 5
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 <223> H-chain of 4-1m antibody

<220>
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 <222> (1).. (1368)

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 Ser Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
 20 25 30
 tac tgg tcc tgg atc cgg cag ttc cct ggc aac aag ctg gaa tgg atg 144
 Tyr Trp Ser Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp Met
 35 40 45
 ggc gag atc aac cac cgg ggc tcc acc aac tct aac ccc agc ctg aag 192
 Gly Glu Ile Asn His Arg Gly Ser Thr Asn Ser Asn Pro Ser Leu Lys
 50 55 60
 tcc cgg atc tcc atc acc gtg gac acc tcc aag aac cag ttc ttt ctg 240
 Ser Arg Ile Ser Ile Thr Val Asp Thr Ser Lys Asn Gln Phe Phe Leu
 65 70 75 80
 cag ctc aac tcc gtg aca acc gag gac acc gcc acc tac tac tgt gcc 288
 Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
 85 90 95
 aga gag ggc atc tct ggc tcc atg ggc atc tac gac tac tcc ggc atg 336
 Arg Glu Gly Ile Ser Gly Ser Met Gly Ile Tyr Asp Tyr Ser Gly Met
 100 105 110
 gat gtg tgg ggc cag ggc aca ctg gtt acc gtg tct gcc gct aag acc 384
 Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Lys Thr
 115 120 125

acc gct cct tcc gtg tat cct ctg gca cct gtg tgt ggc gac acc acc	432
Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro Val Cys Gly Asp Thr Thr	
130 135 140	
gga agt tct gtg acc ctg gga tgt ctg gtc aag ggc tac ttc ccc gag	480
Gly Ser Ser Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu	
145 150 155 160	
cct gtg aca ctg acc tgg aac tct ggc tct ctg tcc tct ggc gtg cac	528
Pro Val Thr Leu Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His	
165 170 175	
acc ttt cca gcc gtg ctg cag tct gac ctg tac acc ctg tct agc tcc	576
Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser	
180 185 190	
gtg acc gtg acc tcc tct acc tgg cct agc cag tcc atc acc tgt aac	624
Val Thr Val Thr Ser Ser Thr Trp Pro Ser Gln Ser Ile Thr Cys Asn	
195 200 205	
gtg gcc cat cct gcc tcc agc acc aag gtg gac aag aag atc gag cct	672
Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Glu Pro	
210 215 220	
cgg ggc cct acc atc aag cct tgt cct cca tgc aag tgc ccc gct cct	720
Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro	
225 230 235 240	
aat ctg ctc gga ggc ccc tcc gtg ttc atc ttc cca cct aag atc aag	768
Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys	
245 250 255	
gac gtg ctg atg atc tcc ctg tct cct atc gtg acc tgc gtg gtg gtg	816
Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val	
260 265 270	
gcc gtg tcc gag gat gat cct gac gtg cag atc agt tgg ttc gtg aac	864
Ala Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn	
275 280 285	
aac gtg gaa gtg cac acc gct cag acc cag aca cac aga gag gac tac	912
Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr	
290 295 300	
aac agc acc ctg aga gtg gtg tct gcc ctg cct atc cag cat cag gat	960
Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp	
305 310 315 320	
tgg atg tcc ggc aaa gag ttc aag tgc aaa gtg aac aac aag gac ctg	1008
Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu	
325 330 335	
cct gct cca atc gag cgg acc atc tct aag cct aag ggc tct gtc agg	1056
Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg	
340 345 350	
gcc cct cag gtg tac gtt ttg cct cca cct gag gaa gag atg acc aag	1104

Ala	Pro	Gln	Val	Tyr	Val	Leu	Pro	Pro	Pro	Glu	Glu	Glu	Met	Thr	Lys		
		355					360					365					
aaa	caa	gtg	acc	ctg	aca	tgc	atg	gtc	acc	gac	ttc	atg	ccc	gag	gac	1152	
Lys	Gln	Val	Thr	Leu	Thr	Cys	Met	Val	Thr	Asp	Phe	Met	Pro	Glu	Asp		
	370					375				380							
atc	tac	gtg	gaa	tgg	acc	aac	aac	ggc	aag	acc	gag	ctg	aac	tac	aag	1200	
Ile	Tyr	Val	Glu	Trp	Thr	Asn	Asn	Gly	Lys	Thr	Glu	Leu	Asn	Tyr	Lys		
385					390					395					400		
aac	acc	gag	cca	gtg	ctg	gac	tcc	gac	ggc	tcc	tac	ttc	atg	tac	tcc	1248	
Asn	Thr	Glu	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Tyr	Phe	Met	Tyr	Ser		
				405					410					415			
aag	ctg	cgc	gtc	gag	aag	aag	aac	tgg	gtc	gag	aga	aac	tcc	tac	tcc	1296	
Lys	Leu	Arg	Val	Glu	Lys	Lys	Asn	Trp	Val	Glu	Arg	Asn	Ser	Tyr	Ser		
			420					425					430				
tgc	tcc	gtg	gtg	cac	gag	ggc	ctg	cac	aat	cac	cac	acc	acc	aag	tcc	1344	
Cys	Ser	Val	Val	His	Glu	Gly	Leu	His	Asn	His	His	Thr	Thr	Lys	Ser		
		435					440					445					
ttc	tct	cgg	acc	cct	ggc	aag	tga									1368	
Phe	Ser	Arg	Thr	Pro	Gly	Lys											
	450					455											

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			20					25					30				
Tyr	Trp	Ser	Trp	Ile	Arg	Gln	Phe	Pro	Gly	Asn	Lys	Leu	Glu	Trp	Met		
		35					40					45					
Gly	Glu	Ile	Asn	His	Arg	Gly	Ser	Thr	Asn	Ser	Asn	Pro	Ser	Leu	Lys		
	50					55					60						
Ser	Arg	Ile	Ser	Ile	Thr	Val	Asp	Thr	Ser	Lys	Asn	Gln	Phe	Phe	Leu		
65					70					75					80		

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

Arg Glu Gly Ile Ser Gly Ser Met Gly Ile Tyr Asp Tyr Ser Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Lys Thr
115 120 125

Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro Val Cys Gly Asp Thr Thr
130 135 140

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

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

Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser
180 185 190

Val Thr Val Thr Ser Ser Thr Trp Pro Ser Gln Ser Ile Thr Cys Asn
195 200 205

Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Glu Pro
210 215 220

Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro
225 230 235 240

Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys
245 250 255

Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val
260 265 270

Ala Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn
275 280 285

Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr
290 295 300

Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp
 305 310 315 320

Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu
 325 330 335

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

Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys
 355 360 365

Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp
 370 375 380

Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys
 385 390 395 400

Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser
 405 410 415

Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser
 420 425 430

Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser
 435 440 445

Phe Ser Arg Thr Pro Gly Lys
 450 455

<210> 7
 <211> 663
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> L-chain of 4-1m antibody

<220>
 <221> CDS
 <222> (1).. (663)

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20 25 30	
tcc aac aac aag aac tac ctg acc tgg tat cag cag aag ccc ggc cag Ser Asn Asn Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln	144
35 40 45	
tct cct aag ctg ctg atc tac tgg gcc tcc acc aga gaa tct ggc gtg Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val	192
50 55 60	
ccc gat aga ttc acc ggc tct ggc tct ggc acc gac ttt acc ctg acc Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr	240
65 70 75 80	
atc tcc tcc gtg aag gcc gag gat ctg gct gtg tac tac tgc cag cag Ile Ser Ser Val Lys Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln	288
85 90 95	
tac tac agc acc cct tac acc ttt ggc tcc ggc acc aag ctg gaa atc Tyr Tyr Ser Thr Pro Tyr Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile	336
100 105 110	
aag aga gct gac gcc gct cct acc gtg tct atc ttc cca cct agc tcc Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser	384
115 120 125	
gag cag ctg acc tct ggc gga gct tct gtc gtg tgc ttc ctg aac aac Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn	432
130 135 140	
ttc tac ccc aag gac atc aac gtg aag tgg aag atc gac ggc tcc gag Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu	480
145 150 155 160	
aga cag aac ggc gtg ctg aac tct tgg acc gac cag gac tcc aag gac Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp	528
165 170 175	
agc acc tac tcc atg tcc tcc aca ctg acc ctg aca aag gac gag tac Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr	576
180 185 190	
gag cgg cac aac tcc tat acc tgc gag gct acc cac aag acc tcc acc Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr	624
195 200 205	
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210 215 220	

<210> 8
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Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser Val Gly
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Glu Lys Val Thr Met Ser Cys Lys Ser Arg Gln Ser Ile Leu Tyr Ser
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Ser Asn Asn Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

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

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

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

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

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

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

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

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

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

Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr
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<400> 9

Ile	Glu	Gly	Arg	Met	Asp	Gly	Gly	Gly
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