

SEQUENCE LISTING

<110> THE UNIVERSITY OF BRITISH COLUMBIA
TXCELL

<120> NOVEL ANTI-HLA-A2 ANTIBODIES AND USES THEREOF

<130> P1526PC00

<140> NOT YET ASSIGNED

<141> 2018-09-20

<150> US 62/560,841

<151> 2017-09-20

<150> US 62/691,027

<151> 2018-06-28

<160> 89

<170> BiSSAP 1.3.6

<210> 1

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> VH-CDR1

<400> 1

Ser Tyr His Ile Gln

1 5

<210> 2

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> VH-CDR2

<400> 2

Trp Ile Tyr Pro Gly Asp Gly Ser Thr Gln Tyr Asn Glu Lys Phe Lys

1 5 10 15

Gly

<210> 3

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> VH-CDR3

<400> 3

Glu Gly Thr Tyr Tyr Ala Met Asp Tyr

1 5

<210> 4

<211> 7

<212> PRT

<213> Artificial Sequence

<220>
 <223> VH-CDR1

 <400> 4
 Gly Tyr Thr Phe Thr Ser Tyr
 1 5

 <210> 5
 <211> 6
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> VH-CDR2

 <400> 5
 Tyr Pro Gly Asp Gly Ser
 1 5

 <210> 6
 <211> 16
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> VL-CDR1

 <400> 6
 Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
 1 5 10 15

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

 <220>
 <223> VL-CDR2

 <400> 7
 Lys Val Ser Asn Arg Phe Ser
 1 5

 <210> 8
 <211> 9
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> VL-CDR3

 <400> 8
 Phe Gln Gly Ser His Val Pro Arg Thr
 1 5

 <210> 9
 <211> 118
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> VH

<400> 9
 Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30
 His Ile Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Gln Tyr Asn Glu Lys Phe
 50 55 60
 Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Glu Gly Thr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
 100 105 110
 Ser Val Thr Val Ser Ser
 115

<210> 10
 <211> 113
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VL

<220>
 <221> SITE
 <222> 2
 <223> X is V or I

<220>
 <221> SITE
 <222> 7
 <223> X is T or S

<220>
 <221> SITE
 <222> 9
 <223> X is L or S or A

<220>
 <221> SITE
 <222> 10
 <223> X is S or T

<220>
 <221> SITE
 <222> 12
 <223> X is P or S

<220>
 <221> SITE
 <222> 14
 <223> X is T or S

<220>
 <221> SITE
 <222> 15
 <223> X is L or P

<220>
 <221> SITE
 <222> 17

<223> X is E or D

<220>

<221> SITE

<222> 18

<223> X is P or R

<220>

<221> SITE

<222> 19

<223> X is A or V

<220>

<221> SITE

<222> 20

<223> X is S or T

<220>

<221> SITE

<222> 42

<223> X is L or Q

<220>

<221> SITE

<222> 48

<223> X is S or A

<220>

<221> SITE

<222> 63

<223> X is V or I

<220>

<221> SITE

<222> 79

<223> X is K or T

<220>

<221> SITE

<222> 83

<223> X is V or L

<220>

<221> SITE

<222> 85

<223> X is A or P

<220>

<221> SITE

<222> 88

<223> X is L or F

<220>

<221> SITE

<222> 89

<223> X is G or A

<400> 10

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

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

Arg

<210> 11
 <211> 113
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VL

<400> 11

Asp	Val	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	Pro	Val	Thr	Leu	Gly		
1				5					10					15			
Glu	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Ile	Val	His	Ser		
		20						25					30				
Asn	Gly	Asn	Thr	Tyr	Leu	Glu	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser		
		35					40					45					
Pro	Arg	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	Arg	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys		
			100					105						110			

Arg

<210> 12
 <211> 113
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VL

<400> 12

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

Arg

<210> 13
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> VL

<400> 13
Asp Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
20 25 30
Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Gln Gln Lys Pro Gly Gln Ala
35 40 45
Pro Arg Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Ile Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
65 70 75 80
Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Phe Gln Gly
85 90 95
Ser His Val Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110
Arg

<210> 14
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> G3S linker

<400> 14
Gly Gly Gly Ser
1

<210> 15
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> G3S linker

<400> 15
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15

<210> 16
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> G4S linker

<400> 16
Gly Gly Gly Gly Gly Ser
1 5

<210> 17
<211> 10

<212> PRT
 <213> Artificial Sequence

 <220>
 <223> G4S linker

 <400> 17
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10

 <210> 18
 <211> 15
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> G4S linker

 <400> 18
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10 15

 <210> 19
 <211> 20
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> G4S linker

 <400> 19
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1 5 10 15
 Gly Gly Gly Ser
 20

 <210> 20
 <211> 16
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Hinge domain

 <400> 20
 Ala Gly Ser Ser Ser Ser Gly Gly Ser Thr Thr Gly Gly Ser Thr Thr
 1 5 10 15

 <210> 21
 <211> 16
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Hinge domain

 <400> 21
 Gly Thr Thr Ala Ala Ser Gly Ser Ser Gly Gly Ser Ser Ser Gly Ala
 1 5 10 15

 <210> 22
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Hinge domain

<400> 22
 Ser Ser Ala Thr Ala Thr Ala Gly Thr Gly Ser Ser Thr Gly Ser Thr
 1 5 10 15

<210> 23
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Hinge domain

<400> 23
 Thr Ser Gly Ser Thr Gly Thr Ala Ala Ser Ser Thr Ser Thr Ser Thr
 1 5 10 15

<210> 24
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Hinge domain

<400> 24
 ggtggcggag gttctggagg tggaggttcc

30

<210> 25
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Hinge domain

<400> 25
 Lys Ile Arg Arg Asp Ser Ser
 1 5

<210> 26
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD8 Hinge domain

<400> 26
 Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
 1 5 10 15
 Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
 20 25 30
 Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
 35 40 45

<210> 27
 <211> 135
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CD8 Hinge domain

<400> 27
 accacgacgc cagcgccgcg accaccaaca ccggcgccca ccacgcgcgc gcagcccctg 60
 tccctgcgcc cagagggcgtg ccggccagcg gcggggggcg cagtgcacac gagggggctg 120
 gacttcgcct gtgat 135

<210> 28
 <211> 230
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IgG4 Hinge domain

<400> 28
 Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
 1 5 10 15
 Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 20 25 30
 Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 35 40 45
 Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
 50 55 60
 Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Gln Phe Asn Ser
 65 70 75 80
 Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 85 90 95
 Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
 100 105 110
 Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 115 120 125
 Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
 130 135 140
 Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 145 150 155 160
 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 165 170 175
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
 180 185 190
 Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
 195 200 205
 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 210 215 220
 Leu Ser Leu Gly Lys Met
 225 230

<210> 29
 <211> 690
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IgG4 Hinge domain

<400> 29
 gagagcaagt acggccctcc ctgccccctt tgccctgccc ccgagttcct gggcggaccc 60
 agcgtgttcc tgttcccccc caagcccaag gacaccctga tgatcagccg gacccccgag 120
 gtgacctgtg tgggtggtgga cgtgtcccag gaggaccccg aggtccagtt caactgggtac 180
 gtggacggcg tggaggtgca caacgccaa accaagcccc gggaggagca gttcaatagc 240
 acctaccggg tgggtgtccgt gctgaccgtg ctgcaccagg actggctgaa cggcaaggaa 300
 tacaagtgtg aggtgtccaa caagggcctg cccagcagca tcgagaaaac catcagcaag 360
 gccaaaggcc agcctcggga gccccaggtg tacaccctgc cccctagcca agaggagatg 420

accaagaacc	aggtgtccct	gacctgcctg	gtgaagggct	tctaccccag	cgacatcgcc	480
gtggagtggg	agagcaacgg	ccagcccag	aacaactaca	agaccacccc	ccctgtgctg	540
gacagcgacg	gcagcttctt	cctgtacagc	cggctgaccg	tggacaagag	ccggtggcag	600
gagggcaacg	tcttttagctg	ctccgtgatg	cacgaggccc	tgcacaacca	ctacaccag	660
aagagcctga	gcctgtccct	gggcaagatg				690

<210> 30
 <211> 282
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IgD Hinge domain

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

<210> 31
 <211> 847
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IgD Hinge domain

<400> 31
 aggtggcccc aaagtcccaa ggcccaggca tctagtgttc ctactgcaca gccccaggca 60
 gaaggcagcc tagccaaagc tactactgca cctgccacta cgcgcaatac tggccgtggc 120
 ggggaggaga agaaaaagga gaaagagaaa gaagaacagg aagagaggga gaccaagacc 180

cctgaatgtc	catcccat	ccagccgctg	ggcgtctatc	tcttgactcc	cgcagtacag	240
gacttggtgc	ttagagataa	ggccaccttt	acatgtttcg	tcgtgggctc	tgacctgaag	300
gatgcccatt	tgacttgga	gggtgccgga	aaggtaccca	cagggggggg	tgaggaaggg	360
ttgctggagc	gccattccaa	tggtctctcag	agccagcaact	caagactcac	ccttccgaga	420
tccctgtgga	acgccgggac	ctctgtcaca	tgtactctaa	atcatcctag	cctgccccca	480
cagcgtctga	tggcccttag	agagccagcc	gccagggcac	cagttaagct	tagcctgaat	540
ctgctcgcca	gtagtgatcc	cccagaggcc	gccagctggc	tcttatgcga	agtgtccggc	600
tttagcccg	ccaacatctt	gctcatgtgg	ctggaggacc	agcgagaagt	gaacaccagc	660
ggcttcgctc	cagcccggcc	cccaccccag	ccgggttcta	ccacattctg	ggcctggagt	720
gtcttaaggg	tcccagcacc	acctagcccc	cagccagcca	catacacctg	tgttgtgtcc	780
catgaagata	gcaggaccct	gctaaatgct	tctaggagtc	tggagggttc	ctacgtgact	840
gaccatt						847

<210> 32

<211> 39

<212> PRT

<213> Artificial Sequence

<220>

<223> CD28 Hinge domain

<400> 32

Ile	Glu	Val	Met	Tyr	Pro	Pro	Pro	Tyr	Leu	Asp	Asn	Glu	Lys	Ser	Asn
1				5					10					15	
Gly	Thr	Ile	Ile	His	Val	Lys	Gly	Lys	His	Leu	Cys	Pro	Ser	Pro	Leu
			20					25					30		
Phe	Pro	Gly	Pro	Ser	Lys	Pro									
		35													

<210> 33

<211> 117

<212> DNA

<213> Artificial Sequence

<220>

<223> CD28 Hinge domain

<400> 33

attgaagtta	tgtatcctcc	tccttaccta	gacaatgaga	agagcaatgg	aaccattatc	60
catgtgaaag	ggaaacacct	ttgtccaagt	cccctatttc	ccggaccttc	taagccc	117

<210> 34

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> CD8 transmembrane domain

<400> 34

Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu
1				5					10					15	
Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys								
			20												

<210> 35

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> CD8 transmembrane domain

<400> 35

atctacatct gggcgccctt ggccgggact tgtgggggtcc ttctcctgtc actgggtatc	60
accctttact gc	72

<210> 36
 <211> 27
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD28 transmembrane domain

<400> 36
 Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
 1 5 10 15
 Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
 20 25

<210> 37
 <211> 81
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CD28 transmembrane domain

<400> 37	
ttttgggtgc tgggtgggtgg tgggtggagtc ctggcttgct atagcttgct agtaacagtg	60
gcctttatta ttttctgggt g	81

<210> 38
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD3zeta

<400> 38
 Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly
 1 5 10 15
 Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
 20 25 30
 Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
 35 40 45
 Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
 50 55 60
 Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
 65 70 75 80
 Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
 85 90 95
 Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 100 105 110

<210> 39
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD3zeta

<400> 39
 Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
 1 5 10 15

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

<210> 40
 <211> 113
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD3zeta

<400> 40

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

Arg

<210> 41
 <211> 113
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD3zeta

<400> 41

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

Arg

<210> 42
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> CD3zeta

<400> 42
agagtgaagt tcagcaggag cgcagacgcc cccgcgtaca agcagggcca gaaccagctc 60
tataacgagc tcaatctagg acgaagagag gactacgatg ttttggacaa gagacgtggc 120
cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 180
gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc 240
cggaggggca aggggcacga tggcctttac cagggctctca gtacagccac caaggacacc 300
tacgacgccc ttcacatgca ggccctgccc cctcgc 336

<210> 43
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> CD3zeta

<400> 43
agagtgaagt tcagcaggag cgcagacgcc cccgcgtacc agcagggcca gaaccagctc 60
tataacgagc tcaatctagg acgaagagag gactacgatg ttttggacaa gagacgtggc 120
cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 180
gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc 240
cggaggggca aggggcacga tggcctttac cagggctctca gtacagccac caaggacacc 300
tacgacgccc ttcacatgca ggccctgccc cctcgc 336

<210> 44
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-1BB intracellular domain

<400> 44
Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
1 5 10 15
Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
20 25 30
Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
35 40

<210> 45
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
<223> CD27 intracellular domain

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

<210> 46
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> CD28 intracellular domain

<400> 46
Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
1 5 10 15
Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
20 25 30
Pro Arg Asp Phe Ala Ala Tyr Arg Ser
35 40

<210> 47
<211> 126
<212> DNA
<213> Artificial Sequence

<220>
<223> 4-1BB intracellular domain

<400> 47
aaacggggca gaaagaaact cctgtatata ttcaaacaac catttatgag accagtacaa 60
actactcaag aggaagatgg ctgtagctgc cgatttccag aagaagaaga aggaggatgt 120
gaactg 126

<210> 48
<211> 144
<212> DNA
<213> Artificial Sequence

<220>
<223> CD27 intracellular domain

<400> 48
caacgaagga aatatagatc aaacaaagga gaaagtcctg tggagcctgc agagccttgt 60
cgttacagct gccccaggga ggaggagggc agcaccatcc ccatccagga ggattaccga 120
aaaccggagc ctgcctgctc cccc 144

<210> 49
<211> 123
<212> DNA
<213> Artificial Sequence

<220>
<223> CD28 intracellular domain

<400> 49
aggagtaaga ggagcaggct cctgcacagt gactacatga acatgactcc ccgccgcccc 60
gggcccaccc gcaagcatta ccagccctat gccccaccac gcgacttcgc agcctatcgc 120
tcc 123

<210> 50
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> CD8 leader sequence

<400> 50
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15
 His Ala Ala Arg Pro
 20

<210> 51
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Tag

<400> 51
 Asn Trp Ser His Pro Gln Phe Glu Lys
 1 5

<210> 52
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Tag

<400> 52
 Ser Ala Trp Ser His Pro Gln Phe Glu Lys
 1 5 10

<210> 53
 <211> 222
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CAR

<400> 53
 Ala Ala Ala Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu
 1 5 10 15
 Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro
 20 25 30
 Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val
 35 40 45
 Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe
 50 55 60
 Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
 65 70 75 80
 Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
 85 90 95
 Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val
 100 105 110
 Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
 115 120 125
 Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
 130 135 140
 Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
 145 150 155 160
 Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
 165 170 175
 Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
 180 185 190
 Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys

	195		200		205
Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg					
210		215		220	

<210> 54
 <211> 223
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CAR

<400> 54
 Ala Ala Ala Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu
 1 5 10 15
 Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro
 20 25 30
 Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val
 35 40 45
 Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe
 50 55 60
 Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
 65 70 75 80
 Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
 85 90 95
 Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val
 100 105 110
 Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
 115 120 125
 Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
 130 135 140
 Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln
 145 150 155 160
 Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
 165 170 175
 Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
 180 185 190
 Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
 195 200 205
 Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 210 215 220

<210> 55
 <211> 223
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CAR

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

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

<210> 56

<211> 236

<212> PRT

<213> Artificial Sequence

<220>

<223> CAR

<400> 56

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

<210> 57

<211> 224

<212> PRT

<213> Artificial Sequence

<220>

<223> CAR

<400> 57

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

<210> 58

<211> 237

<212> PRT

<213> Artificial Sequence

<220>

<223> CAR

<400> 58

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

		195					200					205					
Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp		
	210					215					220						
Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg					
225					230					235							

<210> 59
 <211> 226
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CAR

<400> 59
 Met His Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
 1 5 10 15
 Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
 20 25 30
 Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
 35 40 45
 Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
 50 55 60
 Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His
 65 70 75 80
 Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys
 85 90 95
 His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
 100 105 110
 Thr Arg Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
 115 120 125
 Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
 130 135 140
 Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
 145 150 155 160
 Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
 165 170 175
 Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
 180 185 190
 Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
 195 200 205
 Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
 210 215 220
 Pro Arg
 225

<210> 60
 <211> 227
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CAR

<400> 60
 Met His Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
 1 5 10 15
 Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
 20 25 30
 Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
 35 40 45
 Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
 50 55 60
 Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His

65					70					75					80
Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro	Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys
				85					90					95	
His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser
			100					105					110		
Thr	Arg	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln
			115				120					125			
Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu
			130			135					140				
Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly
					150					155					160
Gly	Lys	Pro	Gln	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu
				165					170					175	
Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys
			180					185					190		
Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu
		195					200					205			
Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu
	210					215					220				
Pro	Pro	Arg													
225															

<210> 61
 <211> 24
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> P2A ribosomal cleavage site

<400> 61
Ala Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly
1 5 10 15
Asp Val Glu Glu Asn Pro Gly Pro
20

<210> 62
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Heavy chain CDR1 of BB7.2

<400> 62
Ser Tyr His Ile Gln
1 5

<210> 63
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Heavy chain CDR2 of BB7.2

<400> 63
Trp Ile Tyr Pro Gly Asp Gly Ser Thr Gln Tyr Asn Glu Lys Phe Lys
1 5 10 15
Gly

<210> 64
 <211> 9

<212> PRT
 <213> Artificial Sequence

 <220>
 <223> Heavy chain CDR3 of BB7.2

 <400> 64
 Glu Gly Thr Tyr Tyr Ala Met Asp Tyr
 1 5

 <210> 65
 <211> 16
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Light chain CDR1 of BB7.2

 <400> 65
 Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
 1 5 10 15

 <210> 66
 <211> 7
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Light chain CDR2 of BB7.2

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

 <210> 67
 <211> 9
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Light chain CDR3 of BB7.2

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

 <210> 68
 <211> 239
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> eGFP

 <400> 68
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys

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

<210> 69
 <211> 246
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> scFv

<220>
 <221> SITE
 <222> 135
 <223> X is for V or I

<220>
 <221> SITE
 <222> 140
 <223> X is for T or S

<220>
 <221> SITE
 <222> 142
 <223> X is for L or S or A

<220>
 <221> SITE
 <222> 143
 <223> X is for S or T

<220>
 <221> SITE
 <222> 145
 <223> X is for P or S

<220>
 <221> SITE
 <222> 147
 <223> X is for T or S

<220>
 <221> SITE
 <222> 148
 <223> X is for L or P

<220>
<221> SITE
<222> 150
<223> X is for E or D

<220>
<221> SITE
<222> 151
<223> X is for P or R

<220>
<221> SITE
<222> 152
<223> X is for A or V

<220>
<221> SITE
<222> 153
<223> X is for S or T

<220>
<221> SITE
<222> 175
<223> X is for L or Q

<220>
<221> SITE
<222> 181
<223> X is for S or A

<220>
<221> SITE
<222> 196
<223> X is for V or I

<220>
<221> SITE
<222> 212
<223> X is for K or T

<220>
<221> SITE
<222> 216
<223> X is for V or L

<220>
<221> SITE
<222> 218
<223> X is for A or P

<220>
<221> SITE
<222> 221
<223> X is for L or F

<220>
<221> SITE
<222> 222
<223> X is for G or A

<400> 69
Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr		
			20					25					30				
His	Ile	Gln	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile		
		35					40					45					
Gly	Trp	Ile	Tyr	Pro	Gly	Asp	Gly	Ser	Thr	Gln	Tyr	Asn	Glu	Lys	Phe		
	50					55					60						
Lys	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Lys	Ser	Thr	Ser	Thr	Ala	Tyr		
65					70				75						80		
Met	Glu	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys		
			85						90					95			
Ala	Arg	Glu	Gly	Thr	Tyr	Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr		
		100						105					110				
Ser	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser		
		115					120					125					
Gly	Gly	Gly	Gly	Ser	Asp	Xaa	Val	Met	Thr	Gln	Xaa	Pro	Xaa	Xaa	Leu		
	130					135					140						
Xaa	Val	Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Ile	Ser	Cys	Arg	Ser	Ser	Gln		
145					150					155					160		
Ser	Ile	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	Glu	Trp	Tyr	Xaa	Gln		
			165					170						175			
Lys	Pro	Gly	Gln	Xaa	Pro	Arg	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg		
		180						185					190				
Phe	Ser	Gly	Xaa	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp		
	195					200					205						
Phe	Thr	Leu	Xaa	Ile	Ser	Arg	Xaa	Glu	Xaa	Glu	Asp	Xaa	Xaa	Val	Tyr		
	210				215					220							
Tyr	Cys	Phe	Gln	Gly	Ser	His	Val	Pro	Arg	Thr	Phe	Gly	Gly	Gly	Thr		
225					230					235					240		
Lys	Leu	Glu	Ile	Lys	Arg												
				245													

<210> 70

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> scFv

<400> 70

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

Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp
		195					200					205			
Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val	Tyr
	210					215					220				
Tyr	Cys	Phe	Gln	Gly	Ser	His	Val	Pro	Arg	Thr	Phe	Gly	Gly	Gly	Thr
225					230					235					240
Lys	Leu	Glu	Ile	Lys	Arg										
				245											

<210> 71
 <211> 246
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> scFv

<400> 71															
Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu	Val	Lys	Lys	Pro	Gly	Ala
1				5					10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr
			20					25					30		
His	Ile	Gln	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile
		35					40					45			
Gly	Trp	Ile	Tyr	Pro	Gly	Asp	Gly	Ser	Thr	Gln	Tyr	Asn	Glu	Lys	Phe
	50					55					60				
Lys	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Lys	Ser	Thr	Ser	Thr	Ala	Tyr
65					70					75					80
Met	Glu	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Arg	Glu	Gly	Thr	Tyr	Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr
			100					105					110		
Ser	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
		115					120					125			
Gly	Gly	Gly	Gly	Ser	Asp	Val	Val	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu
	130					135					140				
Ser	Val	Thr	Leu	Gly	Asp	Arg	Val	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln
145					150					155					160
Ser	Ile	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	Glu	Trp	Tyr	Gln	Gln
			165					170						175	
Lys	Pro	Gly	Gln	Ser	Pro	Arg	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg
			180					185						190	
Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp
		195					200					205			
Phe	Thr	Leu	Thr	Ile	Ser	Arg	Val	Glu	Pro	Glu	Asp	Leu	Gly	Val	Tyr
	210					215					220				
Tyr	Cys	Phe	Gln	Gly	Ser	His	Val	Pro	Arg	Thr	Phe	Gly	Gly	Gly	Thr
225					230					235					240
Lys	Leu	Glu	Ile	Lys	Arg										
				245											

<210> 72
 <211> 246
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> scFv

<400> 72															
Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu	Val	Lys	Lys	Pro	Gly	Ala
1				5					10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr
			20					25					30		

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

<210> 73

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<223> scFv

<220>

<221> SITE

<222> 136

<223> X is V or I

<220>

<221> SITE

<222> 141

<223> X is for T or S

<220>

<221> SITE

<222> 143

<223> X is for L or S or A

<220>

<221> SITE

<222> 144

<223> X is for S or T

<220>

<221> SITE

<222> 146

<223> X is for P or S

<220>

<221> SITE

<222> 148
<223> X is for T or S

<220>
<221> SITE
<222> 149
<223> X is for L or P

<220>
<221> SITE
<222> 151
<223> X is for E or D

<220>
<221> SITE
<222> 152
<223> X is for P or R

<220>
<221> SITE
<222> 153
<223> X is for A or V

<220>
<221> SITE
<222> 154
<223> X is for S or T

<220>
<221> SITE
<222> 176
<223> X is for L or Q

<220>
<221> SITE
<222> 182
<223> X is for S or A

<220>
<221> SITE
<222> 197
<223> X is for V or I

<220>
<221> SITE
<222> 213
<223> X is for K or T

<220>
<221> SITE
<222> 217
<223> X is for V or L

<220>
<221> SITE
<222> 219
<223> X is for A or P

<220>
<221> SITE
<222> 222
<223> X is for L or F

<220>

<221> SITE
 <222> 223
 <223> X is for G or A

<400> 73
 Ser Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly
 1 5 10 15
 Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser
 20 25 30
 Tyr His Ile Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp
 35 40 45
 Ile Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Gln Tyr Asn Glu Lys
 50 55 60
 Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala
 65 70 75 80
 Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr
 85 90 95
 Cys Ala Arg Glu Gly Thr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 115 120 125
 Ser Gly Gly Gly Gly Ser Asp Xaa Val Met Thr Gln Xaa Pro Xaa Xaa
 130 135 140
 Leu Xaa Val Xaa Xaa Gly Xaa Xaa Xaa Xaa Ile Ser Cys Arg Ser Ser
 145 150 155 160
 Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Xaa
 165 170 175
 Gln Lys Pro Gly Gln Xaa Pro Arg Leu Leu Ile Tyr Lys Val Ser Asn
 180 185 190
 Arg Phe Ser Gly Xaa Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
 195 200 205
 Asp Phe Thr Leu Xaa Ile Ser Arg Xaa Glu Xaa Glu Asp Xaa Xaa Val
 210 215 220
 Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Arg Thr Phe Gly Gly Gly
 225 230 235 240
 Thr Lys Leu Glu Ile Lys Arg
 245

<210> 74
 <211> 247
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> scFv

<400> 74
 Ser Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly
 1 5 10 15
 Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser
 20 25 30
 Tyr His Ile Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp
 35 40 45
 Ile Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Gln Tyr Asn Glu Lys
 50 55 60
 Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala
 65 70 75 80
 Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr
 85 90 95
 Cys Ala Arg Glu Gly Thr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 115 120 125
 Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser

130		135		140
Leu Pro Val Thr Leu Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser				
145		150		155
Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu				160
	165		170	175
Gln Lys Pro Gly Gln Ser Pro Arg Leu Leu Ile Tyr Lys Val Ser Asn				
	180		185	190
Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr				
	195		200	205
Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val				
	210		215	220
Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Arg Thr Phe Gly Gly Gly				240
225		230	235	
Thr Lys Leu Glu Ile Lys Arg				
	245			

<210> 75
 <211> 247
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> scFv

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

<210> 76
 <211> 247
 <212> PRT
 <213> Artificial Sequence

<220>

<223> scFv

<400> 76

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

<210> 77

<211> 471

<212> PRT

<213> Artificial Sequence

<220>

<223> CAR

<220>

<221> SITE

<222> 136

<223> X is for V or I

<220>

<221> SITE

<222> 141

<223> X is for T or S

<220>

<221> SITE

<222> 143

<223> X is for L or S or A

<220>

<221> SITE

<222> 144

<223> X is for S or T

<220>
<221> SITE
<222> 146
<223> X is for P or S

<220>
<221> SITE
<222> 148
<223> X is for T or S

<220>
<221> SITE
<222> 149
<223> X is for L or P

<220>
<221> SITE
<222> 151
<223> X is for E or D

<220>
<221> SITE
<222> 152
<223> X is for P or R

<220>
<221> SITE
<222> 153
<223> X is for A or V

<220>
<221> SITE
<222> 154
<223> X is for S or T

<220>
<221> SITE
<222> 176
<223> X is for L or Q

<220>
<221> SITE
<222> 182
<223> X is for S or A

<220>
<221> SITE
<222> 197
<223> X is for V or I

<220>
<221> SITE
<222> 213
<223> X is for K or T

<220>
<221> SITE
<222> 217
<223> X is for V or L

<220>
<221> SITE
<222> 219

<223> X is for A or P

<220>

<221> SITE

<222> 222

<223> X is for L or F

<220>

<221> SITE

<222> 223

<223> X is for G or A

<400> 77

Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu	Val	Lys	Lys	Pro	Gly
1				5					10					15	
Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser
			20					25					30		
Tyr	His	Ile	Gln	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp
		35					40					45			
Ile	Gly	Trp	Ile	Tyr	Pro	Gly	Asp	Gly	Ser	Thr	Gln	Tyr	Asn	Glu	Lys
	50					55					60				
Phe	Lys	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Lys	Ser	Thr	Ser	Thr	Ala
65					70				75						80
Tyr	Met	Glu	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr
				85					90					95	
Cys	Ala	Arg	Glu	Gly	Thr	Tyr	Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly
			100					105					110		
Thr	Ser	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly
		115					120					125			
Ser	Gly	Gly	Gly	Gly	Ser	Asp	Xaa	Val	Met	Thr	Gln	Xaa	Pro	Xaa	Xaa
	130					135					140				
Leu	Xaa	Val	Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Ile	Ser	Cys	Arg	Ser	Ser
145					150					155					160
Gln	Ser	Ile	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	Glu	Trp	Tyr	Xaa
			165						170					175	
Gln	Lys	Pro	Gly	Gln	Xaa	Pro	Arg	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn
		180						185					190		
Arg	Phe	Ser	Gly	Xaa	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr
	195					200					205				
Asp	Phe	Thr	Leu	Xaa	Ile	Ser	Arg	Xaa	Glu	Xaa	Glu	Asp	Xaa	Xaa	Val
	210					215					220				
Tyr	Tyr	Cys	Phe	Gln	Gly	Ser	His	Val	Pro	Arg	Thr	Phe	Gly	Gly	Gly
225				230						235					240
Thr	Lys	Leu	Glu	Ile	Lys	Arg	Arg	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro
			245						250					255	
Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro
			260					265					270		
Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu
		275					280					285			
Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys
	290					295					300				
Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly
305					310					315					320
Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val
			325						330					335	
Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu
			340					345					350		
Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp
		355					360					365			
Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn
						375					380				
Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg
385					390					395					400
Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly

				405					410					415			
Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu		
			420					425					430				
Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu		
		435					440					445					
Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His		
	450					455					460						
Met	Gln	Ala	Leu	Pro	Pro	Arg											
465					470												

<210> 78
 <211> 471
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CAR

<400> 78

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

305					310					315					320
Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val
				325					330					335	
Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu
			340					345					350		
Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp
		355					360					365			
Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn
	370					375					380				
Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg
385					390					395					400
Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly
			405						410					415	
Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu
			420				425						430		
Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu
		435					440					445			
Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His
	450					455					460				
Met	Gln	Ala	Leu	Pro	Pro	Arg									
465					470										

<210> 80

<211> 471

<212> PRT

<213> Artificial Sequence

<220>

<223> CAR

<400> 80

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

<223> X is for T or S

<220>

<221> SITE

<222> 170

<223> X is for L or P

<220>

<221> SITE

<222> 172

<223> X is for E or D

<220>

<221> SITE

<222> 173

<223> X is for P or R

<220>

<221> SITE

<222> 174

<223> X is for A or V

<220>

<221> SITE

<222> 175

<223> X is for S or T

<220>

<221> SITE

<222> 197

<223> X is for L or Q

<220>

<221> SITE

<222> 203

<223> X is for S or A

<220>

<221> SITE

<222> 218

<223> X is for V or I

<220>

<221> SITE

<222> 234

<223> X is for Kor T

<220>

<221> SITE

<222> 238

<223> X is for V or L

<220>

<221> SITE

<222> 240

<223> X is for A or P

<220>

<221> SITE

<222> 243

<223> X is for L or F

<220>

<221> SITE

<222> 244

<223> X is for G or A

<400> 81

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5					10					15	
His	Ala	Ala	Arg	Pro	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu
			20					25					30		
Val	Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly
	35						40				45				
Tyr	Thr	Phe	Thr	Ser	Tyr	His	Ile	Gln	Trp	Val	Arg	Gln	Ala	Pro	Gly
	50					55					60				
Gln	Gly	Leu	Glu	Trp	Ile	Gly	Trp	Ile	Tyr	Pro	Gly	Asp	Gly	Ser	Thr
65				70						75					80
Gln	Tyr	Asn	Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Lys
				85					90					95	
Ser	Thr	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp
			100					105					110		
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Glu	Gly	Thr	Tyr	Tyr	Ala	Met	Asp
	115						120					125			
Tyr	Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly
	130					135					140				
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Xaa	Val	Met	Thr
145					150					155					160
Gln	Xaa	Pro	Xaa	Xaa	Leu	Xaa	Val	Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Ile
				165				170						175	
Ser	Cys	Arg	Ser	Ser	Gln	Ser	Ile	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr
			180					185					190		
Leu	Glu	Trp	Tyr	Xaa	Gln	Lys	Pro	Gly	Gln	Xaa	Pro	Arg	Leu	Leu	Ile
	195						200					205			
Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Xaa	Pro	Asp	Arg	Phe	Ser	Gly
	210					215					220				
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Xaa	Ile	Ser	Arg	Xaa	Glu	Xaa
225					230					235					240
Glu	Asp	Xaa	Xaa	Val	Tyr	Tyr	Cys	Phe	Gln	Gly	Ser	His	Val	Pro	Arg
				245					250					255	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Arg	Thr	Thr	Thr
			260					265					270		
Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro
	275						280					285			
Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val
	290					295					300				
His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro
305				310						315					320
Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu
				325					330					335	
Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro
		340						345					350		
Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys
	355						360					365			
Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe
	370					375					380				
Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu
385					390					395					400
Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp
				405					410					415	
Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys
			420					425					430		
Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala
		435					440					445			
Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys
	450					455					460				
Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr
465					470					475					480

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 82
<211> 492
<212> PRT
<213> Artificial Sequence

<220>
<223> CAR

<400> 82
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15
His Ala Ala Arg Pro Ser Gln Val Gln Leu Val Gln Ser Gly Pro Glu
20 25 30
Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly
35 40 45
Tyr Thr Phe Thr Ser Tyr His Ile Gln Trp Val Arg Gln Ala Pro Gly
50 55 60
Gln Gly Leu Glu Trp Ile Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr
65 70 75 80
Gln Tyr Asn Glu Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Lys
85 90 95
Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp
100 105 110
Thr Ala Val Tyr Tyr Cys Ala Arg Glu Gly Thr Tyr Tyr Ala Met Asp
115 120 125
Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly
130 135 140
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr
145 150 155 160
Gln Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Glu Pro Ala Ser Ile
165 170 175
Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr
180 185 190
Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Arg Leu Leu Ile
195 200 205
Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly
210 215 220
Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
225 230 235 240
Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Arg
245 250 255
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Arg Thr Thr Thr
260 265 270
Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
275 280 285
Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
290 295 300
His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
305 310 315 320
Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
325 330 335
Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro
340 345 350
Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys
355 360 365
Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe
370 375 380
Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
385 390 395 400
Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
405 410 415

Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys
			420					425					430		
Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala
		435					440					445			
Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys
		450				455					460				
Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr
465					470					475					480
Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg				
			485						490						

<210> 83

<211> 492

<212> PRT

<213> Artificial Sequence

<220>

<223> CAR

<400> 83

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

Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys		
		355					360					365					
Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe		
	370					375					380						
Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu		
385					390				395						400		
Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp		
				405					410					415			
Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys		
			420					425					430				
Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala		
		435					440					445					
Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys		
	450					455					460						
Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr		
465					470					475					480		
Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg						
				485					490								

<210> 84

<211> 492

<212> PRT

<213> Artificial Sequence

<220>

<223> CAR

<400> 84

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

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

<210> 85
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> LAGLIDADG motif

<400> 85
 Leu Ala Gly Leu Ile Asp Ala Asp Gly
 1 5

<210> 86
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VH

<400> 86
 caggtccagc tagtacaaag cggccctgaa gtaaagaaac ctggtgcctc tgtgaagggtg 60
 agctgcaagg ccagcggcta caccttcacc agctaccaca tccagtgggt tgcacaggcc 120
 cctggacagg gactagagtg gatcggctgg atctatcctg gcgacggcag caccagctac 180
 aacgagaagt tcaagggcag agttaccatc accgccgaca agagcaccag cacagcctat 240
 atggagctga gcagcctgac cagcgaggac acagctgttt actattgtgc cagagagggc 300
 acctactacg caatggatta ttggggccag gggaccagcg tgaccgtttc ttct 354

<210> 87
 <211> 339
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VL

<400> 87

gatggtgtaa	tgaccagac	acctctgagc	ctgcctgtga	ccctgggaga	accagcatcc	60
atcagctgtc	ggagcagcca	gagcatcggt	cacagcaacg	gcaacaccta	cctggaatgg	120
tatctacaga	agcccggaca	gagccccagg	ctgctgatct	acaagggtgtc	caaccgcttc	180
agtgggtgtgc	ccgatagatt	ttctggcagc	ggctctggca	ccgacttcac	cctgaagatc	240
tccagagtgg	aagccgagga	cctgggctgt	tactactgct	tccaaggcag	ccatgtgcca	300
agaacctttg	gtggaggcac	aaagctggaa	atcaagcgg			339

<210> 88

<211> 339

<212> DNA

<213> Artificial Sequence

<220>

<223> VL

<400> 88

gatggtgtaa	tgaccagag	ccctagtagc	ctgtctgtga	ccctgggaga	tcgagtatcc	60
atcagctgtc	ggagcagcca	gagcatcggt	cacagcaacg	gcaacaccta	cctggaatgg	120
tatcaacaga	agcccggaca	gagccccagg	ctgctgatct	acaagggtgtc	caaccgcttc	180
agtgggtgtgc	ccgatagatt	ttctggcagc	ggctctggca	ccgacttcac	cctgacgatc	240
tccagagtgg	aaccagagga	cctgggctgt	tactactgct	tccaaggcag	ccatgtgcca	300
agaacctttg	gtggaggcac	aaagctggaa	atcaagcgg			339

<210> 89

<211> 339

<212> DNA

<213> Artificial Sequence

<220>

<223> VL

<400> 89

gatattgtaa	tgaccagag	ccctgcaaca	ctgtctgtgt	cccctggaga	acgagcaaca	60
atcagctgtc	ggagcagcca	gagcatcggt	cacagcaacg	gcaacaccta	cctggaatgg	120
tatcaacaga	agcccggaca	ggccccagg	ctgctgatct	acaagggtgtc	caaccgcttc	180
agtggaatac	ccgatagatt	ttctggcagc	ggctctggca	ccgacttcac	cctgacgatc	240
tccagattag	aaccagagga	ctttgcagt	tactactgct	tccaaggcag	ccatgtgcca	300
agaacctttg	gtggaggcac	aaagctggaa	atcaagcgg			339