

SEQUENCE LISTING

<110> CHUGAI SEIYAKU KABUSHIKI KAISHA

<120> Antibody capable of neutralizing substance having activity alternative to function of Coagulation Factor VIII (FVIII)

<130> C1-A1407P

<150> JP 2014-197207

<151> 2014-09-26

<160> 38

<170> PatentIn version 3.5

<210> 1

<211> 124

<212> PRT

<213> Artificial

<220>

<223> AQ8 VH

<400> 1

Glu	Val	Asn	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
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Ser	Met	Ser	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Thr	Asp	Tyr
			20					25					30		

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

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

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

Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Ser Ala Thr Tyr

 85 90 95

Tyr Cys Ala Arg Asp Ser Tyr Tyr Ser Tyr Asp Gly Tyr Ala Met Asp
100 105 110

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

$\langle 210 \rangle$	2
$\langle 211 \rangle$	107
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	Artificial

$\langle 220 \rangle$
 $\langle 223 \rangle$ AQ8 VL

$\langle 400 \rangle$ 2

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

Glu Thr Ile Thr Ile Thr Cys Gln Ala Ser Glu Asn Ile Tyr Phe Ser
20 25 30

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

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

Ser Gly Ser Gly Thr Gln Tyr Ser Met Lys Ile Asn Ser Met Gln Pro
65 70 75 80

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

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

$\langle 210 \rangle$	3
$\langle 211 \rangle$	120
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	Artificial

<220>
 <223> AJ540 VH

<400> 3

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

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

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

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

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

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

Ala Arg Glu Gly Gly Gly Tyr Tyr Trp Tyr Phe Asp Phe Trp Gly Pro
 100 105 110

Gly Thr Met Val Thr Val Ser Ser
 115 120

<210> 4
 <211> 107
 <212> PRT
 <213> Artificial

<220>
 <223> AJ540 VL

<400> 4

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

Asp Arg Val Thr Met Asn Cys Lys Ala Asn Gln Asn Val Asp Phe Asn
 20 25 30

Val Asp Trp Tyr Gln Gln Lys Thr Gly Gln Ser Pro Lys Leu Leu Ile
 35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Asn Met Gln Ala
 65 70 75 80

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

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

<210> 5
 <211> 372
 <212> DNA
 <213> Artificial

<220>
 <223> nucleic acid sequence of AQ8 VH

<400> 5
 gaagtgaacc tgggtgaaag cggcggaggc ctggtgcagc cggaggcag catgtctctg 60
 agctgcgccg ccagcggctt caccttcacc gactactaca tgagctgggt ccgccagccc 120
 cctggcaagg ctctggaatg gctggctctg atcagaaaca aggccaacgg ctacaccacc 180
 gagtacagcg ccagcgtgaa gggccggttc accatcagcc gggacaacag ccagagcatc 240
 ctgtacctgc agatgaacgc cctgcgggcc gaggactcgg ccacctacta ctgcgccaga 300
 gacagctact acagctacga cggctacgcc atggactact ggggccaggg caccagcgtg 360
 accgtgtcta gc 372

<210> 6
 <211> 321
 <212> DNA
 <213> Artificial

<220>
 <223> nucleic acid sequence of AQ8 VL

<400> 6
 gacatccaga tgaccagag ccctgcctcc ctggccgcct ctgtgggcca gacaatcacc 60
 atcacctgtc aggccagcga gaacatctac ttcagcctgg cctggtatca gcagaagcag 120
 ggcaagagcc ccagctgct gatctacaac accgacagcc tgaaggacgg cgtgcccagc 180

agattcagcg gcagcggctc cggcaccag tacagcatga agatcaacag catgcagccc 240
 gaggacaccg ctacctactt ttgccggcag agctacgact tcccctggac cttcggcgga 300
 ggcaccaagc tggaaatcaa g 321

<210> 7
 <211> 360
 <212> DNA
 <213> Artificial

<220>
 <223> nucleic acid sequence of AJ540 VH

<400> 7
 cagatccagc tggcgcagag cggccctgag ctgaagaaac ccggcgagag cgtgaagatc 60
 agctgcaagg ccagcggcta caccttcacc gactacgcca tgcactgggt gaaacagggtg 120
 cccggcaagg gcctgaagtg gatgggctgg atcaacacct acaccggcaa gccacacctac 180
 gccgacgact tcaagggcag attcgtgttc agcctggaag ccagcgccag caccgccaac 240
 ctgcagatca gcaacctgaa gaacgaggac accgccaacg tgttctgcgc cagagagggc 300
 ggaggctact actggtactt cgacttctgg ggccctggca caatggtgac agtgtccagc 360

<210> 8
 <211> 321
 <212> DNA
 <213> Artificial

<220>
 <223> nucleic acid sequence of AJ540 VL

<400> 8
 gacatcgtga tgaccagag ccccaccagc atgagcatca gcgtgggcca cagagtgacc 60
 atgaactgca aggccaacca gaacgtggac ttcaacgtgg actggtatca gcagaaaacc 120
 ggccagtccc ccaagctgct gatctacaag gccagcaacc ggtacacagg cgtgcccgcac 180

agattcacag gcagcggcag cggcaccgac ttacacttca ccacagcaa catgcaggcc 240
gaggacctgg ccgtgtacta ctgcatgcag agcaacagct tccccctgac cttcggctcc 300
ggcaccaacc tggaatcaa g 321

<210> 9
<211> 448
<212> PRT
<213> Artificial

<220>
<223> Artificial sequence

<400> 9

Gln 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 Thr Phe Ser Tyr Tyr
20 25 30

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

Ser Ser Ile Ser Pro Ser Gly Gln Ser Thr Tyr Tyr Arg Arg Glu 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 Arg Thr Gly Arg Glu Tyr Gly Gly Gly Trp Tyr Phe Asp Tyr

	100		105		110										
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly
	115						120					125			
Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser
	130					135					140				
Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val
145					150					155					160
Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe
				165					170					175	
Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val
			180					185					190		
Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Thr	Cys	Asn	Val
	195						200					205			
Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys
210						215					220				
Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	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	Gln	Glu
			260					265						270	

Asp Pro Glu Val Gln 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 Gly Leu Pro Ser Ser 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 Gln Lys Glu Met 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 Glu Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

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

<210> 10
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 <213> Artificial

<220>
 <223> Artificial sequence

<400> 10

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
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Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Arg Asn Ile Glu Arg Gln
 20 25 30

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

Tyr Gln Ala Ser Arg Lys Glu Ser Gly Val Pro Asp Arg Phe Ser Gly
 50 55 60

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

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

Thr Phe Gly Gly Gly Thr Lys Val 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> 11
 <211> 444
 <212> PRT
 <213> Artificial

<220>
 <223> Artificial sequence

<400> 11

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

Asn Met Asp Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

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

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
 210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Phe 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 Gln Glu Asp Pro Glu Val
 260 265 270

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

Asn His Tyr Thr Gln Glu Ser Leu Ser Leu Ser Pro
 435 440

<210> 12
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 <213> Artificial

<220>
 <223> AQ8 heavy chain CDR1

<400> 12

Asp Tyr Tyr Met Ser
 1 5

<210> 13
 <211> 19
 <212> PRT
 <213> Artificial

<220>
 <223> AQ8 heavy chain CDR2

<400> 13

Leu Ile Arg Asn Lys Ala Asn Gly Tyr Thr Thr Glu Tyr Ser Ala Ser
 1 5 10 15

Val Lys Gly

<210> 14
 <211> 13
 <212> PRT
 <213> Artificial

<220>
 <223> AQ8 heavy chain CDR3

<400> 14

Asp	Ser	Tyr	Tyr	Ser	Tyr	Asp	Gly	Tyr	Ala	Met	Asp	Tyr
1				5					10			

<210> 15
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 <212> DNA
 <213> Artificial

<220>
 <223> nucleic acid sequence of AQ8 heavy chain CDR1

<400> 15
 gactactaca tgagc

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<210> 16
 <211> 57
 <212> DNA
 <213> Artificial

<220>
 <223> nucleic acid sequence of AQ8 heavy chain CDR2

<400> 16
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57

<210> 17
 <211> 39
 <212> DNA
 <213> Artificial

<220>
 <223> nucleic acid sequence of AQ8 heavy chain CDR3

<400> 17
 gacagctact acagctacga cggctacgcc atggactac

39

<210> 18
 <211> 11
 <212> PRT
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<220>
 <223> AQ8 light chain CDR1

<400> 18
 Gln Ala Ser Glu Asn Ile Tyr Phe Ser Leu Ala
 1 5 10

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

<220>
 <223> AQ8 light chain CDR2

<400> 19
 Asn Thr Asp Ser Leu Lys Asp
 1 5

<210> 20
 <211> 9

<212> PRT
 <213> Artificial

<220>
 <223> AQ8 light chain CDR3

<400> 20

Arg Gln Ser Tyr Asp Phe Pro Trp Thr
 1 5

<210> 21
 <211> 33
 <212> DNA
 <213> Artificial

<220>
 <223> nucleic acid sequence of AQ8 light chain CDR1

<400> 21
 caggccagcg agaacatcta cttcagcctg gcc 33

<210> 22
 <211> 21
 <212> DNA
 <213> Artificial

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 <223> nucleic acid sequence of AQ8 light chain CDR2

<400> 22
 aacaccgaca gcctgaagga c 21

<210> 23
 <211> 27
 <212> DNA
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<220>
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<400> 23
cggcagagct acgacttccc ctggacc

27

<210> 24
<211> 5
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<223> AJ540 heavy chain CDR1

<400> 24

Asp Tyr Ala Met His
1 5

<210> 25
<211> 17
<212> PRT
<213> Artificial

<220>
<223> AJ540 heavy chain CDR2

<400> 25

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

Gly

<210> 26
<211> 11
<212> PRT
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<223> AJ540 heavy chain CDR3

<400> 26

Glu Gly Gly Gly Tyr Tyr Trp Tyr Phe Asp Phe
1 5 10

<210> 27

<211> 15

<212> DNA

<213> Artificial

<220>

<223> nucleic acid sequence of AJ540 heavy chain CDR1

<400> 27

gactacgccac tgcac

15

<210> 28

<211> 51

<212> DNA

<213> Artificial

<220>

<223> nucleic acid sequence of AJ540 heavy chain CDR2

<400> 28

tggatcaaca cctacaccgg caagcccacc tacgccgacg acttcaaggg c

51

<210> 29

<211> 33

<212> DNA

<213> Artificial

<220>

<223> nucleic acid sequence of AJ540 heavy chain CDR3

<400> 29

gagggcggag gctactactg gtacttcgac ttc

33

<210> 30
 <211> 11
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<220>
 <223> AJ540 light chain CDR1

<400> 30

Lys Ala Asn Gln Asn Val Asp Phe Asn Val Asp
 1 5 10

<210> 31
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 <212> PRT
 <213> Artificial

<220>
 <223> AJ540 light chain CDR2

<400> 31

Lys Ala Ser Asn Arg Tyr Thr
 1 5

<210> 32
 <211> 9
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<220>
 <223> AJ540 light chain CDR3

<400> 32

Met Gln Ser Asn Ser Phe Pro Leu Thr
 1 5

<210> 33
 <211> 33
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<223> nucleic acid sequence of AJ540 light chain CDR1

<400> 33

aaggccaacc agaacgtgga cttcaacgtg gac

33

<210> 34
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<223> nucleic acid sequence of AJ540 light chain CDR2

<400> 34

aaggccagca accggtacac a

21

<210> 35
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<223> nucleic acid sequence of AJ540 light chain CDR3

<400> 35

atgcagagca acagcttccc cctgacc

27

<210> 36
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 <212> PRT
 <213> Artificial

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<400> 36

Gln 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 Thr Phe Ser Tyr Tyr
 20 25 30

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

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

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

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

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

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

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

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

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

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

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

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

Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe 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 Gln Glu
 260 265 270

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

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe 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 Gly Leu Pro Ser Ser Ile Glu
 325 330 335

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

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

Trp 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 Arg Leu Thr Val Asp
 405 410 415

Lys Ser Arg Trp Gln Glu 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 Leu
 435 440 445

<210> 37

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<212> PRT

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<223> artificial sequence

<400> 37

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

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

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

Gly Asp Ile Asn Thr Arg Ser Gly Gly Ser Ile Tyr Asn Glu Glu Phe
 50 55 60

Gln Asp Arg Val Thr Met Thr Ile Asp Lys Ser Thr Gly 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 Arg Arg Ser Tyr Gly Tyr Tyr His Asp Glu Trp Gly Glu Gly
 100 105 110

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

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
 130 135 140

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

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

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

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

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
 210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Phe 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 Gln Glu Asp Pro Glu Val
 260 265 270

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

Lys Pro Arg Glu Glu Gln Phe 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 Gly Leu Pro Ser Ser 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 Gln Cys Glu Met Thr Lys Asn Gln Val Ser Leu Ser Cys Ala 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 Val Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415

Gln Glu 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 Leu
 435 440

<210> 38

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<223> artificial sequence

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Val 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