

SEQUENCE LISTING

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Chou, Chuan-chu

Zhuang, Qiuchuan

Wang, Pingyan

Wang, Lin

Yang, Lei

Hao, Jiaying

<120> Chimeric antigen receptors

based on single-domain antibodies and methods of use thereof

<130> 761422000340

<140> Not Yet Assigned

<141> Concurrently Herewith

<160> 277

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<223> CD19 single-domain antibody VHH CDR1

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Ile Asn Arg Met Gly

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<400> 2

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

1 5 10 15

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Val Ser Ser Asn Arg Asp Pro Asp Tyr
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Ile Gly Thr Met Gly
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1 5 10 15
Gly

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Asp Arg Leu Ser Leu Asp Leu Ser Gly Arg Tyr His Tyr Asn Pro Ala
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Val Tyr Asp Tyr
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Ser Gly Phe Thr Leu Asp Tyr Tyr Ala Ile Gly
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Ser Gly Arg Thr Phe Ser Thr Tyr Gly Met Ala
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Ser Gly Arg Thr Phe Thr Met Gly
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Ser Gly Gly Ile Phe Val Ile Asn Ala Met Gly
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Ser Gly Arg Thr Phe Ser Ser Ile Val Met Gly
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<400> 12
Ser Gly Phe Thr Phe Asp Arg Ala Val Ile Val
1 5 10

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Ser Thr Tyr Thr Val Asn Ser Asp Val Met Gly
1 5 10

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Ser Gly Ala Thr Leu Thr Asn Asp His Met Ala
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Ser	Gly	Gly	Thr	Leu	Ser	Lys	Asn	Thr	Val	Ala
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Ser	Glu	His	Thr	Phe	Ser	Ser	His	Val	Met	Gly
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Ser	Gly	Arg	Ala	Phe	Ser	Thr	Tyr	Phe	Met	Ala
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Cys	Ile	Ser	Arg	Ser	Asp	Gly	Ser	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
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Gly

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Ser Lys Ala Ser Met Asn Tyr Ser Gly Arg Thr Tyr Tyr Ala Asp Ser
1 5 10 15
Val Lys Gly

<213> Artificial Sequence

<223> BCMA 269A37917 VHH CDR2

Ala Ile Ser Leu Ser Pro Thr Leu Ala Tyr Tyr Ala Glu Ser Val Lys
1 5 10 15
Gly

<213> Artificial Sequence

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Ser Ile Arg Gly Leu Gly Arg Thr Asn Tyr Asp Asp Ser Val Lys Gly
1 5 10 15

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<223> BCMA 269A37915 VHH CDR2

Ala Ile Met Trp Asn Asp Gly Ile Thr Tyr Leu Gln Asp Ser Val Lys
1 5 10 15
Gly

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Phe Ile Lys Pro Ser Asp Gly Thr Ile Tyr Tyr Ile Asp Ser Leu Lys
1 5 10 15
Gly

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Ala Ile Met Trp Asn Asp Gly Ile Thr Tyr Leu Gln Asp Ser Val Lys
1 5 10 15
Gly

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Ala Ile Asp Trp Ser Gly Arg Thr Thr Asn Tyr Ala Asp Pro Val Glu
1 5 10 15
Gly

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Ser Ile Thr Trp Asp Gly Arg Thr Thr Tyr Tyr Ala Asp Ser Val Lys
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Gly

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Val Ile Gly Trp Arg Asp Ile Ser Thr Ser Tyr Ala Asp Ser Val Lys
1 5 10 15
Gly

<210> 28
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<400> 28
Gly Ile Ala Trp Ser Gly Gly Ser Thr Ala Tyr Ala Asp Ser Val Lys
1 5 10 15
Gly

<210> 29
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<400> 29
Ala Gly Ala Asp Cys Ser Gly Tyr Leu Arg Asp Tyr Glu Phe
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Ala	Gly	Thr	Gly	Cys	Ser	Thr	Tyr	Gly	Cys	Phe	Asp	Ala	Gln	Ile	Ile
1				5					10					15	
Asp	Tyr														

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<400> 31

Ala	Asp	Arg	Lys	Ser	Val	Met	Ser	Ile	Arg	Pro	Asp	Tyr
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<400> 32

Val	Tyr	Val	Thr	Leu	Leu	Gly	Gly	Val	Asn	Arg	Asp	Tyr
1				5					10			

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Ala	Ser	Lys	Gly	Arg	Tyr	Ser	Glu	Tyr	Glu	Tyr
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<400> 34

Ala Ser Pro Glu Asp Trp Tyr Thr Asp Trp Ile Asp Trp Ser Ile Tyr
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Arg

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<400> 35

Ala Ser Lys Gly Arg Tyr Ser Glu Tyr Glu Tyr
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<400> 36

Val Leu Arg Ala Trp Ile Ser Tyr Asp Asn Asp Tyr
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<400> 37

Asp Leu Gly Lys Trp Pro Ala Gly Pro Ala Asp Tyr
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Ala	Arg	Arg	Ile	Asp	Ala	Ala	Asp	Phe	Asp	Ser
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Ser	Arg	Gly	Ile	Glu	Val	Glu	Glu	Phe	Gly	Ala
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Ser	Gly	Leu	Thr	Phe	Ser	Ser	Tyr	Pro	Met	Met
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<400> 41

Ser	Gly	Phe	Thr	Phe	Ser	Ser	Asn	Trp	Met	Tyr
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<210> 42

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Ser Gly Arg Ile Phe Ser Ile Asn Ala Met Gly
1 5 10

<210> 43
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<400> 43
Ser Gly Ser Ile Phe Lys Val Phe Arg Val Phe Ala Met Ser
1 5 10

<210> 44
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<400> 44
Thr Gly Lys Val Phe Ser Ile Tyr Asp Met Gly
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Ser Ala Ser Ile Phe Thr Arg Leu Pro Met Gly
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<400> 46

Ser Gly Arg Ala Tyr Ala Thr Met Ala
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<400> 47
Ser Gly Leu Thr Phe Ser Ser Tyr Ile Met Gly
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Ser Gln Gly Ile Phe Thr Ile Asn Ala Met Gly
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<400> 49
Ser Gly Arg Thr Phe Ser Ser Tyr Ala Met Ala
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<400> 50
Ser Gly Thr Ile Val Ser Ile Ser Thr Met Gly
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<400> 51
Ser Gly Arg Thr Tyr Ala Met Gly
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<400> 52
Arg Ile Ser Asp Ser Gly Gly Tyr Thr Asn Tyr Asp Asp Ser Val Lys
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Gly

<210> 53
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<400> 53
Thr Ile Ser Thr Asp Gly Arg Gly Thr Tyr Tyr Lys Asp Ser Val Lys
1 5 10 15
Gly

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<400> 54

Ala Ile Ser Thr Ala Gly Ser Thr Asn Tyr Gly Asp Ser Val Lys Gly
1 5 10 15

<210> 55

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<400> 55

Ser Ile Ser Ser Gly Glu Thr Thr Thr Tyr Ala Asp Ser Val Lys Gly
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<210> 56

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<400> 56

Glu Ile Thr Ser Ser Gly Thr Thr His Tyr Asp Asp Phe Val Ser Gly
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<400> 57

Gly Ile Val Pro Ser Gly Arg Ile Asn Tyr Ala Asp Ser Val Lys Gly
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<210> 58

<211> 17

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<400> 58

His Leu Arg Val Ser Gly Asp Thr Thr Tyr Tyr Thr Asp Ser Val Lys
1 5 10 15

Gly

<210> 59
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<212> PRT
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Glu Ile Ser Ser Gly Gly Met Thr Ser Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 60
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Glu Val Ser Ser Gly Gly Arg Thr Asp Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 61
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<400> 61
Ser Ile Ser Thr Ser Gly Gly Ile Thr Asp Tyr Ala Asp Ser Val Lys
1 5 10 15
Gly

<210> 62
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<400> 62

Thr Ile Thr Arg Arg Gly Arg Thr Asn Tyr Thr Asp Ser Val Lys Gly
1 5 10 15

<210> 63

<211> 16

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<400> 63

Thr Ile Ser Gly Ala Gly Asn Thr Lys Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 64

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<400> 64

Ile Leu Gly Leu Pro Thr
1 5

<210> 65

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<400> 65

Lys Glu Pro Arg Val Leu Met Ala Tyr Leu Arg Asn Leu Gly Asp Phe
1 5 10 15
Gly Ser

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<400> 66

Leu Asn Phe Pro Pro Tyr Val Tyr
1 5

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<220>
<223> CD38 38A37331 VHH CDR3

<400> 67
Ala Asp His Thr Phe Thr Gly Asp Phe
1 5

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<220>
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<400> 68
Asn His Val Phe Gly Gly Ser Tyr
1 5

<210> 69
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<400> 69
Ala Asp Thr Phe Pro Leu Pro Thr
1 5

<210> 70
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<400> 70
Gly Pro Tyr Gly Ile Leu Ala Ala Ala Arg Val Ser Asn Pro Gly Asn
1 5 10 15

Tyr Asp Tyr

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<400> 71
Ala Pro Glu Arg Gly Ser Ile Trp Tyr Ser Arg Tyr Glu Tyr Lys Tyr
1 5 10 15

<210> 72
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<212> PRT
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<220>
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<400> 72
Val Ser Gly Trp His Val Phe Val Gly Asp Arg Ile Val
1 5 10

<210> 73
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<400> 73
Ala Arg Thr Trp Tyr Leu Arg Thr Ser Leu Gln Tyr Asp Tyr
1 5 10

<210> 74
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<212> PRT
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<220>
<223> CD38 38A37731 VHH CDR3

<400> 74
Ala Glu Val Gln Leu Asp Ile Trp Ala Ser Ala Tyr Asp Tyr
1 5 10

<210> 75
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<223> CD38 38A37326 VHH CDR3

<400> 75
Ala Gly Lys Trp Phe Pro Ala Ala Asn Glu Tyr
1 5 10

<210> 76
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<223> CD19 single-domain antibody VHH

<400> 76
Gln Val Lys Leu Glu Glu Ser Gly Gly Glu Leu Val Gln Pro Gly Gly
1 5 10 15
Pro Leu Arg Leu Ser Cys Ala Ala Ser Gly Asn Ile Phe Ser Ile Asn
20 25 30
Arg Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Ala Phe Val
35 40 45
Ala Ser Ile Thr Val Arg Gly Ile Thr Asn Tyr Ala Asp Ser Val Lys
50 55 60
Gly Arg Phe Thr Ile Ser Val Asp Lys Ser Lys Asn Thr Ile Tyr Leu
65 70 75 80
Gln Met Asn Ala Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
85 90 95
Ala Val Ser Ser Asn Arg Asp Pro Asp Tyr Trp Gly Gln Gly Thr Gln
100 105 110
Val Thr Val Ser Ser
115

<210> 77
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<220>
<223> CD20 single-domain antibody VHH

<400> 77
Pro Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Asp
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Gly Ile Gly

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

<210> 78

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<220>

<223> BCMA 269A37346 VHH

<400> 78

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

<210> 79

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<400> 79

Gln Val Lys Leu Glu Glu Ser Gly Gly Arg Leu Val Gln Pro Arg Gly

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

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<400> 80

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

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<220>

<223> BCMA 269A37355 VHH

<400> 81

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

<210> 82

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> BCMA 269A37915 VHH

<400> 82

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

<210> 83

<211> 128

<212> PRT

<213> Artificial Sequence

<220>

<223> BCMA 269A37936 VHH

<400> 83

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

<210> 84
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> BCMA 269A37953 VHH

<400> 84															
Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Met	Val	Gln	Ala	Gly	Asp
1				5				10					15		
Ser	Leu	Arg	Leu	Ser	Cys	Val	Gln	Ser	Thr	Tyr	Thr	Val	Asn	Ser	Asp
		20					25					30			
Val	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Glu	Phe	Val
	35					40					45				
Gly	Ala	Ile	Met	Trp	Asn	Asp	Gly	Ile	Thr	Tyr	Leu	Gln	Asp	Ser	Val
	50				55			60							
Lys	Gly	Arg	Phe	Thr	Ile	Phe	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Val	Tyr
65				70				75						80	
Leu	Gln	Met	Asn	Ser	Leu	Lys	Leu	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85					90					95		
Ala	Ala	Ser	Lys	Gly	Arg	Tyr	Ser	Glu	Tyr	Glu	Tyr	Trp	Gly	Gln	Gly
		100					105						110		
Thr	Gln	Val	Thr	Val	Ser	Ser									
		115													

<210> 85
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> BCMA 269A37965 VHH

<400> 85															
Ala	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala	Gly	Asp

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

<210> 86

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> BCMA 269A37972 VHH

<400> 86

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

<210> 87

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> BCMA 269A37353 VHH

<400> 87

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Arg

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

<210> 88

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> BCMA 269A37948 VHH

<400> 88

Ala	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala	Gly	Asp		
1				5				10					15				
Ser	Leu	Arg	Leu	Thr	Cys	Thr	Ala	Ser	Gly	Arg	Ala	Phe	Ser	Thr	Tyr		
		20					25					30					
Phe	Met	Ala	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Glu	Phe	Val		
	35					40					45						
Ala	Gly	Ile	Ala	Trp	Ser	Gly	Gly	Ser	Thr	Ala	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	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys		
			85					90						95			
Ala	Ser	Arg	Gly	Ile	Glu	Val	Glu	Glu	Phe	Gly	Ala	Trp	Gly	Gln	Gly		
		100					105						110				
Thr	Gln	Val	Thr	Val	Ser	Ser											
		115															

<210> 89

<211> 114

<212> PRT

<213> Artificial Sequence

<220>

<223> CD38 38A37333 VHH

<400> 89

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

<210> 90

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> CD38 38A37336 VHH

<400> 90

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

<210> 91

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> CD38 38A37699 VHH

<400> 91

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly

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

<210> 92
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD38 38A37331 VHH

<400> 92																
Gln	Val	Lys	Leu	Glu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Glu	
1				5				10					15			
Ser	Leu	Arg	Leu	Ser	Cys	Ser	Ala	Ser	Gly	Ser	Ile	Phe	Lys	Val	Phe	
			20				25					30				
Arg	Val	Phe	Ala	Met	Ser	Trp	Tyr	Arg	Gln	Gly	Pro	Gly	Lys	Gln	Arg	
		35				40					45					
Glu	Leu	Val	Ala	Ser	Ile	Ser	Ser	Gly	Glu	Thr	Thr	Thr	Tyr	Ala	Asp	
		50				55				60						
Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	
65					70				75						80	
Ala	Tyr	Leu	Gln	Met	Asp	Ser	Leu	Lys	Pro	Glu	Asp	Thr	Ala	Val	Tyr	
			85					90					95			
Tyr	Cys	Asn	Ala	Asp	His	Thr	Phe	Thr	Gly	Asp	Phe	Trp	Gly	Gln	Gly	
			100					105					110			
Thr	Gln	Val	Thr	Val	Ser	Ser										
			115													

<210> 93
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD38 38A37717 VHH

<400> 93																
Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala	Gly	Gly	

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

<210> 94

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> CD38 38A37719 VHH

<400> 94

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

<210> 95

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> CD38 38A37330 VHH

<400> 95

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Asp

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

<210> 96
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD38 38A37334 VHH

<400> 96															
Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala	Gly	Gly
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Leu	Thr	Phe	Ser	Ser	Tyr
			20					25					30		
Ile	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Glu	Glu	Arg	Glu	Leu	Val
		35					40					45			
Ala	Glu	Ile	Ser	Ser	Gly	Gly	Met	Thr	Ser	Tyr	Ala	Asp	Ser	Val	Lys
	50					55					60				
Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Lys	Thr	Gly	Tyr	Leu
65					70					75					80
Gln	Met	Asn	Ser	Leu	Lys	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala
				85					90					95	
Ala	Pro	Glu	Arg	Gly	Ser	Ile	Trp	Tyr	Ser	Arg	Tyr	Glu	Tyr	Lys	Tyr
			100					105					110		
Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser					
			115				120								

<210> 97
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD38 38A37730 VHH

<400> 97															
Ala	Val	Gln	Leu	Val	Asp	Ser	Gly	Gly	Gly	Leu	Ala	Gln	Thr	Gly	Gly

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

<210> 98

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> CD38 38A37340 VHH

<400> 98

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

<210> 99

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> CD38 38A37731 VHH

<400> 99

Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly

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

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

<220>
 <223> CD38 38A37326 VHH

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

<210> 101
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CD19 single-domain antibody VHH

<400> 101
 caggtaaagc tggaggagtc tgggggagaa ttggtgcagc ctggggggcc tctgagactc 60

```

tcctgtgcag cctcgggaaa catcttcagt atcaatcgca tgggctggta ccgccaggct 120
ccagggaagc agcgcgcgtt cgtcgcacat attactgttc gtggtataac aaactatgca 180
gactccgtga agggccgatt caccatttct gtagacaagt ccaaaaacac gatttatctg 240
cagatgaacg cactcaaacc tgaggacacg gccgtctatt attgtaatgc agtgtcttca 300
aacagggacc ccgactactg gggccagggg acccagggtca ccgtctcctc a 351

```

<210> 102

<211> 387

<212> DNA

<213> Artificial Sequence

<220>

<223> CD20 single-domain antibody VHH

<400> 102

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ccggtgcagc tgggtggagtc tgggggaggc ttggtgcagg ctggggattc tctgagactc 60
tcctgtgctg cctctggacg caccttcggt attggtacca tgggctgggt ccgccaacct 120
ccagggaagg agcgtgaatt tgtagcagct attaggtgga gtactgggtg cactcgctat 180
gcagactccg tgaagggccg attcaccatc tcccgagaca acgccaagct cacggtagat 240
ctgcaaatgg acagcctgaa acctgaagac acggccgttt attactgtgc agcagataga 300
ctgtcccttg atttaagtgg tcgttaccac tacaaccccg ccgtgtatga ctattggggc 360
caggggaccc aggtcacctg ctcctca 387

```

<210> 103

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMA 269A37346 VHH

<400> 103

```

caggtgcagc tgggtggagtc tgggggaggc ttggtgcagc ctgggggttc tctgaggctc 60
tcctgtgaag cctctggatt cactttggat tattatgcc a taggctgggt ccgccaggcc 120
ccagggaagg agcgcgaggg ggtcatatgt attagtagaa gtgatggtag cacatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca acgccaagaa aacggtgtat 240
ctgcaaatga tcagcctgaa acctgaggac acggccgctt attactgtgc agcaggggcc 300
gattgttcgg ggtacctacg agattatgag ttccgggggc aggggaccca ggtcacctgc 360
tcctca 366

```

<210> 104

<211> 384

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMA 269A37348 VHH

<400> 104

```

caggtaaagc tggaggagtc tgggggacga ttggtgcagc caaggggctc tctgagactc 60
tcctgtgcag gctctggacg cactttcagt acctatggta tggcctgggt ccgccaggct 120
ccagggaagg agcgtgagtt cgtagcgtct aaagcatcga tgaattacag cggtagaaca 180
tactatgcag actccgtgaa gggccgattc accatcgcca gagacaacgc caagaacatg 240
gtgtttctgc aatgaacaa cctgaagcct gaggacacgg ccgtttatta ctgtgcagcg 300

```

ggcactggat gctcaacata tgggtgtttt gacgccaga taatagacta ctggggcaaa 360
gggaccctgg tcaccgtctc ctca 384

<210> 105

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMA 269A37917 VHH

<400> 105

gaggtgcagc tgggtggagtc tgggggaggc ttggtgcagg ctgggggggtc tctgagactc 60
tcctgtgcag cctctggacg caccttcacc atgggggtggt tccgtcaggc tccagggaag 120
gagcgtgagt ttgtagcagc tattagtttg agtcctactt tagcatatta tgcagagtcc 180
gtgaagggcc gattcaccat cagccgagac aacgccaaga acacggtggt tttgcaaag 240
aacagcctga aacctgagga cacggccctt tattactgtg cagcagaccg gaaatcagta 300
atgtctattc ggcccgacta ctggggccag gggaccagg tcaccgtctc ctca 354

<210> 106

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMA 269A37355 VHH

<400> 106

gccgtgcagc tgggtggattc tgggggaggc ttggtgcagc ctgggggggtc tctgagactc 60
tcctgtgtag cctctggagg tatcttcgtc atcaatgcc a tgggctggta ccgccaggct 120
ccaggaaagc agcgcgagtt ggtcgcactt attcgtggac taggcagaac aaactatgac 180
gactccgtga agggccgatt caccatctcc agagacaacg ccaacaacac ggtgtatctg 240
cagatgaaca gcctggaacc tgaggacacg gccgtctact actgtacagt ctacgttaca 300
ctacttggtg ggggttaatag ggactactgg ggccaggggga cccaggtcac cgtctcctca 360

<210> 107

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMA 269A37915 VHH

<400> 107

gaggtgcagc tgggtggagtc tgggggagga ttggtgcagg ctgggggggtc tctgagactc 60
tcctgtgcag cctctggacg gaccttcagt agcattgtca tgggctgggt ccgccaggct 120
ccagggaagg agcgtgagtt tgtaggagcg attatgtgga atgatggtat tacatacttg 180
caagactccg tgaagggccg atttaccatc ttcagagaca atgccaagaa cacggtgtat 240
ctgcaaatac acagcctgaa acttgaggat acggccgttt attactgtgc agcatccaag 300
ggtagatact cggaatatga gtactggggc caggggaccc aggtcaccgt ctcctca 357

<210> 108

<211> 384

<212> DNA
<213> Artificial Sequence

<220>

<223> BCMA 269A37936 VHH

<400> 108

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gaggtgcagc tgggtggagtc tggggggaggc gtggtgcagg ctgggggggtc tctgacagtc 60
tcctgtacag cctctggatt cactttcgac cgtgctgtca tagtctggtt ccgccaggcc 120
cccgggaagg gccgtgaggg ggtctcattt attaaaccta gtgatggcac catatactac 180
attgactccc tgaagggccg attcacgac tccagtgcac tcgccaagaa tacggtatat 240
ctgcaaataa aaagtctgga atcggaggac tcggccgttt attactgtgc ggcctcgcct 300
gaggactggt acacggattg gatcgactgg agtatatatc ggtggcagca ctggggccag 360
gggaccagc tcactgtctc ctca 384
```

<210> 109

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMA 269A37953 VHH

<400> 109

```
gaggtgcagc tgggtggagtc tggggggagga atggtgcagg ctgggggactc tctgagacta 60
tcctgtgtgc agtctactta caccgtcaat agcgatgtca tgggctgggt ccgccaggct 120
ccagggaagg agcgtgagtt tgtaggagcg attatgtgga atgatgggtat tacatacttg 180
caagactccg tgaagggccg atttaccatc ttcagagaca acgccaagaa cacggtgtat 240
ctgcaaataa acagcctgaa acttgaggat acggccgttt attactgtgc agcatccaag 300
ggtagatact cggaatatga gtactggggc caggggagcc aggtcaccgt ctctctca 357
```

<210> 110

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMA 269A37965 VHH

<400> 110

```
gcggtgcagc tgggtggagtc tggggggagga ttggtgcagg ctgggggactc tctgagactc 60
tcctgtacag cctctggtgc aaccttgact aacgatcaca tggcatgggt ccgccaggct 120
ccagggaagg ggcgtgaatt tgtagcagct attgactgga gtggtcgtac cacaaattac 180
gcagaccccg tagagggccg attcaccatc tccagaaaca acgccaagaa cacggtgtat 240
ctggaaataa acagcctgaa acttgaggac acggccgttt attactgtgc ggtcctccgc 300
gcttggatct catatgacaa tgactactgg ggccagggga cccaggtcac cgtctctctca 360
```

<210> 111

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMA 269A37972 VHH

<400> 111

```
caggtgcagc tgggtggagtc tggggggagga ttggtgcagg ctgggggctc tctgagactc 60
tcctgtgcag cctctggagg caccttaagt aaaaataccg tggcttggtt ccgccaggct 120
ccagggaagg agcgtggggtt tgtagcgtct attacctggg atggctgtac gacatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca acgccaagaa cacagtgtat 240
ctgcaaatga acagcctgaa acctgaggat acggccgttt atgtctgtgc agacttaggg 300
aaatggcctg cgggcccggc ggactactgg ggccagggga cccaggtcac cgtctcctca 360
```

<210> 112

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMA 269A37353 VHH

<400> 112

```
caggtaaagc tggaggagtc tggggggaggc ttggtgcagg ctgggcggtc tctgagactc 60
tcctgtgcag cctctgaaca caccttcagt agccatgtca tgggctgggtt ccgccaggct 120
ccagggaagg agcgtgagtc tgttgagttt attggctgga gagatattag cacaagctat 180
gcagactccg tgaagggccg attcaccatc tccagagaca acgccaagaa gacgctgtat 240
ctgcaaatga atagcctgaa acctgaggac acggccgttt actactgtgc agcacgtcgg 300
atcgacgcag ctgactttga ttcctggggg caggggaccc aggtcaccgt ctcctcg 357
```

<210> 113

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMA 269A37948 VHH

<400> 113

```
gcggtgcagc tgggtggagtc tggggggagga ttggtgcagg ctgggggactc tctgagactc 60
acctgtacag cctctggacg cgccttcagt acctatttca tggcctgggtt ccgccaggct 120
ccagggaagg agcgtgagtt tgtagcagga attgcatgga gtggtggttag cagggcgtat 180
gcagactccg tgaagggccg attcaccatc tccagagaca acgccaagaa cacggtgtat 240
ctgcaaatga acagcctgaa atctgaggac acggccgttt attactgtgc cagcaggggg 300
attgaggtcg aagagtttgg tgcctggggc caggggaccc aggtcaccgt ctcgtcg 357
```

<210> 114

<211> 342

<212> DNA

<213> Artificial Sequence

<220>

<223> CD38 38A37333 VHH

<400> 114

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gatgtgcagc tgggtggagtc tggggggaggc ttggtgcagc ctgggggggtc tctgagactc 60
tcctgtgtag cctctggatt gaccttcagt agctacccca tgatgtgggt ccgccaggct 120
```

```

ccaggaaagg ggctcgagt ggtctcacgt attagcgata gtggtggtta cacaaactat 180
gacgactccg tgaagggccg attcaccatc tccagagaca acgccaagaa cagctgtat 240
ctgcaaataa acagcctgac acctgaggac acggccgtgt attactgtag aatcctgggg 300
ttgcccacca cgggccaggg gaccaggtc accgtctcct ca 342

```

<210> 115

<211> 378

<212> DNA

<213> Artificial Sequence

<220>

<223> CD38 38A37336 VHH

<400> 115

```

gaggtgcagc tgggtggagtc tgggggagggc ctggtgcagc ctgggggggtc tctgagactc 60
tcctgtgcag cctctggatt caccttcagt agcaactgga tgtattgggt ccgtcaggct 120
ccagggaagg ggctcgagt ggtcgcaact attagtactg atggtcgtgg aacatactat 180
aaagactctg tgaagggccg attcaccgtc tccagagaca acgcatgag tacgtgctt 240
ctgcaaataa acaatctgaa atctgaagat acggccgtgt attattgtgc aaaagagccg 300
aggggtgtga tggcttacct gcggaacctg ggtgactttg gttcctgggg ccaggggacc 360
caggtcaccg tctcctcg 378

```

<210> 116

<211> 345

<212> DNA

<213> Artificial Sequence

<220>

<223> CD38 38A37699 VHH

<400> 116

```

caggtgcagc tgggtggagtc tgggggagggc ttggtgcagg ctgggggggtc tctgagactc 60
tcctgtgcag cctctggaag gatcttcagt atcaatgcca tgggctggta ccgccaggct 120
ccagggaagc agcgcgagtt ggtcgccgct attagtacgg ctggtagcac aaactatgga 180
gactccgtga agggccgatt caccatctcc agagacaac ccaagaacac ggtgtatctg 240
caaatgaaca gcctgaaacc tgaggacaca gctgtttatt actgtaattt aaattttccc 300
ccgtatgtgt actggggcca ggggacccag gtcaccgtct cctca 345

```

<210> 117

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> CD38 38A37331 VHH

<400> 117

```

caggtaaagc tggaggagtc tgggggaggt ctggtgcagc ctggggagtc tctgagactc 60
tcctgttcag cctctggaag catcttcaaa gttttcagag tctttgccat gagctgttac 120
cgccagggtc ccgggaaaca gcgcgagttg gtcgcatcca ttagtagtgg cgagaccaca 180
acctatgcag actccgtgaa gggccgattc accatctcca gagacaacgc caagaatacg 240
gcgtatctgc aaatggacag cctgaaacct gaggacacgg ccgtctatta ctgtaatgcg 300
gatcacacct ttacaggaga cttctggggc caggggaccc aggtcaccgt ctcctca 357

```

<210> 118
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<223> CD38 38A37717 VHH

<400> 118
gaggtgcagc tgggtggaaag cggggggggga ctggtgcagg caggcgggtc actgagactg 60
tcattgtatcg caactgggaa ggtgttttagc atctacgaca tgggctggta taggcaggca 120
ccaggaaagc agaggggagct ggtggccgag atcaccagct ccggcaccac acactacgac 180
gatttcgtgt ctggccggtt taccatcagc agagacaacg ccaagaatac agtgtatctg 240
cagatgaaca ccctgaaggc cgaggataca gccgtgtact attgccgggc taatcacgtc 300
ttcggcggct cctactgggg gcagggaact caggtcactg tgtcatcc 348

<210> 119
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> CD38 38A37719 VHH

<400> 119
caggtaaagc tggaggagtc tggggggaggc tcggtgcaga ctgggggggtc tctgagactc 60
tcctgtgcag cctctgcaag catcttcact aggctgccc a tgggctggta ccgccaggct 120
ccagggaagc agcgcgagtt ggtcgtaggc attgttccta gtggtaggat aaactatgca 180
gactccgtga agggccgatt caccatctcc agagacaacg ccaagaacac ggtgtatctg 240
caaatgaaca gcctgcgccc tgaggacaca gccgtctatt actgccgcgc cgataccttc 300
cccttgccca cctggggcca ggggaccag gtcaccgtct cctca 345

<210> 120
<211> 378
<212> DNA
<213> Artificial Sequence

<220>
<223> CD38 38A37330 VHH

<400> 120
caggtgcagc tgggtggagtc tggggggagga ttggtgcagg ctgggggactc tctgagactc 60
tcctgtgcag cctctggacg cgcctacgct acgatggcct gggtccgcca ggctccaggg 120
aaggagcgtg agttttagc acatctgcgc gtgagtgggtg ataccactta ctatacagac 180
tccgtgaagg gccgattcac catctccaga gacaacgcca agaacacggc gtatctgcaa 240
atgaacatgt tgaaacctga ggacacggcc gtttattact gtgcagcggg accgtatggc 300
attcttgccg ctgccagggt cagtaatcca ggaaattatg attattgggg ccaggggacc 360
caggtcaccg tctcctca 378

<210> 121
<211> 369
<212> DNA
<213> Artificial Sequence

<220>

<223> CD38 38A37334 VHH

<400> 121

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gaggtgcagc  tgggtggagtc  tggggggagga  ttggtgcagg  ctgggggctc  tctgagactc  60
tcctgtgcag  cctctggact  caccttcagt  agttatatta  tgggctgggt  ccgccaggct  120
ccaggcgagg  agcgcgagtt  ggtcgcggaa  attagtagcg  gtggtatgac  atcgtatgca  180
gactccgtga  agggccgatt  caccatctcc  agagacaacg  ccaagaagac  ggggtatctg  240
caaatgaaca  gcctgaaacc  tgaggacacg  gccgtttact  attgtgcagc  ccctgagagg  300
ggtagtatct  ggtacagccg  ctacgaatat  aagtactggg  gccaggggac  ccaggtcacc  360
gtctcctca
```

<210> 122

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> CD38 38A37730 VHH

<400> 122

```
gccgtgcagc  tgggtggattc  tggggggaggc  ttggcgcaga  ctgggggggtc  tctgagactc  60
tcctgtgcag  cctctcaagg  gatcttcact  atcaatgcca  tgggctggta  ccgccagggt  120
ccagggaagc  agcgggagtt  ggtcgcagaa  gttagtagtg  gtggccgcac  agactatgca  180
gactccgtga  agggccgatt  caccatctcc  agagacaacg  ccaagaacac  ggtgtacctg  240
caaatgaaca  gcctgaaacc  tgaggacaca  ggcgctctatt  attgtcgagt  ttctggatgg  300
catgtgtttg  tcggtgaccg  catagtttgg  ggccagggca  ccctggtcac  tgtctcctca  360
```

<210> 123

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<223> CD38 38A37340 VHH

<400> 123

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gatgtgcagc  tgggtggagtc  tggggggagga  ttggtgcagg  ctgggggactc  tctgagactc  60
tcctgtgcag  cctctggacg  caccttcagt  agctatgcca  tggcctgggt  ccgccaggct  120
ccagggaagg  agcgtgagat  tgtttcgtct  atcagtacca  gtggtgggtat  cacagactat  180
gcagactccg  tgaagggccg  attcaccatc  tccaaagaca  gcgcgaagat  gaacacgggt  240
tatctgcaaa  tgaatagcct  agaacctgag  gacacggccg  tttactactg  tgcggcccgt  300
acatgggtacc  ttcgtacttc  tctccaatat  gactattggg  gccaggggac  ccaggtcacc  360
gtctcctca
```

<210> 124

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> CD38 38A37731 VHH

<400> 124
caggtaaagc tggaggagtc tgggggaggc ttggtgcagg ctgggggggtc tctgagactc 60
tcctgtgtag cctctggaac catcgtcagt atcagtacca tgggctggta ccgccaggct 120
ccagggaagc agcgcgagtt ggtcgcgact ataaccaggc gtggacgcac gaactataca 180
gactccgtga agggccgatt caccatctcc agagacaacg ccaaaaacac ggtgtatctg 240
caaatgaaca gcctgaaacc tgaggacaca gccgtctatt actgtaatgc agagggtgcaa 300
ctggatatat gggcatctgc gtatgactac tggggccagg ggacccagggt caccgtcgcc 360
tca 363

<210> 125
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> CD38 38A37326 VHH

<400> 125
gaggtgcagc tgggtggagtc tgggggagga ttggtgcagg ctggggggctc tctgagactc 60
tcctgtgcag cctctggacg cacctatgcc atgggctgggt atcgccaggc tccagggaag 120
cagcgcgact tggtcgcaac tattagtgggt gcgggtaaca caaagtatgc agactccgtg 180
aagggccgat tcaccatctc cagagacaac gccagaaca caatgtatct gcaaatgaac 240
agcctgaaac ctgaggacac ggccgtttat tactgtgccg cgggtaaata gttccctgct 300
gcgaatgagt actggggcca ggggaccag gtcaccgtct cctca 345

<210> 126
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Kozak nucleic acid sequence

<400> 126
gccgccacc 9

<210> 127
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> CD8alpha signal peptide

<400> 127
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> 128
<211> 63
<212> DNA

<213> Artificial Sequence

<220>

<223> CD8alpha signal peptide nucleic acid sequence 1

<400> 128

```
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60
ccg                                                                 63
```

<210> 129

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> CD8alpha signal peptide nucleic acid sequence 2

<400> 129

```
atggctctgc ccgtcactgc tctgctgctg cccctggctc tgctgctgca cgccgcaaga 60
ccc                                                                 63
```

<210> 130

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> CD8alpha hinge

<400> 130

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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> 131

<211> 135

<212> DNA

<213> Artificial Sequence

<220>

<223> CD8alpha hinge

<400> 131

```
accacgacgc cagcgccgcg accaccaaca ccggcgccca ccatcgcgtc gcagcccctg 60
tccctgcgcc cagaggcgtg ccggccagcg gcggggggcg cagtgcacac gaggggggctg 120
gacttcgcct gtgat                                                                 135
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<210> 132

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> CD8alpha transmembrane

<400> 132

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> 133

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> CD28 transmembrane

<400> 133

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> 134

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> CD8alpha transmembrane

<400> 134

atctacatct	gggcgccctt	ggccgggact	tgtgggggtcc	ttctcctgtc	actggttatac	60
accctttact	gc					72

<210> 135

<211> 81

<212> DNA

<213> Artificial Sequence

<220>

<223> CD28 transmembrane

<400> 135

ttttgggtgc	tggtgggtggt	tggtggagtc	ctggcttgct	atagcttgct	agtaacagtg	60
gcctttatta	tttctgggt	g				81

<210> 136

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> CD28 cytoplasmic aa sequence

<400> 136

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> 137

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> CD137 cytoplasmic domain

<400> 137

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> 138

<211> 123

<212> DNA

<213> Artificial Sequence

<220>

<223> CD28 cytoplasmic na sequence

<400> 138

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

<210> 139

<211> 126

<212> DNA

<213> Artificial Sequence

<220>

<223> CD137 cytoplasmic domain

<400> 139

aaacggggca	gaaagaaact	cctgtatata	ttcaaacaac	catttatgag	accagtacaa	60
------------	------------	------------	------------	------------	------------	----

actactcaag aggaagatgg ctgtagctgc cgatttccag aagaagaaga aggaggatgt 120
gaactg 126

<210> 140

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> wt CD3z cytoplasmic domain

<400> 140

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> 141

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Q65K CD3z cytoplasmic domain

<400> 141

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> 142
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> wt CD3z cytoplasmic domain

<400> 142
agagtgaagt tcagcaggag cgcagacgcc cccgcgtacc agcagggcca gaaccagctc 60
tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc 120
cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 180
gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc 240
cggaggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc 300
tacgacgccc ttcacatgca ggccctgccc cctcgc 336

<210> 143
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Q65K CD3z cytoplasmic domain

<400> 143
agagtgaagt tcagcaggag cgcagacgcc cccgcgtaca agcagggcca gaaccagctc 60
tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc 120
cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 180
gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc 240
cggaggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc 300
tacgacgccc ttcacatgca ggccctgccc cctcgc 336

<210> 144
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> linker sequence 1

<400> 144
Gly Gly Gly Gly Ser
1 5

<210> 145
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> linker sequence 2

<400> 145

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 146

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> linker sequence 3

<400> 146

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15

<210> 147

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> linker sequence 4

<400> 147

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Gly
1 5 10 15
Ser Gly Ser Gly Gly Gly Gly Ser
20

<210> 148

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

<223> linker sequence 5

<400> 148

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Gly
1 5 10 15
Ser Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
20 25 30
Gly Ser

<210> 149

<211> 15

<212> PRT
<213> Artificial Sequence

<220>
<223> Linker sequence 6

<400> 149
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 150
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker sequence 7

<400> 150
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> 151
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker sequence 8

<400> 151
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15
Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25

<210> 152
<211> 420
<212> PRT
<213> Artificial Sequence

<220>
<223> BCMA 269A37346 CAR

<400> 152
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 Val Asn Arg Thr Arg Arg Met His Gln Val Gln
20 25 30

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

<210> 153

<211> 426

<212> PRT

<213> Artificial Sequence

<220>

<223> BCMA 269A37348 CAR

<400> 153

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

370		375		380
Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His				
385		390		395
Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp				
	405		410	415
Ala Leu His Met Gln Ala Leu Pro Pro Arg				
	420		425	

<210> 154
 <211> 416
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> BCMA 269A37917 CAR

<400> 154

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

Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu
	290					295					300				
Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Lys	Gln	Gly
305					310					315					320
Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr
				325					330					335	
Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys
			340					345					350		
Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys
		355					360					365			
Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg
	370					375					380				
Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala
385					390					395					400
Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg
				405					410					415	

<210> 155

<211> 418

<212> PRT

<213> Artificial Sequence

<220>

<223> BCMA 269A37355 CAR

<400> 155

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

210		215		220
Ser Lys Arg Ser Arg	Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro			
225	230	235		240
Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro				
	245	250		255
Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu				
	260	265		270
Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu				
	275	280		285
Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys				
	290	295		300
Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys				
305	310	315		320
Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu				
	325	330		335
Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly				
	340	345		350
Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu				
	355	360		365
Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly				
	370	375		380
Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser				
385	390	395		400
Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro				
	405	410		415
Pro Arg				

<210> 156
 <211> 417
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> BCMA 269A37915 CAR

<400> 156
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 Val Asn Arg Thr Arg Arg Met His Glu Val Gln
20 25 30
Leu Val Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly Ser Leu Arg
35 40 45
Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Ser Ile Val Met Gly
50 55 60
Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Gly Ala Ile
65 70 75 80
Met Trp Asn Asp Gly Ile Thr Tyr Leu Gln Asp Ser Val Lys Gly Arg
85 90 95
Phe Thr Ile Phe Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu Gln Met
100 105 110
Asn Ser Leu Lys Leu Glu Asp Thr Ala Val Tyr Tyr Cys Ala Ala Ser
115 120 125

Lys Gly Arg Tyr Ser Glu Tyr Glu Tyr Trp Gly Gln Gly Thr Gln Val
 130 135 140
 Thr Val Ser Ser Thr Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
 145 150 155 160
 Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
 165 170 175
 Cys Arg Pro Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
 180 185 190
 Ala Cys Asp Phe Trp Val Leu Val Val Gly Gly Val Leu Ala Cys
 195 200 205
 Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser
 210 215 220
 Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
 225 230 235 240
 Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
 245 250 255
 Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr
 260 265 270
 Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
 275 280 285
 Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu
 290 295 300
 Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln
 305 310 315 320
 Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
 325 330 335
 Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
 340 345 350
 Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
 355 360 365
 Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
 370 375 380
 Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
 385 390 395 400
 Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
 405 410 415
 Arg

<210> 157

<211> 426

<212> PRT

<213> Artificial Sequence

<220>

<223> BCMA 269A37936 CAR

<400> 157

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 Val Asn Arg Thr Arg Arg Met His Glu Val Gln
 20 25 30
 Leu Val Glu Ser Gly Gly Gly Val Val Gln Ala Gly Gly Ser Leu Thr

<213> Artificial Sequence

<220>

<223> BCMA 269A37953 CAR

<400> 158

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

Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr
385					390					395					400
Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro
				405					410					415	

Arg

<210> 159

<211> 418

<212> PRT

<213> Artificial Sequence

<220>

<223> BCMA 269A37965 CAR

<400> 159

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

290		295		300
Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys				
305		310		315
Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu				
	325		330	335
Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly				
	340		345	350
Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu				
	355		360	365
Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly				
	370		375	380
Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser				
385		390		395
Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro				
	405		410	415
Pro Arg				

<210> 160
 <211> 418
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> BCMA 269A37972 CAR

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

Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Phe	Trp	Val	Arg
210						215					220				
Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro
225					230					235					240
Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro
				245					250					255	
Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser	Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu
		260						265					270		
Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu
	275						280					285			
Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys
290						295					300				
Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Lys
305					310					315					320
Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu
			325					330						335	
Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly
		340					345					350			
Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu
	355					360						365			
Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly
370					375						380				
Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser
385					390				395						400
Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro
			405					410					415		
Pro	Arg														

<210> 161
 <211> 417
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> BCMA 269A37353 CAR

<400> 161

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

<212> PRT

<213> Artificial Sequence

<220>

<223> CD38 38A37333 CAR

<400> 163

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

370	375	380
His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr		
385	390	395
Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg		400
405	410	

<210> 164
 <211> 423
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD38 38A37336 CAR

<400> 164

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

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

<210> 165

<211> 412

<212> PRT

<213> Artificial Sequence

<220>

<223> CD38 38A37699 CAR

<400> 165

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

210		215		220
Leu His Ser Asp Tyr Met	Asn Met Thr Pro Arg	Arg Pro Gly Pro Thr		
225	230	235		240
Arg Lys His Tyr Gln Pro	Tyr Ala Pro Pro Arg	Asp Phe Ala Ala Tyr		
	245	250		255
Arg Ser Lys Arg Gly Arg	Lys Lys Leu Leu Tyr	Ile Phe Lys Gln Pro		
	260	265		270
Phe Met Arg Pro Val Gln	Thr Thr Gln Glu Glu	Asp Gly Cys Ser Cys		
	275	280		285
Arg Phe Pro Glu Glu Glu	Glu Gly Gly Cys Glu	Leu Arg Val Lys Phe		
	290	295		300
Ser Arg Ser Ala Asp Ala	Pro Ala Tyr Lys Gln	Gly Gln Asn Gln Leu		
305	310	315		320
Tyr Asn Glu Leu Asn Leu	Gly Arg Arg Glu Glu	Tyr Asp Val Leu Asp		
	325	330		335
Lys Arg Arg Gly Arg Asp	Pro Glu Met Gly Gly	Lys Pro Arg Arg Lys		
	340	345		350
Asn Pro Gln Glu Gly Leu	Tyr Asn Glu Leu Gln	Lys Asp Lys Met Ala		
	355	360		365
Glu Ala Tyr Ser Glu Ile	Gly Met Lys Gly Glu	Arg Arg Arg Gly Lys		
	370	375		380
Gly His Asp Gly Leu Tyr	Gln Gly Leu Ser Thr	Ala Thr Lys Asp Thr		
385	390	395		400
Tyr Asp Ala Leu His Met	Gln Ala Leu Pro Pro	Arg		
	405	410		

<210> 166

<211> 416

<212> PRT

<213> Artificial Sequence

<220>

<223> CD38 38A37331 CAR

<400> 166

Met Ala Leu Pro Val Thr	Ala Leu Leu Leu Pro	Leu Ala Leu Leu Leu
1	5	10
His Ala Ala Arg Pro	Val Asn Gln Val Lys	Leu Glu Glu Ser Gly Gly
	20	25
Gly Leu Val Gln Pro	Gly Glu Ser Leu Arg	Leu Ser Cys Ser Ala Ser
	35	40
Gly Ser Ile Phe Lys	Val Phe Arg Val Phe	Ala Met Ser Trp Tyr Arg
	50	55
Gln Gly Pro Gly Lys	Gln Arg Glu Leu Val	Ala Ser Ile Ser Ser Gly
65	70	75
Glu Thr Thr Thr Tyr	Ala Asp Ser Val Lys	Gly Arg Phe Thr Ile Ser
	85	90
Arg Asp Asn Ala Lys	Asn Thr Ala Tyr Leu	Gln Met Asp Ser Leu Lys
	100	105
Pro Glu Asp Thr Ala	Val Tyr Tyr Cys Asn	Ala Asp His Thr Phe Thr
	115	120
Gly Asp Phe Trp Gly	Gln Gly Thr Gln Val	Thr Val Ser Ser Thr Arg
	130	135
		140

Arg	Met	His	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro
145					150					155					160
Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys
				165					170						175
Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala
			180					185					190		
Cys	Asp	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	Cys	Tyr
	195					200						205			
Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Phe	Trp	Val	Arg	Ser	Lys
	210					215					220				
Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro	Arg	Arg
225					230					235					240
Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	Arg	Asp
				245					250						255
Phe	Ala	Ala	Tyr	Arg	Ser	Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile
			260					265					270		
Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp
	275						280					285			
Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu
	290					295					300				
Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Lys	Gln	Gly
305					310					315					320
Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr
				325				330						335	
Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys
			340				345					350			
Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys
	355					360					365				
Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg
	370					375				380					
Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala
385					390					395					400
Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg
				405				410						415	

<210> 167

<211> 413

<212> PRT

<213> Artificial Sequence

<220>

<223> CD38 38A37717 CAR

<400> 167

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

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

<210> 168
 <211> 412
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD38 38A37719 CAR

<400> 168

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

<210> 169
 <211> 423
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD38 38A37330 CAR

<400> 169

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

Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	
		275					280					285				
Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	
	290					295					300					
Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	
305					310					315					320	
Tyr	Lys	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	
				325					330					335		
Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	
			340					345					350			
Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	
		355					360					365				
Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	
		370				375					380					
Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	
385					390					395					400	
Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	
				405					410					415		
Leu	Pro	Pro	Arg													
			420													

<210> 171

<211> 417

<212> PRT

<213> Artificial Sequence

<220>

<223> CD38 38A37730 CAR

<400> 171

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

Ser	Ala	Lys	Met	Asn	Thr	Val	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Glu	Pro
			100					105					110		
Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Arg	Thr	Trp	Tyr	Leu	Arg
		115					120					125			
Thr	Ser	Leu	Gln	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val
		130				135						140			
Ser	Ser	Thr	Arg	Arg	Met	His	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg
145					150					155					160
Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg
			165						170					175	
Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly
			180					185					190		
Leu	Asp	Phe	Ala	Cys	Asp	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val
		195					200					205			
Leu	Ala	Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Phe	Trp
		210				215					220				
Val	Arg	Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met
225					230					235					240
Thr	Pro	Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala
				245					250					255	
Pro	Pro	Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser	Lys	Arg	Gly	Arg	Lys	Lys
			260					265					270		
Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr
		275					280					285			
Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly
		290				295					300				
Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala
305					310					315					320
Tyr	Lys	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg
				325					330					335	
Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu
			340					345					350		
Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn
		355					360					365			
Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met
		370				375					380				
Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly
385					390					395					400
Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala
				405					410					415	
Leu	Pro	Pro	Arg												
			420												

<210> 173
 <211> 418
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD38 38A37731 CAR

<400> 173
 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	Val	Asn	Gln	Val	Lys	Leu	Glu	Glu	Ser	Gly	Gly				
			20					25					30						
Gly	Leu	Val	Gln	Ala	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Val	Ala	Ser				
		35					40					45							
Gly	Thr	Ile	Val	Ser	Ile	Ser	Thr	Met	Gly	Trp	Tyr	Arg	Gln	Ala	Pro				
		50				55					60								
Gly	Lys	Gln	Arg	Glu	Leu	Val	Ala	Thr	Ile	Thr	Arg	Arg	Gly	Arg	Thr				
65				70					75						80				
Asn	Tyr	Thr	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn				
				85					90					95					
Ala	Lys	Asn	Thr	Val	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Lys	Pro	Glu	Asp				
			100					105					110						
Thr	Ala	Val	Tyr	Tyr	Cys	Asn	Ala	Glu	Val	Gln	Leu	Asp	Ile	Trp	Ala				
		115					120					125							
Ser	Ala	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ala	Ser				
		130				135					140								
Thr	Arg	Arg	Met	His	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro				
145				150					155					160					
Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu				
				165					170					175					
Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp				
			180					185					190						
Phe	Ala	Cys	Asp	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala				
		195					200					205							
Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Phe	Trp	Val	Arg				
		210				215				220									
Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro				
225				230					235					240					
Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro				
				245					250					255					
Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser	Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu				
			260					265					270						
Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu				
		275					280					285							
Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys				
		290				295					300								
Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Lys				
305				310						315				320					
Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu				
				325					330					335					
Glu	Tyr	Asp	Val	Leu	Asp</														

<210> 174
 <211> 412
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD38 38A37326 CAR

<400> 174
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 His Ala Ala Arg Pro Val Asn Glu Val Gln Leu Val Glu Ser Gly Gly
 20 25 30
 Gly Leu Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
 35 40 45
 Gly Arg Thr Tyr Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln
 50 55 60
 Arg Asp Leu Val Ala Thr Ile Ser Gly Ala Gly Asn Thr Lys Tyr Ala
 65 70 75 80
 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
 85 90 95
 Thr Met Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val
 100 105 110
 Tyr Tyr Cys Ala Ala Gly Lys Trp Phe Pro Ala Ala Asn Glu Tyr Trp
 115 120 125
 Gly Gln Gly Thr Gln Val Thr Val Ser Ser Thr Arg Arg Met His Thr
 130 135 140
 Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
 145 150 155 160
 Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
 165 170 175
 Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe Trp
 180 185 190
 Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
 195 200 205
 Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu
 210 215 220
 Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr
 225 230 235 240
 Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr
 245 250 255
 Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro
 260 265 270
 Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys
 275 280 285
 Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe
 290 295 300
 Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu
 305 310 315 320
 Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
 325 330 335
 Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
 340 345 350

Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala
	355						360					365			
Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys
370						375					380				
Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr
385					390					395					400
Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg				
			405					410							

<210> 175
 <211> 1263
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> BCMA 269A37346 CAR

<400> 175
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 gtgcagcctg ggggttctct gaggctctcc tgtgaagcct ctggattcac tttggattat 180
 tatgccatag gctggttccg ccaggcccca gggaaggagc gcgaggggggt catatgtatt 240
 agtagaagtg atggtagcac atactatgca gactccgtga agggccgatt caccatctcc 300
 agagacaacg ccaagaaaac ggtgtatctg caaatgatca gcctgaaacc tgaggacacg 360
 gccgcttatt actgtgcagc agggggccgat tgttcggggg acctacgaga ttatgagttc 420
 cggggggcagg ggaccaggt caccgtctcc tcaactagta ccacgacgcc agcgccgcga 480
 ccaccaacac cggcgccac catcgctcg cagcccctgt ccctgcgccc agaggcgtgc 540
 cggccagcgg cggggggcgc agtgcacacg agggggctgg acttcgcctg tgatttttgg 600
 gtgctggtgg tggttggtgg agtcctggct tgctatagct tgctagtaac agtggccttt 660
 attattttct gggtagaggag taagaggagc aggcctctgc acagtgacta catgaacatg 720
 actccccgcc gccccgggac caccgcaag cattaccagc cctatgcccc accacgcgac 780
 ttcgcagcct atcgctccaa acggggcaga aagaaactcc tgtatatatt caaacaacca 840
 tttatgagac cagtacaaac tactcaagag gaagatggct gtagctgccg atttccagaa 900
 gaagaagaag gaggatgtga actgagagtg aagttcagca ggagcgcaga cgccccgcg 960
 tacaagcagg gccagaacca gctctataac gagctcaatc taggacgaag agaggagtac 1020
 gatgttttgg acaagagacg tggccgggac cctgagatgg ggggaaagcc gagaaggaag 1080
 aaccctcagg aaggcctgta caatgaactg cagaaagata agatggcgga ggcctacagt 1140
 gagattggga tgaaaggcga gcgccggagg ggcaaggggc acgatggcct ttaccagggt 1200
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 tga 1263

<210> 176
 <211> 1281
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> BCMA 269A37348 CAR

<400> 176
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 ccggttaacc gcacgcgtcg catgcatcag gtaaagctgg aggagtctgg gggacgattg 120
 gtgcagccaa ggggctctct gagactctcc tgtgcaggct ctggacgcac tttcagtacc 180

tatggtatgg	cctggttccg	ccaggctcca	gggaaggagc	gtgagttcgt	agcgtctaaa	240
gcatcgatga	attacagcgg	tagaacatac	tatgcagact	ccgtgaaggg	ccgattcacc	300
atcgccagag	acaacgcaa	gaacatggtg	tttctgcaaa	tgaacaacct	gaagcctgag	360
gacacggccg	tttattactg	tgcagcgggc	actggatgct	caacatatgg	gtgttttgac	420
gcccagataa	tagactactg	gggcaaaggg	accctggtca	ccgtctcctc	aactagtacc	480
acgacgccag	cgccgcgacc	accaacaccg	gcgcccacca	tcgcgtcgca	gcccctgtcc	540
ctgcgccag	aggcgtgccg	gccagcggcg	gggggcgcag	tgcacacgag	ggggctggac	600
ttcgctgtg	atTTTTGGGT	gctggtggtg	gttggaggag	tcctggcttg	ctatagcttg	660
ctagtaacag	tggcctttat	tattttctgg	gtgaggagta	agaggagcag	gctcctgcac	720
agtgactaca	tgaacatgac	tccccgccgc	cccgggcccc	cccgcaagca	ttaccagccc	780
tatgccccac	cacgcgactt	cgcagcctat	cgctccaaac	ggggcagaaa	gaaactcctg	840
tatatattca	aacaaccatt	tatgagacca	gtacaaacta	ctcaagagga	agatggctgt	900
agctgccgat	ttccagaaga	agaagaagga	ggatgtgaac	tgagagtga	gttcagcagg	960
agcgagacg	ccccgcgta	caagcagggc	cagaaccagc	tctataacga	gctcaatcta	1020
ggacgaagag	aggagtacga	tgTTTTGGAC	aagagacgtg	gccgggaccc	tgagatgggg	1080
ggaaagccga	gaaggaagaa	ccctcaggaa	ggcctgtaca	atgaactgca	gaaagataag	1140
atggcggagg	cctacagtga	gattgggatg	aaaggcgagc	gccggagggg	caaggggcac	1200
gatggccttt	accagggtct	cagtacagcc	accaaggaca	cctacgacgc	ccttcacatg	1260
caggccctgc	cccctcgctg	a				1281

<210> 177

<211> 1251

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMA 269A37917 CAR

<400> 177

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ccggttaacc	gcacgcgtcg	catgcatgag	gtgcagctgg	tggagtctgg	gggaggcttg	120
gtgcaggctg	gggggtctct	gagactctcc	tgtgcagcct	ctggacgcac	cttcaccatg	180
gggtggttcc	gtcaggctcc	agggaaggag	cgtgagtttg	tagcagctat	tagtttgagt	240
cctacttttag	catattatgc	agagtccgtg	aagggccgat	tcaccatcag	ccgagacaac	300
gccaagaaca	cggtggtttt	gcaaatgaac	agcctgaaac	ctgaggacac	ggccctttat	360
tactgtgcag	cagaccggaa	atcagtaatg	tctattcggc	ccgactactg	gggccagggg	420
accaggtca	ccgtctcctc	aactagtacc	acgacgccag	cgccgcgacc	accaacaccg	480
gcgcccacca	tcgcgtcgca	gcccctgtcc	ctgcgccag	aggcgtgccg	gccagcggcg	540
gggggcgcag	tgcacacgag	ggggctggac	ttcgctgtg	atTTTTGGGT	gctggtggtg	600
gttggaggag	tcctggcttg	ctatagcttg	ctagtaacag	tggcctttat	tattttctgg	660
gtgaggagta	agaggagcag	gctcctgcac	agtgactaca	tgaacatgac	tccccgccgc	720
cccgggcccc	cccgcaagca	ttaccagccc	tatgccccac	cacgcgactt	cgcagcctat	780
cgctccaaac	ggggcagaaa	gaaactcctg	tatatattca	aacaaccatt	tatgagacca	840
gtacaaacta	ctcaagagga	agatggctgt	agctgccgat	ttccagaaga	agaagaagga	900
ggatgtgaac	tgagagtga	gttcagcagg	agcgagacg	ccccgcgta	caagcagggc	960
cagaaccagc	tctataacga	gctcaatcta	ggacgaagag	aggagtacga	tgTTTTGGAC	1020
aagagacgtg	gccgggaccc	tgagatgggg	ggaaagccga	gaaggaagaa	ccctcaggaa	1080
ggcctgtaca	atgaactgca	gaaagataag	atggcggagg	cctacagtga	gattgggatg	1140
aaaggcgagc	gccggagggg	caaggggcac	gatggccttt	accagggtct	cagtacagcc	1200
accaaggaca	cctacgacgc	ccttcacatg	caggccctgc	cccctcgctg	a	1251

<210> 178

<211> 1257

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMA 269A37355 CAR

<400> 178

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gtgcagcctg gggggtctct gagactctcc tgtgtagcct ctggagggtat cttcgtcatc 180
aatgccatgg gctggtaccg ccaggctcca ggaaagcagc gcgagttggt cgcatctatt 240
cgtggactag gcagaacaaa ctatgacgac tccgtgaagg gccgattcac catctccaga 300
gacaacgcca acaacacggt gtatctgcag atgaacagcc tggaacctga ggacacggcc 360
gtctactact gtacagtcta cgttacacta cttggtgggg ttaataggga ctactggggc 420
caggggaccc aggtcaccgt ctcctcaact agtaccacga cgccagcgcc gcgaccacca 480
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gcggcggggg gcgcagtgca cacgaggggg ctggacttcg cctgtgattt ttgggtgctg 600
gtggtggttg gtggagtcct ggcttgctat agcttgctag taacagtggc ctttattatt 660
ttctgggtga ggagtaagag gagcaggctc ctgcacagtg actacatgaa catgactccc 720
cgccgccccg ggcccacccg caagcattac cagccctatg cccaccacg cgacttcgca 780
gcctatcgct ccaaacgggg cagaaagaaa ctcctgtata tattcaaaca accatttatg 840
agaccagtac aaactactca agaggaagat ggctgtagct gccgatttcc agaagaagaa 900
gaaggaggat gtgaactgag agtgaagttc agcaggagcg cagacgcccc cgctgacaag 960
cagggccaga accagctcta taacgagctc aatctaggac gaagagagga gtacgatgtt 1020
ttggacaaga gacgtggccg ggaccctgag atggggggaa agccgagaag gaagaacctt 1080
caggaaggcc tgtacaatga actgcagaaa gataagatgg cggaggccta cagtgagatt 1140
gggatgaaag gcgagcgccg gaggggcaag gggcacgatg gcctttacca gggctctcagt 1200
acagccacca aggacaccta cgacgccctt cacatgcagg ccctgcccc tcgctga 1257
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<210> 179

<211> 1254

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMA 269A37915 CAR

<400> 179

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ccggttaacc gcacgcgtcg catgcatgag gtgcagctgg tggagtctgg gggaggattg 120
gtgcaggctg ggggctctct gagactctcc tgtgcagcct ctggacggac cttcagtagc 180
attgtcatgg gctggttccg ccaggctcca gggaaggagc gtgagtttgt aggagcgatt 240
atgtggaatg atggtattac atacttgcaa gactccgtga agggccgatt taccatcttc 300
agagacaatg ccaagaacac ggtgtatctg caaatgaaca gcctgaaact tgaggatacg 360
gccgtttatt actgtgcagc atccaagggt agatactcgg aatatgagta ctggggccag 420
gggaccaggg tcaccgtctc ctcaactagt accacgacgc cagcgccgcg accaccaaca 480
ccggcgccca ccatcgcgtc gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg 540
gcggggggcg cagtgcacac gagggggctg gacttcgcct gtgatttttg ggtgctggtg 600
gtggttggtg gagtcttggt ttgctatagc ttgctagtaa cagtggcctt tattattttc 660
tgggtgagga gtaagaggag caggctcctg cacagtgact acatgaacat gactccccgc 720
cgccccgggc ccacccgcaa gcattaccag ccctatgccc caccacgcga cttcgcagcc 780
tatcgctcca aacggggcag aaagaaactc ctgtatatat tcaaacaacc atttatgaga 840
ccagtacaaa ctactcaaga ggaagatggc tgtagctgcc gatttccaga agaagaagaa 900
ggaggatgtg aactgagagt gaagttcagc aggagcgag acgccccgc gtacaagcag 960
ggccagaacc agctctataa cgagctcaat ctaggacgaa gagaggagta cgatgttttg 1020
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gacaagagac	gtggccggga	ccctgagatg	gggggaaagc	cgagaaggaa	gaaccctcag	1080
gaaggcctgt	acaatgaact	gcagaaagat	aagatggcgg	aggcctacag	tgagattggg	1140
atgaaaggcg	agcgccggag	gggcaagggg	cacgatggcc	tttaccaggg	tctcagtaca	1200
gccaccaagg	acacctacga	cgcccttcac	atgcaggccc	tgccccctcg	ctga	1254

<210> 180

<211> 1281

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMA 269A37936 CAR

<400> 180

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ccggttaacc	gcacgcgtcg	catgcatgag	gtgcagctgg	tgaggtctgg	gggaggcgtg	120
gtgcaggctg	gggggtctct	gacagtctcc	tgtacagcct	ctggattcac	tttcgaccgt	180
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agtgacatcg	ccaagaatac	ggtatatctg	caaatgaaaa	gtctggaatc	ggaggactcg	360
gccgtttatt	actgtgcggc	ctcgcctgag	gactggtaca	cggattggat	cgactggagt	420
atatatcggg	ggcagcactg	gggccagggg	acccagggtc	ctgtctcctc	aactagtacc	480
acgacgccag	cgccgcgacc	accaacaccg	gcgcccacca	tcgcgtcgca	gccccgtgcc	540
ctgcgcccag	aggcgtgccg	gccagcggcg	gggggcgcag	tgcacacgag	ggggctggac	600
ttcgctgtg	atTTTTGGGT	gctgggtggg	gttgggtggg	tcctggcttg	ctatagcttg	660
ctagtaacag	tggcctttat	tattttctgg	gtgaggagta	agaggagcag	gctcctgcac	720
agtgactaca	tgaacatgac	tccccgccgc	cccgggcccc	cccgcaagca	ttaccagccc	780
tatgccccac	cacgcgactt	cgcagcctat	cgctccaaac	ggggcagaaa	gaaactcctg	840
tatatattca	aacaaccatt	tatgagacca	gtacaaacta	ctcaagagga	agatggctgt	900
agctgccgat	ttccagaaga	agaagaagga	ggatgtgaac	tgagagtga	gttcagcagg	960
agcgagacg	ccccgcgcta	caagcagggc	cagaaccagc	tctataacga	gctcaatcta	1020
ggacgaagag	aggagtacga	tgTTTTGGAC	aagagacgtg	gccgggaccc	tgagatgggg	1080
ggaaagccga	gaaggaagaa	ccctcaggaa	ggcctgtaca	atgaactgca	gaaagataag	1140
atggcggagg	cctacagtga	gattgggatg	aaaggcgagc	gccggagggg	caaggggcac	1200
gatggccttt	accagggtct	cagtacagcc	accaaggaca	cctacgacgc	ccttcacatg	1260
caggccctgc	cccctcgctg	a				1281

<210> 181

<211> 1254

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMA 269A37953 CAR

<400> 181

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ccggttaacc	gcacgcgtcg	catgcatgag	gtgcagctgg	tgaggtctgg	gggagggaatg	120
gtgcaggctg	gggactctct	gagactatcc	tgtgtgcagt	ctacttacac	cgtaaatagc	180
gatgtcatgg	gctggttccg	ccaggctcca	gggaaggagc	gtgagtttgt	aggagcgatt	240
atgtggaatg	atggtattac	atacttgcaa	gactccgtga	agggccgatt	taccatcttc	300
agagacaacg	ccaagaacac	ggtgtatctg	caaatgaaca	gcctgaaact	tgaggatacg	360
gccgtttatt	actgtgcagc	atccaagggt	agatactcgg	aatatgagta	ctggggccag	420
gggacccagg	tcaccgtctc	ctcaactagt	accacgacgc	cagcgccgcg	accaccaaca	480

ccggcgccca	ccatcgcgtc	gcagcccctg	tccttgcgcc	cagaggcgtg	ccggccagcg	540
gcggggggcg	cagtgcacac	gagggggctg	gacttcgcct	gtgatttttg	ggtgctggtg	600
gtggttggtg	gagtcctggc	ttgctatagc	ttgctagtaa	cagtggcctt	tattattttc	660
tgggtgagga	gtaagaggag	caggctcctg	cacagtgact	acatgaacat	gactccccgc	720
cgccccgggc	ccacccgcaa	gcattaccag	ccctatgccc	caccacgcga	cttcgcagcc	780
tatcgctcca	aacggggcag	aaagaaactc	ctgtatatat	tcaaacaacc	atttatgaga	840
ccagtacaaa	ctactcaaga	ggaagatggc	tgtagctgcc	gatttccaga	agaagaagaa	900
ggaggatgtg	aactgagagt	gaagttcagc	aggagcgcag	acgccccgcg	gtacaagcag	960
ggccagaacc	agctctataa	cgagctcaat	ctaggacgaa	gagaggagta	cgatgttttg	1020
gacaagagac	gtggccggga	ccctgagatg	gggggaaagc	cgagaaggaa	gaaccctcag	1080
gaaggcctgt	acaatgaact	gcagaaagat	aagatggcgg	aggcctacag	tgagattggg	1140
atgaaaggcg	agcgccggag	gggcaagggg	cacgatggcc	tttaccaggg	tctcagtaca	1200
gccaccaagg	acacctacga	cgcccttcac	atgcaggccc	tgccccctcg	ctga	1254

<210> 182

<211> 1257

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMA 269A37965 CAR

<400> 182

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ccggttaacc	gcacgcgtcg	catgcatgcg	gtgcagctgg	tggagtctgg	gggaggattg	120
gtgcaggctg	gggactctct	gagactctcc	tgtacagcct	ctggtgcaac	cttgactaac	180
gatcacatgg	catggttccg	ccaggctcca	gggaaggggc	gtgaatttgt	agcagctatt	240
gactggagtg	gtcgtaccac	aaattacgca	gaccccgtag	agggccgatt	caccatctcc	300
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<400> 183

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<212> DNA

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<223> BCMA 269A37353 CAR

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<220>
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<220>
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<210> 187

<211> 1272

<212> DNA

<213> Artificial Sequence

<220>

<223> CD38 38A37336 CAR

<400> 187

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<212> DNA

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<220>

<223> CD38 38A37669 CAR

<400> 188

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<212> DNA

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<220>

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<223> CD38 38A37717 CAR

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<212> DNA

<213> Artificial Sequence

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<223> CD38 38A37719 CAR

<400> 191

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cggaggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc 1200
tacgacgccc ttcacatgca ggccctgccc cctcgtcga 1239
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<210> 192
<211> 1272
<212> DNA
<213> Artificial Sequence

<220>
<223> CD38 38A37330 CAR

<400> 192
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ctgagactct cctgtgcagc ctctggacgc gcctacgcta cgatggcctg gttccgccag 180
gctccaggga aggagcgtga gttttagtagca catctgcgcg tgagtgggtga taccacttac 240
tatacagact ccgtgaaggg ccgattcacc atctccagag acaacgcca gaacacggcg 300
tatctgcaaa tgaacatggt gaaacctgag gacacggccg tttattactg tgcagcggga 360
ccgtatggca ttcttgccgc tgccagggtc agtaatccag gaaattatga ttattggggc 420
caggggaccc aggtcaccgt ctctcaacg cgtcgcacgc atactagtac cagcagcca 480
gcgccgcgac caccaacacc ggcgcccacc atcgcgtcgc agcccctgtc cctgcgcca 540
gaggcgtgcc ggccagcggc ggggggcgca gtgcacacga gggggctgga cttcgctgt 600
gatttttggg tgctgggtgt ggttgggtgga gtcctggctt gctatagctt gctagtaaca 660
gtggccttta ttattttctg ggtgaggagt aagaggagca ggctcctgca cagtgactac 720
atgaacatga ctccccgccg ccccgggccc acccgcaagc attaccagcc ctatgcccc 780
ccacgcgact tcgcagccta tcgctccaaa cggggcagaa agaaactcct gtatatattc 840
aaacaacat ttatgagacc agtacaact actcaagagg aagatggctg tagctgccga 900
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gccccgcgt acaagcaggg ccagaaccag ctctataacg agctcaatct aggacgaaga 1020
gaggagtacg atgttttgga caagagacgt ggccgggacc ctgagatggg gggaaagccg 1080
agaaggaaga accctcagga aggcctgtac aatgaactgc agaaagataa gatggcggag 1140
gcctacagtg agattgggat gaaaggcgag cgccggaggg gcaaggggca cgatggcctt 1200
taccagggtc tcagtacagc caccaaggac acctacgacg cccttcacat gcaggccctg 1260
ccccctcgct ga 1272

<210> 193
<211> 1263
<212> DNA
<213> Artificial Sequence

<220>
<223> CD38 38A37334 CAR

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ctgagactct cctgtgcagc ctctggactc accttcagta gttatattat gggctgggtc 180
cgccaggctc caggcgagga gcgcgagttg gtcgcggaaa ttagtagcgg tggtagaca 240
tcgtatgcag actccgtgaa gggccgattc accatctcca gagacaacgc caagaagacg 300
gggtatctgc aaatgaacag cctgaaacct gaggacacgg ccgtttacta ttgtgcagcc 360
cctgagaggg gtagtatctg gtacagccgc tacgaatata agtactgggg ccaggggacc 420
caggtcaccg tctctcaac gcgtcgcacg catactagta ccacgacgcc agcgccgcga 480
ccaccaacac cggcgcccac catcgcgtcg cagcccctgt ccctgcgccc agaggcgtgc 540
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gtgctgggtg tgggtgggtg agtcctggct tgctatagct tgctagtaac agtggccttt 660
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tacaagcagg	gccagaacca	gctctataac	gagctcaatc	taggacgaag	agaggagtac	1020
gatgttttgg	acaagagacg	tggccgggac	cctgagatgg	ggggaaagcc	gagaaggaag	1080
aaccctcagg	aaggcctgta	caatgaactg	cagaaagata	agatggcgga	ggcctacagt	1140
gagattggga	tgaaaggcga	gcgccggagg	ggcaaggggc	acgatggcct	ttaccagggg	1200
ctcagtacag	ccaccaagga	cacctacgac	gcccttcaca	tgcaggccct	gccccctcgc	1260
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<210> 194

<211> 1254

<212> DNA

<213> Artificial Sequence

<220>

<223> CD38 38A37730 CAR

<400> 194

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ctgagactct	cctgtgcagc	ctctcaaggg	atcttcacta	tcaatgccat	gggctggtac	180
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gactatgcag	actccgtgaa	gggccgattc	accatctcca	gagacaacgc	caagaacacg	300
gtgtacctgc	aaatgaacag	cctgaaacct	gaggacacag	gcgtctatta	ttgtcgagtt	360
tctggatggc	atgtgtttgt	cggtgaccgc	atagtttggg	gccagggcac	cctggtcact	420
gtctcctcaa	cgctcgcgac	gcatactagt	accacgacgc	cagcgccgcg	accaccaaca	480
ccggcgccca	ccatcgcgtc	gcagcccctg	tccctgcgcc	cagaggcggtg	ccggccagcg	540
gcggggggcg	cagtgcacac	gagggggctg	gacttcgcct	gtgatttttg	ggtgctgggtg	600
gtggttgggtg	gagtcctggc	ttgctatagc	ttgctagtaa	cagtggcctt	tattattttc	660
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ccagtacaaa	ctactcaaga	ggaagatggc	tgtagctgcc	gatttccaga	agaagaagaa	900
ggaggatgtg	aactgagagt	gaagttcagc	aggagcgag	acgccccgc	gtacaagcag	960
ggccagaacc	agctctataa	cgagctcaat	ctaggacgaa	gagaggagta	cgatgttttg	1020
gacaagagac	gtggccggga	ccctgagatg	gggggaaagc	cgagaaggaa	gaaccctcag	1080
gaaggcctgt	acaatgaact	gcagaaagat	aagatggcgg	aggcctacag	tgagattggg	1140
atgaaaggcg	agcgccggag	gggcaagggg	cacgatggcc	tttaccaggg	tctcagtaca	1200
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<210> 195

<211> 1263

<212> DNA

<213> Artificial Sequence

<220>

<223> CD38 38A37340 CAR

<400> 195

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ctgagactct	cctgtgcagc	ctctggacgc	accttcagta	gctatgccat	ggcctggttc	180

cgccaggctc	caggggaagga	gcgtgagatt	gtttcgtcta	tcagtaccag	tggtggtatc	240
acagactatg	cagactccgt	gaagggccga	ttcaccatct	ccaaagacag	cgcgaagatg	300
aacacggtgt	atctgcaaat	gaatagccta	gaacctgagg	acacggccgt	ttactactgt	360
gcggcccgta	catggtacct	tcgtacttct	ctccaatatg	actattgggg	ccaggggacc	420
caggtcaccg	tctcctcaac	gcgtcgcgatg	catactagta	ccacgacgcc	agcgccgcga	480
ccaccaacac	cggcgcccac	catcgcgtcg	cagcccctgt	ccctgcgccc	agaggcgtgc	540
cggccagcgg	cggggggcgc	agtgcacacg	agggggctgg	acttcgcctg	tgatttttgg	600
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gatgttttgg	acaagagacg	tggccgggac	cctgagatgg	ggggaaagcc	gagaaggaag	1080
aaccctcagg	aaggcctgta	caatgaactg	cagaaagata	agatggcgga	ggcctacagt	1140
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ctcagtacag	ccaccaagga	cacctacgac	gcccttcaca	tgcaggccct	gccccctcgc	1260
tga						1263

<210> 196

<211> 1257

<212> DNA

<213> Artificial Sequence

<220>

<223> CD38 38A37731 CAR

<400> 196

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ctgagactct	cctgtgtagc	ctctggaacc	atcgtcagta	tcagtaccat	gggctggtac	180
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aactatacag	actccgtgaa	gggccgattc	accatctcca	gagacaacgc	caaaaaacacg	300
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accgtcgcct	caacgcgtcg	catgcatact	agtaccacga	cgccagcgcc	gcgaccacca	480
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<210> 197

<211> 1239

<212> DNA

<213> Artificial Sequence

<220>

<223> CD38 38A37326 CAR

<400> 197

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cggaggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc 1200
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<210> 198

<211> 495

<212> PRT

<213> Artificial Sequence

<220>

<223> BCMAx2 269A37946 GSI5014 CAR

<400> 198

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20     25     30
Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe
35     40     45
Thr Leu Asp Tyr Tyr Ala Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys
50     55     60
Glu Arg Glu Gly Val Ile Cys Ile Ser Arg Ser Asp Gly Ser Thr Tyr
65     70     75     80
Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
85     90     95
Lys Lys Thr Val Tyr Leu Gln Met Ile Ser Leu Lys Pro Glu Asp Thr
100    105    110
Ala Ala Tyr Tyr Cys Ala Ala Gly Ala Asp Cys Ser Gly Tyr Leu Arg
115    120    125
Asp Tyr Glu Phe Arg Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly
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130		135		140	
Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val					
145		150		155	160
Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr					
	165		170		175
Leu Asp Tyr Tyr Ala Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu					
	180		185		190
Arg Glu Gly Val Ile Cys Ile Ser Arg Ser Asp Gly Ser Thr Tyr Tyr					
	195		200		205
Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys					
	210		215		220
Lys Thr Val Tyr Leu Gln Met Ile Ser Leu Lys Pro Glu Asp Thr Ala					
225		230		235	240
Ala Tyr Tyr Cys Ala Ala Gly Ala Asp Cys Ser Gly Tyr Leu Arg Asp					
	245		250		255
Tyr Glu Phe Arg Gly Gln Gly Thr Gln Val Thr Val Ser Ser Thr Ser					
	260		265		270
Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala					
	275		280		285
Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly					
	290		295		300
Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile					
305		310		315	320
Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val					
	325		330		335
Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe					
	340		345		350
Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly					
	355		360		365
Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg					
	370		375		380
Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln					
385		390		395	400
Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp					
	405		410		415
Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro					
	420		425		430
Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp					
	435		440		445
Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg					
	450		455		460
Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr					
465		470		475	480
Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg					
	485		490		495

<210> 199

<211> 622

<212> PRT

<213> Artificial Sequence

<220>

<223> BCMaX3 269A37946 GSI5015 CAR

<400> 199

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			20					25					30		
Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Glu	Ala	Ser	Gly	Phe
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Thr	Leu	Asp	Tyr	Tyr	Ala	Ile	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys
	50					55					60				
Glu	Arg	Glu	Gly	Val	Ile	Cys	Ile	Ser	Arg	Ser	Asp	Gly	Ser	Thr	Tyr
65					70					75					80
Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala
				85					90					95	
Lys	Lys	Thr	Val	Tyr	Leu	Gln	Met	Ile	Ser	Leu	Lys	Pro	Glu	Asp	Thr
			100					105					110		
Ala	Ala	Tyr	Tyr	Cys	Ala	Ala	Gly	Ala	Asp	Cys	Ser	Gly	Tyr	Leu	Arg
		115					120					125			
Asp	Tyr	Glu	Phe	Arg	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Gly
	130					135					140				
Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val
145					150					155					160
Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Glu	Ala	Ser	Gly	Phe	Thr
				165					170					175	
Leu	Asp	Tyr	Tyr	Ala	Ile	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu
			180					185					190		
Arg	Glu	Gly	Val	Ile	Cys	Ile	Ser	Arg	Ser	Asp	Gly	Ser	Thr	Tyr	Tyr
		195					200					205			
Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys
	210					215					220				
Lys	Thr	Val	Tyr	Leu	Gln	Met	Ile	Ser	Leu	Lys	Pro	Glu	Asp	Thr	Ala
225					230					235					240
Ala	Tyr	Tyr	Cys	Ala	Ala	Gly	Ala	Asp	Cys	Ser	Gly	Tyr	Leu	Arg	Asp
				245					250					255	
Tyr	Glu	Phe	Arg	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Gly	Gly
			260					265					270		
Gly	Gly	Ser	Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln
		275					280					285			
Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Glu	Ala	Ser	Gly	Phe	Thr	Leu
	290					295					300				
Asp	Tyr	Tyr	Ala	Ile	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg
305					310					315					320
Glu	Gly	Val	Ile	Cys	Ile	Ser	Arg	Ser	Asp	Gly	Ser	Thr	Tyr	Tyr	Ala
				325					330					335	
Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Lys
			340					345					350		
Thr	Val	Tyr	Leu	Gln	Met	Ile	Ser	Leu	Lys	Pro	Glu	Asp	Thr	Ala	Ala
		355					360						365		
Tyr	Tyr	Cys	Ala	Ala	Gly	Ala	Asp	Cys	Ser	Gly	Tyr	Leu	Arg	Asp	Tyr
	370					375					380				
Glu	Phe	Arg	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Thr	Ser	Thr
385					390					395					400
Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser
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Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	
			420					425					430			
Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	
		435					440					445				
Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	
	450					455					460					
Thr	Leu	Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	
465					470					475					480	
Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	
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Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	
			500					505					510			
Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	
		515					520					525				
Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	
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Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	
545					550					555					560	
Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	
				565					570					575		
Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	
			580					585					590			
Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	
		595					600					605				
Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg			
	610					615					620					

<210> 200

<211> 483

<212> PRT

<213> Artificial Sequence

<220>

<223> CD38x2 38A37717 GSI5016 CAR

<400> 200

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

130		135		140											
Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala	Gly	Gly	Ser	Leu
145					150					155					160
Arg	Leu	Ser	Cys	Ile	Ala	Thr	Gly	Lys	Val	Phe	Ser	Ile	Tyr	Asp	Met
				165						170					175
Gly	Trp	Tyr	Arg	Gln	Ala	Pro	Gly	Lys	Gln	Arg	Glu	Leu	Val	Ala	Glu
				180						185					190
Ile	Thr	Ser	Ser	Gly	Thr	Thr	His	Tyr	Asp	Asp	Phe	Val	Ser	Gly	Arg
		195					200					205			
Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Val	Tyr	Leu	Gln	Met
	210					215					220				
Asn	Thr	Leu	Lys	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Arg	Ala	Asn
225					230					235					240
His	Val	Phe	Gly	Gly	Ser	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val
				245						250					255
Ser	Ser	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala
			260					265					270		
Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg
		275					280					285			
Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys
	290					295					300				
Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu
305					310					315					320
Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys	Leu
				325					330						335
Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln
			340					345					350		
Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly
		355					360					365			
Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr
	370					375					380				
Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg
385				390						395					400
Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met
				405					410					415	
Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu
			420					425					430		
Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys
		435					440					445			
Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu
	450					455				460					
Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu
465					470					475					480
Pro	Pro	Arg													

<210> 201

<211> 604

<212> PRT

<213> Artificial Sequence

<220>

<223> CD38x3 38A37717 GSI5017 CAR

<400> 201

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

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

<210> 202

<211> 1488

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMAX2 269A37946 GSI5014 CAR

<400> 202

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ctgtcctgcg aggcctctgg cttcaccctg gactactatg ccatacgctg gtttaggcag 180
gcacctggaa aggagaggga gggagtgatc tgtatctctc gcagcgacgg cagcacatac 240
tatgccgatt ccgtgaaggg ccggttcacc atcagcagag acaacgcaa gaagacagt 300
tacctgcaga tgatctccct gaagcctgag gataccgcag catactattg cgcagcagga 360
gcagactgta gcggatacct gagggattat gagtttaggg gacagggaac ccaggtgaca 420
gtgagctccg gaggaggagg ctcccagggtg cagctggtgg agtctggagg cggcctggtg 480
cagcctggag gcagcctgag actgagctgt gaagcttccg gatttaccct ggactactat 540
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gataatgcca agaagacagt ctatctgcag atgattagcc tgaagcccga ggacacagcc 720
gcctattact gcgcagcagg agcagattgt agtgggtatc tgagggacta tgagtttcgg 780
gggcagggga cacaggtgac agtgagttct actagtagca cgacgccagc gccgcgacca 840
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ccagcggcgg ggggcgcagt gcacacgagg gggctggact tcgcctgtga tatctacatc 960
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tgcaaacggg gcagaaagaa actcctgtat atattcaaac aaccatttat gagaccagta 1080
caaactactc aagaggaaga tggctgtagc tgccgatttc cagaagaaga agaaggagga 1140

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tgtgaactga	gagtgaagtt	cagcaggagc	gcagacgccc	ccgcgtacca	gcagggccag	1200
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agacgtggcc	gggaccctga	gatgggggga	aagccgagaa	ggaagaacc	tcaggaaggc	1320
ctgtacaatg	aactgcagaa	agataagatg	gcggaggcct	acagtgagat	tgggatgaaa	1380
ggcgagcgcc	ggagggggcaa	ggggcacgat	ggcctttacc	agggtctcag	tacagccacc	1440
aaggacacct	acgacgccct	tcacatgcag	gccctgcccc	ctcgctaa		1488

<210> 203

<211> 1869

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMAX3 269A37946 GSI5015 CAR

<400> 203

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ctgtcttgcg	aggccagcgg	cttcaccctg	gactactatg	ccatcggctg	gttttaggcag	180
gcacctggaa	aggagagggga	gggagtgatc	tgtatctcca	gatctgacgg	ctccacatac	240
tatgccgatt	ctgtgaaggg	ccggttcacc	atctctagag	acaacgcaa	gaagacagtg	300
tacctgcaga	tgatcagcct	gaagcccag	gataccgcag	catactattg	cgcagcagga	360
gcagactgtt	ccggatacct	gagggattat	gagtttaggg	gacagggaac	ccaggtgaca	420
gtgagctccg	gaggaggagg	ctcccaggtg	cagctgggtg	agtctggagg	cggcctgggtg	480
cagcctggag	gctccctgag	gctgtcttgc	gaggcaagcg	gcttcaccct	ggattactat	540
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cgctccgacg	gcagtaccta	ctatgccgat	tccgtcaaag	gccggttcac	catctccaga	660
gacaatgcc	agaagacagt	ctatctgcag	atgatctctc	tgaagcctga	ggatacagcc	720
gcctattact	gtgccgcagg	agcagactgt	agtggctatc	tgagagatta	tgagtttcgc	780
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ggatttactc	tggattatta	cgctattgga	tggttcagac	aggcccctgg	caaagaaaga	960
gaaggggtga	tctgtatctc	tcggagcgac	ggctctacat	actatgccga	tagcgtcaag	1020
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ctgaagcccg	aggacactgc	cgcctattac	tgtgcagcag	gagcagattg	tagcgggtat	1140
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tactggtta	tcacccttta	ctgcaaacgg	ggcagaaaga	aactcctgta	tatattcaaa	1440
caaccattta	tgagaccagt	acaaactact	caagaggaag	atggctgtag	ctgccgattt	1500
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cccgctacc	agcagggccca	gaaccagctc	tataacgagc	tcaatctagg	acgaagagag	1620
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cagggtctca	gtacagccac	caaggacacc	tacgacgccc	ttcacatgca	ggccctgccc	1860
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<210> 204

<211> 1452

<212> DNA

<213> Artificial Sequence

<220>

<223> CD38x2 38A37717 GSI5016 CAR

<400> 204

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ctgtcctgca tcgccaccgg caaggtgttc agcatctacg acatgggatg gtataggcag 180
gcaccaggaa agcagagaga gctgggtggcc gagatcacia gctccggcac cacacactac 240
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<210> 205

<211> 1815

<212> DNA

<213> Artificial Sequence

<220>

<223> CD38x3 38A37717 GSI5017 CAR

<400> 205

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gacgatttcg tgtccggccg gtttaccatc tctagagaca acgccaagaa tacagtgtat 300
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gtgttcggag gatcctactg gggacaggga acccagggtga cagtgtctag cggaggagga 420
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ggcggcagtg aagtgcagct ggtggagtcc ggagggggcc tgggtgcaggc cggcggctct 840
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gaggcctaca gtgagattgg gatgaaaggc gagcgccgga ggggcaaggg gcacgatggc 1740
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<210> 206

<211> 502

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19XCD20 single-domain antibody-based bispecific CAR

<400> 206

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

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Ser Arg Asp Asn Ala Lys Leu Thr Val Asp Leu Gln Met Asp Ser Leu
 225 230 235 240
 Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala Ala Asp Arg Leu Ser
 245 250 255
 Leu Asp Leu Ser Gly Arg Tyr His Tyr Asn Pro Ala Val Tyr Asp Tyr
 260 265 270
 Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ile Glu Val Met Tyr
 275 280 285
 Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His
 290 295 300
 Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser
 305 310 315 320
 Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr
 325 330 335
 Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys
 340 345 350
 Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg
 355 360 365
 Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp
 370 375 380
 Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
 385 390 395 400
 Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
 405 410 415
 Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
 420 425 430
 Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu
 435 440 445
 Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
 450 455 460
 Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
 465 470 475 480
 Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
 485 490 495
 Gln Ala Leu Pro Pro Arg
 500

<210> 207

<211> 489

<212> PRT

<213> Artificial Sequence

<220>

<223> CD38xBCMA 38A37717 269A37346 GSI5001 CAR

<400> 207

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 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
 20 25 30
 Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Ile Ala Thr Gly Lys
 35 40 45
 Val Phe Ser Ile Tyr Asp Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys

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

<210> 208
 <211> 494
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD38xBCMA 38A37717 269A37346 GSI5002 CAR

<400> 208

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

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

<210> 209

<211> 500

<212> PRT

<213> Artificial Sequence

<220>

<223> CD38xBCMA 38A37717 269A37346 GSI5003 CAR

<400> 209

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

His	Ala	Ala	Arg	Pro	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu
Val	Gln	Ala	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ile	Ala	Thr	Gly	Lys
Val	Phe	Ser	Ile	Tyr	Asp	Met	Gly	Trp	Tyr	Arg	Gln	Ala	Pro	Gly	Lys
Gln	Arg	Glu	Leu	Val	Ala	Glu	Ile	Thr	Ser	Ser	Gly	Thr	Thr	His	Tyr
65					70					75					80
Asp	Asp	Phe	Val	Ser	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys
				85					90					95	
Asn	Thr	Val	Tyr	Leu	Gln	Met	Asn	Thr	Leu	Lys	Ala	Glu	Asp	Thr	Ala
			100					105					110		
Val	Tyr	Tyr	Cys	Arg	Ala	Asn	His	Val	Phe	Gly	Gly	Ser	Tyr	Trp	Gly
		115					120					125			
Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly
	130					135					140				
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Gly	Gly	Ser	Gly	Ser	Gly	Gly	Gly	Gly
145				150						155					160
Ser	Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly
				165					170					175	
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Glu	Ala	Ser	Gly	Phe	Thr	Leu	Asp	Tyr
			180					185					190		
Tyr	Ala	Ile	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Glu	Gly
		195					200					205			
Val	Ile	Cys	Ile	Ser	Arg	Ser	Asp	Gly	Ser	Thr	Tyr	Tyr	Ala	Asp	Ser
	210					215					220				
Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Lys	Thr	Val
225					230					235					240
Tyr	Leu	Gln	Met	Ile	Ser	Leu	Lys	Pro	Glu	Asp	Thr	Ala	Ala	Tyr	Tyr
				245					250					255	
Cys	Ala	Ala	Gly	Ala	Asp	Cys	Ser	Gly	Tyr	Leu	Arg	Asp	Tyr	Glu	Phe
			260					265					270		
Arg	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Thr	Ser	Thr	Thr	Thr
			275				280					285			
Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro
					295						300				
Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val
305					310					315					320
His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro
				325					330					335	
Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu
			340					345					350		
Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro
		355					360					365			
Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys
		370				375					380				
Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe
385</															

Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala
	450					455					460				
Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys
465					470					475					480
Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr
				485					490					495	
Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg				
			500					505							

<210> 211

<211> 518

<212> PRT

<213> Artificial Sequence

<220>

<223> CD38xBCMA 38A37717 269A37346 GSI5005 CAR

<400> 211

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

		275				280				285					
Val	Thr	Val	Ser	Ser	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro
	290					295					300				
Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu
305					310					315					320
Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp
				325					330					335	
Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly
			340					345					350		
Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly	Arg
	355						360					365			
Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln
	370					375					380				
Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu
385					390					395					400
Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala
				405					410					415	
Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu
			420					425					430		
Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp
	435					440						445			
Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu
	450					455					460				
Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile
465					470					475					480
Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr
				485					490					495	
Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met
			500					505					510		
Gln	Ala	Leu	Pro	Pro	Arg										
		515													

<210> 212

<211> 489

<212> PRT

<213> Artificial Sequence

<220>

<223> BCMAxCD38 269A37346 38A37717 GSI5006 CAR

<400> 212

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

Lys	Lys	Thr	Val	Tyr	Leu	Gln	Met	Ile	Ser	Leu	Lys	Pro	Glu	Asp	Thr		
			100					105					110				
Ala	Ala	Tyr	Tyr	Cys	Ala	Ala	Gly	Ala	Asp	Cys	Ser	Gly	Tyr	Leu	Arg		
		115					120					125					
Asp	Tyr	Glu	Phe	Arg	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Gly		
	130					135					140						
Gly	Gly	Gly	Ser	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val		
145					150					155					160		
Gln	Ala	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ile	Ala	Thr	Gly	Lys	Val		
				165					170					175			
Phe	Ser	Ile	Tyr	Asp	Met	Gly	Trp	Tyr	Arg	Gln	Ala	Pro	Gly	Lys	Gln		
			180					185					190				
Arg	Glu	Leu	Val	Ala	Glu	Ile	Thr	Ser	Ser	Gly	Thr	Thr	His	Tyr	Asp		
		195					200					205					
Asp	Phe	Val	Ser	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn		
	210					215					220						
Thr	Val	Tyr	Leu	Gln	Met	Asn	Thr	Leu	Lys	Ala	Glu	Asp	Thr	Ala	Val		
225					230					235					240		
Tyr	Tyr	Cys	Arg	Ala	Asn	His	Val	Phe	Gly	Gly	Ser	Tyr	Trp	Gly	Gln		
				245					250					255			
Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro		
		260						265					270				
Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu		
		275					280					285					
Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg		
	290					295				300							
Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly		
305					310					315					320		
Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys		
				325					330					335			
Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg		
			340					345					350				
Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro		
		355					360					365					
Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser		
	370				375						380						
Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu		
385					390					395					400		
Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg		
				405					410					415			
Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln		
			420					425					430				
Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr		
		435					440					445					
Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp		
	450					455					460						
Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala		
465					470					475					480		
Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg									
				485													

<210> 213

<211> 494

<212> PRT

<213> Artificial Sequence

<220>

<223> BCMAxCD38 269A37346 38A37717 GSI5007 CAR

<400> 213

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

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

<210> 214

<211> 500

<212> PRT

<213> Artificial Sequence

<220>

<223> BCMAxCD38 269A37346 38A37717 GSI5008 CAR

<400> 214

Met Ala Leu Pro Val	Thr Ala Leu Leu Leu	Pro Leu Ala Leu Leu
1	5	10
His Ala Ala Arg	Pro Gln Val Gln	Leu Val Glu Ser
	20	25
Val Gln Pro Gly	Gly Ser Leu Arg	Leu Ser Cys Glu
	35	40
Thr Leu Asp Tyr	Tyr Ala Ile Gly	Trp Phe Arg Gln
	50	55
Glu Arg Glu Gly	Val Ile Cys Ile	Ser Arg Ser Asp
65	70	75
Tyr Ala Asp Ser	Val Lys Gly Arg	Phe Thr Ile Ser
	85	90
Lys Lys Thr Val	Tyr Leu Gln Met	Ile Ser Leu Lys
	100	105
Ala Ala Tyr Tyr	Cys Ala Ala Gly	Ala Asp Cys Ser
	115	120
Asp Tyr Glu Phe	Arg Gly Gln Gly	Thr Gln Val Thr
	130	135
Gly Gly Ser Gly	Gly Gly Ser Gly	Gly Gly Gly Ser
145	150	155
Val Gln Leu Val	Glu Ser Gly Gly	Gly Leu Val Gln
	165	170
Leu Arg Leu Ser	Cys Ile Ala Thr	Gly Lys Val Phe
	180	185
Met Gly Trp Tyr	Arg Gln Ala Pro	Gly Lys Gln Arg
	195	200
Glu Ile Thr Ser	Ser Gly Thr Thr	His Tyr Asp Asp
	210	215
		220

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu Gln
 225 230 235 240
 Met Asn Thr Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys Arg Ala
 245 250 255
 Asn His Val Phe Gly Gly Ser Tyr Trp Gly Gln Gly Thr Gln Val Thr
 260 265 270
 Val Ser Ser Thr Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
 275 280 285
 Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
 290 295 300
 Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
 305 310 315 320
 Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
 325 330 335
 Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys
 340 345 350
 Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr
 355 360 365
 Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Gly
 370 375 380
 Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
 385 390 395 400
 Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
 405 410 415
 Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
 420 425 430
 Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
 435 440 445
 Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
 450 455 460
 Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
 465 470 475 480
 Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
 485 490 495
 Leu Pro Pro Arg
 500

<210> 215

<211> 510

<212> PRT

<213> Artificial Sequence

<220>

<223> BCMAXCD38 269A37346 38A37717 GSI5009 CAR

<400> 215

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 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu
 20 25 30
 Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe
 35 40 45
 Thr Leu Asp Tyr Tyr Ala Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys

50		55		60
Glu Arg Glu Gly Val Ile Cys Ile Ser Arg Ser Asp Gly Ser Thr Tyr				
65		70		75
Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala				
	85		90	
Lys Lys Thr Val Tyr Leu Gln Met Ile Ser Leu Lys Pro Glu Asp Thr				
	100		105	
Ala Ala Tyr Tyr Cys Ala Ala Gly Ala Asp Cys Ser Gly Tyr Leu Arg				
	115		120	
Asp Tyr Glu Phe Arg Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly				
	130		135	
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser				
145		150		155
Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly				
	165		170	
Gly Leu Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Ile Ala Thr				
	180		185	
Gly Lys Val Phe Ser Ile Tyr Asp Met Gly Trp Tyr Arg Gln Ala Pro				
	195		200	
Gly Lys Gln Arg Glu Leu Val Ala Glu Ile Thr Ser Ser Gly Thr Thr				
	210		215	
His Tyr Asp Asp Phe Val Ser Gly Arg Phe Thr Ile Ser Arg Asp Asn				
225		230		235
Ala Lys Asn Thr Val Tyr Leu Gln Met Asn Thr Leu Lys Ala Glu Asp				
	245		250	
Thr Ala Val Tyr Tyr Cys Arg Ala Asn His Val Phe Gly Gly Ser Tyr				
	260		265	
Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Thr Ser Thr Ser Thr				
	275		280	
Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser				
	290		295	
Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly				
305		310		315
Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp				
	325		330	
Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile				
	340		345	
Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys				
	355		360	
Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys				
	370		375	
Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val				
385		390		395
Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn				
	405		410	
Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val				
	420		425	
Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg				
	435		440	
Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys				
	450		455	
Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg				
465		470		475
Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys				
	480			

				485					490					495
Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg	
			500					505					510	

<210> 216
 <211> 518
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> BCMAxCD38 269A37346 38A37717 GSI5010 CAR

<400> 216

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

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
 325 330 335
 Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
 340 345 350
 Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg
 355 360 365
 Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln
 370 375 380
 Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu
 385 390 395 400
 Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
 405 410 415
 Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
 420 425 430
 Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
 435 440 445
 Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu
 450 455 460
 Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
 465 470 475 480
 Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
 485 490 495
 Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
 500 505 510
 Gln Ala Leu Pro Pro Arg
 515

<210> 217

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> CD19XCD20 single-domain antibody-based bispecific CAR

<400> 217

gccgccacca tggccttacc agtgaccgcc ttgctcctgc cgctggcctt gctgctccac 60
 gccgccaggc cgcaggtaaa gctggaggag tctgggggag aattggtgca gcctggggggg 120
 cctctgagac tctcctgtgc agcctcggga aacatcttca gtatcaatcg catgggctgg 180
 taccgccagg ctccagggaa gcagcgcgcg ttcgtcgcgt ctattactgt tcgtgggtata 240
 acaaactatg cagactccgt gaagggccga ttcaccattt ctgtagacaa gtccaaaaaac 300
 acgatttatc tgcagatgaa cgcactcaaa cctgaggaca cggccgtcta ttattgtaat 360
 gcagtgtctt caaacaggga ccccactac tggggccagg ggaccaggt caccgtctcc 420
 tcaggcggcg gcagcggcgg cggcagcggc ggcggcagcg gcggcggcag cccggtgcag 480
 ctgggtggagt ctgggggagg cttggtgcag gctggggatt ctctgagact ctctgtgtct 540
 gcctctggac gcaccttcgg tattggtacc atgggctggt tccgccaacc tccaggaag 600
 gagcgtgaat ttgtagcagc tattaggtgg agtactgggt gcactcgcta tgcagactcc 660
 gtgaagggcc gattcacat ctcccgagac aacgccaagc tcacggtaga tctgcaaagt 720
 gacagcctga aacctgaaga cacggccgtt tattactgtg cagcagatag actgtccctt 780
 gatttaagtg gtcgttacca ctacaacccc gccgtgtatg actattgggg ccaggggacc 840
 caggtcaccg tctcctcaat tgaagttatg tatcctcctc cttacctaga caatgagaag 900
 agcaatggaa ccattatcca tgtgaaaggg aaacacctt gtccaagtcc cctatttccc 960
 ggaccttcta agcccttttg ggtgctggtg gtggttggtg gagtccctggc ttgctatagc 1020

ttgctagtaa	cagtggcctt	tattatatttc	tgggtgagga	gtaagaggag	caggctcctg	1080
cacagtgact	acatgaacat	gactccccgc	cgccccgggc	ccacccgcaa	gcattaccag	1140
ccctatgccc	caccacgcga	cttcgcagcc	tatcgctcca	gagtgaagtt	cagcaggagc	1200
gcagacgccc	ccgcgtacca	gcagggccag	aaccagctct	ataacgagct	caatctagga	1260
cgaagagagg	agtacgatgt	tttgacaag	agacgtggcc	gggaccctga	gatgggggga	1320
aagccgagaa	ggaagaaccc	tcaggaaggc	ctgtacaatg	aactgcagaa	agataagatg	1380
gcggaggcct	acagtgaat	tgggatgaaa	ggcgagcgcc	ggaggggcaa	ggggcacgat	1440
ggcctttacc	agggtctcag	tacagccacc	aaggacacct	acgacgccct	tcacatgcag	1500
gccctgcccc	ctcgtgata	a				1521

<210> 218

<211> 1470

<212> DNA

<213> Artificial Sequence

<220>

<223> CD38xBCMA 38A37717 269A37346 GSI5001 CAR

<400> 218

atggctctgc	ccgtcactgc	tctgctgctg	cccctggctc	tgctgctgca	cgccgcaaga	60
cccgaagtcc	agctggtgga	atctggcgga	ggcctggtgc	aggcaggagg	cagcctgagg	120
ctgtcctgca	tcgccaccgg	caaggtgttc	tccatctacg	acatgggctg	gtatcggcag	180
gccccaggca	agcagagaga	gctggtggcc	gagatcacia	gctccggcac	cacacactac	240
gacgatttcg	tgtctggccg	gtttaccatc	agcagagaca	acgccaagaa	tacagtgtat	300
ctgcagatga	acacctgaa	ggccgaggat	acagccgtgt	actattgtcg	ggccaatcac	360
gtgtttggag	gaagctactg	gggacaggga	accaggtga	cagtgtctag	cggaggagga	420
ggcagccagg	tgcagctggt	ggagtccgga	ggaggcctgg	tgcagccagg	aggctctctg	480
aggctgagct	gcgaggcatc	cggattcacc	ctggactact	atgccatcgg	ctggtttagg	540
caggcacctg	gaaaggagag	ggagggagtg	atctgtatct	ccagatctga	cggctccaca	600
tactatgccg	attctgtgaa	gggcaggttc	accatctctc	gcgataacgc	caagaagaca	660
gtctacctgc	agatgatcag	cctgaagccc	gaggacaccg	cagcactacta	ttgcgcagca	720
ggagcagatt	gtagtggcta	tctgagggac	tacgagttcc	gagggcaggg	gacacaggtg	780
accgtgagca	gcactagtag	cacgacgcca	gcgccgcgac	caccaacacc	ggcgcccacc	840
atcgctgcgc	agccccctgtc	cctgcgcccc	gaggcgtgcc	ggccagcggc	ggggggcgca	900
gtgcacacga	gggggctgga	cttcgcctgt	gatatctaca	tctgggcgcc	cttggccggg	960
acttgtgggg	tccttctcct	gtcactgggt	atcacccttt	actgcaaacg	gggcagaaaag	1020
aaactcctgt	atatattcaa	acaaccattt	atgagaccag	tacaaactac	tcaaggaggaa	1080
gatggctgta	gctgccgatt	tccagaagaa	gaagaaggag	gatgtgaact	gagagtgaag	1140
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<210> 219

<211> 1485

<212> DNA

<213> Artificial Sequence

<220>

<223> CD38xBCMA 38A37717 269A37346 GSI5002 CAR

<400> 219

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<210> 220

<211> 1503

<212> DNA

<213> Artificial Sequence

<220>

<223> CD38xBCMA 38A37717 269A37346 GSI5003 CAR

<400> 220

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<210> 221

<211> 1527

<212> DNA

<213> Artificial Sequence

<220>

<223> CD38xBCMA 38A37717 269A37346 GSI5004 CAR

<400> 221

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<210> 222

<211> 1557

<212> DNA

<213> Artificial Sequence

<220>

<223> CD38xBCMA 38A37717 269A37346 GSI5005 CAR

<400> 222

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<210> 223

<211> 1470

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMAXCD38 269A37346 38A37717 GSI5006 CAR

<400> 223

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<210> 224

<211> 1485

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMAXCD38 269A37346 38A37717 GSI5007 CAR

<400> 224

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<210> 225

<211> 1503

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMAXCD38 269A37346 38A37717 GSI5008 CAR

<400> 225

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<210> 226

<211> 1533

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMAXCD38 269A37346 38A37717 GSI5009 CAR

<400> 226

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aagaaactcc	tgtatatatt	caaacaacca	tttatgagac	cagtacaaac	tactcaagag	1140
gaagatggct	gtagctgccg	atttccagaa	gaagaagaag	gaggatgtga	actgagagt	1200
aagttcagca	ggagcgcgaga	cgcggcgcg	taccagcagg	gccagaacca	gctctataac	1260

gagctcaatc	taggacgaag	agaggagtac	gatgttttgg	acaagagacg	tggccggggac	1320
cctgagatgg	ggggaaagcc	gagaaggaag	aaccctcagg	aaggcctgta	caatgaactg	1380
cagaaagata	agatggcgga	ggcctacagt	gagattggga	tgaaaggcga	gcgccggagg	1440
ggcaaggggc	acgatggcct	ttaccagggt	ctcagtacag	ccaccaagga	cacctacgac	1500
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<210> 227

<211> 1557

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMAxCD38 269A37346 38A37717 GSI5010 CAR

<400> 227

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ctgagctgcg	aggcatccgg	attcaccctg	gactactatg	ccatcggctg	gttttaggcag	180
gcacctggaa	aggagaggga	gggagtgtat	tgtatctccc	gctctgacgg	cagcacatac	240
tatgccgatt	ccgtgaaggg	ccggttcacc	atctccagag	acaacgcaa	gaagacagtg	300
tacctgcaga	tgatctctct	gaagccagag	gataccgcag	catactattg	cgcagcagga	360
gcagactgta	gcggatacct	gagggattat	gagtttaggg	gacagggaac	ccaggtgaca	420
gtgagctccg	gaggaggagg	atccggcgga	ggaggctctg	gaggcggcgg	cgccggcagc	480
ggctcaggag	gcggaggaa	cgccggcggc	ggctccggcg	gcggcggctc	tgagggtgcag	540
ctggtggaga	gcggaggagg	cctggtgcag	gcaggaggct	ctctgcggct	gagctgcatc	600
gccaccggca	aggtgttctc	catctacgat	atgggatggt	ataggcaggc	accaggaaag	660
cagagagagc	tggtggccga	gatcacatct	agcggcacca	cacactacga	cgatttctgt	720
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gaaggaggat	gtgaactgag	agtgaagttc	agcaggagcg	cagacgcccc	cgcgtaccag	1260
cagggccaga	accagctcta	taacgagctc	aatctaggac	gaagagagga	gtacgatgtt	1320
ttggacaaga	gacgtggccg	ggaccctgag	atggggggaa	agccgagaag	gaagaacctt	1380
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gggatgaaag	gcgagcgccg	gaggggcaag	gggcacgatg	gcctttacca	gggtctcagt	1500
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<210> 228

<211> 663

<212> DNA

<213> Artificial Sequence

<220>

<223> CD28 TM and CD28-CD3 zeta intracellular signaling domain

<400> 228

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catgtgaaag	ggaaacacct	ttgtccaagt	cccctatttc	ccggaccttc	taagcccttt	120
tgggtgctgg	tggtggttgg	tggagtcctg	gcttgctata	gcttgctagt	aacagtggcc	180

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tttattattt tctgggtgag gagtaagagg agcaggctcc tgcacagtga ctacatgaac 240
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gacttcgcag cctatcgctc cagagtgaag ttcagcagga gcgcagacgc ccccgctac 360
cagcagggcc agaaccagct ctataacgag ctcaatctag gacgaagaga ggagtacgat 420
gttttggaca agagacgtgg ccgggaccct gagatggggg gaaagccgag aaggaagaac 480
cctcaggaag gcctgtacaa tgaactgcag aaagataaga tggcggaggc ctacagttag 540
attgggatga aaggcgagcg ccggaggggc aaggggcacg atggccttta ccagggtctc 600
agtacagcca ccaaggacac ctacgacgcc cttcacatgc aggccctgcc ccctcgctga 660
taa

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<210> 229
<211> 23
<212> DNA
<213> Artificial Sequence

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<220>
<223> upstream primer CALL001

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<400> 229
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<210> 230
<211> 23
<212> DNA
<213> Artificial Sequence

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<220>
<223> downstream primer CALL002

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<400> 230
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<210> 231
<211> 29
<212> DNA
<213> Artificial Sequence

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<220>
<223> upstream primer BACK-1

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<400> 231
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<210> 232
<211> 29
<212> DNA
<213> Artificial Sequence

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<220>
<223> downstream primer BACK-2

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<400> 232
gatgtgcagc tgcaggagtc tgggggagg 29

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<213> Artificial Sequence	
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<223> downstream primer PMCF	
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<210> 234	
<211> 6	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> EcoRI restriction site	
<400> 234	
gaattc	6
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<211> 6	
<212> DNA	
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<220>	
<223> SpeI restriction site	
<400> 235	
actagt	6
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<212> DNA	
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<220>	
<223> HpaI restriction site	
<400> 236	
gttaac	6
<210> 237	
<211> 6	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> MluI restriction site	
<400> 237	
acgcgt	6

<210> 238
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> NsiI restriction site

<400> 238
atgcat

6

<210> 239
<211> 2307
<212> DNA
<213> Artificial Sequence

<220>
<223> tandem BCMA, CD38 269A37346 38A37717 GSI5013 CAR

<400> 239
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ccggttaacg aggtgcagct ggtggaaagc ggggggggac tgggtgcaggc aggcgggtca 120
ctgagactgt catgtatcgc aactgggaag gtgttttagca tctacgacat gggctggtat 180
aggcaggcac caggaaagca gagggagctg gtggccgaga tcaccagctc cggcaccaca 240
cactacgacg atttcgtgtc tggccggttt accatcagca gagacaacgc caagaatata 300
gtgtatctgc agatgaacac cctgaaggcc gaggatacag ccgtgtacta ttgccgggct 360
aatcacgtct tcggcgggctc ctactggggg cagggaactc aggtcactgt gtcatccacg 420
cgtcgcgtgc atactagtag cacgacgcca gcgccgcgac caccaacacc ggcgcccacc 480
atcgcgtcgc agcccctgtc cctgcgcca gaggcgtgcc ggccagcggc ggggggcgca 540
gtgcacacga gggggctgga cttcgcctgt gatattctaca tctgggcgcc cttggccggg 600
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aaactcctgt atatatcaa acaaccattt atgagaccag taaaaactac tcaagaggaa 720
gatggctgta gctgccgatt tccagaagaa gaagaaggag gatgtgaact gagagtgaag 780
ttcagcagga gcgcagacgc ccccgcgtag cagcagggcc agaaccagct ctataacgag 840
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gagatggggg gaaagccgag aaggaagaac cctcaggaag gcctgtacaa tgaactgcag 960
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tgtgggggtc ttctcctgtc actggttatc accctttact gcaaacgggg cagaaagaaa 1860
ctcctgtata tattcaaaca accatttatg agaccagtac aaactactca agaggaagat 1920
ggctgtagct gccgatttcc agaagaagaa gaaggaggat gtgaactgag agtgaagttc 1980

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agcaggagcg cagacgcccc cgcgtaccag cagggccaga accagctcta taacgagctc 2040
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atgggggggaa agccgagaag gaagaaccct caggaaggcc tgtacaatga actgcagaaa 2160
gataagatgg cggaggccta cagtgaattt gggatgaaag gcgagcgccg gaggggcaag 2220
gggcacgatg gcctttacca ggggtctcagt acagccacca aggacaccta cgacgccctt 2280
cacatgcagg ccctgcccc tcgctaa                                     2307

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<210> 240
 <211> 30
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD19 VHH FR1

<400> 240
 Gln Val Lys Leu Glu Glu Ser Gly Gly Glu Leu Val Gln Pro Gly Gly
 1 5 10 15
 Pro Leu Arg Leu Ser Cys Ala Ala Ser Gly Asn Ile Phe Ser
 20 25 30

<210> 241
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD19 VHH FR2

<400> 241
 Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Ala Phe Val Ala
 1 5 10

<210> 242
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD19 VHH FR3

<400> 242
 Arg Phe Thr Ile Ser Val Asp Lys Ser Lys Asn Thr Ile Tyr Leu Gln
 1 5 10 15
 Met Asn Ala Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn Ala
 20 25 30

<210> 243
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>

<223> CD19 VHH FR4

<400> 243

Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
1 5 10

<210> 244

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> CD20 VHH FR1

<400> 244

Pro Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Asp
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Gly
20 25 30

<210> 245

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> CD20 VHH FR2

<400> 245

Trp Phe Arg Gln Pro Pro Gly Lys Glu Arg Glu Phe Val Ala
1 5 10

<210> 246

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> CD20 VHH FR3

<400> 246

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

<210> 247

<211> 11

<212> PRT
<213> Artificial Sequence

<220>
<223> CD20 VHH FR4

<400> 247
Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
1 5 10

<210> 248
<211> 357
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 CAR

<400> 248
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 Gln Val Lys Leu Glu Glu Ser Gly Gly Glu Leu
20 25 30
Val Gln Pro Gly Gly Pro Leu Arg Leu Ser Cys Ala Ala Ser Gly Asn
35 40 45
Ile Phe Ser Ile Asn Arg Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys
50 55 60
Gln Arg Ala Phe Val Ala Ser Ile Thr Val Arg Gly Ile Thr Asn Tyr
65 70 75 80
Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Val Asp Lys Ser Lys
85 90 95
Asn Thr Ile Tyr Leu Gln Met Asn Ala Leu Lys Pro Glu Asp Thr Ala
100 105 110
Val Tyr Tyr Cys Asn Ala Val Ser Ser Asn Arg Asp Pro Asp Tyr Trp
115 120 125
Gly Gln Gly Thr Gln Val Thr Val Ser Ser Ile Glu Val Met Tyr Pro
130 135 140
Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val
145 150 155 160
Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys
165 170 175
Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
180 185 190
Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
195 200 205
Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
210 215 220
Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
225 230 235 240
Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
245 250 255
Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
260 265 270

Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro
		275					280					285			
Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr
	290					295					300				
Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly
305					310					315					320
Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln
				325					330					335	
Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln
			340					345					350		
Ala	Leu	Pro	Pro	Arg											
		355													

<210> 249

<211> 369

<212> PRT

<213> Artificial Sequence

<220>

<223> CD20 CAR

<400> 249

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

				245					250				255				
Ser	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln		
			260					265					270				
Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu		
		275					280					285					
Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly		
	290					295					300						
Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln		
305					310					315					320		
Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu		
			325						330					335			
Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr		
		340					345						350				
Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro		
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Arg

<210> 250
 <211> 1077
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CD19 CAR

<400> 250
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 ctctcctgtg cagcctcggg aaacatcttc agtatcaatc gcatgggctg gtaccgccag 180
 gctccaggga agcagcgcgc gttcgtcgca tctattactg ttcgtggtat aacaaactat 240
 gcagactccg tgaagggccg attcaccatt tctgtagaca agtccaaaaa cacgatttat 300
 ctgcagatga acgcactcaa acctgaggac acggccgtct attattgtaa tgcagtgtct 360
 tcaaacaggg accccgacta ctggggccag gggaccagg tcaccgtctc ctcaattgaa 420
 gttatgtatc ctctctctta cctagacaat gagaagagca atggaacat tatccatgtg 480
 aaagggaac acctttgtcc aagtcctcta tttcccgac cttctaagcc cttttgggtg 540
 ctggtggtgg ttggtggagt cctggcttgc tatagcttgc tagtaacagt ggcctttatt 600
 attttctggg tgaggagtaa gaggagcagg ctctgcaca gtgactacat gaacatgact 660
 ccccgccgcc ccggggccac ccgcaagcat taccagccct atgccccacc acgcgacttc 720
 gcagcctatc gctccagagt gaagttcagc aggagcgcag acgccccgcg gtaccagcag 780
 ggccagaacc agctctataa cgagctcaat ctaggacgaa gagaggagta cgatgttttg 840
 gacaagagac gtggccggga ccctgagatg gggggaaagc cgagaaggaa gaaccctcag 900
 gaaggcctgt acaatgaact gcagaaagat aagatggcgg aggcctacag tgagattggg 960
 atgaaaggcg agcgccggag gggcaagggg cacgatggcc tttaccaggg tctcagtaca 1020
 gccaccaagg acacctacga cgcccttcac atgcaggccc tgccccctcg ctgataa 1077

<210> 251
 <211> 1113
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CD20 CAR

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<400> 251
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ctctcctgtg ctgcctctgg acgcaccttc ggtattggta ccatgggctg gttccgcaa 180
cctccaggga aggagcgtga atttgtagca gctattaggt ggagtactgg tggcactcgc 240
tatgcagact ccgtgaaggg ccgattcacc atctcccag acaacgcaa gctcacgta 300
gatctgcaaa tggacagcct gaaacctgaa gacacggccg tttattactg tgcagcagat 360
agactgtccc ttgatttaag tggtcgttac cactacaacc ccgccgtgta tgactattgg 420
ggccagggga cccaggtcac cgtctcctca attgaagtta tgtatcctcc tccttaccta 480
gacaatgaga agagcaatgg aaccattatc catgtgaaag ggaaacacct ttgtccaagt 540
cccctatttc ccggaccttc taagcccttt tgggtgctgg tgggtggttg tggagtcctg 600
gcttgctata gcttgctagt aacagtggcc tttattatct tctgggtgag gagtaagagg 660
agcaggctcc tgcacagtga ctacatgaac atgactcccc gccgccccgg gccacccgc 720
aagcattacc agccctatgc cccaccacgc gacttcgcag cctatcgctc cagagtgaag 780
ttcagcagga gcgcagacgc ccccgctac cagcagggcc agaaccagct ctataacgag 840
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aaagataaga tggcggaggc ctacagttag attgggatga aaggcgagcg ccggaggggc 1020
aaggggcacg atggccttta ccagggtctc agtacagcca ccaaggacac ctacgacgcc 1080
cttcacatgc aggccctgcc ccctcgctga taa 1113

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<210> 252
<211> 23
<212> DNA
<213> Artificial Sequence

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<220>
<223> 137P2F primer

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<400> 252
gtccttctcc tgtcactggt tat 23

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<210> 253
<211> 23
<212> DNA
<213> Artificial Sequence

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<220>
<223> 137P2R primer

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<400> 253
tcttcttctt ctggaaatcg gca 23

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<210> 254
<211> 48
<212> DNA
<213> Artificial Sequence

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<220>
<223> Linker sequence 3

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<400> 254
ggcggcggca gcggcggcgg cagcggcggc ggcagcggcg gcggcagc 48

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<210> 255
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> T2A

<400> 255
Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu
1 5 10 15
Glu Asn Pro Gly Pro
20

<210> 256
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> T2A

<400> 256
ggcagtggag agggcagagg aagtctgcta acatgcggtg acgtcgagga gaatcctggc 60
cca 63

<210> 257
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> GSI5011 CAR 269A37346

<400> 257
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 Val Asn Arg Thr Arg Arg Met His Gln Val Gln
20 25 30
Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
35 40 45
Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Asp Tyr Tyr Ala Ile Gly
50 55 60
Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Val Ile Cys Ile
65 70 75 80
Ser Arg Ser Asp Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg
85 90 95
Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr Leu Gln Met
100 105 110
Ile Ser Leu Lys Pro Glu Asp Thr Ala Ala Tyr Tyr Cys Ala Ala Gly
115 120 125
Ala Asp Cys Ser Gly Tyr Leu Arg Asp Tyr Glu Phe Arg Gly Gln Gly

130		135		140											
Thr	Gln	Val	Thr	Val	Ser	Ser	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg
145					150					155					160
Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg
				165					170						175
Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly
			180					185					190		
Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr
		195					200					205			
Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg
	210					215					220				
Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro
225					230					235					240
Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu
				245					250						255
Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala
			260					265					270		
Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu
		275					280					285			
Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly
	290					295					300				
Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu
305					310					315					320
Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser
			325						330					335	
Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly
		340						345					350		
Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu
		355					360					365			
His	Met	Gln	Ala	Leu	Pro	Pro	Arg								
	370					375									

<210> 258

<211> 373

<212> PRT

<213> Artificial Sequence

<220>

<223> GSI5019 CAR 269A37353

<400> 258

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

Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Lys	Thr	Leu	Tyr	Leu	Gln	Met
			100					105					110		
Asn	Ser	Leu	Lys	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Arg
		115					120					125			
Arg	Ile	Asp	Ala	Ala	Asp	Phe	Asp	Ser	Trp	Gly	Gln	Gly	Thr	Gln	Val
	130					135					140				
Thr	Val	Ser	Ser	Thr	Ser	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	
145					150				155					160	
Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala
			165					170					175		
Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe
			180					185					190		
Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val
		195					200					205			
Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly	Arg	Lys
	210					215					220				
Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr
225					230					235					240
Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu
				245					250					255	
Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro
			260					265					270		
Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly
		275					280					285			
Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro
	290					295					300				
Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr
305					310					315					320
Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly
				325				330						335	
Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln
			340					345					350		
Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln
		355					360					365			
Ala	Leu	Pro	Pro	Arg											
			370												

<210> 259

<211> 372

<212> PRT

<213> Artificial Sequence

<220>

<223> GSI5020 CAR 269A37917

<400> 259

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	Val	Asn	Arg	Thr	Arg	Arg	Met	His	Glu	Val	Gln
			20					25					30		
Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala	Gly	Gly	Ser	Leu	Arg
		35					40					45			
Leu	Ser	Cys	Ala	Ala	Ser	Gly	Arg	Thr	Phe	Thr	Met	Gly	Trp	Phe	Arg

50		55		60											
Gln	Ala	Pro	Gly	Lys	Glu	Arg	Glu	Phe	Val	Ala	Ala	Ile	Ser	Leu	Ser
65				70					75					80	
Pro	Thr	Leu	Ala	Tyr	Tyr	Ala	Glu	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile
			85						90					95	
Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Val	Val	Leu	Gln	Met	Asn	Ser	Leu
			100					105					110		
Lys	Pro	Glu	Asp	Thr	Ala	Leu	Tyr	Tyr	Cys	Ala	Ala	Asp	Arg	Lys	Ser
		115					120					125			
Val	Met	Ser	Ile	Arg	Pro	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr
	130					135					140				
Val	Ser	Ser	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro
145					150					155					160
Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys
				165					170					175	
Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala
			180					185					190		
Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu
	195					200						205			
Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys
	210					215					220				
Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr
225					230					235					240
Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly
			245						250					255	
Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala
			260					265					270		
Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg
	275					280						285			
Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu
	290				295						300				
Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn
305				310					315					320	
Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met
			325					330					335		
Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly
	340					345						350			
Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala
	355					360					365				
Leu	Pro	Pro	Arg												
	370														

<210> 260

<211> 369

<212> PRT

<213> Artificial Sequence

<220>

<223> GSI5012 CAR 38A37717

<400> 260

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

Arg

<210> 261

<211> 1131

<212> DNA

<213> Artificial Sequence

<220>

<223> GSI5011 CAR 269A37346

<400> 261

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ccggttaacc gcacgcgtcg catgcatcag gtgcagctgg tggagtctgg gggaggcttg 120
gtgcagcctg ggggttctct gaggcctctc tgtgaagcct ctggattcac tttggattat 180
tatgccatag gctggttccg ccaggcccca gggaaggagc gcgagggggg catatgtatt 240
agtagaagtg atggtagcac atactatgca gactccgtga agggccgatt caccatctcc 300
agagacaacg ccaagaaaac ggtgtatctg caaatgatca gcctgaaacc tgaggacacg 360
gccgcttatt actgtgcagc aggggccgat tgttcggggg acctacgaga ttatgagttc 420
cggggggcagg ggaccaggt caccgtctcc tcaactagta ccacgacgcc agcgccgcga 480
ccaccaacac cggcgccac catcgcgtcg cagcccctgt ccctgcgcc agaggcgtgc 540
cggccagcgg cggggggcgc agtgcacac agggggctgg acttcgcctg tgatatctac 600
atctgggccc cttggccgg gacttgtggg gtccttctcc tgtcactggg tatcaccctt 660
tactgcaaac ggggcagaaa gaaactcctg tatatatcca aacaaccatt tatgagacca 720
gtacaaacta ctcaagagga agatggctgt agctgccgat ttccagaaga agaagaagga 780
ggatgtgaac tgagagtga gttcagcagg agcgagacg ccccgcgta ccagcagggc 840
cagaaccagc tctataacga gctcaatcta ggacgaagag aggagtacga tgttttggac 900
aagagacgtg gccgggaccc tgagatgggg ggaaagccga gaaggaagaa ccctcaggaa 960
ggcctgtaca atgaactgca gaaagataag atggcggagg cctacagtga gattgggatg 1020
aaaggcgagc gccggagggg caaggggcac gatggccttt accagggtct cagtacagcc 1080
accaaggaca cctacgacgc cttcacatg caggccctgc cccctcgcta a 1131
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<210> 262

<211> 1122

<212> DNA

<213> Artificial Sequence

<220>

<223> GSI5019 CAR 269A37353

<400> 262

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ccggttaacc gcacgcgtcg catgcatcag gtaaagctgg aggagtctgg gggaggcttg 120
gtgcaggctg ggcggtctct gagactctcc tgtgcagcct ctgaacacac cttcagtagc 180
catgtcatgg gctggttccg ccaggctcca gggaaggagc gtgagtctgt tgcagttatt 240
ggctggagag atattagcac aagctatgca gactccgtga agggccgatt caccatctcc 300
agagacaacg ccaagaagac gctgtatctg caaatgaata gcctgaaacc tgaggacacg 360
gccgtttact actgtgcagc acgtcggatc gacgcagctg actttgattc ctgggggcag 420
gggaccaggg tcaccgtctc ctgcactagt accacgacgc cagcgccgcg accaccaaca 480
ccggcgccca ccacgcgtc gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg 540
gcggggggcg cagtgcacac gagggggctg gacttcgcct gtgatattcta catctgggcg 600
cccttggccg ggacttgtgg ggtccttctc ctgtcactgg ttatcaccct ttactgcaaa 660
cggggcagaa agaaactcct gtatatattc aaacaaccat ttatgagacc agtacaaact 720
actcaagagg aagatggctg tagctgccga tttccagaag aagaagaagg aggatgtgaa 780
ctgagagtga agttcagcag gagcgagac gccccgcgt accagcaggg ccagaaccag 840
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ggccgggacc ctgagatggg gggaaagccg agaaggaaga accctcagga aggcctgtac 960
aatgaactgc agaaagataa gatggcggag gcctacagtg agattgggat gaaaggcgag 1020
cgccggaggg gcaaggggca cgatggcctt taccagggtc tcagtacagc caccaaggac 1080
acctacgacg cccttcacat gcaggccctg cccctcgct aa 1122
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<210> 263

<211> 1119

<212> DNA

<213> Artificial Sequence

<220>

<223> GSI5020 CAR 269A37917

<400> 263

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ccggttaacc gcacgcgtcg catgcatgag gtgcagctgg tggagtctgg gggaggcttg 120
gtgcaggctg gggggtctct gagactctcc tgtgcagcct ctggacgcac cttcaccatg 180
gggtggttcc gtcaggctcc aggggaaggag cgtgagtttg tagcagctat tagtttgagt 240
cctacttttag catattatgc agagtccgtg aagggccgat tcaccatcag ccgagacaac 300
gccaagaaca cggtgggtttt gcaaataaac agcctgaaac ctgaggacac ggccctttat 360
tactgtgcag cagaccggaa atcagtaatg tctattcggc ccgactactg gggccagggg 420
accaggtca ccgtctcctc aactagtacc acgacgccag cgccgcgacc accaacaccg 480
gcgcccacca tcgcgtcgca gcccctgtcc ctgcgccag aggcgtgccg gccagcggcg 540
gggggcgcag tgcacacgag ggggctggac ttgcctgtg atatctacat ctgggcgccc 600
ttggccggga cttgtggggt cttctcctg tctactggtta tcacccttta ctgcaaacgg 660
ggcagaaaga aactcctgta tatattcaaa caaccattta tgagaccagt acaaactact 720
caagaggaag atggctgtag ctgccgattt ccagaagaag aagaaggagg atgtgaactg 780
agagtgaagt tcagcaggag cgcagacgcc cccgcgtacc agcagggccca gaaccagctc 840
tataacgagc tcaatctagg acgaagagag gactacgatg ttttgacaa gagacgtggc 900
cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 960
gaactgcaga aagataagat ggccggaggcc tacagtgaga ttgggatgaa aggcgagcgc 1020
cggaggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc 1080
tacgacgccc ttcacatgca ggccctgccc ctcgctaa 1119
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<210> 264

<211> 1110

<212> DNA

<213> Artificial Sequence

<220>

<223> GSI5012 CAR 38A37717

<400> 264

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ccggttaacg aggtgcagct ggtggaagc ggggggggac tgggtgcaggc aggcgggtca 120
ctgagactgt catgtatcgc aactgggaag gtgttttagca tctacgacat gggctggtat 180
aggcaggcac caggaaagca gagggagctg gtggccgaga tcaccagctc cggcaccaca 240
cactacgacg atttcgtgtc tggccggttt accatcagca gagacaacgc caagaataca 300
gtgtatctgc agatgaacac cctgaaggcc gaggatacag ccgtgtacta ttgccgggct 360
aatcacgtct tcggcgggctc ctactggggg cagggaactc aggtcactgt gtcatccacg 420
cgtcgcgtgc atactagtac cacgacgcca gcgccgcgac caccaacacc ggcgcccacc 480
atcgcgtcgc agccccgtc cctgcgcca gaggcgtgcc ggccagcggc ggggggcgca 540
gtgcacacga gggggctgga cttgcctgt gatattctaca tctgggcgcc cttggccggg 600
acttgtgggg tccttctcct gtcactggtt atcacccttt actgcaaacg gggcagaaag 660
aaactcctgt atatatcaa acaaccattt atgagaccag taaaaactac tcaagaggaa 720
gatggctgta gctgccgatt tccagaagaa gaagaaggag gatgtgaact gagagtgaag 780
ttcagcagga gcgcagacgc cccgcgtac cagcagggcc agaaccagct ctataacgag 840
ctcaatctag gacgaagaga ggagtacgat gttttggaca agagacgtgg ccgggaccct 900
gagatggggg gaaagccgag aaggaagaac ctcaggaag gcctgtacaa tgaactgcag 960
aaagataaga tggcggaggc ctacagttag attgggatga aaggcgagcg ccggaggggc 1020
aaggggcacg atggccttta ccagggtctc agtacagcca ccaaggacac ctacgacgcc 1080
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cttcacatgc aggccctgcc ccctcgctaa

1110

<210> 265

<211> 488

<212> PRT

<213> Artificial Sequence

<220>

<223> GSI5021 CAR

<400> 265

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

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

<210> 266

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> GSI5022 CAR

<400> 266

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

Pro	Gly	Lys	Glu	Arg	Glu	Phe	Val	Ala	Ala	Ile	Ser	Leu	Ser	Pro	Thr
	195						200					205			
Leu	Ala	Tyr	Tyr	Ala	Glu	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg
	210					215					220				
Asp	Asn	Ala	Lys	Asn	Thr	Val	Val	Leu	Gln	Met	Asn	Ser	Leu	Lys	Pro
225					230					235					240
Glu	Asp	Thr	Ala	Leu	Tyr	Tyr	Cys	Ala	Ala	Asp	Arg	Lys	Ser	Val	Met
			245						250					255	
Ser	Ile	Arg	Pro	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser
			260					265					270		
Ser	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro
		275					280					285			
Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro
	290					295					300				
Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp
305					310					315					320
Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu
				325					330					335	
Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu
			340					345					350		
Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu
	355						360					365			
Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys
	370					375					380				
Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln
385					390					395					400
Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu
				405					410					415	
Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly
			420					425					430		
Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu
		435					440					445			
Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly
	450					455					460				
Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser
465					470					475					480
Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro
				485					490					495	

Pro Arg

<210> 267

<211> 508

<212> PRT

<213> Artificial Sequence

<220>

<223> GSI5023 CAR

<400> 267

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	Gln	Val	Lys	Leu	Glu	Glu	Ser	Gly	Gly	Gly	Leu

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

450		455		460											
Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys
465				470		475				480					
Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr
				485				490						495	
Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg				
			500					505							

<210> 268
 <211> 493
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> GSI5024 CAR

<400> 268

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

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

<210> 269

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> GSI5025 CAR

<400> 269

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

130		135		140													
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gln	Val	Lys	Leu	Glu	Glu		
145		150		155						155					160		
Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala	Gly	Arg	Ser	Leu	Arg	Leu	Ser	Cys		
		165		170											175		
Ala	Ala	Ser	Glu	His	Thr	Phe	Ser	Ser	His	Val	Met	Gly	Trp	Phe	Arg		
		180		185											190		
Gln	Ala	Pro	Gly	Lys	Glu	Arg	Glu	Ser	Val	Ala	Val	Ile	Gly	Trp	Arg		
		195		200											205		
Asp	Ile	Ser	Thr	Ser	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile		
		210		215											220		
Ser	Arg	Asp	Asn	Ala	Lys	Lys	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu		
225				230						235					240		
Lys	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Arg	Arg	Ile	Asp		
				245						250					255		
Ala	Ala	Asp	Phe	Asp	Ser	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser		
			260							265					270		
Ser	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro		
		275								280					285		
Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro		
		290				295									300		
Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp		
305				310						315					320		
Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu		
				325						330					335		
Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu		
			340							345					350		
Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu		
		355													360		
Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys		
		370				375									380		
Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln		
385				390						395					400		
Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu		
			405							410					415		
Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly		
		420								425					430		
Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu		
		435								440					445		
Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly		
		450				455									460		
Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser		
465				470						475					480		
Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro		
			485							490					495		
Pro	Arg																

<210> 270

<211> 503

<212> PRT

<213> Artificial Sequence

<220>

<223> GSI5026 CAR

<400> 270

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

Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn
				405				410						415	
Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg
			420					425					430		
Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly
		435					440					445			
Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu
	450					455					460				
Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu
465					470					475					480
Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His
			485					490						495	
Met	Gln	Ala	Leu	Pro	Pro	Arg									
			500												

<210> 271

<211> 1467

<212> DNA

<213> Artificial Sequence

<220>

<223> GSI5021 CAR

<400> 271

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ctgagctgcg	cagcatccga	gcacaccttc	agctcccacg	tgatgggctg	gtttcggcag	180
gccccaggca	aggagagaga	gagcgtggcc	gtgatcggct	ggagggacat	ctccacatct	240
tacgccgatt	ccgtgaaggg	ccggttcacc	atcagccggg	acaacgcaa	gaagacactg	300
tatctgcaga	tgaacagcct	gaagcccgag	gacaccgccg	tgtactattg	cgcagcaagg	360
agaatcgacg	cagcagactt	tgattcctgg	ggccagggca	cccagggtgac	agtgtctagc	420
ggaggaggag	gatctgaggt	gcagctggtg	gagagcggag	gcggcctggt	gcaggccgga	480
ggctctctga	ggctgagctg	tgcagcatcc	ggaagaacct	tcacaatggg	ctggttttagg	540
caggcaccag	gaaaggagag	ggagtctctg	gcagcaatca	gcctgtcccc	taccctggcc	600
tactatgccg	agagcgtgaa	gggcagggtt	accatctccc	gcgataacgc	caagaataca	660
gtgggtgctg	agatgaatc	cctgaaacct	gaggacacag	ccctgtacta	ttgtgccgcc	720
gatcggaaga	gcgtgatgag	cattagacca	gactattggg	ggcagggaac	acaggtgacc	780
gtgagcagca	ctagtaccac	gacgccagcg	ccgcgaccac	caacaccggc	gcccaccatc	840
gcgtcgcagc	ccctgtccct	gcgcccagag	gcgtgccggc	cagcggcggg	gggcgcagtg	900
cacacgaggg	ggctggactt	cgcctgtgat	atctacatct	gggcgccctt	ggccgggact	960
tgtgggggtcc	ttctcctgtc	actggttatc	accctttact	gcaaacgggg	cagaaagaaa	1020
ctcctgtata	tattcaaaca	accatttatg	agaccagtac	aaactactca	agaggaagat	1080
ggctgtagct	gccgatttcc	agaagaagaa	gaaggaggat	gtgaactgag	agtgaagttc	1140
agcaggagcg	cagacgcccc	cgcgtaccag	cagggccaga	accagctcta	taacgagctc	1200
aatctaggac	gaagagagga	gtacgatgtt	ttggacaaga	gacgtggccg	ggaccctgag	1260
atgggggggaa	agccgagaag	gaagaacct	cagggaaggcc	tgtacaatga	actgcagaaa	1320
gataagatgg	cggaggccta	cagtgaagatt	gggatgaaag	gcgagcgccg	gaggggcaag	1380
gggcacgatg	gcctttacca	gggtctcagt	acagccacca	aggacaccta	cgacgccctt	1440
cacatgcagg	ccctgcccc	tcgctaa				1467

<210> 272

<211> 1497

<212> DNA

<213> Artificial Sequence

<220>

<223> GSI5022 CAR

<400> 272

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cctcaggtca aactggaaga aagtggggga ggcctggtgc aggcaggacg gagcctgcgc 120
ctgagctgcg cagcatccga gcacaccttc agctcccacg tgatgggctg gtttcggcag 180
gccccaggca aggagagaga gtccgtggcc gtgacggctt ggagggacat ctccacatct 240
tacgccgatt ctgtgaaggg ccggttcacc atcagcagag acaacgcaa gaagacactg 300
tatctgcaga tgaatagcct gaagcccgag gacaccgccg tgtactattg cgcagcaagg 360
agaatcgacg cagcagactt tgattcctgg ggccagggca cccaggtgac agtgtctagc 420
ggaggaggag gatctggagg aggaggaagc ggaggaggag gatccgaggt gcagctggtg 480
gagtctggag gcggcctggt gcaggccgga ggctctctga ggctgagctg tgcagcatcc 540
ggaagaacct tcacaatggg ctggtttagg caggcaccag gaaaggagag ggagttcgtg 600
gcagcaatca gcctgtcccc taccctggcc tactatgccg agtccgtgaa gggcaggttt 660
accatctctc gcgataacgc caagaatata gtggtgctgc agatgaacag cctgaaacct 720
gaggacacag ccctgtacta ttgtgccgcc gatcggaaga gcgtgatgag cattagacc 780
gattattggg gacagggcac acaggtgaca gtgagtagca ctagtaccac gacgccagcg 840
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accctttact gcaaacgggg cagaaagaaa ctctgtata tattcaaaca accatttatg 1080
agaccagtac aaactactca agaggaagat ggctgtagct gccgatttcc agaagaagaa 1140
gaaggaggat gtgaactgag agtgaagttc agcaggagcg cagacgcccc cgcgtaccag 1200
cagggccaga accagctcta taacgagctc aatctaggac gaagagagga gtacgatgtt 1260
ttggacaaga gacgtggccg ggaccctgag atggggggaa agccgagaag gaagaacctt 1320
caggaaggcc tgtacaatga actgcagaaa gataagatgg cggaggccta cagtgagatt 1380
gggatgaaag gcgagcgccg gaggggcaag gggcacgatg gcctttacca ggggtctcagt 1440
acagccacca aggacaccta cgacgccctt cacatgcagg ccctgcccc tcgctaa 1497
```

<210> 273

<211> 1527

<212> DNA

<213> Artificial Sequence

<220>

<223> GSI5023 CAR

<400> 273

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ccacaggtca aactggaaga atcaggagga ggcctggtgc aggcaggacg gagcctgcgc 120
ctgagctgcg cagcatccga gcacaccttc agctcccacg tgatgggctg gtttcggcag 180
gccccaggca aggagagaga gtccgtggcc gtgacggctt ggagggacat ctccacatct 240
tacgccgatt ccgtgaaggg ccggttcacc atcagccggg acaacgcaa gaagacactg 300
tatctgcaga tgaacagcct gaagcccgag gacaccgccg tgtactattg cgcagcaagg 360
agaatcgacg cagcagactt tgatagctgg ggccagggca cccaggtgac agtgtctagc 420
ggaggaggag gatctggagg aggaggaagc ggaggaggag gaagcggcgg cggcggctct 480
ggcggcggcg gcagcgaggt gcagctggtg gagagcggcg gcggcctggt gcaggccggc 540
ggctctctga ggctgagctg tgcagcatcc ggaagaacct tcacaatggg ctggtttagg 600
caggcaccag gaaaggagag ggagttcgtg gcagcaatca gcctgtcccc taccctggcc 660
tactatgccg agagcgtgaa gggcaggttt accatctccc gcgataacgc caagaatata 720
gtggtgttac aaatgaacag cctgaaacct gaggacacag ccctgtacta ttgtgccgcc 780
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gatcgggaaga	gcgtgatgag	cattagaccc	gattattggg	ggcagggggac	acaggtgacc	840
gtgagcagca	ctagtaccac	gacgccagcg	ccgcgaccac	caacaccggc	gcccaccatc	900
gcgtcgcagc	ccctgtccct	gcgcccagag	gcgtgccggc	cagcggcggg	gggcgagtg	960
cacacgaggg	ggctggactt	cgcctgtgat	atctacatct	gggcgccctt	ggccgggact	1020
tgtgggggtcc	ttctcctgtc	actggttatc	accctttact	gcaaacgggg	cagaaagaaa	1080
ctcctgtata	tattcaaaca	accatttatg	agaccagtac	aaactactca	agaggaagat	1140
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agcaggagcg	cagacgcccc	cgcgtaccag	cagggccaga	accagctcta	taacgagctc	1260
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gataagatgg	cggaggccta	cagtgaagatt	gggatgaaag	gcgagcgccg	gaggggcaag	1440
gggcacgatg	gcctttacca	gggtctcagt	acagccacca	aggacaccta	cgacgccctt	1500
cacatgcagg	ccctgcccc	tcgctaa				1527

<210> 274

<211> 1482

<212> DNA

<213> Artificial Sequence

<220>

<223> GSI5024 CAR

<400> 274

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cctgaagtcc	agctggtgga	atccggggga	ggcctggtgc	aggcaggagg	ctccctgagg	120
ctgtcttgcg	cagcaagcgg	aagaaccttc	acaatgggct	ggtttaggca	ggcaccagga	180
aaggagaggg	agttcgtggc	cgccatctcc	ctgtctccta	ccctggccta	ctatgccgag	240
agcgtgaagg	gcagggtttac	catctcccgc	gacaacgcca	agaatacagt	ggtgctgcag	300
atgaacagcc	tgaagccaga	ggacacagcc	ctgtactatt	gcgccgccga	tcggaagtct	360
gtgatgagca	tcagacccga	ttactggggc	cagggcaccc	aggtgacagt	gagctccgga	420
ggaggaggat	ccggcggagg	aggctctcag	gtgaagctgg	aggagtccgg	aggcggcctg	480
gtgcaggccg	gacggtccct	gagactgtct	tgtgccgcca	gcgagcacac	cttctctagc	540
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ggatggaggg	acatcagcac	atcctacgcc	gattctgtga	agggccggtt	caccatcagc	660
agagacaacg	ccaagaagac	actgtatttta	caaatgaaca	gcctgaagcc	cgaggatacc	720
gccgtgtact	attgtgccgc	ccggcggatt	gacgccgcag	actttgactc	atgggggcag	780
ggaactcagg	tgaccgtgtc	ctcaactagt	accacgacgc	cagcgccgcg	accaccaaca	840
ccggcgccca	ccatcgctc	gcagcccctg	tccctgcgcc	cagaggcgtg	ccggccagcg	900
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cgccggaggg	gcaaggggca	cgatggcctt	taccagggtc	tcagtacagc	caccaaggac	1440
acctacgacg	cccttcacat	gcaggccctg	ccccctcgct	aa		1482

<210> 275

<211> 1497

<212> DNA

<213> Artificial Sequence

<220>

<223> GSI5025 CAR

<400> 275

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ctgtcttgcg cagcaagcgg aagaaccttc acaatgggct ggtttaggca ggcaccagga 180
aaggagaggg agttcgtggc cgccatctcc ctgtctccta ccctggccta ctatgccgag 240
tccgtgaagg gcaggtttac catctctcgc gacaacgcca agaatacagt ggtgctgcag 300
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gtgatgagca tcagaccgga ttactggggc cagggcaccc aggtgacagt gagctccgga 420
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agcggaggcg gcctgggtgca ggccggacgg tccctgagac tgtcttggtc cgccagcgag 540
cacaccttct ctagccacgt gatgggatgg ttcaggcagg cacctggaaa ggagagggag 600
tctgtggccg tgatcggctg gagggacatc agcacatcct acgccgatag cgtgaagggc 660
cggttcacca tctccagaga caacgccaag aagacactgt atctgcagat gaatagcctg 720
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gggatgaaag gcgagcgccg gaggggcaag gggcacgatg gcctttacca ggggtctcagt 1440
acagccacca aggacaccta cgacgccctt cacatgcagg ccctgcccc tcgctaa 1497
```

<210> 276

<211> 1512

<212> DNA

<213> Artificial Sequence

<220>

<223> GSI5026 CAR

<400> 276

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cctgaagtcc agctgggtgga atctggcgga ggcctgggtgc aggcaggagg ctccctgagg 120
ctgtcttgcg cagcaagcgg aagaaccttc acaatgggct ggtttaggca ggcaccagga 180
aaggagaggg agttcgtggc cgccatctcc ctgtctccta ccctggccta ctatgccgag 240
tctgtgaagg gcaggtttac catcagccgc gacaacgcca agaatacagt ggtgctgcag 300
atgaacagcc tgaagccaga ggacacagcc ctgtactatt gcgccgccga tcggaagtct 360
gtgatgagca tcagaccgga ttactggggc cagggcaccc aggtgacagt gagctccgga 420
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gtgaagctgg aggagtccgg aggcggcctg gtgcaggccg gacggtccct gagactgtct 540
tgtgccgcca gcgagcacac cttctctagc cacgtgatgg gatggttcag gcaggcacct 600
ggaaaggaga gggagagcgt ggcagtgatc ggatggaggg acatcagcac atcctacgcc 660
gattccgtga agggccggtt caccatcagc cgggacaacg ccaagaagac actgtattta 720
caaatgaaca gcctgaagcc cgaggatacc gccgtgtact attgtgccgc ccggcggatt 780
gatgccgcag actttgatag ttggggacag gggactcagg tcaccgtcag cagcactagt 840
accacgacgc cagcgcgcgc accaccaaca ccggcgccca ccatcgctc gcagcccctg 900
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gacttcgcct gtgatatcta catctgggcg cccttggccg ggacttgtgg ggtccttctc 1020
ctgtcactgg ttatcacctt ttactgcaaa cggggcagaa agaaactcct gtatatattc 1080
aaacaaccat ttatgagacc agtacaaact actcaagagg aagatggctg tagctgccga 1140
tttccagaag aagaagaagg aggatgtgaa ctgagagtga agttcagcag gagcgagac 1200
gccccgcgt accagcaggg ccagaaccag ctctataacg agctcaatct aggacgaaga 1260
gaggagtacg atgttttgga caagagacgt ggccgggacc ctgagatggg gggaaagccg 1320
agaaggaaga accctcagga aggcctgtac aatgaactgc agaaagataa gatggcggag 1380
gcctacagtg agattgggat gaaaggcgag cgccggaggg gcaaggggca cgatggcctt 1440
taccagggtc tcagtacagc caccaaggac acctacgacg cccttcacat gcaggccctg 1500
ccccctcgct aa 1512

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<210> 277

<211> 768

<212> PRT

<213> Artificial Sequence

<220>

<223> tandem BCMA, CD38 269A37346 38A37717 GSI5013 CARs

<400> 277

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

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Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly
			290				295				300				
Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln
			305				310				315				
Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu
			320				325				330				
Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr
			335				340				345				
Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro
			350				355				360				
Arg	Gly	Ser	Gly	Glu	Gly	Arg	Gly	Ser	Leu	Leu	Thr	Cys	Gly	Asp	Val
			365				370				375				
Glu	Glu	Asn	Pro	Gly	Pro	Gly	Ser	Met	Ala	Leu	Pro	Val	Thr	Ala	Leu
			380				385				390				
Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu	His	Ala	Ala	Arg	Pro	Val	Asn	Arg
			395				400				405				
Thr	Arg	Arg	Met	His	Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu
			410				415				420				
Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Glu	Ala	Ser	Gly	Phe
			425				430				435				
Thr	Leu	Asp	Tyr	Tyr	Ala	Ile	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys
			440				445				450				
Glu	Arg	Glu	Gly	Val	Ile	Cys	Ile	Ser	Arg	Ser	Asp	Gly	Ser	Thr	Tyr
			455				460				465				
Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala
			470				475				480				
Lys	Lys	Thr	Val	Tyr	Leu	Gln	Met	Ile	Ser	Leu	Lys	Pro	Glu	Asp	Thr
			485				490				495				
Ala	Ala	Tyr	Tyr	Cys	Ala	Ala	Gly	Ala	Asp	Cys	Ser	Gly	Tyr	Leu	Arg
			500				505				510				
Asp	Tyr	Glu	Phe	Arg	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Thr
			515				520				525				
Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile
			530				535				540				
Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala
			545				550				555				
Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr
			560				565				570				
Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu
			575				580				585				
Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile
			590				595				600				
Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp
			605				610				615				
Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu
			620				625				630				
Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly
			635				640				645				
Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr
			650				655				660				
Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys
			665				670				675				

690					695					700					
Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys
705					710					715					720
Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg
				725					730						735
Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala
				740					745						750
Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg
		755					760					765			