

SEQUENCE LISTING

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Ala	Gln	Phe	Pro	Gly	Ala	Cys	Gly	Leu	Arg	Tyr	Arg	Asn	Pro	Val	Ser	35	40	45	
Gln	Cys	Met	Arg	Gly	Val	Arg	Leu	Val	Glu	Gly	Ile	Leu	His	Ala	Pro	50	55	60	
Asp	Ala	Gly	Trp	Gly	Asn	Leu	Val	Tyr	Val	Val	Asn	Tyr	Pro	Lys	Asp	65	70	75	80
Asn	Lys	Arg	Lys	Met	Asp	Glu	Thr	Asp	Ala	Ser	Ser	Ala	Val	Lys	Val	85	90	95	
Lys	Arg	Ala	Val	Gln	Lys	Thr	Ser	Asp	Leu	Ile	Val	Leu	Gly	Leu	Pro	100	105	110	
Trp	Lys	Thr	Thr	Glu	Gln	Asp	Leu	Lys	Glu	Tyr	Phe	Ser	Thr	Phe	Gly	115	120	125	
Glu	Val	Leu	Met	Val	Gln	Val	Lys	Lys	Asp	Leu	Lys	Thr	Gly	His	Ser	130	135	140	
Lys	Gly	Phe	Gly	Phe	Val	Arg	Phe	Thr	Glu	Tyr	Glu	Thr	Gln	Val	Lys	145	150	155	160
Val	Met	Ser	Gln	Arg	His	Met	Ile	Asp	Gly	Arg	Trp	Cys	Asp	Cys	Lys	165	170	175	
Leu	Pro	Asn	Ser	Lys	Gln	Ser	Gln	Asp	Glu	Pro	Leu	Arg	Ser	Arg	Lys	180	185	190	
Val	Phe	Val	Gly	Arg	Cys	Thr	Glu	Asp	Met	Thr	Glu	Asp	Glu	Leu	Arg	195	200	205	
Glu	Phe	Phe	Ser	Gln	Tyr	Gly	Asp	Val	Met	Asp	Val	Phe	Ile	Pro	Lys	210	215	220	
Pro	Phe	Arg	Ala	Phe	Ala	Phe	Val	Thr	Phe	Ala	Asp	Asp	Gln	Ile	Ala	225	230	235	240
Gln	Ser	Leu	Cys	Gly	Glu	Asp	Leu	Ile	Ile	Lys	Gly	Ile	Ser	Val	His	245	250	255	

Ile	Ser	Asn	Ala	Glu	Pro	Lys	His	Asn	Ser	Asn	Arg	Gln	Leu	Glu	Arg
			260					265					270		
Ser	Gly	Arg	Phe	Gly	Gly	Asn	Pro	Gly	Gly	Phe	Gly	Asn	Gln	Gly	Gly
		275				280						285			
Phe	Gly	Asn	Ser	Arg	Gly	Gly	Gly	Ala	Gly	Leu	Gly	Asn	Asn	Gln	Gly
	290				295						300				
Ser	Asn	Met	Gly	Gly	Gly	Met	Asn	Phe	Gly	Ala	Phe	Ser	Ile	Asn	Pro
305				310						315					320
Ala	Met	Met	Ala	Ala	Ala	Gln	Ala	Ala	Leu	Gln	Ser	Ser	Trp	Gly	Met
			325						330					335	
Met	Gly	Met	Leu	Ala	Ser	Gln	Gln	Asn	Gln	Ser	Gly	Pro	Ser	Gly	Asn
			340					345					350		
Asn	Gln	Asn	Gln	Gly	Asn	Met	Gln	Arg	Glu	Pro	Asn	Gln	Ala	Phe	Gly
		355					360					365			
Ser	Gly	Asn	Asn	Ser	Tyr	Ser	Gly	Ser	Asn	Ser	Gly	Ala	Ala	Ile	Gly
	370				375						380				
Trp	Gly	Ser	Ala	Ser	Asn	Ala	Gly	Ser	Gly	Ser	Gly	Phe	Asn	Gly	Gly
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1 5 10 15
Ser Val Lys Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr
20 25 30
Ser Ile His Trp Val Lys Gln Ser His Gly Glu Ser Leu Glu Trp Ile
35 40 45
Gly Gly Ile Asn Pro Asp Asn Gly Gly Thr Arg 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 Asp Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Glu Ser Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
100 105 110

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Gly Ile Asn Pro Asp Asn Gly Gly Thr Arg Tyr Asn Gln Lys Phe Lys
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<220>
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Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn 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 Val Ser Lys Leu Asp Ser Arg Ile 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 Gly
85 90 95
Thr His Phe Pro His Thr Phe Gly Ser Gly Thr Lys Leu Glu Leu Lys
100 105 110

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<220>
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Leu Val Ser Lys Leu Asp Ser
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<400> 17
Trp Gln Gly Thr His Phe Pro His Thr
1 5

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catggagaga gccttgagtg gattggaggt attaatcctg acaatggtgg tactaggtac 180
aaccagaagt tcaagggcaa ggcgacattg actgtagaca agtcctccag cacagcctac 240
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ttgttacaga ggccaggcca gtctccaaag cgcctaactct atctggtgtc taaactggac    180
tctagaatcc ctgacagggt cactggcagt ggatcaggga cagatttcac actgaaaatc    240
agcagagtgg aggctgagga tttgggagtt tattattgct ggcaaggtag acattttcct    300
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<400> 20

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Ser Val Lys Ile Ser Cys Lys Thr Ser Gly Phe Thr Phe Thr Glu Tyr
      20      25      30
Ser Met His Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
      35      40      45
Gly Gly 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 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 Glu Ser Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
      100     105     110
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Glu Tyr Ser Met His
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Gly

<210> 23
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<220>
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<400> 23
Glu Ser Xaa Xaa Xaa
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Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His 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 Val Ser Lys Leu Asp Ser Arg Ile 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 Gly
85 90 95
Thr His Phe Pro His Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105 110

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<400> 27
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catggaaaga gccttgagt gattggaggt attaatccta acaatgggtg tactagctac 180
aaccagaagt tcaagggcaa ggccacattg actgtagaca agtcctccag cacagcctac 240
atggagctcc gcagcctaac atctgaggat tctgcagtct attactgtgc aagagagtcc 300

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ttgttacaga ggccaggcca gtctccaaag cgcctaactct atctgggtgtc taaactggac 180

tctagaatcc ctgacagggt cactggcagt ggatcaggga cagatttcac actgaaaatc 240

agcagagtgg aggctgagga tttgggagtt tattattgct ggcaagggtac acattttcct 300

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<223> ACI-7069-634H10-Ab2 VH

<400> 30

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

Ser Val Arg Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

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

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

Gln Gly Lys Ala Thr Ile Thr Ser Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

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

Ala Arg Phe Tyr Gly Gly Ser His Trp Tyr Phe Asp Val Trp Gly Ala
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

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Asp Thr Tyr Met His
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<400> 32
Arg Ile Asp Pro Ala Asn Ser Asn Thr Lys Phe Asp Pro Lys Phe Gln
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Gly

<210> 33
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<220>
<223> ACI-7069-634H10-Ab2 VH CDR3

<400> 33
Phe Tyr Gly Gly Ser His Trp Tyr Phe Asp Val
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<210> 34
<211> 107
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<223> ACI-7069-634H10-Ab2 VL

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Asp Ile Lys Met Thr Gln Ser Pro Ser Ser Met Tyr Ala Ser Leu Gly
1 5 10 15
Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Lys Ser Tyr
20 25 30

Leu	Ser	Trp	Tyr	Gln	His	Lys	Pro	Trp	Lys	Ser	Pro	Lys	Ala	Leu	Ile
		35					40					45			
Tyr	Tyr	Ala	Thr	Ser	Leu	Ala	Asp	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				
Ser	Gly	Ser	Gly	Gln	Asp	Tyr	Ser	Leu	Thr	Ile	Ser	Ser	Leu	Glu	Ser
65					70					75					80
Asp	Asp	Thr	Ala	Thr	Tyr	Tyr	Cys	Leu	Gln	Gln	Gly	Glu	Ser	Pro	Tyr
				85					90					95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys					
			100					105							

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Tyr	Ala	Thr	Ser	Leu	Ala	Asp
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Leu	Gln	Gln	Gly	Glu	Ser	Pro	Tyr	Thr
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cctgaacagg gcctggaatg gattggaagg attgatacctg cgaatagtaa tactaaattt	180
gacccgaagt tccagggcaa ggccactata acatcagaca catcctcaa cacagcctac	240
ctgcagctca gcagcctgac atctgaggac actgccgtct attactgtgc tagattctac	300
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tggaaatctc ctaaggccct gatctattat gctacaagct tggcagatgg ggtcccatca	180
agattcagtg gcagtggatc tgggcaagat tattctctaa ccatcagcag cctggagtct	240
gacgatacag caacttacta ctgtctacag caaggtgaga gcccgtagac gttcggaggg	300
gggaccaagc tggaaataaa a	321

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<400> 40

Glu	Val	His	Leu	Val	Glu	Ser	Gly	Gly	Asp	Leu	Val	Met	Pro	Gly	Gly
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Ser	Leu	Lys	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Asn	Tyr
			20					25					30		
Gly	Met	Ser	Trp	Val	Arg	Gln	Thr	Pro	Asp	Lys	Arg	Leu	Glu	Trp	Val
		35					40					45			
Ala	Thr	Ile	Ser	Ser	Gly	Gly	Lys	Tyr	Ile	Asn	Tyr	Leu	Asp	Ser	Leu
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr
65					70					75					80
Leu	Gln	Met	Ser	Ser	Leu	Lys	Ser	Glu	Asp	Thr	Ala	Met	Tyr	Tyr	Cys
				85					90					95	
Ala	Lys	Asp	Tyr	Gly	Ser	Gly	Trp	Ala	Trp	Phe	Ala	Tyr	Trp	Gly	Gln
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Gly	Thr	Leu	Val	Thr	Val	Ser	Ala								
		115					120								

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 Asn Tyr Gly Met Ser
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<210> 42
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 Thr Ile Ser Ser Gly Gly Lys Tyr Ile Asn Tyr Leu Asp Ser Leu Lys
 1 5 10 15
 Gly

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<220>
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1 5 10

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1 5 10 15
Ser Ala Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser Thr Tyr Thr
20 25 30
Ile Glu Trp Tyr Gln Gln Gln Pro Leu Lys Pro Pro Lys Tyr Val Met
35 40 45
Glu Leu Lys Lys Asp Gly Ser His Ser Thr Gly Asp Gly Ile Pro Asp
50 55 60
Arg Phe Ser Gly Ser Ser Ser Gly Ala Asp Arg Tyr Leu Ser Ile Ser
65 70 75 80
Asn Ile Gln Pro Glu Asp Glu Ala Ile Tyr Ile Cys Gly Val Gly Asp
85 90 95
Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Gly Thr Lys Val
100 105 110
Thr Val Leu
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<220>
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Thr Leu Ser Ser Gln His Ser Thr Tyr Thr Ile Glu
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Gly Ser His Ser Thr Gly Asp
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<220>
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Gly Val Gly Asp Thr Ile Lys Glu Gln Phe Val Tyr Val
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tcctgtgcag cctctggatt cactttcagt aactatggca tgtcttgggt tcgccagact 120
ccagacaaga ggctggagtg ggtcgcaacc attagtagtg gtggtaaata tatcaactac 180
ttagacagtt tgaaggggcg attcaccatc tccagagaca atgccaagaa caccctatac 240
ctgcaaatga gcagtctgaa gtctgaggat acagccatgt attactgtgc aaaagactac 300
ggtagtggct gggcctgggt tgcttactgg ggccaaggga ctctggtcac tgtctctgca 360

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acgtgcacct tgagtagtca gcacagtacg tacaccattg aatggatatca gcaacagcca 120
ctcaagcctc ctaagtatgt gatggagctt aagaaagatg gaagccacag cacaggtgat 180
gggattcctg atcgcttctc tggatccagc tctggtgctg atcgctacct tagcatttcc 240

aacatccagc ctgaagatga agcaatatac atctgtggtg tgggtgatac aattaaggaa 300
caattttgtgt atgttttcgg cgggtggaacc aaggtcactg tccta 345

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Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln
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Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30
Gly Val His Trp Val Arg Gln Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45
Gly Leu Met Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60
Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
65 70 75 80
Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Val
85 90 95
Ile Tyr Arg Thr Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110
Val Ser Ala
115

<210> 61

<211> 5

<212> PRT

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<220>

<223> ACI-7069-641H1-Ab2 VH CDR1

<400> 61

Asn Tyr Gly Val His
1 5

<210> 62

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> ACI-7069-641H1-Ab2 VH CDR2

<400> 62

Leu Met Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met Ser
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<210> 63

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> ACI-7069-641H1-Ab2 VH CDR3

<400> 63

Tyr Arg Thr Gly Phe Ala Tyr
1 5

<210> 64

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> ACI-7069-641H1-Ab2 VL

<400> 64

Asp Val Leu 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 Ile Val His Thr
20 25 30
Ile Gly Asn Thr Tyr Leu Glu 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 Tyr Cys Phe Gln Gly
85 90 95
Ser His Val Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 65

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> ACI-7069-641H1-Ab2 VL CDR1

<400> 65

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

<210> 66

<211> 7

<212> PRT

<213> Artificial Sequence

<220>
<223> ACI-7069-641H1-Ab2 VL CDR2

<400> 66
Lys Val Ser Asn Arg Phe Ser
1 5

<210> 67
<211> 9
<212> PRT
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<220>
<223> ACI-7069-641H1-Ab2 VL CDR3

<400> 67
Phe Gln Gly Ser His Val Pro Phe Thr
1 5

<210> 68
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
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acttgtactg tctctggggtt ttcattaacc aactatgggtg tacactgggt tcgccagcct 120
ccaggaaagg gtctgggagtg gctggggacta atgtgggctg gtggaagcac aaattataat 180
tcggctctca tgtccagact gagcatcagc aaagacaact ccaagagtca agttttctta 240
aaaatgaaca gtctgcaaac tgatgacaca gccatgtact actgtgtcat ctataggacg 300
gggtttgctt actggggcca agggactctg gtcactgtct ctgca 345

<210> 69
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> ACI-7069-641H1-Ab2 VL

<400> 69
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atctcttgca gatctagtca gagcattgta catactattg gaaacaccta tttagaatgg 120
 tacctgcaga aaccaggcca gtctccaaag ctcctgatct acaaagtttc caaccggttt 180
 tctgggggtcc cagacagggtt cagtggcagt ggatcaggga cagatttcac actcaagatc 240
 agcagagtgg aggctgagga tctgggagtt tattactgct ttcaaggttc acatgttcca 300
 ttcactttcg gctcggggac aaagttggaa ataaaa 336

<210> 70
 <211> 113
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ACI-7069-642A10-ab1 VH

<400> 70
 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 Lys Tyr
 20 25 30
 Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Glu Ile Asn Pro Ser Asn Gly Arg Thr Asn Tyr Asn Glu Lys Phe
 50 55 60
 Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Tyr Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
 100 105 110
 Ser

<210> 71
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ACI-7069-642A10-ab1 VH CDR1

<400> 71
 Lys Tyr Trp Met His
 1 5

<210> 72
 <211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> ACI-7069-642A10-ab1 VH CDR2

<400> 72
Glu Ile Asn Pro Ser Asn Gly Arg Thr Asn Tyr Asn Glu Lys Phe Lys
1 5 10 15
Ser

<210> 73
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> ACI-7069-642A10-ab1 VH CDR3

<400> 73
Tyr Met Asp Tyr
1

<210> 74
<211> 112
<212> PRT
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<220>
<223> ACI-7069-642A10-ab1 VL

<400> 74
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 Phe Asp Arg
 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 Val 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 Gly
 85 90 95
Thr His Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 75

<211> 16
<212> PRT
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<220>
<223> ACI-7069-642A10-ab1 VL CDR1

<400> 75
Lys Ser Ser Gln Ser Leu Phe Asp Arg Asp Gly Lys Thr Tyr Leu Asn
1 5 10 15

<210> 76
<400> 76
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<210> 77
<211> 9
<212> PRT
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<220>
<223> ACI-7069-642A10-ab1 VL CDR3

<400> 77
Trp Gln Gly Thr His Phe Pro Trp Thr
1 5

<210> 78
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> ACI-7069-642A10-ab1 VH

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tcctgcaagg cttctggcta caccttcacc aagtactgga tgcactgggt gaagcagagg 120
cctggacaag gccttgagtg gattggagag attaatccta gcaacggtcg tactaactac 180
aatgagaagt tcaagagcaa ggccacactg actgtagaca aatcctccag cacagcctac 240
atgcaactca gcagcctgac atctgaggac tctgcggtct attactgtgc aagatatatg 300
gactactggg gtcaaggaac ctcagtcacc gtctcctca 339

<210> 79
 <211> 336
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> ACI-7069-642A10-ab1 VL

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 atctcttgca agtcaagtca gaggcctctt gatcgtgatg gaaagacata tttgaattgg 120
 ttgttacaga ggccaggcca gtctccaaag cgcctaattct atctggtgtc taaactggac 180
 tctggagtcc ctgacaggtt cactggcagt ggatcaggga cagatttcac actgaaaatc 240
 agcagagtgg aggctgagga tttgggagtt tattattgct ggcaaggtag acattttccg 300
 tggacgttcg gtggaggcac caagctggaa atcaaa 336

<210> 80
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ACI-7069-642D12-Ab1 VH

<400> 80
 Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Arg Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Pro
 20 25 30
 Tyr Met His Trp Val Arg Gln Arg Pro Lys Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr Lys Tyr Asp Pro Lys Phe
 50 55 60
 Gln Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Asn Val Ala Tyr
 65 70 75 80
 Leu His Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Phe Tyr Gly Ser Ser His Trp Tyr Phe Asp Val Trp Gly Ala
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 81
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>

<223> ACI-7069-642D12-Ab1 VH CDR1

<400> 81

Asp Pro Tyr Met His

1 5

<210> 82

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> ACI-7069-642D12-Ab1 VH CDR2

<400> 82

Arg Ile Asp Pro Ala Asp Gly Asn Thr Lys Tyr Asp Pro Lys Phe Gln

1 5 10 15

Gly

<210> 83

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> ACI-7069-642D12-Ab1 VH CDR3

<400> 83

Phe Tyr Gly Ser Ser His Trp Tyr Phe Asp Val

1 5 10

<210> 84

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> ACI-7069-642D12-Ab1 VL

<400> 84

Asp Ile Lys Met Thr Gln Ser Pro Ser Ser Met Tyr Ala Ser Leu Gly

1 5 10 15

Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Lys Arg Tyr

20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Trp Lys Ser Pro Lys Ile Leu Ile

35 40 45

Tyr Tyr Ala Thr Ser Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly

50						55						60					
Thr	Gly	Ser	Gly	Gln	Asp	Tyr	Ser	Leu	Thr	Ile	Ser	Ser	Leu	Glu	Ser		
65					70					75					80		
Asp	Asp	Val	Ala	Thr	Tyr	Tyr	Cys	Leu	Gln	Gln	Gly	Glu	Ser	Pro	Tyr		
				85					90					95			
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys							
			100					105									

<210> 85
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<220>
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<400> 85													
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1				5					10				

<210> 86
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 <212> PRT
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<220>
 <223> ACI-7069-642D12-Ab1 VL CDR2

<400> 86						
Tyr	Ala	Thr	Ser	Leu	Ala	Asp
1				5		

<210> 87
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ACI-7069-642D12-Ab1 VL CDR3

<400> 87								
Leu	Gln	Gln	Gly	Glu	Ser	Pro	Tyr	Thr
1				5				

<210> 88
 <211> 360
 <212> DNA
 <213> Artificial Sequence

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<223> ACI-7069-642D12-Ab1 VH

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tcctgcacag cttctggcctt caacattaata gaccctata tgcactgggt caggcagagg	120
cctaaacagg gcctggagt gattggaagg attgacctg cggatggtaa tactaaatat	180
gacccgaagt tccagggcaa ggccacttta acagcagaca catcctcaa tgtagcctac	240
ctgcacctca gcagcctgac atctgaggac actgccgtct attactgtgc tagattctac	300
ggtagtagcc actggtatct cgatgtgtgg ggcgcaggga ccacggtcac cgtctcctca	360

<210> 89

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> ACI-7069-642D12-Ab1 VL

<400> 89

gacatcaaga tgaccagtc tccatcctcc atgtatgcat cgttgggaga gagagtcact	60
atcacttgca aggcgagtc ggacattaata aggtatttaa gctgggtacca gcagaaacca	120
tggaatctc ctaagatcct gatctattat gcaacaagct tggcagatgg ggtcccatca	180
agattcagtg gactggatc tggacaagat tattctctaa ccatcagcag cctggagtct	240
gacgatgtag caacttacta ctgtctacag caaggtgaga gcccgtagac gttcggaggg	300
gggaccaagc tggaaataaa a	321

<210> 90

<400> 90

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<210> 91

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<210> 92

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<210> 99
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<210> 100
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> ACI-7069-646B7-Ab1 VH

<400> 100
Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln
1 5 10 15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Phe
20 25 30
Gly Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45
Gly Ile Met Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60
Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
65 70 75 80
Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Val
85 90 95
Ile Tyr Lys Thr Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110
Val Ser Ala
115

<210> 101
<211> 5

<212> PRT
<213> Artificial Sequence

<220>
<223> ACI-7069-646B7-Ab1 VH CDR1

<400> 101
Asn Phe Gly Val His
1 5

<210> 102
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> ACI-7069-646B7-Ab1 VH CDR2

<400> 102
Ile Met Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met Ser
1 5 10 15

<210> 103
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> ACI-7069-646B7-Ab1 VH CDR3

<400> 103
Tyr Lys Thr Gly Phe Ala Tyr
1 5

<210> 104
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> ACI-7069-646B7-Ab1 VL

<400> 104
Asp Val Leu 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 Ile Val His Ala
20 25 30
Ile Gly Asn Thr Tyr Leu Glu 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	Tyr	Cys	Phe	Gln	Gly		
			85						90					95			
Ser	His	Val	Pro	Phe	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu	Ile	Lys		
		100					105						110				

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

<220>
 <223> ACI-7069-646B7-Ab1 VL CDR1

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

<210> 106
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ACI-7069-646B7-Ab1 VL CDR2

Lys	Val	Ser	Asn	Arg	Phe	Ser											
1			5														

<210> 107
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ACI-7069-646B7-Ab1 VL CDR2

Phe	Gln	Gly	Ser	His	Val	Pro	Phe	Thr									
1			5														

<210> 108

<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> ACI-7069-646B7-Ab1 VH

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acttgacttg tctctggatt ttcattaacc aactttgggtg tacactgggt tcgccagcct 120
ccaggaaagg gtctggagtg gctgggaata atgtgggctg gtggaagcac aaattataat 180
tcggctctca tgtccagact gagcatcagc aaagacaact ccaagagtca agttttctta 240
aaaatgaaca gtctccaaac tgatgacaca gccatgtact actgtgtcat ctataagacg 300
gggtttgctt actggggcca agggactctg gtcactgtct ctgca 345

<210> 109
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> ACI-7069-646B7-Ab1 VL

<400> 109
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atctcttgca gatctagtca gagcattgta catgctattg gaaacaccta tttagaatgg 120
tacctgcaga aaccaggcca gtctccaaag ctctgatct acaaagtttc caaccggttt 180
tctgggggtcc cagacagggt cagtggcagt ggatcaggga cagatttcac actcaagatc 240
agcagagtgg aggctgagga tctgggagtt tattactgct ttcaaggttc acatgttcca 300
ttcacgttcg gctcggggac aaagttggaa ataaaa 336

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<210> 120
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> ACI-7071-712A6-Ab1 VH

<400> 120
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Thr
1 5 10 15
Ser Val Lys Leu Ser Cys Lys Ala Ser Ala Tyr Thr Phe Thr Glu Tyr
 20 25 30
Thr Ile His Trp Ile Lys Gln Lys Ser Gly Gln Gly Leu Glu Trp Ile
 35 40 45
Gly Trp Phe His Pro Glu Asn Asp Asn Ile Lys Tyr Asn Glu Asn Phe
50 55 60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Arg Ser Ser Ser Thr Val Tyr
65 70 75 80
Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95
Ala Gly Thr Ser Gly Tyr Gly Asp Tyr Trp Gly Gln Gly Thr Thr Leu

100 105 110
Thr Val Ser Ser
115

<210> 121
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> ACI-7071-712A6-Ab1 VH CDR1

<400> 121
Glu Tyr Thr Ile His
1 5

<210> 122
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> ACI-7071-712A6-Ab1 VH CDR2

<400> 122
Trp Phe His Pro Glu Asn Asp Asn Ile Lys Tyr Asn Glu Asn Phe Lys
1 5 10 15
Asp

<210> 123
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> ACI-7071-712A6-Ab1 VH CDR3

<400> 123
Thr Ser Gly Tyr Gly Asp Tyr
1 5

<210> 124
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> ACI-7071-712A6-Ab1 VL

<400> 124

Asp	Val	Val	Met	Thr	Gln	Ile	Pro	Leu	Thr	Leu	Ser	Ile	Thr	Ile	Gly
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Gln	Pro	Ala	Ser	Ile	Ser	Cys	Lys	Ser	Ser	Gln	Ser	Leu	Leu	Pro	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	Val	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	Asp	Asp	Leu	Gly	Val	Tyr	Tyr	Cys	Trp	Gln	Gly
				85					90					95	
Thr	His	Phe	Pro	Pro	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys
			100					105					110		

<210> 125

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> ACI-7071-712A6-Ab1 VL CDR1

<400> 125

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

<210> 126

<400> 126

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<210> 127

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> ACI-7071-712A6-Ab1 VL CDR3

<400> 127

Trp	Gln	Gly	Thr	His	Phe	Pro	Pro	Thr
1				5				

<210> 128

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<223> ACI-7071-712A6-Ab1 VH

<400> 128

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tcctgtaagg cttctgccta caccttcact gaatatacta tacactggat aaagcagaaa	120
tctggacagg gtcttgagtg gattgggtgg tttcacctg aaaatgataa tataaagtac	180
aatgagaatt tcaaggacaa ggccacattg actgcggaca gacacctcag cacagtctat	240
atggaactta gtagattgac atctgaagac tctgcggtct atttctgtgc agggacgtca	300
ggctacggag actactgggg ccaaggcacc actctcacag tctcttca	348

<210> 129

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> ACI-7071-712A6-Ab1 VL

<400> 129

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ttgttacaga ggccaggcca gtctccaaag cgcctaactct atctggtgtc taaactggac	180
tctggagtcc ctgacagggt cactggcagt ggatcaggga cagatttcac actgaaaatc	240
agcagagtgg aggctgacga tttgggagtt tattattgct ggcaaggtac acattttcct	300
cctacgttcg gtgctgggac caagctggaa ctgaaa	336

<210> 130

<400> 130

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<210> 131

<400> 131

000

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<210> 140
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> ACI-7071-809D9-Ab2 VH

<400> 140
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Val
1 5 10 15
Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Lys Phe Thr Asp Tyr
20 25 30
Ser Met His Trp Val Lys Gln Ser His Thr Lys Ser Leu Glu Trp Ile
35 40 45
Gly Val Ile Ser Thr Tyr Tyr Gly Asp Thr Thr Tyr Asn Gln Lys Phe
50 55 60
Lys Gly Lys Ala Thr Ile Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys
85 90 95
Ala Thr Tyr Gly Asn Phe Pro Ala Ser Phe Ser Tyr Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ala
115

<210> 141
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> ACI-7071-809D9-Ab2 VH CDR1

<400> 141
Asp Tyr Ser Met His
1 5

<210> 142
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> ACI-7071-809D9-Ab2 VH CDR2

<400> 142
Val Ile Ser Thr Tyr Tyr Gly Asp Thr Thr Tyr Asn Gln Lys Phe Lys
1 5 10 15
Gly

<210> 143
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> ACI-7071-809D9-Ab2 VH CDR3

<400> 143
Tyr Gly Asn Phe Pro Ala Ser Phe Ser Tyr
1 5 10

<210> 144
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> ACI-7071-809D9-Ab2 VL

<400> 144
Asp Ile Val Met Thr Gln Ala Ala Pro Ser Ile Pro Val Thr Pro Gly
1 5 10 15

Glu	Ser	Val	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Lys	Ser	Leu	Leu	His	Ser
			20					25					30		
Asn	Gly	Asn	Thr	Tyr	Leu	Tyr	Trp	Phe	Leu	Gln	Arg	Pro	Gly	Gln	Ser
		35					40					45			
Pro	Gln	Leu	Leu	Ile	Tyr	Arg	Met	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro
	50					55					60				
Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ala	Phe	Thr	Leu	Arg	Ile
65				70						75				80	
Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Met	Gln	His
			85					90					95		
Leu	Glu	Tyr	Pro	Phe	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu	Ile	Lys
			100					105					110		

<210> 145
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ACI-7071-809D9-Ab2 VL CDR1

<400> 145
Arg Ser Ser Lys Ser Leu Leu His Ser Asn Gly Asn Thr Tyr Leu Tyr
1 5 10 15

<210> 146
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ACI-7071-809D9-Ab2 VL CDR2

<400> 146
Arg Met Ser Asn Leu Ala Ser
1 5

<210> 147
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ACI-7071-809D9-Ab2 VL CDR3

<400> 147
Met Gln His Leu Glu Tyr Pro Phe Thr

<210> 148

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> ACI-7071-809D9-Ab2 VH

<400> 148

caggtccagc tgcagcagtc tggggctgag ctggtgaggc ctggggctctc agtgaagatt	60
tcctgcaagg gttctggcta caaattcact gattattcta tgcactgggt gaaacagagt	120
catacaaaga gtctagagtg gattggagtt attagtactt actatggtga tactacctac	180
aaccagaaat tcaagggcaa ggccacaatc actgtagaca aatcctccag cacagcctat	240
atggaacttg ccagactgac atctgaggat tctgccatct attactgtgc aacgtacggt	300
aacttcccgg cctcattttc ttactggggc caagggactc tggtcactgt ctctgca	357

<210> 149

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> ACI-7071-809D9-Ab2 VL

<400> 149

gatattgtga tgactcaggc tgcaccctct atacctgtca ctcttgaga gtcagtatcc	60
atctcctgca ggtctagtaa gagtctcctg catagtaatg gcaacactta cttgtattgg	120
ttcctgcaga ggccaggcca gtctcctcag ctctgatata atcggtatgc caaccttgcc	180
tcaggagtcc cagacagggt cagtggcagt gggtcaggaa ctgctttcac actgagaatc	240
agtagagtgg aggctgagga tgtgggtgtt tattactgta tgcaacatct agaatatcca	300
ttcacgttcg gctcggggac aaagttggaa ataaaa	336

<210> 150

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> ACI-7071-809F12-Ab1 VH

<400> 150

Gln	Val	Gln	Leu	Lys	Glu	Ser	Gly	Pro	Gly	Leu	Val	Ala	Pro	Ser	Gln
1				5					10					15	
Ser	Leu	Ser	Ile	Thr	Cys	Thr	Val	Ser	Gly	Phe	Ser	Leu	Asn	Arg	Asn
			20					25					30		
Gly	Val	Gln	Trp	Val	Arg	Gln	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Leu	
		35					40				45				
Gly	Val	Ile	Trp	Pro	Gly	Gly	Ser	Thr	Asn	Cys	Asn	Ser	Ala	Leu	Met
		50				55					60				
Ser	Arg	Leu	Ser	Ile	Ser	Lys	Asp	Asn	Ser	Lys	Ser	Gln	Val	Phe	Leu
65					70				75					80	
Lys	Met	Asn	Ser	Leu	His	Thr	Asp	Asp	Thr	Gly	Ile	Tyr	Tyr	Cys	Ala
				85					90					95	
Arg	Val	Gly	Gly	Asn	Tyr	Val	Trp	Asp	Tyr	Asn	Asn	Tyr	Ala	Trp	Gly
			100					105					110		
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ala							
		115					120								

<210> 151

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> ACI-7071-809F12-Ab1 VH CDR1

<400> 151

Arg	Asn	Gly	Val	Gln
1				5

<210> 152

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> ACI-7071-809F12-Ab1 VH CDR2

<400> 152

Val	Ile	Trp	Pro	Gly	Gly	Ser	Thr	Asn	Cys	Asn	Ser	Ala	Leu	Met	Ser
1				5					10					15	

<210> 153

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> ACI-7071-809F12-Ab1 VH CDR3

<400> 153

Val Gly Gly Asn Tyr Val Trp Asp Tyr Asn Asn Tyr Ala
1 5 10

<210> 154

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> ACI-7071-809F12-Ab1 VL

<400> 154

Asp Val Leu 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 Asn Ile Val His Ser
20 25 30
Ile Gly Asn Thr Tyr Leu Glu 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 Tyr Cys Phe Gln Gly
85 90 95
Ser His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Arg
100 105 110

<210> 155

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> ACI-7071-809F12-Ab1 VL CDR1

<400> 155

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

<210> 156

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> ACI-7071-809F12-Ab1 VL CDR2

<400> 156

Lys Val Ser Asn Arg Phe Ser

1 5

<210> 157

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> ACI-7071-809F12-Ab1 VL CDR3

<400> 157

Phe Gln Gly Ser His Val Pro Tyr Thr

1 5

<210> 158

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> ACI-7071-809F12-Ab1 VH

<400> 158

cagggtgcagc tgaaggagtc aggacctggc ctggtggcgc cctcacagag cctgtccatc 60

acttgcaactg tctctggggtt ttcgttaaagc agaaatgggtg tacagtgggt tcgccagcct 120

ccaggaaaagg gtctggagtg gctgggagta atatggcctg gcggaagcac aaattgtaat 180

tcggctctca tgtccagact gagcatcagc aaagacaact ccaagagtca agttttctta 240

aaaatgaaca gtctgcacac tgatgacaca ggcatatatt actgtgccag agtagggggt 300

aactacgtgt gggactataa taactacgcc tggggccaag ggactctggt cactgtctct 360

gca 363

<210> 159

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> ACI-7071-809F12-Ab1 VL

<400> 159

gatgttttga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaggcctcc	60
atctcttgca gatctagtca gaacattgta catagtattg gaaacaccta tttagagtgg	120
tacctgcaga aaccaggcca gtctccaaag ctcctgatct acaaagtttc caaccgattt	180
tctgggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaagatc	240
agcagagtgg aggctgagga tctgggagtt tattactgct ttcaaggttc acatgttccg	300
tacacgttcg gaggggggac caagctagaa ataaga	336