

SEQUENCE LISTING

<110> CHIA TAI TIANQING PHARMACEUTICAL GROUP CO., LTD.

<120> MULTI-SPECIFIC ANTIBODY TARGETING BCMA

<150> CN202110405638.3

<151> 2021-04-15

<160> 84

<170> PatentIn version 3.5

<210> 1

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide linker

<400> 1

Gly Gly Gly Gly Ser

1 5

<210> 2

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide linker

<400> 2

Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly

1 5 10

<210> 3

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Hinge region

<400> 3

Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro

1 5 10 15

<210> 4
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Hinge region

<400> 4
 Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1 5 10 15

<210> 5
 <211> 232
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Human IgG1 constant region

<400> 5
 Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1 5 10 15
 Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 20 25 30
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 35 40 45
 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95
 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 100 105 110
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

	195		200		205										
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys
	210					215					220				
Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys								
225					230										

<210> 6
 <211> 183
 <212> PRT
 <213> *Macaca fascicularis*

<220>
 <223> Full-length cynomolgus monkey BCMA

<400> 6															
Met	Leu	Gln	Met	Ala	Arg	Gln	Cys	Ser	Gln	Asn	Glu	Tyr	Phe	Asp	Ser
1				5					10					15	
Leu	Leu	His	Asp	Cys	Lys	Pro	Cys	Gln	Leu	Arg	Cys	Ser	Ser	Thr	Pro
			20					25						30	
Pro	Leu	Thr	Cys	Gln	Arg	Tyr	Cys	Asn	Ala	Ser	Met	Thr	Asn	Ser	Val
		35					40					45			
Lys	Gly	Met	Asn	Ala	Ile	Leu	Trp	Thr	Cys	Leu	Gly	Leu	Ser	Leu	Ile
	50					55					60				
Ile	Ser	Leu	Ala	Val	Phe	Val	Leu	Thr	Phe	Leu	Leu	Arg	Lys	Met	Ser
65					70					75				80	
Ser	Glu	Pro	Leu	Lys	Asp	Glu	Phe	Lys	Asn	Thr	Gly	Ser	Gly	Leu	Leu
				85					90					95	
Gly	Met	Ala	Asn	Ile	Asp	Leu	Glu	Lys	Gly	Arg	Thr	Gly	Asp	Glu	Ile
			100					105					110		
Val	Leu	Pro	Arg	Gly	Leu	Glu	Tyr	Thr	Val	Glu	Glu	Cys	Thr	Cys	Glu
		115					120					125			
Asp	Cys	Ile	Lys	Asn	Lys	Pro	Lys	Val	Asp	Ser	Asp	His	Cys	Phe	Pro
	130					135					140				
Leu	Pro	Ala	Met	Glu	Glu	Gly	Ala	Thr	Ile	Leu	Val	Thr	Thr	Lys	Thr
145					150					155					160
Asn	Asp	Tyr	Cys	Asn	Ser	Leu	Ser	Ala	Ala	Leu	Ser	Val	Thr	Glu	Ile
				165					170					175	
Glu	Lys	Ser	Ile	Ser	Ala	Arg									
			180												

<210> 7
 <211> 5
 <212> PRT
 <213> *Camelus bactrianus*

<220>
 <223> 1A1 single variable domain CDR1

<400> 7
 Gly Trp Asn Lys His
 1 5

<210> 8
 <211> 16
 <212> PRT
 <213> Camelus bactrianus

<220>
 <223> 1A1 single variable domain CDR2

<400> 8
 Ser Ile Phe Arg Asp Gly Lys Thr Ala Tyr Thr Asp Ser Val Lys Gly
 1 5 10 15

<210> 9
 <211> 10
 <212> PRT
 <213> Camelus bactrianus

<220>
 <223> 1A1 single variable domain CDR3

<400> 9
 Asp Leu Pro Gly Ser Gly Leu Pro Ala Phe
 1 5 10

<210> 10
 <211> 5
 <212> PRT
 <213> Camelus bactrianus

<220>
 <223> 1A10 single variable domain CDR1

<400> 10
 Val Ala Cys Met Ala
 1 5

<210> 11
 <211> 17
 <212> PRT
 <213> Camelus bactrianus

<220>
 <223> 1A10 single variable domain CDR2

<400> 11
 Thr Ile Val Ala Asp Phe Gly Thr Thr Asn Tyr Ala Ala Ser Val Lys
 1 5 10 15
 Gly

<210> 12
 <211> 14
 <212> PRT
 <213> Camelus bactrianus

<220>
 <223> 1A10 single variable domain CDR3

<400> 12
 Thr Gln Arg Gly Gly Ile Asp Trp Cys Asp Glu Ile Asn Tyr
 1 5 10

<210> 13
 <211> 5
 <212> PRT
 <213> Camelus bactrianus

<220>
 <223> 1A11 single variable domain CDR1

<400> 13
 Ser Ala Cys Met Gly
 1 5

<210> 14
 <211> 17
 <212> PRT
 <213> Camelus bactrianus

<220>
 <223> 1A11 single variable domain CDR2

<400> 14
 Arg Ile Glu Thr Gly Tyr Gly Gly Thr Val Tyr Ala Asp Ser Val Lys
 1 5 10 15
 Gly

<210> 15

<211> 17
<212> PRT
<213> Camelus bactrianus

<220>
<223> 1A11 single variable domain CDR3

<400> 15
Lys Arg Ser Trp Cys Thr Pro Thr Trp Trp His Glu Leu Asp Tyr Asn
1 5 10 15
Tyr

<210> 16
<211> 5
<212> PRT
<213> Camelus bactrianus

<220>
<223> 1B10 single variable domain CDR1

<400> 16
Gly Trp Asn Lys His
1 5

<210> 17
<211> 16
<212> PRT
<213> Camelus bactrianus

<220>
<223> 1B10 single variable domain CDR2

<400> 17
Ser Ile Phe Arg Asp Gly Lys Thr Ala Tyr Thr Asp Ser Val Lys Gly
1 5 10 15

<210> 18
<211> 10
<212> PRT
<213> Camelus bactrianus

<220>
<223> 1B10 single variable domain CDR3

<400> 18

Asp Leu Pro Gly Ser Gly Leu Pro Glu Phe
 1 5 10

<210> 19
 <211> 118
 <212> PRT
 <213> Camelus bactrianus

<220>
 <223> 1A1 single variable domain

<400> 19
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Ser Val Gln Ala Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Tyr Thr Phe Arg Gly Trp
 20 25 30
 Asn Lys His Trp Tyr Arg Gln Ala Pro Gly Lys Glu Arg Glu Leu Val
 35 40 45
 Ser Ser Ile Phe Arg Asp Gly Lys Thr Ala Tyr Thr Asp Ser Val Lys
 50 55 60
 Gly Arg Phe Thr Ile Ser Gln Asp Asn Ala Asp Ala Thr Val Tyr Leu
 65 70 75 80
 Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Met Tyr Tyr Cys Lys
 85 90 95
 Tyr Asp Leu Pro Gly Ser Gly Leu Pro Ala Phe Trp Gly Gln Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ser
 115

<210> 20
 <211> 354
 <212> DNA
 <213> Camelus bactrianus

<220>
 <223> 1A1 single variable domain

<400> 20
 caggtgcagc tgggtggagtc tgggggaggc tcggtgcagg ccggagggtc tctgagactc 60
 tcctgtacag cctctggata caccttcagg ggctggaaca agcactggta ccgccaggct 120
 ccagggaagg agcgcgagtt ggtctcgagc atctttcgtg atgggaagac agcctataca 180
 gactccgtga agggccgatt caccatctct caagacaacg ccgacgcaac ggtgtatctg 240
 caaatgaaca gcctgaaacc tgaggacacg gccatgtatt actgtaaata cgatctgcct 300
 ggatctggtc ttctgcatt ctggggccag gggaccctgg tcactgtctc atca 354

<210> 21
 <211> 123
 <212> PRT

<213> Camelus bactrianus

<220>

<223> 1A10 single variable domain

<400> 21

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

<210> 22

<211> 369

<212> DNA

<213> Camelus bactrianus

<220>

<223> 1A10 single variable domain

<400> 22

caggtgcagc	tggtggagtc	tgggggaggc	tcggtgcagg	ctggagggtc	gctgagactc	60
tcctgtgccg	cctccgata	cagcagtaat	gtggcatgca	tggcctggta	ccgccaggct	120
ccagggaagg	agcgcgagt	ggtcgcaact	attgttgctg	atttcggtac	cacaaactat	180
gccgcctccg	tgaagggccg	attcaccatc	tccaagaca	acgccaagaa	cacggtgtat	240
ctgcaaata	acagcctgaa	acctgaggac	tctgccatgt	actactgtgc	ggcaaccag	300
agggggggta	ttgactgggt	tgatgaaatt	aattactggg	gccaggggac	cctggtcact	360
gtctcatca						369

<210> 23

<211> 126

<212> PRT

<213> Camelus bactrianus

<220>

<223> 1A11 single variable domain

<400> 23
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Ser Val Gln Ala Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Ser Ala
 20 25 30
 Cys Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Val
 35 40 45
 Ala Arg Ile Glu Thr Gly Tyr Gly Gly Thr Val Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Ala Ala Lys Arg Ser Trp Cys Thr Pro Thr Trp Trp His Glu Leu Asp
 100 105 110
 Tyr Asn Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
 115 120 125

<210> 24
 <211> 378
 <212> DNA
 <213> Camelus bactrianus

<220>
 <223> 1A11 single variable domain

<400> 24
 caggtgcagc tggtggagtc tgggggaggc tcggtgcagg ctggagggtc tctgagactc 60
 tcctgtgcag cctctggagt cacttttaat agcgcagtga tgggttggtt ccgccaggct 120
 ccaggaagg agcgcgaggg ggtcgcacgt attgaaactg gttatggtgg cactgtctat 180
 gccgactccg tgaagggacg attcaccatc tcccgagaca acgccaagaa cacggtgtat 240
 ctgcaaatga acagcctaaa acctgaggac actgccatgt actactgtgc ggctaagaga 300
 tcctggtgta ctcctacgtg gtggcacgaa cttgactata actactgggg acaggggacc 360
 caggtcactg tctcatca 378

<210> 25
 <211> 118
 <212> PRT
 <213> Camelus bactrianus

<220>
 <223> 1B10 single variable domain

<400> 25
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Ser Val Gln Ala Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Tyr Thr Phe Arg Gly Trp

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

<210> 26

<211> 354

<212> DNA

<213> Camelus bactrianus

<220>

<223> 1B10 single variable domain

<400> 26

gaggtgcagc	tggtggagtc	tgggggaggc	tcggtgcagg	ccggagggtc	tctgagactc	60
tcctgtacag	cctctggata	caccttcagg	ggctggaaca	agcactggta	ccgccaggct	120
ccagggaagg	agcgcgagtt	ggtctcgagt	atctttcgtg	atgggaagac	agcctataca	180
gactccgtga	agggccgatt	caccatctct	caagacagcg	ccgacgcaac	ggtgtatctg	240
caaataaaca	gcctgaaacc	tgaggacacg	gccatgtatt	actgtaaata	cgatctgcct	300
ggatctggtc	ttcctgagtt	ctggggccag	gggaccctgg	tcactgtctc	atca	354

<210> 27

<211> 350

<212> PRT

<213> Artificial Sequence

<220>

<223> 1A1-Fc

<400> 27

Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Ser	Val	Gln	Ala	Gly	Gly		
1			5				10				15						
Ser	Leu	Arg	Leu	Ser	Cys	Thr	Ala	Ser	Gly	Tyr	Thr	Phe	Arg	Gly	Trp		
		20					25				30						
Asn	Lys	His	Trp	Tyr	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Glu	Leu	Val		
	35					40			45								
Ser	Ser	Ile	Phe	Arg	Asp	Gly	Lys	Thr	Ala	Tyr	Thr	Asp	Ser	Val	Lys		
	50				55				60								
Gly	Arg	Phe	Thr	Ile	Ser	Gln	Asp	Asn	Ala	Asp	Ala	Thr	Val	Tyr	Leu		

65					70					75					80
Gln	Met	Asn	Ser	Leu	Lys	Pro	Glu	Asp	Thr	Ala	Met	Tyr	Tyr	Cys	Lys
				85					90					95	
Tyr	Asp	Leu	Pro	Gly	Ser	Gly	Leu	Pro	Ala	Phe	Trp	Gly	Gln	Gly	Thr
			100					105					110		
Leu	Val	Thr	Val	Ser	Ser	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr
		115					120					125			
Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe
	130					135					140				
Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro
145				150						155					160
Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val
				165					170					175	
Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr
		180						185					190		
Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val
	195						200					205			
Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys
	210					215					220				
Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser
225					230					235					240
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro
				245					250					255	
Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val
		260						265					270		
Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly
	275						280					285			
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp
	290					295					300				
Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp
305					310					315					320
Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His
			325						330					335	
Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys		
		340						345					350		

<210> 28
 <211> 1050
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 1A1-Fc

<400> 28	
caagtgcacac tggaggagtc tggaggcggt tccgtgcagg ccggcggtc cctgagactg	60
tcctgcaccg cttccggcta caccttcaga ggctggaaca agcactggta tcggcaggct	120
cctggcaaaag aaagagagct ggtgtcctcc atcttcggg acggcaagac cgcctacacc	180
gactccgtga agggcagatt caccatctct caggacaacg ccgacgccac agtgtacctg	240

cagatgaact	ctctgaagcc	cgaggacacc	gccatgtact	actgcaagta	cgacctgcct	300
ggatctggcc	tgcccgctt	ctggggccaa	ggcaccctgg	taaccgtgtc	gtccgagccc	360
aagtcttgcg	acaagaccca	cacctgtcct	ccttgtcctg	ctccggaact	gctgggcggc	420
ccttccgtgt	ttctgtttcc	tccaaagcct	aaggacacac	tgatgatcag	ccggaccctt	480
gaggtgacct	gcgtggtcgt	ggatgtctct	cacgaggatc	ctgaggtgaa	gttcaactgg	540
tacgtggatg	gagtgggaagt	gcataacgct	aaaaccaagc	ctagagaaga	gcagtacaac	600
tccacctaca	gagtgggtgc	cgtgctgacc	gtgctgcacc	aggattggct	gaacggcaaa	660
gagtacaagt	gcaaggtgtc	caacaaggct	ctgcctgccc	ctatcgagaa	gaccatctcc	720
aaggccaagg	gccagcctcg	ggagcctcaa	gtgtacaccc	tgccctcctt	tcgcgacgag	780
ctgaccaaga	accaggtgtc	tctgacctgc	ctggtgaaag	gcttctaccc	ctccgacatc	840
gccgtggaat	gggagtccaa	tggccagccc	gagaacaact	acaagaccac	cccacctgtg	900
ctggactctg	atggctcctt	cttcctgtac	tccaagctga	ccgtggacaa	gtccagatgg	960
cagcagggca	acgtgttctc	ctgttctgtg	atgcacgagg	ccctgcacaa	ccactacaca	1020
cagaagtccc	tgagcctgtc	tcctggcaag				1050

<210> 29
 <211> 355
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 1A10-Fc

<400> 29

Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Ser	Val	Gln	Ala	Gly	Gly
1				5				10						15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Tyr	Ser	Ser	Asn	Val	Ala
			20					25					30		
Cys	Met	Ala	Trp	Tyr	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Glu	Trp	Val
		35					40					45			
Ala	Thr	Ile	Val	Ala	Asp	Phe	Gly	Thr	Thr	Asn	Tyr	Ala	Ala	Ser	Val
	50					55				60					
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Gln	Asp	Asn	Ala	Lys	Asn	Thr	Val	Tyr
65					70				75					80	
Leu	Gln	Met	Asn	Ser	Leu	Lys	Pro	Glu	Asp	Ser	Ala	Met	Tyr	Tyr	Cys
			85					90					95		
Ala	Ala	Thr	Gln	Arg	Gly	Gly	Ile	Asp	Trp	Cys	Asp	Glu	Ile	Asn	Tyr
		100					105					110			
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Glu	Pro	Lys	Ser	Cys
	115					120					125				
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly
	130				135					140					
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
145				150					155					160	
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His
			165				170						175		
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
	180						185					190			
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr

<210> 31
 <211> 358
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 1A11-Fc

<400> 31
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Ser Val Gln Ala Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Ser Ala
 20 25 30
 Cys Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Val
 35 40 45
 Ala Arg Ile Glu Thr Gly Tyr Gly Gly Thr Val Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Ala Ala Lys Arg Ser Trp Cys Thr Pro Thr Trp Trp His Glu Leu Asp
 100 105 110
 Tyr Asn Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Glu Pro
 115 120 125
 Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
 130 135 140
 Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 145 150 155 160
 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 165 170 175
 Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
 180 185 190
 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
 195 200 205
 Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
 210 215 220
 Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
 225 230 235 240
 Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
 245 250 255
 Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
 260 265 270
 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 275 280 285
 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 290 295 300
 Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys

305		310		315		320									
Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys
				325					330					335	
Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu
			340					345					350		
Ser	Leu	Ser	Pro	Gly	Lys										
			355												

<210> 32
 <211> 1074
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 1A11-Fc

<400> 32

caggtgcagt	tggttgaatc	tggcggcgga	tctgtgcagg	ctggcggatc	tctgagactg	60
tcctgtgccg	cttccggcgt	caccttcaac	tccgcttgca	tgggatgggt	cagacaggcc	120
cctggcaaag	agagagaggg	cgtcgctagg	atcgagaccg	gctatggcgg	aaccgtctac	180
gccgactccg	tcaagggcag	gttcaccatc	agcagagaca	acgccaagaa	caccgtgtac	240
ctgcagatga	actcccctgaa	gcccaggagc	accgccatgt	actactgtgc	tgccaagaga	300
agctgggtgca	cccctacctg	gtggcacgag	ctggactaca	actactgggg	ccagggcaca	360
caggtcaccg	tgtcctctga	gcctaagtcc	tgcgacaaga	cccacacctg	tcctccatgt	420
cctgctccag	aactgctcgg	cggaccttcc	gtgttcctgt	ttcctccaaa	gcctaaggat	480
accctgatga	tctctcggac	ccctgaagtg	acctgcgtgg	tggatggatgt	gtctcacgag	540
gatcccgaag	tgaagttcaa	ttggtacgtg	gacggcgtgg	aagtgcacaa	tgctaagacc	600
aagcctagag	aggaacagta	caactccacc	tatagagtgg	tgtccgtgct	gaccgtgctg	660
caccaggatt	ggctgaacgg	caaagagtac	aagtgcgaagg	tgtccaacaa	ggccctgcct	720
gctcctatcg	aaaagaccat	ctccaaggcc	aagggccagc	ctagggaacc	ccagggtttac	780
accttgccctc	catctcggga	cgagctgacc	aagaaccagg	tgtccctgac	ctgtctgggtc	840
aagggcttct	acccctccga	tatcgccgtg	gaatgggagt	ctaattggcca	gccagagaac	900
aactacaaga	caaccctcc	tgtgctggac	tccgacggct	cattcttcct	gtactccaag	960
ctgacagtgg	acaagtccag	atggcagcag	ggcaacgtgt	tctcctgctc	cgtgatgcac	1020
gaggccctgc	acaatcacta	caccagaag	tccctgtctc	tgagccccgg	caaa	1074

<210> 33
 <211> 350
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 1B10-Fc

<400> 33

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Ser	Val	Gln	Ala	Gly	Gly
1				5				10					15		
Ser	Leu	Arg	Leu	Ser	Cys	Thr	Ala	Ser	Gly	Tyr	Thr	Phe	Arg	Gly	Trp

			20					25					30				
Asn	Lys	His	Trp	Tyr	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Glu	Leu	Val		
		35					40					45					
Ser	Ser	Ile	Phe	Arg	Asp	Gly	Lys	Thr	Ala	Tyr	Thr	Asp	Ser	Val	Lys		
	50					55					60						
Gly	Arg	Phe	Thr	Ile	Ser	Gln	Asp	Ser	Ala	Asp	Ala	Thr	Val	Tyr	Leu		
65				70					75					80			
Gln	Met	Asn	Ser	Leu	Lys	Pro	Glu	Asp	Thr	Ala	Met	Tyr	Tyr	Cys	Lys		
			85					90					95				
Tyr	Asp	Leu	Pro	Gly	Ser	Gly	Leu	Pro	Glu	Phe	Trp	Gly	Gln	Gly	Thr		
		100					105						110				
Leu	Val	Thr	Val	Ser	Ser	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr		
		115					120					125					
Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe		
	130					135					140						
Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro		
145				150					155						160		
Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val		
			165					170						175			
Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr		
		180					185						190				
Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val		
	195					200					205						
Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys		
	210				215					220							
Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser		
225				230						235					240		
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro		
			245					250						255			
Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val		
		260					265						270				
Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly		
	275					280						285					
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp		
	290				295						300						
Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp		
305				310						315					320		
Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His		
			325					330						335			
Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys				
			340				345						350				

<210> 34
 <211> 1050
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 1B10-Fc

<400> 34
gaggtgcaac tgggtggagtc tggaggcggt tccgtgcagg ccggcggctc cctgagactg 60
tcctgcaccg cttccggcta caccttcaga ggctggaaca agcactggta tcggcaggct 120
cctggcaaag aaagagagct ggtgtcctcc atcttcggg acggcaagac cgcctacacc 180
gactccgtga agggcagatt caccatctct caggactctg ccgacgccac agtgtacctg 240
cagatgaact ctctgaagcc cgaggacacc gccatgtact actgcaagta cgacctgcct 300
ggatctggcc tgcccagatt ctggggccaa ggcaccctgg taaccgtgtc gtccgagccc 360
aagtcttgcg acaagaccca cacctgtcct ccttgtcctg ctccggaact gctgggcggc 420
ccttccgtgt ttctgtttcc tccaaagcct aaggacacac tgatgatcag ccggaccctt 480
gaggtgacct gcgtggtcgt ggatgtctct cacgaggatc ctgaggtgaa gttcaactgg 540
tacgtggatg gagtgggaagt gcataacgct aaaaccaagc ctagagaaga gcagtacaac 600
tccacctaca gagtgggtgtc cgtgctgacc gtgctgcacc aggattggct gaacggcaaa 660
gagtacaagt gcaagggtgtc caacaaggct ctgcctgccc ctatcgagaa gaccatctcc 720
aaggccaagg gccagcctcg ggagcctcaa gtgtacacc tgccctcttc tcgcgacgag 780
ctgaccaaga accaggtgtc tctgacctgc ctggtgaaag gcttctatcc ctccgacatc 840
gccgtggaat gggagtccaa tggccagccc gagaacaact acaagaccac cccacctgtg 900
ctggactctg atggctcctt cttcctgtac tccaagctga ccgtggacaa gtccagatgg 960
cagcagggca acgtgttctc ctgttctgtg atgcacgagg ccctgcacaa ccactacaca 1020
cagaagtccc tgagcctgtc tcctggcaag 1050

<210> 35
<211> 54
<212> PRT
<213> Homo sapiens

<220>
<223> Human BCMA extracellular region

<400> 35
Met Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser
1 5 10 15
Leu Leu His Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr
20 25 30
Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser
35 40 45
Val Lys Gly Thr Asn Ala
50

<210> 36
<211> 53
<212> PRT
<213> Macaca fascicularis

<220>
<223> Cynomolgus monkey BCMA extracellular region

<400> 36

Met Leu Gln Met Ala Arg Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser
1 5 10 15
Leu Leu His Asp Cys Lys Pro Cys Gln Leu Arg Cys Ser Ser Thr Pro
20 25 30
Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Met Thr Asn Ser Val
35 40 45
Lys Gly Met Asn Ala
50

<210> 37
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A10-V1 single variable domain

<400> 37
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 Tyr Ser Ser Asn Val Ala
20 25 30
Cys Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Thr Ile Val Ala Asp Phe Gly Thr Thr Asn Tyr Ala Ala Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Gln Asp Asn Ser Lys Asn Thr Val 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 Ala Thr Gln Arg Gly Gly Ile Asp Trp Cys Asp Glu Ile Asn Tyr
100 105 110
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 38
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A10-V2 single variable domain

<400> 38
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 Tyr Ser Ser Asn Val Ala
20 25 30

Cys	Met	Ala	Trp	Tyr	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Glu	Trp	Val
	35						40					45			
Ser	Thr	Ile	Val	Ala	Asp	Phe	Gly	Thr	Thr	Asn	Tyr	Ala	Ala	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Gln	Asp	Asn	Ser	Lys	Asn	Thr	Val	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	Ala	Thr	Gln	Arg	Gly	Gly	Ile	Asp	Trp	Cys	Asp	Glu	Ile	Asn	Tyr
			100					105					110		
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser					
		115					120								

<210> 39
 <211> 126
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 1A11-V1 single variable domain

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	Asn	Ser	Ala
			20					25					30		
Cys	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Arg	Glu	Gly	Val
		35				40						45			
Ser	Arg	Ile	Glu	Thr	Gly	Tyr	Gly	Gly	Thr	Val	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Val	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	Ala	Lys	Arg	Ser	Trp	Cys	Thr	Pro	Thr	Trp	Trp	His	Glu	Leu	Asp
			100					105					110		
Tyr	Asn	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser		
		115					120					125			

<210> 40
 <211> 126
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 1A11-V2 single variable domain

<400> 40

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	Asn	Ser	Ala
			20					25					30		
Cys	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Glu	Gly	Val
		35					40					45			
Ser	Arg	Ile	Glu	Thr	Gly	Tyr	Gly	Gly	Thr	Val	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Val	Tyr
65					70				75						80
Leu	Gln	Met	Asn	Ser	Leu	Lys	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Ala	Ala	Lys	Arg	Ser	Trp	Cys	Thr	Pro	Thr	Trp	Trp	His	Glu	Leu	Asp
			100					105					110		
Tyr	Asn	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser		
		115					120					125			

<210> 41
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (11)
 <223> Xaa is S or L

<220>
 <221> UNSURE
 <222> (14)
 <223> Xaa is P or A

<220>
 <221> UNSURE
 <222> (44)
 <223> Xaa is G or E

<220>
 <221> UNSURE
 <222> (45)
 <223> Xaa is R or L

<220>
 <221> UNSURE
 <222> (49)
 <223> Xaa is A or S

<220>
 <221> UNSURE
 <222> (75)
 <223> Xaa is A or S

<220>
 <221> UNSURE
 <222> (87)
 <223> Xaa is R or K

<220>
 <221> UNSURE
 <222> (88)
 <223> Xaa is A or P

<220>
 <221> UNSURE
 <222> (91)
 <223> Xaa is T or S

<220>
 <221> UNSURE
 <222> (93)
 <223> Xaa is V or M

<220>
 <223> BCMA-binding single variable domain

<400> 41
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Xaa Val Gln Xaa Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Ser Ser Asn Val Ala
 20 25 30
 Cys Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Xaa Xaa Glu Trp Val
 35 40 45
 Xaa Thr Ile Val Ala Asp Phe Gly Thr Thr Asn Tyr Ala Ala Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Gln Asp Asn Xaa Lys Asn Thr Val Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Xaa Xaa Glu Asp Xaa Ala Xaa Tyr Tyr Cys
 85 90 95
 Ala Ala Thr Gln Arg Gly Gly Ile Asp Trp Cys Asp Glu Ile Asn Tyr

			100					105		110
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser
		115					120			

<210> 42
 <211> 126
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (11)
 <223> Xaa is S or L

<220>
 <221> UNSURE
 <222> (14)
 <223> Xaa is P or A

<220>
 <221> UNSURE
 <222> (27)
 <223> Xaa is F or V

<220>
 <221> UNSURE
 <222> (44)
 <223> Xaa is E or G

<220>
 <221> UNSURE
 <222> (49)
 <223> Xaa is A or S

<220>
 <221> UNSURE
 <222> (75)
 <223> Xaa is A or S

<220>
 <221> UNSURE
 <222> (87)
 <223> Xaa is R or K

<220>
 <221> UNSURE
 <222> (88)
 <223> Xaa is A or P

<220>
 <221> UNSURE
 <222> (93)
 <223> Xaa is V or M

<220>
 <223> BCMA-binding single variable domain

<400> 42
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Xaa Val Gln Xaa Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Xaa Thr Phe Asn Ser Ala
 20 25 30
 Cys Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Xaa Arg Glu Gly Val
 35 40 45
 Xaa Arg Ile Glu Thr Gly Tyr Gly Gly Thr Val Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Xaa Lys Asn Thr Val Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Xaa Xaa Glu Asp Thr Ala Xaa Tyr Tyr Cys
 85 90 95
 Ala Ala Lys Arg Ser Trp Cys Thr Pro Thr Trp Trp His Glu Leu Asp
 100 105 110
 Tyr Asn Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
 115 120 125

<210> 43
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD3-HCDR1

<400> 43
 Thr Tyr Ala Met Asn
 1 5

<210> 44
 <211> 19

<212> PRT
<213> Artificial Sequence

<220>
<223> CD3-HCDR2

<400> 44
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15
Val Lys Asp

<210> 45
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3-HCDR3

<400> 45
His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr
1 5 10

<210> 46
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3-LCDR1

<400> 46
Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 47
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3-LCDR2

<400> 47
Gly Thr Asn Lys Arg Ala Pro

1

5

<210> 48

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3-LCDR3

<400> 48

Ala Leu Trp Tyr Ser Asn Leu Trp Val

1

5

<210> 49

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3-VH

<400> 49

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

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr

20

25

30

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

35

40

45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp

50

55

60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr

65

70

75

80

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Met Tyr

85

90

95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe

100

105

110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115

120

125

<210> 50

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3-VL

<400> 50

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

<210> 51

<211> 356

<212> PRT

<213> Artificial Sequence

<220>

<223> 1A10-V1

<400> 51

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	Tyr	Ser	Ser	Asn	Val	Ala
			20					25					30		
Cys	Met	Ala	Trp	Tyr	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			
Ala	Thr	Ile	Val	Ala	Asp	Phe	Gly	Thr	Thr	Asn	Tyr	Ala	Ala	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Gln	Asp	Asn	Ser	Lys	Asn	Thr	Val	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	Ala	Thr	Gln	Arg	Gly	Gly	Ile	Asp	Trp	Cys	Asp	Glu	Ile	Asn	Tyr
			100					105					110		
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Glu	Pro	Lys	Ser
			115					120					125		
Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu
	130					135					140				
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
145					150					155					160
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser
				165					170					175	
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu

gtggataagt cccggtggca gcagggcaat gtgttcagct gttccgtgat gcacgaggct	1020
ctgcacaacc actataccca gaagtcctg tccctgagcc ccggcaag	1068

<210> 53
 <211> 356
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 1A10-V2

<400> 53

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	Tyr	Ser	Ser	Asn	Val	Ala	20	25	30	
Cys	Met	Ala	Trp	Tyr	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Glu	Trp	Val	35	40	45	
Ser	Thr	Ile	Val	Ala	Asp	Phe	Gly	Thr	Thr	Asn	Tyr	Ala	Ala	Ser	Val	50	55	60	
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Gln	Asp	Asn	Ser	Lys	Asn	Thr	Val	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	Ala	Thr	Gln	Arg	Gly	Gly	Ile	Asp	Trp	Cys	Asp	Glu	Ile	Asn	Tyr	100	105	110	
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Glu	Pro	Lys	Ser	115	120	125	
Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	130	135	140	
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	145	150	155	160
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	165	170	175	
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	180	185	190	
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	195	200	205	
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	210	215	220	
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	225	230	235	240
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	245	250	255	
Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	260	265	270	
Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	275	280	285	
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro				

290	295	300
Pro Val Leu Asp Ser	Asp Gly Ser Phe Phe Leu	Tyr Ser Lys Leu Thr
305	310	315
Val Asp Lys Ser Arg Trp	Gln Gln Gly Asn Val	Phe Ser Cys Ser Val
325	330	335
Met His Glu Ala Leu His	Asn His Tyr Thr Gln	Lys Ser Leu Ser Leu
340	345	350
Ser Pro Gly Lys		
355		

<210> 54
 <211> 1068
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 1A10-V2

<400> 54	
caggtgcagc tgggtggagtc cggcggcgga ctggtgcagc ctggaggatc tctgcggctg	60
tcctgcgccg ccagcggata ctccagcaac gtggcttgca tggcctggta tcggcaggcc	120
cctggcaagg agcgggagtg ggtgagcacc atcgtggctg acttcggcac caccaattat	180
gccgctagcg tgaagggccg gttcaccatc agccaggata actccaagaa taccgtgtat	240
ctgcagatga atagcctgcg ggccgaggat accgccgtgt attattgtgc cgctaccag	300
cggggcggca tcgactggtg tgatgagatc aactattggg gccagggcac cctggtgacc	360
gtgtcctccg gcgagcctaa gtcctccgac aagaccaca cctgccctcc ttgtcccgcc	420
cctgagctgc tgggcggacc atctgtgttc ctgttcctc ccaagcccaa ggacaccctg	480
atgatctcca ggaccctga ggtgacctgc gtgggtgggg atgtgtccca cgaggacct	540
gaggtgaagt tcaactggta cgtggacggc gtggagggtgc acaatgctaa gaccaagccc	600
cgggaggagc agtataacag cacctaccgg gtgggtgagcg tgctgaccgt gctgcaccag	660
gattggctga atggcaagga gtacaagtgt aaggtgtcca acaaggctct gcctgcccc	720
atcgagaaga ccatctccaa ggccaagggc cagcctcggg agccccaggt gtataccctg	780
ccccctcca gggacgagct gaccaagaac caggtgagcc tgacctgtct ggtgaagggc	840
ttctatcctt ccgacatcgc cgtggagtgg gagtccaacg gccagcctga gaataactac	900
aagaccacc cccctgtgct ggatagcgac ggctccttc tcctgtattc caagctgacc	960
gtggataagt cccggtggca gcagggaat gtgttcagct gttccgtgat gcacgaggct	1020
ctgcacaacc actataccca gaagtccttg tccctgagcc cgggcaag	1068

<210> 55
 <211> 359
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 1A11-V1

<400> 55
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

<220>

<223> 1A11-V1

<400> 56

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cagggtgcagc tgggtggagtc cggcggcgga ctggtgcagc caggaggatc tctgcggctg      60
tcctgtgccg cttccggctt cacccttcaat tccgcttgca tgggctgggt caggcaggcc      120
cctggcaagg gcagggaggg agtgtccagg atcgagaccg gctacggcgg caccgtgtac      180
gctgacagcg tgaagggcgg gttcaccatc agccgggata actccaagaa caccgtgtat      240
ctgcagatga atagcctgag ggctgaggat accgccgtgt actattgtgc tgctaagcgg      300
tcctgggtgta cccccacctg gtggcacgag ctggactaca attactgggg ccagggcacc      360
caggtgaccg tgagctccgg cgagcctaag tcctccgaca agaccacac ctgccctcct      420
tgtcccggcc ctgagctgct gggcggacca tctgtgttcc tgttccctcc caagcccaag      480
gacaccctga tgatctccag gaccctgag gtgacctgcg tgggtggtgga tgtgtccac      540
gaggaccctg aggtgaagtt caactggtac gtggacggcg tggaggtgca caatgctaag      600
accaagcccc gggaggagca gtataacagc acctaccggg tggtgagcgt gctgaccgtg      660
ctgcaccagg attggctgaa tggcaaggag tacaagtgtg aggtgtccaa caaggctctg      720
cctgccccca tcgagaagac catctccaag gcccaaggcc agcctcgga gcccagggtg      780
tataccctgc cccctccag ggacgagctg accaagaacc aggtgagcct gacctgtctg      840
gtgaagggtc tctatcctt cgacatcgcc gtggagtggg agtccaacgg ccagcctgag      900
aataactaca agaccacccc ccctgtgctg gatagcgac gctccttctt cctgtattcc      960
aagctgaccg tggataagtc ccggtggcag cagggaatg tgttcagctg ttccgtgatg     1020
cacgaggctc tgcacaacca ctataccag aagtccctgt ccctgagccc cggcaag      1077
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<210> 57

<211> 359

<212> PRT

<213> Artificial Sequence

<220>

<223> 1A11-V2

<400> 57

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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 Asn Ser Ala
          20          25          30
Cys Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Val
          35          40          45
Ser Arg Ile Glu Thr Gly Tyr Gly Gly Thr Val Tyr Ala Asp Ser Val
          50          55          60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
65          70          75          80
Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
          85          90          95
Ala Ala Lys Arg Ser Trp Cys Thr Pro Thr Trp Trp His Glu Leu Asp
          100          105          110
Tyr Asn Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Glu
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gacaccctga	tgatctccag	gaccctgag	gtgacctgcg	tggtggtgga	tgtgtcccac	540
gaggaccctg	aggtgaagtt	caactggtag	gtggacggcg	tgtaggtgca	caatgctaag	600
accaagcccc	gggaggagca	gtataacagc	acctaccggg	tggtgagcgt	gctgaccgtg	660
ctgcaccagg	attggctgaa	tggcaaggag	tacaagtgtg	aggtgtccaa	caaggctctg	720
cctgccccca	tcgagaagac	catctccaag	gccaaaggcc	agcctcggga	gccccagggtg	780
tataccctgc	ccccctccag	ggacgagctg	accaagaacc	aggtgagcct	gacctgtctg	840
gtgaagggct	tctatccttc	cgacatcgcc	gtggagtggg	agtccaacgg	ccagcctgag	900
aataactaca	agaccacccc	ccctgtgctg	gatagcgacg	gctccttctt	cctgtattcc	960
aagctgaccg	tggataagtc	ccggtggcag	cagggcaatg	tgttcagctg	ttccgtgatg	1020
cacgaggctc	tgcaacaacca	ctataccag	aagtccctgt	ccctgagccc	cggcaag	1077

<210> 59
 <211> 492
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A10-linker-A11-Fc

<400> 59

Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Ser	Val	Gln	Ala	Gly	Gly
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Tyr	Ser	Ser	Asn	Val	Ala
			20					25					30		
Cys	Met	Ala	Trp	Tyr	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Glu	Trp	Val
		35					40					45			
Ala	Thr	Ile	Val	Ala	Asp	Phe	Gly	Thr	Thr	Asn	Tyr	Ala	Ala	Ser	Val
	50				55					60					
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Gln	Asp	Asn	Ala	Lys	Asn	Thr	Val	Tyr
65					70				75					80	
Leu	Gln	Met	Asn	Ser	Leu	Lys	Pro	Glu	Asp	Ser	Ala	Met	Tyr	Tyr	Cys
			85					90					95		
Ala	Ala	Thr	Gln	Arg	Gly	Gly	Ile	Asp	Trp	Cys	Asp	Glu	Ile	Asn	Tyr
			100				105						110		
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser
	115					120					125				
Gly	Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Ser
	130				135					140					
Val	Gln	Ala	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Val
145					150				155					160	
Thr	Phe	Asn	Ser	Ala	Cys	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys
			165				170						175		
Glu	Arg	Glu	Gly	Val	Ala	Arg	Ile	Glu	Thr	Gly	Tyr	Gly	Gly	Thr	Val
	180					185					190				
Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala
	195				200						205				
Lys	Asn	Thr	Val	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Lys	Pro	Glu	Asp	Thr
	210				215					220					
Ala	Met	Tyr	Tyr	Cys	Ala	Ala	Lys	Arg	Ser	Trp	Cys	Thr	Pro	Thr	Trp

225					230					235				240
Trp	His	Glu	Leu	Asp	Tyr	Asn	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val
				245					250				255	
Val	Ser	Ser	Gly	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Cys
			260					265					270	
Pro	Cys	Pro	Ala	Pro	Glu	Ala	Ala	Gly	Gly	Pro	Ser	Val	Phe	Leu
			275				280					285		
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu
		290				295				300				
Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys
305					310					315				320
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys
				325					330					335
Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu
			340					345					350	
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys
		355					360					365		
Ser	Asn	Lys	Ala	Leu	Ala	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys
		370				375					380			
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Cys	Thr	Leu	Pro	Pro	Ser
385					390					395				400
Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Ser	Cys	Ala	Val	Lys
				405				410						415
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln
			420					425					430	
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly
		435					440					445		
Phe	Phe	Leu	Val	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln
		450				455						460		
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn
465					470					475				480
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys			
				485					490					

<210> 60
 <211> 1476
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> A10-linker-A11-Fc

<400> 60	
caggtgcagc	60
tggtggagag	
cggcggcgga	
tccgtgcagg	
ctggaggaag	
cctgcggctg	120
tcctgtgccg	
cctccgata	
ctcctccaac	
gtggcctgta	
tggcttggtg	
caggcaggct	180
cctggcaagg	
agcgggagtg	
ggtggctacc	
atcgtggccg	
acttcggcac	
caccaattac	240
gctgctagcg	
tgaagggcag	
gttcaccatc	
agccaggata	
acgctaagaa	
taccgtgtac	300
ctgcagatga	
atagcctgaa	
gcccaggagc	
tccgctatgt	
actattgtgc	
cgctacccag	360
aggggcggca	
tcgattgggt	
cgacgagatc	
aattattggg	
gccagggcac	
cctggtgacc	

gtgagcagcg	gcggaggcgg	aagcggagga	ggaggaagcc	aggtgcagct	cgtggagtcc	420
ggcggcgga	gcgtgcaggc	tggtggaagc	ctgaggctgt	cctgtgctgc	tagcggcgtg	480
accttcaact	ccgcttgtat	gggctggttc	cggcaggctc	ccggcaagga	gagagagggc	540
gtggccagga	tcgagaccgg	ctatggcggc	accgtgtacg	ccgacagcgt	gaagggacgg	600
ttcaccatct	ccagggataa	cgctaaaaac	accgtgtatc	tgcagatgaa	cagcctgaag	660
ccagaggata	ccgctatgta	ttactgtgct	gccaaagcga	gctgggtgtac	ccctacctgg	720
tggcacgagc	tggactacaa	ctattggggc	cagggaaccc	aggtgaccgt	gtccagcggc	780
gagcccaagt	ccagcgacaa	gaccacaccc	tgtcctcctt	gccctgctcc	agaggccgct	840
ggcggaccta	gcgtgttcct	gttcctcctt	aagcctaagg	acaccctgat	gatctccaga	900
acacctgaag	tgacctgcgt	ggtcgtggat	gtttctcacg	aggaccctga	ggtgaagttc	960
aactggtacg	tggacggcgt	ggaagtgcac	aacgccaaga	ccaagcctcg	ggaggaacag	1020
tacaactcca	cctacagagt	ggtgtccgtg	ctgaccgtgc	tgcaccagga	ctggctgaac	1080
ggaaaagagt	acaagtgcaa	ggtgtccaac	aaggccctgg	ccgctcctat	cgagaagact	1140
atctccaagg	ctaagggccca	gcctagagag	cctcaagtgt	gcaccctgcc	tccatctcgg	1200
gaagagatga	ccaagaacca	ggtgtctctg	tcttgcgccg	tcaagggtct	ctacccttcc	1260
gacatcgccg	tggaatggga	gtctaacggc	cagcctgaga	acaactacaa	gaccaccctt	1320
cctgtgctgg	actctgacgg	ctccttcttc	ctcgtgtcca	agctgaccgt	ggacaagtct	1380
cggtggcagc	agggcaacgt	gttctcctgc	tctgtgatgc	acgaggctct	gcacaaccac	1440
tacaccacaga	agtcctgtgc	cctgtcccct	ggcaag			1476

<210> 61
 <211> 455
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> anti-CD3-HC-Fc

<400> 61
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr
 20 25 30
 Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
 50 55 60
 Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
 65 70 75 80
 Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Met Tyr
 85 90 95
 Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
 100 105 110
 Ala Tyr Trp Gly Gln Gly Thr Leu 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
 Ala 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 Cys Arg Glu Glu Met Thr Lys
 355 360 365
 Asn Gln Val Ser Leu Trp 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
 420 425 430
 Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser
 435 440 445
 Leu Ser Leu Ser Pro Gly Lys
 450 455

<210> 62
 <211> 1365
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> anti-CD3-HC-Fc

<400> 62
 gaggtgcagc tggtggaatc tggcggaggc ctcgtgcagc ccggcggctc tctgagactg

60

tcttgcgccg	cttctggcctt	taccttcaat	acctatgcc	tgaattgggt	gcggcaggcc	120
cctggcaagg	gcctggaatg	ggtcgccaga	atcagatcca	agtacaacaa	ctacgccacc	180
tactacgccg	attctgtgaa	agacagattc	accatctctc	gggacgactc	taagaacacc	240
gcctacctgc	agatgaacaa	cctgaagacc	gaggacaccg	ctatgtacta	ctgcgtgaga	300
cacggcaact	tcggcaactc	ctacgtgtcc	tggttcgcct	actggggcca	gggcaccctg	360
gtcacagttt	cttctgcctc	taccaagggc	ccttccgtgt	tccctctggc	ccctagcagc	420
aaaagcacct	ccggcggaac	cgccgccctg	ggctgtctgg	tgaaggacta	cttccccgag	480
cctgtgacgg	tgtcttgga	ctccggcgct	ctgacctctg	gcgtgcatac	ctttcctgcc	540
gtgctgcagt	ccagcggact	gtactccctg	tcctccgtcg	tgacagttcc	ctcctctagc	600
ctgggcacac	agacctacat	ctgcaacgtg	aaccacaagc	cttctaacac	caaagtggac	660
aagaaggtgg	aacccaaatc	ctgcgacaag	acacacacct	gtcctccttg	ccctgctcct	720
gaggccgctg	gcggccctag	cgtgtttctg	tttcctccta	agcccaagga	cacactgatg	780
atctccagaa	ccccagaagt	gacctgcgta	gtgggtggacg	tgtcccacga	ggatcctgag	840
gtgaagttca	actggtacgt	ggatggcgctg	gaagtgcaca	acgccaagac	caagcctaga	900
gaagagcagt	acaactccac	ctacagagtg	gtgtccgtgc	tgaccgtgct	gcaccaggac	960
tggctgaacg	gcaaagagta	caagtgcgaag	gtgtccaaca	aggccctggc	tgctcctatc	1020
gagaagacca	tctccaaggc	taaggacag	cctcggaac	ctcaagtgtg	caccctgcct	1080
cctttagtag	aggaaatgac	caagaaccag	gtgtctctgt	ggcgcctggg	caagggtctt	1140
tacccttctg	acatcgccgt	ggagtggggag	tccaacggcc	agcctgagaa	caactacaaa	1200
accacccctc	cagtgtctgga	ctccgacggc	tccttcttcc	tgtactccaa	gctgacagtg	1260
gataagtcta	gatggcagca	gggcaatgtg	ttctcctgct	ccgtgatgca	cgaggctctg	1320
cacaaccggt	tcaccagaa	gtccctgtcc	ctgtccctg	gcaag		1365

<210> 63
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> anti-CD3-LC

<400> 63
 Glu Leu Val Val Thr Gln Glu Pro Ser Leu Thr Thr Ser Pro Gly Gly
 1 5 10 15
 Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
 20 25 30
 Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
 35 40 45
 Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Thr Pro Ala Arg Phe
 50 55 60
 Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Thr Gly Val
 65 70 75 80
 Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
 85 90 95
 Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
 100 105 110
 Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu
 115 120 125
 Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro

130	135	140
Gly Ala Val Thr Val	Ala Trp Lys Ala Asp	Gly Ser Pro Val Lys Ala
145	150	155
Gly Val Glu Thr Thr	Lys Pro Ser Lys Gln Ser	Asn Asn Lys Tyr Ala
165	170	175
Ala Ser Ser Tyr Leu Ser Leu Thr	Pro Glu Gln Trp Lys Ser	His Arg
180	185	190
Ser Tyr Ser Cys Gln Val Thr	His Glu Gly Ser Thr	Val Glu Lys Thr
195	200	205
Val Ala Pro Thr Glu Cys Ser		
210	215	

<210> 64
 <211> 645
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> anti-CD3-LC

<400> 64	
gagctggtgg tgaccagga gccatccctg accacaagcc caggaggaac cgtgacactg	60
acctgtagat ccagcaccgg cgccgtgacc acaagcaact acgctaattg ggtgcagcag	120
aagcctggac aggctccaag gggactgata ggaggaacca acaagagagc ccccggaaca	180
ccagctcggg tttccggcag cctgctggga ggcaaggccg ctctgacaat caccggcgtg	240
cagccagagg acgaggccga gtactattgc gctctgtggt attctaattc gtgggtgttt	300
ggaggaggaa caaagctgac cgtgctggga cagcccaagg ctaaccctac agtgaccctg	360
ttccccctt cttccgagga gctgcaggcc aataaggcca ccctggtgtg cctgatctct	420
gacttttacc caggagctgt gacagtggct tggaaggctg atggctcccc tgtgaaggct	480
ggcgtggaga ccacaaagcc aagcaagcag tctaacaata agtacgccgc tagctcttat	540
ctgtctctga ccccgagca gtggaagtcc cacaggtctt attcctgcca ggtgacacat	600
gagggcagca cagtggagaa gaccgtggcc cctacagagt gttct	645

<210> 65
 <211> 492
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> anti-BCMA-A10-v1-linker-A11-v1-Fc

<400> 65
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 Tyr Ser Ser Asn Val Ala
20 25 30
Cys Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala	Thr	Ile	Val	Ala	Asp	Phe	Gly	Thr	Thr	Asn	Tyr	Ala	Ala	Ser	Val
50						55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Gln	Asp	Asn	Ser	Lys	Asn	Thr	Val	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	Ala	Thr	Gln	Arg	Gly	Gly	Ile	Asp	Trp	Cys	Asp	Glu	Ile	Asn	Tyr
			100					105					110		
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser
	115						120					125			
Gly	Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu
	130					135					140				
Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe
145					150					155					160
Thr	Phe	Asn	Ser	Ala	Cys	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys
				165					170					175	
Gly	Arg	Glu	Gly	Val	Ser	Arg	Ile	Glu	Thr	Gly	Tyr	Gly	Gly	Thr	Val
			180					185					190		
Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser
		195					200					205			
Lys	Asn	Thr	Val	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr
	210					215					220				
Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Lys	Arg	Ser	Trp	Cys	Thr	Pro	Thr	Trp
225					230					235					240
Trp	His	Glu	Leu	Asp	Tyr	Asn	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr
				245					250					255	
Val	Ser	Ser	Gly	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro
			260					265					270		
Pro	Cys	Pro	Ala	Pro	Glu	Ala	Ala	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe
		275					280					285			
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val
	290					295					300				
Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe
305					310					315					320
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro
				325					330					335	
Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr
			340					345					350		
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val
		355					360					365			
Ser	Asn	Lys	Ala	Leu	Ala	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala
					375						380				
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Cys	Thr	Leu	Pro	Pro	Ser	Arg
385					390					395					400
Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Ser	Cys	Ala	Val	Lys	Gly
				405					410					415	
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro
			420					425					430		
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser
		435					440					445			

Phe	Phe	Leu	Val	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln
450						455					460				
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His
465					470					475				480	
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys				
			485					490							

<210> 66
 <211> 1476
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> anti-BCMA-A10-v1-linker-A11-v1-Fc

<400> 66

caagtgcagc	tggtcgagtc	cggcggcgga	ctggtgcagc	caggcggctc	cctccggctg	60
tcctgtgccg	cctccggcta	ctcctctaac	gtggcctgca	tggcctggta	tagacaggct	120
cctggcaagg	gcctggaatg	ggtggccacc	attgtggccg	acttcggcac	caccaactac	180
gccgcttccg	tcaagggcag	attcaccatc	tcccaggata	actccaagaa	caccgtgtac	240
ctgcagatga	actccctgag	ggctgaagat	accgctgtgt	actactgtgc	tgccacacag	300
agaggcggca	tcgattgggtg	cgacgagatc	aactattggg	gacagggcac	tttggtgacc	360
gtgtccagcg	gaggcggcgg	ctccggcggg	ggcggctctc	aggttcagct	ggtcgagtc	420
ggcgggtggc	tggtgcagcc	cggcggaagc	ctgagactgt	cctgcgccgc	ctctggcttt	480
accttcaact	ctgcctgtat	gggctggttt	cggcaagccc	ctgggaaagg	cagagagggc	540
gtgagccgga	tcgagacagg	ctacggcggc	acagtttacg	ctgactctgt	gaagggaaga	600
ttcaccatca	gccgggacaa	ttccaaaaat	accgtgtacc	tgcagatgaa	cagcctgcgg	660
gccgaggaca	cagctgtcta	ctactgcgcg	gccaaagcgt	cttggtgtac	ccctacctgg	720
tggcacgagc	tggactacaa	ctactggggc	cagggaactc	aggtgaccgt	gtcctccggc	780
gagcccaagt	cctctgacaa	gacacacacc	tgtcctccat	gccctgctcc	tgaggccgct	840
ggcggacctt	ccgtgttctt	gtttcctcct	aagcccaagg	acaccctgat	gatctctcgg	900
acccctgagg	tgacctgcgt	ggtggtggac	gtgtctcatg	aggatcctga	agtgaagtcc	960
aactggtacg	tggatggcgt	ggaagtgcac	aacgccaaga	ccaagcctag	agaagaacag	1020
tacaactcca	cctacagagt	ggtcagcgtg	ctgaccgtgc	tgcatacagga	ctggctgaac	1080
ggaaaagagt	acaagtgcaa	ggtgtccaac	aaggctctgg	ctgcccctat	cgagaagacc	1140
atctccaagg	ccaagggcca	gccccgcgag	cctcaggtgt	gcaccctgcc	tccatctaga	1200
gaagagatga	ccaagaacca	ggtctccctc	agctgcgccg	tgaagggctt	ctacccttct	1260
gacatcgctg	tggaatggga	aagcaatggc	caacccgaga	acaactacaa	gaccaccccc	1320
cctgtgctgg	actccgacgg	cagcttcttc	ctggtgtcaa	agctgacagt	ggacaagtcc	1380
agatggcagc	agggcaacgt	gttcagctgc	agtgtgatgc	acgaggccct	gcacaaccac	1440
tacaccaga	aatctctgtc	tctgtctcct	ggcaaa			1476

<210> 67
 <211> 482
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> anti-CD3-scFv-Fc

<400> 67

Glu	Leu	Val	Val	Thr	Gln	Glu	Pro	Ser	Leu	Thr	Thr	Ser	Pro	Gly	Gly
1				5					10					15	
Thr	Val	Thr	Leu	Thr	Cys	Arg	Ser	Ser	Thr	Gly	Ala	Val	Thr	Thr	Ser
			20					25					30		
Asn	Tyr	Ala	Asn	Trp	Val	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Gly
		35				40						45			
Leu	Ile	Gly	Gly	Thr	Asn	Lys	Arg	Ala	Pro	Gly	Thr	Pro	Ala	Arg	Phe
50					55					60					
Ser	Gly	Ser	Leu	Leu	Gly	Gly	Lys	Ala	Ala	Leu	Thr	Ile	Thr	Gly	Val
65				70					75					80	
Gln	Pro	Glu	Asp	Glu	Ala	Glu	Tyr	Tyr	Cys	Ala	Leu	Trp	Tyr	Ser	Asn
			85					90						95	
Leu	Trp	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	Gly	Gly
			100					105					110		
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Val	Gln	Leu
		115				120					125				
Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu
130					135					140					
Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Asn	Thr	Tyr	Ala	Met	Asn	Trp
145				150					155					160	
Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Arg	Ile	Arg
			165					170						175	
Ser	Lys	Tyr	Asn	Asn	Tyr	Ala	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Asp
			180					185					190		
Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Asn	Thr	Ala	Tyr	Leu	Gln
		195				200						205			
Met	Asn	Asn	Leu	Lys	Thr	Glu	Asp	Thr	Ala	Met	Tyr	Tyr	Cys	Val	Arg
210					215					220					
His	Gly	Asn	Phe	Gly	Asn	Ser	Tyr	Val	Ser	Trp	Phe	Ala	Tyr	Trp	Gly
225				230					235					240	
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Glu	Pro	Lys	Ser	Ser	Asp
			245					250					255		
Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala	Ala	Gly	Gly
		260					265					270			
Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile
		275				280						285			
Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu
290					295						300				
Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His
305				310					315					320	
Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg
			325					330					335		
Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys
		340					345					350			
Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Ala	Ala	Pro	Ile	Glu
	355					360					365				
Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr

370		375		380
Thr Leu Pro Pro Cys Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu				
385		390		400
Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp				
	405		410	415
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val				
	420		425	430
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp				
	435		440	445
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His				
	450		455	460
Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu Ser Pro				
465		470		480
Gly Lys				

<210> 68
 <211> 1446
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> anti-CD3-scFv-Fc

<400> 68

gagctggctcg	tcaccaaga	gccctctctg	accacaagcc	ctggcggaac	cgtgaccctg	60
acctgtaggt	cctccaccgg	cgctgtgacc	acctcgaact	atgccaactg	ggtgcaacag	120
aagcccggcc	aggcaccag	aggcctgac	ggcggcacca	acaagcgcgc	ccccggcaca	180
cctgccagat	tctctggctc	tctgctgggc	ggaaaggccg	ccctgaccat	caccggcgctc	240
cagcccagg	acgaggccga	gtactactgc	gctctgtggt	actccaacct	gtgggtgttt	300
ggcggcggca	ccaagctgac	cgtgctgggc	ggcgggtggct	ctggaggagg	cggatctggt	360
ggcggaggct	ctgaagtgca	gctcgttgag	agcggcggcg	gcctggtgca	gcctggcggc	420
tccctgagac	tgtcttgcg	cgcttccggc	ttcaccttca	acacctatgc	catgaattgg	480
gtccggcagg	ccccggcaa	gggactggaa	tgggtggcta	gaatcagatc	caagtacaac	540
aactacgcta	cctactacgc	cgactctgtg	aaggaccggt	tcaccatctc	tcgggacgac	600
tccaagaaca	ccgcctacct	gcagatgaac	aatctgaaga	ccgaggatac	cgctatgtac	660
tactgtgtgc	ggcacggcaa	cttcggcaac	tcctacgtgt	cctggttcgc	ctactggggc	720
cagggcactc	tcgtgaccgt	gtccagcggc	gagcccaagt	cctctgacaa	gacccacacc	780
tgccctccat	gtcctgctcc	tgaggctgct	ggcggccctt	ccgtgtttct	gttccctcct	840
aagcctaaag	atacactgat	gatctcccgg	accctgaag	ttacatgcgt	ggtggtggac	900
gtgtctcacg	aggaccccga	agtgaagttc	aactggtatg	tggatggcgt	ggaagtgcac	960
aatgccaaaa	ccaagcctcg	ggaggaacag	tacaactcta	cctacagagt	ggtaagcgtg	1020
ctgaccgtgc	tgcaccagga	ctggctgaac	ggcaaagagt	acaagtgcaa	ggtgtctaac	1080
aaggctctgg	ccgcccctat	cgagaagaca	atttccaagg	ccaagggcca	gcctagagaa	1140
cctcaggtgt	acaccctgcc	tccttgca	gaagagatga	ccaagaacca	ggttagccta	1200
tggtgcctgg	tgaagggttt	ctacccttct	gacatcgccg	tggagtggga	gtccaatggc	1260
caaccagaga	acaactacaa	gacaacacca	cctgtgctgg	actccgatgg	ctccttcttc	1320
ctgtactcta	agctgacagt	ggacaagtcc	agatggcagc	agggcaacgt	gttctcctgc	1380
tccgtgatgc	atgaagctct	gcacaaccgg	ttcaccaga	aatccctgag	cctgtctcct	1440

ggaaaa

1446

<210> 69
<211> 356
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-BCMA-A10-v1-Fc

<400> 69
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 Tyr Ser Ser Asn Val Ala
20 25 30
Cys Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Thr Ile Val Ala Asp Phe Gly Thr Thr Asn Tyr Ala Ala Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Gln Asp Asn Ser Lys Asn Thr Val 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 Ala Thr Gln Arg Gly Gly Ile Asp Trp Cys Asp Glu Ile Asn Tyr
100 105 110
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Glu Pro Lys Ser
115 120 125
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
130 135 140
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
145 150 155 160
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
165 170 175
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
180 185 190
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
195 200 205
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
210 215 220
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Ala Ala Pro
225 230 235 240
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
245 250 255
Val Cys Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
260 265 270
Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
275 280 285
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
290 295 300

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr
 305 310 315 320
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 325 330 335
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 340 345 350
 Ser Pro Gly Lys
 355

<210> 70
 <211> 1068
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> anti-BCMA-A10-v1-Fc

<400> 70
 caagtccagc tggttgagtc cggcggaggc ctggtgcagc caggcggctc cctgagactg 60
 tcttgtgctg cctctggcta ctctctaat gtggcctgca tggcctggta ccggcaggcc 120
 cctggcaagg gcctggaatg ggtggctact atcgtggccg acttcggcac caccaattat 180
 gctgcctctg tgaagggacg gttcaccatc tcccaggaca actccaagaa caccgtgtac 240
 ctgcagatga acagcctgcg ggccgaggac acagccgtgt actactgtgc cgctacacag 300
 agaggcggca tcgactgggtg cgacgagatc aactactggg gccaaaggaac cctggtgaca 360
 gtgtcttctg gcgagcccaa atcctccgat aaaacacaca cctgtcctcc ttgccctgct 420
 cccgaggccg ccggcggccc tagcgtattc ctgtttcccc ctaagcctaa ggacacattg 480
 atgatctctc ggacacccga agtgacctgc gtggctcgtg acgtgtctca cgaagatcct 540
 gaggtgaagt tcaactggta tgtggatggc gtggaagtgc ataacgcaa gaccaagccc 600
 agagaggaac agtacaactc tacctacaga gtgggtgtccg tcctgaccgt gctgcatcag 660
 gattggctga acggcaaaga gtacaagtgc aagggtgtcta acaaggctct ggccgctccc 720
 attgagaaga ccatctccaa ggctaagggt cagcctagag agcctcaagt gtgcaccctg 780
 cctccatcta gagaagagat gaccaagaac caggctcagcc tgtcttgtgc agtgaaaggc 840
 ttctacccaa gcgacatcgc cgtggaatgg gagtctaatt gccagcctga aaacaactac 900
 aagaccacc ctcctgtgct cgactccgac ggctccttct tcctgggtgtc caagctgacc 960
 gtggacaagt cccgctggca gcagggcaac gtgttctcct gctccgtgat gcacgaggct 1020
 ctgcacaacc actacacca gaagagcctg agcctgtccc ctggaaag 1068

<210> 71
 <211> 613
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> anti-BCMA-A11-v1-linker-anti-CD3-scFv-Fc

<400> 71
 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	Asn	Ser	Ala	20	25	30
Cys	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Arg	Glu	Gly	Val	35	40	45
Ser	Arg	Ile	Glu	Thr	Gly	Tyr	Gly	Gly	Thr	Val	Tyr	Ala	Asp	Ser	Val	50	55	60
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Val	Tyr	65	70	75
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	85	90	95
Ala	Ala	Lys	Arg	Ser	Trp	Cys	Thr	Pro	Thr	Trp	Trp	His	Glu	Leu	Asp	100	105	110
Tyr	Asn	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Gly	Gly	115	120	125
Gly	Gly	Ser	Glu	Leu	Val	Val	Thr	Gln	Glu	Pro	Ser	Leu	Thr	Thr	Ser	130	135	140
Pro	Gly	Gly	Thr	Val	Thr	Leu	Thr	Cys	Arg	Ser	Ser	Thr	Gly	Ala	Val	145	150	155
Thr	Thr	Ser	Asn	Tyr	Ala	Asn	Trp	Val	Gln	Gln	Lys	Pro	Gly	Gln	Ala	165	170	175
Pro	Arg	Gly	Leu	Ile	Gly	Gly	Thr	Asn	Lys	Arg	Ala	Pro	Gly	Thr	Pro	180	185	190
Ala	Arg	Phe	Ser	Gly	Ser	Leu	Leu	Gly	Gly	Lys	Ala	Ala	Leu	Thr	Ile	195	200	205
Thr	Gly	Val	Gln	Pro	Glu	Asp	Glu	Ala	Glu	Tyr	Tyr	Cys	Ala	Leu	Trp	210	215	220
Tyr	Ser	Asn	Leu	Trp	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	225	230	235
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	245	250	255
Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	260	265	270
Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Asn	Thr	Tyr	Ala	275	280	285
Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	290	295	300
Arg	Ile	Arg	Ser	Lys	Tyr	Asn	Asn	Tyr	Ala	Thr	Tyr	Tyr	Ala	Asp	Ser	305	310	315
Val	Lys	Asp	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Asn	Thr	Ala	325	330	335
Tyr	Leu	Gln	Met	Asn	Asn	Leu	Lys	Thr	Glu	Asp	Thr	Ala	Met	Tyr	Tyr	340	345	350
Cys	Val	Arg	His	Gly	Asn	Phe	Gly	Asn	Ser	Tyr	Val	Ser	Trp	Phe	Ala	355	360	365
Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Glu	Pro	Lys	370	375	380
Ser	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala	385	390	395
Ala	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	405	410	415

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 420 425 430
 Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 435 440 445
 Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
 450 455 460
 Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 465 470 475 480
 Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Ala Ala
 485 490 495
 Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 500 505 510
 Gln Val Tyr Thr Leu Pro Pro Cys Arg Glu Glu Met Thr Lys Asn Gln
 515 520 525
 Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 530 535 540
 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 545 550 555 560
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 565 570 575
 Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 580 585 590
 Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu Ser
 595 600 605
 Leu Ser Pro Gly Lys
 610

<210> 72

<211> 1839

<212> DNA

<213> Artificial Sequence

<220>

<223> anti-BCMA-A11-v1-linker-anti-CD3-scFv-Fc

<400> 72

caggtgcagc	tcgtggaatc	cggcggcggc	ctggtgcagc	ctggcggctc	tctgagactg	60
tcttgtgctg	cctctggctt	tactttcaac	tccgcctgca	tgggctgggt	cagacaggcc	120
cccggaaagg	gccgggaggg	cgtgtctcgg	atcgagacag	gctacggcgg	taccgtgtac	180
gccgactctg	tgaaggcag	attcaccatc	tccagagaca	actccaagaa	taccgtctac	240
ctgcagatga	atagcctccg	cgccgaggac	accgctgtgt	actactgcgc	cgctaagaga	300
tcttggtgca	ccccacctg	gtggcacgag	ctggactaca	actactgggg	ccaggggaacc	360
caggtgaccg	tgtccagcgg	cggaggcggc	tctgaactgg	tgggtgacca	agagccttcc	420
ctgaccacct	cccctggcgg	cacagtgaca	ctgacctgta	gatactccac	cggcgccgtg	480
accacctcta	actatgctaa	ctgggtgcag	cagaaacctg	gccaggcacc	tcggggactg	540
atcggcggca	ccaacaagcg	ggctcctgga	acacctgcta	gattctccgg	ctccttgctg	600
ggcggcaagg	ccgccctgac	catcaccggg	gtgcaacctg	aggacgaggc	tgagtattac	660
tgcgctctgt	ggtactccaa	cctgtgggtc	tttggcggcg	gaaccaagct	gaccgtgctg	720
ggcggcggcg	gctccggcgg	aggcggctcc	ggaggaggcg	gcagcgaggt	gcagctggtc	780

gagtctggcg	gcggcctggt	gcagcccggc	ggctcgctgc	ggctgagctg	tgccgcctcc	840
ggcttcacat	tcaataccta	cgccatgaac	tggttcaggc	aggctcctgg	caaaggcctg	900
gaatgggtgg	ccagaatccg	gagcaagtac	aacaactatg	ccacctacta	cgccgattct	960
gtgaaggaca	gattcacaat	ctcccgggac	gactctaaga	acaccgctta	cctgcagatg	1020
aacaacctga	agaccgagga	tacagctatg	tactactgtg	tgcggcacgg	caacttcggc	1080
aattcctacg	tgtcctgggt	cgctactagg	ggacaaggca	ccttggtgac	agtttctagc	1140
ggcgagccca	agtcttctga	caagacacac	acctgccctc	cttgtcctgc	ccctgaggcc	1200
gctggcggac	cttctgtgtt	tctgtttcca	cctaagccta	aggataccct	gatgatctct	1260
agaacccccg	aggtgacctg	cgtggtcgtg	gacgtgagcc	atgaagatcc	tgaagtgaag	1320
ttcaactggt	atgtggacgg	cgtggaagtg	cacaatgcc	agaccaagcc	tagagaagag	1380
cagtacaact	ctacctacag	agtgggtgtcc	gtgctgaccg	ttctgcatca	ggactggctg	1440
aacggcaaag	agtacaagt	caaggtgtct	aacaaggctc	tggctgcccc	tatcgagaag	1500
accatttcca	aggccaaggg	ccagccacgc	gaacctcaag	tgtacaccct	gccaccttgc	1560
agagaggaga	tgaccaagaa	ccaggtgagc	ctgtgggtgcc	tggtgaaagg	cttctacccc	1620
agcgacatcg	ccgtggaatg	ggagtccaac	ggccagcccg	agaacaacta	caaaaccacc	1680
cctcctgtgc	tggattctga	tggttccttc	ttcctgtact	ctaagctgac	cgtggacaag	1740
tcccgggtggc	agcagggcaa	cgtgttcagc	tgctccgtga	tgcacgaagc	cctgcacaac	1800
cggttcaccc	agaaatccct	gtctctgtct	ccaggcaag			1839

<210> 73
 <211> 359
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> anti-BCMA-A11-v1-Fc

<400> 73
 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 Asn Ser Ala
 20 25 30
 Cys Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Gly Arg Glu Gly Val
 35 40 45
 Ser Arg Ile Glu Thr Gly Tyr Gly Gly Thr Val Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val 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 Ala Lys Arg Ser Trp Cys Thr Pro Thr Trp Trp His Glu Leu Asp
 100 105 110
 Tyr Asn Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Glu
 115 120 125
 Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
 130 135 140
 Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 145 150 155 160
 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val


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gtcaagggt tctacccttc tgacatcgcc gtggaatggg agtctaacgg ccagcccgag      900
aacaactata agaccacccc ccccggtgctg gattctgatg gctccttctt cctcgtgtcc      960
aagctgaccg tggacaagtc cagatggcag cagggcaacg tgttctcctg ctctgtgatg     1020
cacgaggcac tgcacaacca ctacaccag aagtcctta gcctgtctcc tggcaag          1077

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<210> 75
<211> 343
<212> PRT
<213> Artificial Sequence

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<220>
<223> anti-BCMA-A10-v1-linker-anti-CD3-VL

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<400> 75
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 Tyr Ser Ser Asn Val Ala
20     25     30
Cys Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35     40     45
Ala Thr Ile Val Ala Asp Phe Gly Thr Thr Asn Tyr Ala Ala Ser Val
50     55     60
Lys Gly Arg Phe Thr Ile Ser Gln Asp Asn Ser Lys Asn Thr Val 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 Ala Thr Gln Arg Gly Gly Ile Asp Trp Cys Asp Glu Ile Asn Tyr
100    105    110
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115    120    125
Glu Leu Val Val Thr Gln Glu Pro Ser Leu Thr Thr Ser Pro Gly Gly
130    135    140
Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
145    150    155    160
Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
165    170    175
Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Thr Pro Ala Arg Phe
180    185    190
Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Thr Gly Val
195    200    205
Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
210    215    220
Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
225    230    235    240
Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu
245    250    255
Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro
260    265    270
Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys Ala

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	275		280		285	
Gly	Val	Glu	Thr	Thr	Lys	Pro
	290				295	
Ala	Ser	Ser	Tyr	Leu	Ser	Leu
305				310		
Ser	Tyr	Ser	Cys	Gln	Val	Thr
				325		
Val	Ala	Pro	Thr	Glu	Cys	Ser
				340		

<210> 76
 <211> 1029
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> anti-BCMA-A10-v1-linker-anti-CD3-VL

<400> 76
 caagtgcagc tgggtggaatc tggcggcgga ctggtgcagc caggcggctc cctgagactg 60
 tcctgtgctg cttctggcta ctcgtccaac gtggcctgca tggcctggta tcgccaggct 120
 cctggcaaag gcctggaatg ggtggctacc atcgtggccg acttcggcac tacaaactac 180
 gccgcctccg tgaagggcag attcaccatc tctcaggaca actccaagaa caccgtgtac 240
 ctgcagatga acagcctgcg ggctgaggac accgccgtgt actactgtgc cgctaccag 300
 cggggaggca tcgactgggt cgacgagatc aactactggg gccagggaac cttggttaca 360
 gtgtccagcg gcggaggcgg ctccgaactg gtggtgacct aagagccttc tctgaccacc 420
 tcccctggcg gcacagtac cctgacctgt agatcctcta ccggtgccgt gacaacctct 480
 aattacgcca actgggtcca gcagaagccc ggccaagccc cttagaggcct gatcggcggg 540
 acgaacaagc gggctcctgg caccctgcc cggttcagcg gctctctgct gggcggcaag 600
 gctgccctga caatcaccgg cgtgcagcct gaggatgagg ccgagtacta ctgcgctctg 660
 tggatatagca acctgtgggt gttcggagga ggcacaaagc tgaccgtgct gggccagcct 720
 aaggccaatc ctaccgtgac cctgtttcct ccatcttctg aagagctgca ggccaacaaa 780
 gccaccctcg tgtgcctgat ctccgacttc taccgccg cgctgtgaccgt ggcatggaag 840
 gccgatggct cccctgtgaa agctggcgctc gaaaccacca agcctagcaa gcagtccaac 900
 aacaagtacg ctgcctcttc ctacctgtct ctgacccccg agcagtggaa gtcccataga 960
 agctactctt gccaggtgac ccacgagggc tccaccgtcg agaagaccgt ggccccacc 1020
 gagtgtctcc 1029

<210> 77
 <211> 446
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> anti-BCMA-HC-Fc

<400> 77
 Glu Val Gln Leu Leu 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	Ser	Tyr	
			20					25					30			
Ala	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35				40						45				
Ser	Ala	Ile	Ser	Gly	Ser	Gly	Gly	Ser	Thr	Tyr	Tyr	Ala	Asp	Ser	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	Lys	Val	Leu	Gly	Trp	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	
			100					105					110			
Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	
		115					120					125				
Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	
	130					135					140					
Val	Glu	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	
145					150					155					160	
Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	
				165					170					175		
Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	
			180					185					190			
Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	
		195				200						205				
Lys	Val	Asp	Glu	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	
	210					215					220					
Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala	Ala	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	His	Glu	Asp	Pro	Glu	Val	
			260					265					270			
Lys	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	Ala	Leu	Gly	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	
			325						330					335		
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Cys	Thr	Leu	Pro	Pro	
			340					345					350			
Ser	Arg	Asp	Glu	Leu	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	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	

				405					410					415			
Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His		
			420					425					430				
Asn	Arg	Phe	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys				
		435					440					445					

<210> 78
 <211> 1338
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> anti-BCMA-HC-Fc

<400> 78

gaggtgcagc	tgctggaatc	tggaggcggc	ctggtgcaac	ccggcggatc	tctgagactg	60
tcttgtgccg	cttctggcctt	caccttttcc	tcctacgcc	tgtcctgggt	cagacaggcc	120
cctggaaagg	gactggaatg	ggtgtctgcc	atctccggct	ctggcggctc	tacatactac	180
gccgacagcg	tgaagggcag	attcaccatc	agccgggaca	actccaagaa	caccctctac	240
ctgcagatga	actctctgcg	ggccgaggat	accgccgtgt	actactgcgc	caaagtgctg	300
ggatggttcg	actactgggg	ccaaggcacg	ctcgtgaccg	tgtcctccgc	ctccaccaa	360
ggaccttccg	tgtttctct	ggccccttcc	agcaagtcca	cctccggcgg	taccgctgcc	420
ctgggctgcc	tggtcgagga	ctacttccct	gagcccgtga	ccgtgtcttg	gaactccggc	480
gctctgacct	ctggcgtgca	caccttcccc	gctgttctgc	agtccagcgg	cctgtactcc	540
ctgtcctctg	tggtgacagt	gcctagctct	tctctgggca	cccagaccta	catctgcaac	600
gtgaaccaca	agccctccaa	caccaagggtg	gatgagaaag	tggaacccaa	gtcttgcgac	660
aagacacata	cctgtcctcc	ttgccctgct	cctgaggccg	ctggcggccc	ttctgtgttc	720
ctgttcccac	ccaagcctaa	ggacaccctg	atgatctctc	ggacccctga	ggtcacctgc	780
gtggtcgtgg	acgtgtccca	tgaagatcct	gaagtgaagt	tcaactggta	cgtggatggc	840
gtggaagtgc	acaacgcaa	gaccaagcct	cgggaagagc	agtacaactc	cacatacaga	900
gtggtgagcg	tgctgaccgt	gctgcaccag	gactggctga	acggcaaaga	gtacaagtgc	960
aagggtgtcca	acaaggctct	cggcgccccc	atcgagaaga	caatctccaa	ggccaagggc	1020
cagcctagag	agcctcaggt	gtgcaccctg	cctccatctc	gcgacgagct	gactaagaac	1080
caggtgtccc	tgctctgtgc	tggtgaaaggc	ttctaccctt	ctgacatcgc	cgtggagtgg	1140
gagtctaacg	gccagcccga	gaacaactac	aagaccacac	ctcctgttct	ggactccgac	1200
ggctccttct	tcctgggtgc	taagctgacc	gtggacaagt	ccagatggca	gcagggaac	1260
gtgttctcct	gctccgtgat	gcacgaggct	ctgcacaaca	gattcaccca	gaagtctctc	1320
agcctgtccc	ctggcaag					1338

<210> 79
 <211> 216
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> anti-BCMA-LC

<400> 79

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45
 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Tyr Pro Pro
 85 90 95
 Asp Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val
 100 105 110
 Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Arg Lys Leu Lys
 115 120 125
 Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
 130 135 140
 Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
 145 150 155 160
 Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
 165 170 175
 Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
 180 185 190
 Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
 195 200 205
 Lys Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 80

<211> 648

<212> DNA

<213> Artificial Sequence

<220>

<223> anti-BCMA-LC

<400> 80

gagatcgtgc	tgaccagtc	tcctggaaca	ctgtctctgt	cccctggcga	gagagctacc	60
ctgagctgca	gagcctctca	gtccgtgtcc	tcctcctacc	tggcctggta	ccagcagaag	120
cctggccagg	cccctcggct	gctgatctac	ggcgctagct	ctcgggccac	cggcatccct	180
gacagattct	ccggctccgg	ctctggcaca	gattttaccc	tgaccatctc	cagactggaa	240
cctgaggact	tcgccgtgta	ctactgccag	cagtacggct	accccccca	cttcaccttc	300
ggccaaggca	ccaaagtgga	aatcaagcgg	accgtggctg	ctccttctgt	gttcattcttc	360
cctccttccg	accggaagct	gaagtctgga	accgcctccg	tgggtgtgcct	gctgaacaac	420
ttctacccta	gagaggccaa	ggtgcagtgg	aagggtggaca	acgccctgca	gagcggcaac	480
tcccaagagt	ccgtcaccga	gcaggactct	aaggactcca	cctactccct	gtcctctacc	540
ctgacactgt	ccaaggccga	ctacgagaag	cacaaggtgt	acgcctgcga	ggtgaccac	600
cagggcctgt	cttctcctgt	gaccaagtcc	ttcaacagag	gcgaatgt		648

<210> 81
 <211> 671
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> anti-BCMA-VH-anti-CD3-VL-Fc

<400> 81
 Glu Val Gln Leu Leu 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 Ser Tyr
 20 25 30
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser 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 Lys Val Leu Gly Trp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
 115 120 125
 Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
 130 135 140
 Val Glu Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
 145 150 155 160
 Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
 165 170 175
 Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
 180 185 190
 Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
 195 200 205
 Lys Val Asp Glu Lys Val Glu Pro Lys Ser Cys Asp Gly Gly Gly Gly
 210 215 220
 Ser Gly Gly Gly Gly Ser Gln Ala Val Val Thr Gln Glu Pro Ser Leu
 225 230 235 240
 Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr
 245 250 255
 Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro
 260 265 270
 Gly Gln Ala Phe Arg Gly Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro
 275 280 285
 Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala
 290 295 300
 Leu Thr Leu Ser Gly Ala Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys

305					310					315					320
Ala	Leu	Trp	Tyr	Ser	Asn	Leu	Trp	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu
				325					330					335	
Thr	Val	Leu	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu
			340					345					350		
Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys
		355					360				365				
Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser
	370					375				380					
Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser
385					390				395					400	
Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser
				405				410						415	
Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn
			420					425					430		
Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His
	435						440					445			
Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala	Ala	Gly	Gly	Pro	Ser	Val
	450					455					460				
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr
465					470				475					480	
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu
				485				490						495	
Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys
			500					505					510		
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser
		515					520					525			
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys
	530					535					540				
Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Gly	Ala	Pro	Ile	Glu	Lys	Thr	Ile
545					550				555					560	
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro
				565				570						575	
Pro	Cys	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Trp	Cys	Leu
			580					585					590		
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn
	595						600					605			
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser
	610					615					620				
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg
625					630				635					640	
Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu
				645				650						655	
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	
			660					665					670		

<210> 82
 <211> 2013
 <212> DNA
 <213> Artificial Sequence

<220>

<223> anti-BCMA-VH-anti-CD3-VL-Fc

<400> 82

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cctggcaagg	gactggagtg	ggtctccgcc	atctctgggt	ccggaggctc	cacctactac	180
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ctgcagatga	actccctgag	agccgaggac	accgccgtgt	actactgcgc	caaggtgctg	300
ggatggttcg	actactgggg	ccagggcacc	ttagtgaccg	tgtcaagcgc	cagcacaaag	360
ggacctagcg	tatttcctct	ggcccctagc	tctaagtcca	cctctgggtg	caccgcagcc	420
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ctgtcctctg	ttgtcacagt	gcccagttct	tctctgggca	cccagacata	catctgtaac	600
gtgaaccaca	agccttccaa	caccaaagtg	gacgagaaag	tggaacctaa	gtcctgcgat	660
ggcggcgggc	ggtccgggtg	agggggatct	caggctgtgg	tcacccaaga	gccctccctg	720
accgtgtccc	ctggcggcac	cgtgacactg	acctgcggct	cttcacagg	cgccgtgacc	780
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gccctgtggg	attccaacct	gtgggtcttc	ggcgggtggc	ccaagctgac	cgtgctgtct	1020
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atcgccgtgg	aatgggagtc	caatggacag	cccgagaaca	actacaagac	cacacctcca	1860
gtgctggact	ccgacggctc	cttcttcctg	tacagcaagc	tgacagtgga	caagtccaga	1920
tggcagcagg	gcaacgtggt	ctcctgctcc	gtgatgcacg	aggctctgca	caaccactac	1980
accagaaggt	ccctgtccct	gtctcctgga	aag			2013

<210> 83

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-CD3-VH-CL

<400> 83
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 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
 20 25 30
 Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
 50 55 60
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
 65 70 75 80
 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 85 90 95
 Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
 100 105 110
 Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Val
 115 120 125
 Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
 130 135 140
 Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
 145 150 155 160
 Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
 165 170 175
 Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
 180 185 190
 Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
 195 200 205
 Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
 210 215 220
 Lys Ser Phe Asn Arg Gly Glu Cys
 225 230

<210> 84
 <211> 696
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> anti-CD3-VH-CL

<400> 84
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 cccggcaagg gcctggaatg ggtgtccaga atcagatcca agtacaacaa ctacgccacc 180
 tactacgccg attccgtgaa gggacggttc accatctccc gggacgactc caagaacaca 240
 ctgtacctgc agatgaacag cctgagagcc gaggacaccg ccgtgtacta ctgcgtgcgg 300
 cacggcaact tcggcaattc ctacgtgtcc tggttcgctt actggggcca gggcaccttg 360
 gtcaccgtgt cttccgcctc tgtggccgct cttctgtgt tcatcttccc tccttccgac 420
 gagcagctga agtctggcac agcttctgtg gtgtgcctgc tgaacaactt ctaccctaga 480

gaggccaagg	tgcaagtggaa	ggtggacaac	gccctgcagt	ccggcaactc	ccaagagtcc	540
gtgaccgagc	aggactctaa	ggactctacc	tactccctgt	cctccaccct	gaccctgagc	600
aaggccgact	acgagaagca	caaagtgtac	gcctgcgaag	tgaccaccca	gggcctgtcc	660
tctcctgtga	ccaagtcctt	caacagaggc	gagtgc			696