

SEQUENCE LISTING

<110> Nanjing Legend Biotech Co., Ltd.
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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
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 Ser Ile Thr Val Arg Gly Ile Thr Asn Tyr Ala Asp Ser Val Lys Gly
 1 5 10 15

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<400> 3

Val Ser Ser Asn Arg Asp Pro Asp Tyr
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Ile Gly Thr Met Gly
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Ala Ile Arg Trp Ser Thr Gly Gly Thr Arg Tyr Ala Asp Ser Val Lys
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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Ser Gly Arg Thr Phe Ser Thr Tyr Gly Met Ala
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Ser Gly Gly Ile Phe Val Ile Asn Ala Met Gly
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 Ser Gly Phe Thr Phe Asp Arg Ala Val Ile Val
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 Ser Thr Tyr Thr Val Asn Ser Asp Val Met Gly
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 Ser Gly Ala Thr Leu Thr Asn Asp His Met Ala
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Ser Glu His Thr Phe Ser Ser His Val Met Gly
1 5 10

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Ser Gly Arg Ala Phe Ser Thr Tyr Phe Met Ala
1 5 10

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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
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Val Lys Gly

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Ala	Ile	Ser	Leu	Ser	Pro	Thr	Leu	Ala	Tyr	Tyr	Ala	Glu	Ser	Val	Lys
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Gly

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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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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
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Gly

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<400> 24

Ala	Ile	Met	Trp	Asn	Asp	Gly	Ile	Thr	Tyr	Leu	Gln	Asp	Ser	Val	Lys
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Gly

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Ala	Ile	Asp	Trp	Ser	Gly	Arg	Thr	Thr	Asn	Tyr	Ala	Asp	Pro	Val	Glu
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Gly

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

Gly

<210> 27
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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

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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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 <212> PRT
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<400> 29
 Ala Gly Ala Asp Cys Ser Gly Tyr Leu Arg Asp Tyr Glu Phe
 1 5 10

<210> 30
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<400> 30
 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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Val Tyr Val Thr Leu Leu Gly Gly Val Asn Arg Asp Tyr
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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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 Asp Leu Gly Lys Trp Pro Ala Gly Pro Ala Asp Tyr
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 <400> 40
 Ser Gly Leu Thr Phe Ser Ser Tyr Pro Met Met
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<223> CD38 38A37336 VHH CDR1

<400> 41

Ser	Gly	Phe	Thr	Phe	Ser	Ser	Asn	Trp	Met	Tyr
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Ser	Gly	Arg	Ile	Phe	Ser	Ile	Asn	Ala	Met	Gly
1				5					10	

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<223> CD38 38A37331 VHH CDR1

<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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Thr	Gly	Lys	Val	Phe	Ser	Ile	Tyr	Asp	Met	Gly
1				5					10	

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Ser	Ala	Ser	Ile	Phe	Thr	Arg	Leu	Pro	Met	Gly
1				5					10	

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Ser Gly Arg Ala Tyr Ala Thr Met Ala
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<210> 47
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Ser Gly Leu Thr Phe Ser Ser Tyr Ile Met Gly
1 5 10

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Ser Gln Gly Ile Phe Thr Ile Asn Ala Met Gly
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Ser Gly Arg Thr Phe Ser Ser Tyr Ala Met Ala
1 5 10

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 Ser Gly Thr Ile Val Ser Ile Ser Thr Met Gly
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 Gly

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

<210> 54
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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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<210> 56
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 Glu Ile Thr Ser Ser Gly Thr Thr His Tyr Asp Asp Phe Val Ser Gly
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<210> 57
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 Gly Ile Val Pro Ser Gly Arg Ile Asn Tyr Ala Asp Ser Val Lys Gly
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<210> 58
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 Gly

<210> 59
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 Glu Ile Ser Ser Gly Gly Met Thr Ser Tyr Ala Asp Ser Val Lys Gly
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 <400> 60
 Glu Val Ser Ser Gly Gly Arg Thr Asp Tyr Ala Asp Ser Val Lys Gly
 1 5 10 15

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 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
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<212> PRT
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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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 Ile Leu Gly Leu Pro Thr
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 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
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<400> 67

Ala Asp His Thr Phe Thr Gly Asp Phe
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Asn His Val Phe Gly Gly Ser Tyr
1 5

<210> 69

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<212> PRT

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<400> 69

Ala Asp Thr Phe Pro Leu Pro Thr
1 5

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

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

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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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<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	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	
		115					120					125				
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	
1				5					10					15		
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									

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<223> BCMA 269A37348 VHH

<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				

<210> 80

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<223> BCMA 269A37917 VHH

<400> 80

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	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												

<210> 81
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> BCMA 269A37355 VHH

Ala	Val	Gln	Leu	Val	Asp	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
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

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

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

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

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

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

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

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 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

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

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	ctgggggggcc	tctgagactc	60									
tcctgtgcag	cctcgggaaa	catcttcagt	atcaatcgca	tgggctggta	ccgccaggct	120									
ccagggaagc	agcgcgcgtt	cgtcgcatct	attactgttc	gtggtataac	aaactatgca	180									
gactccgtga	agggccgatt	caccatttct	gtagacaagt	ccaaaaacac	gatttatctg	240									
cagatgaacg	cactcaaacc	tgaggacacg	gccgtctatt	attgtaatgc	agtgtcttca	300									
aacagggacc	ccgactactg	gggccagggg	accaggtca	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 ctgggggattc tctgagactc 60
tcctgtgctg cctctggacg caccttcggt attggtacca tgggctgggt ccgccaacct 120
ccagggaagg agcgtgaatt tgtagcagct attaggtgga gtactgggtg cactcgctat 180
gcagactccg tgaagggccg attcaccatc tcccagagaca acgccaagct cacggtagat 240
ctgcaaatgg acagcctgaa acctgaagac acggccggtt attactgtgc agcagataga 300
ctgtcccttg atttaagtgg tcgttaccac tacaaccccg ccgtgtatga ctattggggc 360
caggggaccc aggtcaccgt ctctca 387
```

<210> 103

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMA 269A37346 VHH

<400> 103

```
caggtgcagc tgggtggagtc tgggggaggc ttggtgcagc ctggggggttc 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 agcagggggc 300
gattgttcgg ggtacctacg agattatgag ttccgggggc aggggaccca ggtcaccgtc 360
tcctca 366
```

<210> 104

<211> 384

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMA 269A37348 VHH

<400> 104

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caggtaaagc tggaggagtc tgggggacga ttggtgcagc caagggggtc tctgagactc 60
tcctgtgcag gctctggacg cactttcagt acctatggta tggcctgggt ccgccaggct 120
ccagggaagg agcgtgagtt cgtagcgtct aaagcatcga tgaattacag cggtagaaca 180
tactatgcag actccgtgaa gggccgattc accatcgcca gagacaacgc caagaacatg 240
gtgtttctgc aaatgaacaa cctgaagcct gaggacacgg ccgtttatta ctgtgcagcg 300
ggcactggat gctcaacata tgggtgtttt gacgcccaga taatagacta ctgggggcaa 360
gggaccctgg tcaccgtctc ctca 384
```

<210> 105

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMA 269A37917 VHH

<400> 105

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gaggtgcagc tgggtggagtc tgggggaggc ttggtgcagg ctgggggggtc tctgagactc 60
tcctgtgcag cctctggacg caccttcacc atggggtggt tccgtcaggc tccagggaag 120
gagcgtgagt ttgtagcagc tattagtttg agtcctactt tagcatatta tgcagagtcc 180
gtgaagggcc gattcaccat cagccgagac aacgccaaga acacggtggt tttgcaaatg 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 ggtcgcattc attcgtggac taggcagaac aaactatgac 180
gactccgtga agggccgatt caccatctcc agagacaacg ccaacaacac ggtgtatctg 240
cagatgaaca gcctggaacc tgaggacacg gccgtctact actgtacagt ctacgttaca 300
ctacttggtg gggttaatag ggactactgg ggccagggga cccagggtcac 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 ttaggagcgc attatgtgga atgatgggat tacatacttg 180
caagactccg tgaagggccg atttaccatc ttcagagaca atgccaagaa cacggtgtat 240
ctgcaaatga acagcctgaa acttgaggat acggccggtt attactgtgc agcatccaag 300
ggtagatact cggaatatga gtactggggc cagggggaccc aggtcacccg ctccctca 357

<210> 108
<211> 384
<212> DNA
<213> Artificial Sequence

<220>
<223> BCMA 269A37936 VHH

<400> 108
gaggtgcagc tgggtggagtc tgggggaggc gtggtgcagg ctgggggggtc tctgacagtc 60
tcctgtacag cctctggatt cactttcgac cgtgctgtca tagtctgggt ccgccaggcc 120
cccgggaagg gccgtgaggg ggtctcattt attaaacct a gtgatggcac catatactac 180
attgactccc tgaagggccg attcacgac tccagtgaca tcgccaagaa tacgggtatat 240
ctgcaaatga aaagtctgga atcggaggac tcggccggtt attactgtgc ggctcgcct 300
gaggactggt acacggattg gatcgactgg agtatatatc ggtggcagca ctggggccag 360
gggaccagg tcactgtctc ctca 384

<210> 109
<211> 357
<212> DNA
<213> Artificial Sequence

<220>

<223> BCMA 269A37953 VHH

<400> 109

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gaggtgcagc tgggtggagtc tgggggagga atggtgcagg ctgggggactc tctgagacta 60
tcctgtgtgc agtctactta caccgtcaat agcgatgtca tgggctgggt cgcgcaggct 120
ccagggaagg agcgtgagtt tgtaggagcg attatgtgga atgatgggtat tacatacttg 180
caagactccg tgaagggccg atttaccatc ttcagagaca acgccaagaa cacggtgtat 240
ctgcaaatga acagcctgaa acttgaggat acggccgttt attactgtgc agcatccaag 300
ggtagatact cggaatatga gtactggggc caggggaccc aggtcaccgt ctcctca 357
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<210> 110

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMA 269A37965 VHH

<400> 110

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gcggtgcagc tgggtggagtc tgggggagga ttggtgcagg ctgggggactc tctgagactc 60
tcctgtacag cctctgggtgc aaccttgact aacgatcaca tggcatgggt cgcgcaggct 120
ccagggaagg ggcgtgaatt tgtagcagct attgactgga gtggtcgtac cacaattac 180
gcagaccccg tagagggccg attcaccatc tccagaaaca acgccaagaa cacggtgtat 240
ctggaaaatga acagcctgaa acttgaggac acggccgttt attactgtgc ggtcctccgc 300
gcttggatct catatgacaa tgactactgg ggccagggga cccaggtcac cgtctcctca 360
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<210> 111

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMA 269A37972 VHH

<400> 111

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caggtgcagc tgggtggagtc tgggggagga ttggtgcagg ctgggggctc tctgagactc 60
tcctgtgcag cctctggagg caccttaagt aaaaataccg tggcttgggt cgcgcaggct 120
ccagggaagg agcgtgggtt tgtagcgtct attacctggg atggtcgtac gacatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca acgccaagaa cacagtgtat 240
ctgcaaatga acagcctgaa acctgaggat acggccgttt atgtctgtgc agacttaggg 300
aaatggcctg cgggcccggc ggactactgg ggccagggga cccaggtcac cgtctcctca 360
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<210> 112

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMA 269A37353 VHH

<400> 112

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caggtaaagc tggaggagtc tgggggaggc ttggtgcagg ctgggcggtc tctgagactc 60
tcctgtgcag cctctgaaca caccttcagt agccatgtca tgggctgggt cgcgcaggct 120
ccagggaagg agcgtgagtc tggtgcagtt 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 tgggggagga ttggtgcagg ctgggggactc tctgagactc 60
acctgtacag cctctggacg cgccttcagt acctatttca tggcctgggt cgcaggct 120
ccagggaagg agcgtgagtt tgtagcagga attgcatgga gtggtggtag cacggcgtat 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
gatgtgcagc tgggtggagtc tgggggaggc ttggtgcagc ctgggggggtc tctgagactc 60
tcctgtgtag cctctggatt gaccttcagt agctacccca tgatgtgggt cgcaggct 120
ccaggaaagg ggctcgagtg ggtctcacgt attagcgata gtggtgggta cacaactat 180
gacgactccg tgaagggccg attcaccatc tccagagaca acgccaagaa cacgctgtat 240
ctgcaaatga acagcctgac acctgaggac acggccgtgt attactgtag aatcctgggg 300
ttgcccacca cgggccaggg gaccagggtc accgtctcct ca 342

<210> 115
<211> 378
<212> DNA
<213> Artificial Sequence

<220>
<223> CD38 38A37336 VHH

<400> 115
gaggtgcagc tgggtggagtc tgggggaggc ctggtgcagc ctgggggggtc tctgagactc 60
tcctgtgcag cctctggatt caccttcagt agcaactgga tgtattgggt ccgtcaggct 120
ccagggaagg ggctcgagtg ggtcgcaact attagtactg atggtcgtgg aacatactat 180
aaagactctg tgaagggccg attcaccgtc tccagagaca acgcatgag tacgctgctt 240
ctgcaaatga acaatctgaa atctgaagat acggccgtgt attattgtgc aaaagagccg 300
aggggtgttg 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

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caggtgcagc tggaggagtc tgggggaggc ttggtgcagg ctgggggggtc tctgagactc 60
tcctgtgcag cctctggaag gatcttcagt atcaatgccca tgggctggta ccgccaggct 120
ccagggaagc agcgcgagtt ggtcgccgct attagtagcg ctggtagcac aaactatgga 180
gactccgtga agggccgatt caccatctcc agagacaacg ccaagaacac ggtgtatctg 240
caaatagaaca gcctgaaacc tgaggacaca gctgtttatt actgtaattt aaattttccc 300
ccgtatgtgt actggggcca ggggaccagc gtcaccgtct cctca 345
```

<210> 117

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> CD38 38A37331 VHH

<400> 117

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caggtaaagc tggaggagtc tgggggaggt ctggtgcagc ctggggagtc tctgagactc 60
tcctgttcag cctctggaag catcttcaaa gttttcagag tctttgccat gagctggtag 120
cgccagggtc ccgggaaaca gcgcgagttg gtcgcatcca ttagtagtggt cgagaccaca 180
acctatgcag actccgtgaa gggccgattc accatctcca gagacaacgc caagaatacg 240
gcgtatctgc aaatggacag cctgaaacct gagggacacg ccgtctatta ctgtaatgcg 300
gatcacacct ttacaggaga cttctggggc caggggaccc aggtcacctg ctccctca 357
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<210> 118

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<223> CD38 38A37717 VHH

<400> 118

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gaggtgcagc tggaggaaag cgggggggga ctggtgcagc caggcgggtc actgagactg 60
tcatgtatcg caactgggaa ggtgttttagc atctacgaca tgggctggta taggcaggca 120
ccaggaaagc agaggagagc ggtggccgag atcaccagct ccggcaccac aactacgac 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

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caggtaaagc tggaggagtc tgggggaggc tcggtgcaga ctgggggggtc tctgagactc 60
tcctgtgcag cctctgcaag catcttcact aggctgcccc tgggctggta ccgccaggct 120
ccagggaagc agcgcgagtt ggtcgtaggc attgttccta gtggtaggat aaactatgca 180
gactccgtga agggccgatt caccatctcc agagacaacg ccaagaacac ggtgtatctg 240
caaatagaaca gcctgcgccc tgaggacaca gccgtctatt actgccgcgc cgataccttc 300
cccttgcccc cctggggcca ggggaccagc gtcaccgtct cctca 345
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<210> 120
 <211> 378
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CD38 38A37330 VHH

<400> 120
 caggtgcagc tgggtggagtc tgggggagga ttggtgcagg ctgggggactc tctgagactc 60
 tcctgtgcag cctctggacg cgcctacgt acgatggcct gggtccgcca ggctccagg 120
 aaggagcgtg agtttgtagc 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
 gaggtgcagc tgggtggagtc tgggggagga ttggtgcagg ctggggggctc tctgagactc 60
 tcctgtgcag cctctggact caccttcagt agttatatta tgggctgggt cgcgcaggct 120
 ccaggcgagg agcgcgagtt ggtcgcggaa attagtagcg gtggatgac atcgtatgca 180
 gactccgtga agggccgatt caccatctcc agagacaacg ccaagaagac ggggtatctg 240
 caaatgaaca gcctgaaacc tgaggacacg gccgtttact attgtgcagc ccctgagagg 300
 ggtagtatct ggtacagccg ctacgaatat aagtactggg gccagggggac ccaggtcacc 360
 gtctcctca 369

<210> 122
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CD38 38A37730 VHH

<400> 122
 gccgtgcagc tgggtggattc tgggggaggc ttggcgcaga ctgggggggtc tctgagactc 60
 tcctgtgcag cctctcaagg gatcttcact atcaatgccca tgggctggta ccgccagggt 120
 ccagggaagc agcgggagtt ggtcgcagaa gttagtagtg gtggccgcac agactatgca 180
 gactccgtga agggccgatt caccatctcc agagacaacg ccaagaacac ggtgtacctg 240
 caaatgaaca gcctgaaacc tgaggacaca ggcgtctatt attgtcgagt ttctggatgg 300
 catgtgtttg tcggtgaccg catagtttgg ggccagggca ccctgggtcac tgtctcctca 360

<210> 123
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CD38 38A37340 VHH

<400> 123
gatgtgcagc tgggtggagtc tggggggagga ttggtgcagg ctgggggactc tctgagactc 60
tcctgtgcag cctctggacg caccttcagt agctatgcc a tggcctgggtt ccgccaggct 120
ccagggaagg agcgtgagat tgtttcgtct atcagtagca gtggtgggtat cacagactat 180
gcagactccg tgaagggccg attcaccatc tccaaagaca gcgcgaagat gaacacggtg 240
tatctgcaaa tgaatagcct agaacctgag gacacggccg ttactactg tgcggcccgt 300
acatggtacc ttcgtacttc tctccaatat gactattggg gccagggggac ccaggtcacc 360
gtctcctca 369

<210> 124
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> CD38 38A37731 VHH

<400> 124
caggtaaagc tggaggagtc tggggggagga ttggtgcagg ctgggggggctc tctgagactc 60
tcctgtgtag cctctggaac catcgtcagt atcagtagca tgggctggta ccgccaggct 120
ccagggaagg agcgcgagtt ggtcgcgact ataaccaggc gtggacgcac gaactataca 180
gactccgtga agggccgatt caccatctcc agagacaacg ccaaaaacac ggtgtatctg 240
caaatgaaca gcctgaaacc tgaggacaca gccgtctatt actgtaatgc agaggtgcaa 300
ctggatatat gggcatctgc gtatgactac tgggggccagg ggaccagggt caccgtcgcc 360
tca 363

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

<220>
<223> CD38 38A37326 VHH

<400> 125
gaggtgcagc tgggtggagtc tggggggagga ttggtgcagg ctgggggggctc tctgagactc 60
tcctgtgcag cctctggacg cacctatgcc atgggctggt atcgccaggc tccagggaag 120
cagcgcgact tggtcgcaac tattagtggg gcgggtaaca caaagtatgc agactccgtg 180
aagggccgat tcaccatctc cagagacaac gccagaaca caatgtatct gcaaatgaac 240
agcctgaaac ctgaggacac ggccgtttat tactgtgccg cgggtaaatg 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

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

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

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> CD8alpha transmembrane

<400> 132

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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

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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

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atctacatct gggcgccctt ggccgggact tgtgggggtcc ttctcctgtc actggttatc 60
accctttact gc 72
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<210> 135

<211> 81

<212> DNA

<213> Artificial Sequence

<220>

<223> CD28 transmembrane

<400> 135

ttttgggtgc tgggtgggtggg tgggtggagtc ctggcttgct atagcttgct agtaacagtg 60
gcctttatta ttttctgggt 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
gggccacccc 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 caggggtctca gtacagccac caaggacacc 300
 tacgacgccc ttcacatgca ggcctgccc 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 caggggtctca gtacagccac caaggacacc 300
 tacgacgccc ttcacatgca ggcctgccc 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	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							400		
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

<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	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> 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
35 40 45
Val Ser Cys Thr Ala Ser Gly Phe Thr Phe Asp Arg Ala Val Ile Val
50 55 60
Trp Phe Arg Gln Ala Pro Gly Lys Gly Arg Glu Gly Val Ser Phe Ile
65 70 75 80
Lys Pro Ser Asp Gly Thr Ile Tyr Tyr Ile Asp Ser Leu Lys Gly Arg
85 90 95
Phe Thr Ile Ser Ser Asp Ile Ala Lys Asn Thr Val Tyr Leu Gln Met
100 105 110
Lys Ser Leu Glu Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Ala Ser
115 120 125
Pro Glu Asp Trp Tyr Thr Asp Trp Ile Asp Trp Ser Ile Tyr Arg Trp
130 135 140
Gln His Trp Gly Gln Gly Thr Gln 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 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					400		
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> 158
 <211> 417
 <212> PRT
 <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
				245					250					255
Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser	Lys	Arg	Gly	Arg	Lys	Lys	Leu
			260					265					270	
Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln
		275					280					285		
Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly
	290					295					300			Cys
Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr
305					310					315				Lys
Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg
			325					330						Glu
Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met
		340					345					350		Gly
Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu
	355					360						365		Leu
Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys
370					375					380				Gly
Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu
385					390					395				Ser
Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu
			405						410				415	Pro
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	

		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	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> 162
 <211> 417
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> BCMA 269A37948 CAR

<400> 162
 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 Thr Cys Thr Ala Ser Gly Arg Ala Phe Ser Thr Tyr Phe Met Ala
 50 55 60

Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Glu	Phe	Val	Ala	Gly	Ile	
65					70					75					80	
Ala	Trp	Ser	Gly	Gly	Ser	Thr	Ala	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	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ser	Arg	
	115				120						125					
Gly	Ile	Glu	Val	Glu	Glu	Phe	Gly	Ala	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> 163
 <211> 411
 <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					400		
Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg							
				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 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
Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg				400
	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	15	
His Ala Ala Arg Pro Val Asn Gln Val Lys Leu Glu Glu Ser Gly Gly				
	20	25	30	
Gly Leu Val Gln Pro Gly Glu Ser Leu Arg Leu Ser Cys Ser Ala Ser				
	35	40	45	
Gly Ser Ile Phe Lys Val Phe Arg Val Phe Ala Met Ser Trp Tyr Arg				
	50	55	60	
Gln Gly Pro Gly Lys Gln Arg Glu Leu Val Ala Ser Ile Ser Ser Gly				
65	70	75	80	
Glu Thr Thr Thr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser				
	85	90	95	
Arg Asp Asn Ala Lys Asn Thr Ala Tyr Leu Gln Met Asp Ser Leu Lys				
	100	105	110	
Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn Ala Asp His Thr Phe Thr				
	115	120	125	
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 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 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	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
His Ala Ala Arg Pro Val	Asn Gln Val Lys Leu	Glu Glu Ser Gly Gly
	20	25
Gly Ser Val Gln Thr Gly	Gly Ser Leu Arg Leu	Ser Cys Ala Ala Ser
	35	40
Ala Ser Ile Phe Thr Arg	Leu Pro Met Gly Trp	Tyr Arg Gln Ala Pro
	50	55
Gly Lys Gln Arg Glu Leu	Val Val Gly Ile Val	Pro Ser Gly Arg Ile
65	70	75
Asn Tyr Ala Asp Ser Val	Lys Gly Arg Phe Thr	Ile Ser Arg Asp Asn
	85	90
Ala Lys Asn Thr Val Tyr	Leu Gln Met Asn Ser	Leu Arg Pro Glu Asp
	100	105
Thr Ala Val Tyr Tyr Cys	Arg Ala Asp Thr Phe	Pro Leu Pro Thr Trp
	115	120
Gly Gln Gly Thr Gln Val	Thr Val Ser Ser Thr	Arg Arg Met His Thr
	130	135
Ser Thr Thr Thr Pro Ala	Pro Arg Pro Pro Thr	Pro Ala Pro Thr Ile
145	150	155
Ala Ser Gln Pro Leu Ser	Leu Arg Pro Glu Ala	Cys Arg Pro Ala Ala
	165	170
Gly Gly Ala Val His Thr	Arg Gly Leu Asp Phe	Ala Cys Asp Phe Trp
	180	185
Val Leu Val Val Val Gly	Gly Val Leu Ala Cys	Tyr Ser Leu Leu Val
	195	200
Thr Val Ala Phe Ile Ile	Phe Trp Val Arg Ser	Lys Arg Ser Arg Leu
	210	215
Leu His Ser Asp Tyr Met	Asn Met Thr Pro Arg	Arg Pro Gly Pro Thr
225	230	235
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		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		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		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> 170
 <211> 420
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD38 38A37334 CAR

<400> 170

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 Ala Ala Ser				
	35	40	45	
Gly Leu Thr Phe Ser Ser Tyr Ile Met Gly Trp Phe Arg Gln Ala Pro				
	50	55	60	
Gly Glu Glu Arg Glu Leu Val Ala Glu Ile Ser Ser Gly Gly Met Thr				
65	70	75	80	
Ser Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn				
	85	90	95	
Ala Lys Lys Thr Gly Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp				
	100	105	110	
Thr Ala Val Tyr Tyr Cys Ala Ala Pro Glu Arg Gly Ser Ile Trp Tyr				
	115	120	125	
Ser Arg Tyr Glu Tyr Lys Tyr Trp Gly Gln Gly Thr Gln Val Thr Val				
	130	135	140	
Ser Ser Thr Arg Arg Met His Thr Ser 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> 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	
		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> 172
 <211> 420
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD38 38A37340 CAR

<400> 172
 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 Ala Gly Asp Ser Leu Arg Leu Ser Cys Ala Ala Ser
 35 40 45

<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	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> 174

<220>
<223> CD38 38A37326 CAR

Met 1	Ala	Leu	Pro	Val 5	Thr	Ala	Leu	Leu	Leu 10	Pro	Leu	Ala	Leu	Leu 15
His	Ala	Ala	Arg	Pro 20	Val	Asn	Glu	Val	Gln	Leu	Val	Glu	Ser 30	Gly Gly
Gly	Leu	Val	Gln	Ala 35	Gly	Gly	Ser 40	Leu	Arg	Leu	Ser	Cys 45	Ala	Ala Ser
Gly	Arg	Thr	Tyr	Ala 50	Met	Gly 55	Trp	Tyr	Arg	Gln	Ala 60	Pro	Gly	Lys Gln
Arg 65	Asp	Leu	Val	Ala 70	Thr	Ile	Ser	Gly	Ala	Gly 75	Asn	Thr	Lys	Tyr Ala 80
Asp	Ser	Val	Lys	Gly 85	Arg	Phe	Thr	Ile	Ser 90	Arg	Asp	Asn	Ala	Lys Asn 95
Thr	Met	Tyr	Leu 100	Gln	Met	Asn	Ser	Leu 105	Lys	Pro	Glu	Asp	Thr	Ala Val
Tyr	Tyr	Cys 115	Ala	Ala	Gly	Lys	Trp 120	Phe	Pro	Ala	Ala	Asn 125	Glu	Tyr Trp
Gly	Gln	Gly	Thr	Gln 130	Val	Thr 135	Val	Ser	Ser	Thr	Arg 140	Arg	Met	His Thr
Ser 145	Thr	Thr	Thr	Pro 150	Ala	Pro	Arg	Pro	Pro	Thr 155	Pro	Ala	Pro	Thr Ile 160
Ala	Ser	Gln	Pro	Leu 165	Ser	Leu	Arg	Pro	Glu 170	Ala	Cys	Arg	Pro	Ala Ala 175
Gly	Gly	Ala	Val 180	His	Thr	Arg	Gly 185	Leu	Asp	Phe	Ala	Cys 190	Asp	Phe Trp 195
Val	Leu	Val	Val 195	Val	Gly	Gly	Val 200	Leu	Ala	Cys	Tyr	Ser 205	Leu	Leu Val
Thr	Val 210	Ala	Phe	Ile	Ile	Phe 215	Trp	Val	Arg	Ser	Lys 220	Arg	Ser	Arg Leu
Leu 225	His	Ser	Asp	Tyr	Met 230	Asn	Met	Thr	Pro	Arg	Arg 235	Pro	Gly	Pro Thr 240
Arg	Lys	His	Tyr	Gln 245	Pro	Tyr	Ala	Pro	Pro	Arg	Asp 250	Phe	Ala	Ala Tyr 255
Arg	Ser	Lys	Arg	Gly 260	Arg	Lys	Lys	Leu 265	Leu	Tyr	Ile	Phe	Lys	Gln Pro 270
Phe	Met	Arg 275	Pro	Val	Gln	Thr	Thr 280	Gln	Glu	Glu	Asp 285	Gly	Cys	Ser Cys 290
Arg	Phe 290	Pro	Glu	Glu	Glu	Glu 295	Gly	Gly	Cys	Glu	Leu 300	Arg	Val	Lys Phe 305
Ser 305	Arg	Ser	Ala	Asp	Ala 310	Pro	Ala	Tyr	Lys	Gln 315	Gly	Gln	Asn	Gln Leu 320
Tyr	Asn	Glu	Leu	Asn 325	Leu	Gly	Arg	Arg	Glu 330	Glu	Tyr	Asp	Val	Leu Asp 335
Lys	Arg	Arg	Gly 340	Arg	Asp	Pro	Glu 345	Met	Gly	Gly	Lys	Pro	Arg	Arg Lys 350
Asn	Pro	Gln	Glu	Gly 355	Leu	Tyr	Asn 360	Glu	Leu	Gln	Lys	Asp 365	Lys	Met Ala 370
Glu	Ala 370	Tyr	Ser	Glu	Ile	Gly 375	Met	Lys	Gly	Glu	Arg 380	Arg	Arg	Gly Lys 385
Gly 385	His	Asp	Gly	Leu	Tyr 390	Gln	Gly	Leu	Ser	Thr 395	Ala	Thr	Lys	Asp Thr 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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ccggttaacc gcacgcgtcg catgcatcag gtgcagctgg tggagtctgg gggaggcttg 120
gtgcagcctg ggggttctct gaggtctctc tgtgaagcct ctggattcac tttggattat 180
tatgccatag gctggttccg ccaggcccca ggggaaggagc gcgagggggg catatgtatt 240
agtagaagtg atggtagcac atactatgca gactccgtga agggccgatt caccatctcc 300
agagacaacg ccaagaaaac ggtgtatctg caaatgatca gcctgaaacc tgaggacacg 360
gccgcttatt actgtgcagc aggggccgat tgttcggggg acctacgaga ttatgagttc 420
cgggggagcagg ggaccaggt caccgtctcc tcaactagta ccacgacgcc agcgccgcga 480
ccaccaaacac cggcgcccac catcgcgctcg cagcccctgt ccctgcgccc agaggcgtgc 540
cggccagcgg cggggggcgc agtgcacacg agggggctgg acttcgcctg tgatttttgg 600
gtgctggtgg tggttggtgg agtcctggct tgctatagct tgctagtaac agtggccttt 660
attattttct gggtgaggag taagaggagc aggtcctgc acagtgacta catgaacatg 720
actccccgcc gcccggggcc caccgcgaag cattaccagc cctatgcccc accacgcgac 780
ttcgcagcct atcgctccaa acggggcaga aagaaactcc tgtatatatt caaacaacca 840
tttatgagac cagtacaaac tactcaagag gaagatggct gtagctgccg atttccagaa 900
gaagaagaag gaggatgtga actgagagtg aagttcagca ggagcgaga cgccccgcg 960
tacaagcagg gccagaacca gctctataac gagctcaatc taggacgaag agaggagtac 1020
gatgttttgg acaagagacg tggccgggac cctgagatgg ggggaaagcc gagaagggaag 1080
aaccctcagg aaggcctgta caatgaactg cagaaagata agatggcgga ggcctacagt 1140
gagattggga tgaaaggcga gcgccggagg ggcaaggggc acgatggcct ttaccagggt 1200
ctcagtacag ccaccaagga cacctacgac gcccttcaca tgcaggccct gccccctcgc 1260
tga 1263

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

<220>
<223> BCMA 269A37348 CAR

<400> 176
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60
ccggttaacc gcacgcgtcg catgcatcag gtaaagctgg aggagtctgg gggacgattg 120
gtgcagccaa ggggtctctc gagactctcc tgtgcaggct ctggacgcac tttcagtacc 180
tatggtatgg cctggttccg ccaggctcca ggggaaggagc gtgagttcgt agcgtctaaa 240
gcatcgatga attacagcgg tagaacatac tatgcagact ccgtgaaggg ccgattcacc 300
atcgccagag acaacgcca gaacatggtg tttctgcaaa tgaacaacct gaagcctgag 360
gacacggccg tttattactg tgcagcgggc actggatgct caacatatgg gtgttttgac 420
gccagataa tagactactg gggcaaagg accctgggtc ccgtctctc aactagtacc 480
acgacgccag cgccgcgacc accaacaccg gcgcccacca tcgcgtcgca gccctgtcc 540
ctgcgcccag aggcgtgccg gccagcggcg gggggcgagc tgcacacgag ggggtggac 600
ttcgctgtg atttttgggt gctggtggtg gttggtggag tcttggcttg ctatagcttg 660
ctagtaacag tggcctttat tattttctgg gtgaggagta agaggagcag gctcctgcac 720
agtgactaca tgaacatgac tccccgcgcg cccgggccca cccgcaagca ttaccagccc 780

tatgccccac	cacgcgactt	cgcagcctat	cgctccaaac	ggggcagaaa	gaaactcctg	840
tatatattca	aacaaccatt	tatgagacca	gtacaaacta	ctcaagagga	agatggctgt	900
agctgccgat	ttccagaaga	agaagaagga	ggatgtgaac	tgagagtga	gttcagcagg	960
agcgcagacg	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	accagggctt	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

atggccttac	cagtgaccgc	cttgctcctg	ccgctggcct	tgctgctcca	cgccgccagg	60
ccggttaacc	gcacgcgtcg	catgcatgag	gtgcagctgg	tggagtctgg	gggaggcttg	120
gtgcaggctg	gggggtctct	gagactctcc	tgtgcagcct	ctggacgcac	cttcaccatg	180
gggtggttcc	gtcaggctcc	agggaaggag	cgtgagtttg	tagcagctat	tagtttgagt	240
cctacttttag	catattatgc	agagtcctgt	aagggccgat	tcaccatcag	ccgagacaac	300
gccaaagaaca	cggtgggtttt	gcaaataaac	agcctgaaac	ctgaggacac	ggccctttat	360
tactgtgcag	cagaccggaa	atcagtaatg	tctattcggc	ccgactactg	gggccagggg	420
accagagtca	ccgtctcctc	aactagtacc	acgacgccag	cgccgcgacc	accaacaccg	480
gcgcccacca	tcgcgtcgca	gcccctgtcc	ctgcgcccag	aggcgtgccg	gccagcggcg	540
gggggcgag	tgacacagag	ggggctggac	ttcgcctgtg	atTTTTTggg	gctgggtggg	600
gTtggtggag	tCctggcttg	ctatagcttg	ctagtaacag	tggcctttat	tattttcttg	660
gtgaggagta	agaggagcag	gctcctgcac	agtgactaca	tgaacatgac	tccccgccgc	720
cccgggccca	cccgcgaagc	ttaccagccc	tatgccccac	cacgcgactt	cgcagcctat	780
cgctccaaac	ggggcagaaa	gaaactcctg	tatatattca	aacaaccatt	tatgagacca	840
gtacaaacta	ctcaagagga	agatggctgt	agctgccgat	ttccagaaga	agaagaagga	900
ggatgtgaac	tgagagtga	gttcagcagg	agcgcagacg	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	accagggctt	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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ccggttaacc	gcacgcgtcg	catgcatgcc	gtgcagctgg	tggattcttg	gggaggcttg	120
gtgcagcctg	gggggtctct	gagactctcc	tgtgtagcct	ctggagggtat	cttcgtcatc	180
aatgccatgg	gctggtaccg	ccaggctcca	ggaaagcagc	gcgagttggg	cgcattctatt	240
cgtggactag	gcagaacaaa	ctatgacgac	tccgtgaagg	gccgattcac	catctccaga	300
gacaacgcc	acaacacggg	gtatctgcag	atgaacagcc	tggaaacctga	ggacacggcc	360
gtctactact	gtacagtcta	cgttacacta	cttggtgggg	ttaataggga	ctactggggc	420
caggggaccc	aggtcaccgt	ctcctcaact	agtaccacga	cgccagcgcc	gcgaccacca	480

acaccggcgc	ccaccatcgc	gtcgcagccc	ctgtccctgc	gcccagaggc	gtgccggcca	540
gcggcggggg	gcgcagtgca	cacgaggggg	ctggacttcg	cctgtgattt	ttgggtgctg	600
gtgggtggtg	gtggagtcct	ggcttgctat	agcttgctag	taacagtggc	ctttattatt	660
ttctgggtga	ggagtaagag	gagcaggctc	ctgcacagtg	actacatgaa	catgactccc	720
cgccgccccg	ggcccacccg	caagcattac	cagccctatg	ccccaccacg	cgacttcgca	780
gcctatcgct	ccaaacgggg	cagaaagaaa	ctcctgtata	tattcaaaca	accatttatg	840
agaccagtac	aaactactca	agaggaagat	ggctgtagct	gccgatttcc	agaagaagaa	900
gaaggaggat	gtgaactgag	agtgaagttc	agcaggagcg	cagacgcccc	cgcgtaacaag	960
cagggccaga	accagctcta	taacgagctc	aatctaggac	gaagagagga	gtacgatgtt	1020
ttggacaaga	gacgtggccg	ggaccctgag	atggggggaa	agccgagaag	gaagaaccct	1080
caggaaggcc	tgtacaatga	actgcagaaa	gataagatgg	cggaggccta	cagtgaattt	1140
gggatgaaag	gcgagcgccg	gaggggcaag	gggcacgatg	gcctttacca	gggtctcagt	1200
acagccacca	aggacaccta	cgacgccctt	cacatgcagg	ccctgcccc	tcgctga	1257

<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	caaataaaca	gcctgaaact	tgaggatacg	360
gccgtttatt	actgtgcagc	atccaagggt	agataactcg	aatatgagta	ctggggccag	420
gggacccagg	tcaccgtctc	ctcaactagt	accacgacgc	cagcgccgcg	accaccaaca	480
ccggcgccca	ccatcgcgctc	gcagcccctg	tccctgcgcc	cagaggcgctg	ccggccagcg	540
gcggggggcg	cagtgcacac	gagggggctg	gacttcgcct	gtgatttttg	ggtgctgggtg	600
gtgggtgggtg	gagtcctggc	ttgctatagc	ttgctagtaa	cagtggcctt	tattattttc	660
tgggtgagga	gtaagaggag	caggctcctg	cacagtgact	acatgaacat	gactccccgc	720
cgccccgggc	ccaccgcgaa	gcattaccag	ccctatgccc	caccacgcga	cttcgcagcc	780
tatcgctcca	aacggggcag	aaagaaactc	ctgtatatat	tcaaacaacc	atttatgaga	840
ccagtacaaa	ctactcaaga	ggaagatggc	tgtagctgcc	gatttccaga	agaagaagaa	900
ggaggatgtg	aactgagagt	gaagttcagc	aggagcgagc	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> 180

<211> 1281

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMA 269A37936 CAR

<400> 180

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ccggttaacc	gcacgcgtcg	catgcatgag	gtgcagctgg	tggagtctgg	gggaggcgctg	120
gtgcaggctg	gggggtctct	gacagtctcc	tgtacagcct	ctggattcac	tttcgaccgt	180
gctgtcatag	tctggttccg	ccaggccccc	gggaagggcc	gtgagggggg	ctcattttatt	240

aaacctagt	atggcaccat	atactacatt	gactccctga	agggccgatt	cacgatctcc	300
agtgacatcg	ccaagaatac	ggtatatctg	caaataaaaa	gtctggaatc	ggaggactcg	360
gccgtttatt	actgtgcggc	ctgcctgag	gactggtaca	cggattggat	cgactggagt	420
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<211> 1254

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMA 269A37953 CAR

<400> 181

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<210> 182

<211> 1257

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMA 269A37965 CAR

<400> 182

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<211> 1257

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMA 269A37972 CAR

<400> 183

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<211> 1254

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMA 269A37353 CAR

<400> 184

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gtgcaggctg	ggcggctctt	gagactctcc	tgtgcagcct	ctgaacacac	cttcagtagc	180
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<211> 1254

<212> DNA

<213> Artificial Sequence

<220>

<223> BCMA 269A37948 CAR

<400> 185

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CD38 38A37333 CAR

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<210> 187
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 <212> DNA
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<220>
 <223> CD38 38A37336 CAR

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<210> 188
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CD38 38A37669 CAR

<400> 188

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 <212> DNA
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<220>
 <223> CD38 38A37331 CAR

<400> 189

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<211> 1242

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<213> Artificial Sequence

<220>

<223> CD38 38A37717 CAR

<400> 190

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cgtcgcatgc	atactagtag	cacgacgcca	gcgccgcgac	caccaacacc	ggcgccacc	480
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<210> 191

<211> 1239

<212> DNA

<213> Artificial Sequence

<220>

<223> CD38 38A37719 CAR

<400> 191

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cggaggggca	aggggcacga	tggcctttac	caggggtctca	gtacagccac	caaggacacc	1200
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<223> CD38 38A37330 CAR

<400> 192

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<211> 1263

<212> DNA

<213> Artificial Sequence

<220>

<223> CD38 38A37334 CAR

<400> 193

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cctgagaggg	gtagtatctg	gtacagccgc	tacgaatata	agtactgggg	ccaggggacc	420
caggtcaccg	tctcctcaac	gcgtcgcgatg	catactagta	ccacgacgcc	agcgccgcga	480
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<210> 194

<211> 1254

<212> DNA

<213> Artificial Sequence

<220>

<223> CD38 38A37730 CAR

<400> 194

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<210> 195

<211> 1263

<212> DNA

<213> Artificial Sequence

<220>

<223> CD38 38A37340 CAR

<400> 195

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<210> 196

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<212> DNA

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<220>

<223> CD38 38A37731 CAR

<400> 196

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<210> 197

<211> 1239

<212> DNA

<213> Artificial Sequence

<220>

<223> CD38 38A37326 CAR

<400> 197

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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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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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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
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Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly		
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Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg		
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Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln		
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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			
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<210> 199
 <211> 622
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> BCMAX3 269A37946 GSI5015 CAR

<400> 199
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 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	
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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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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	
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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				
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	210					215					220					
Lys	Thr	Val	Tyr	Leu	Gln	Met	Ile	Ser	Leu	Lys	Pro	Glu	Asp	Thr	Ala	
225					230					235					240	
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				245				250						255		
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			260					265					270			
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305					310					315					320	
Glu	Gly	Val	Ile	Cys	Ile	Ser	Arg	Ser	Asp	Gly	Ser	Thr	Tyr	Tyr	Ala	
				325					330					335		
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			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	
				405					410					415		
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	
				485					490					495		
Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	
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Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn
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Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val
	530					535					540				
Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg
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Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys
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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
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Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg		
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<210> 200

<211> 483

<212> PRT

<213> Artificial Sequence

<220>

<223> CD38x2 38A37717 GSI5016 CAR

<400> 200

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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
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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

Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala	Gly	Gly	Ser	Leu
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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
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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	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				
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<210> 202
 <211> 1488
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> BCMaX2 269A37946 GSI5014 CAR

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 ctgtcctgcg aggcctctgg cttcaccctg gactactatg ccatcggtcg gtttaggcag 180
 gcacctggaa aggagaggga gggagtgatc tgtatctctc gcagcgacgg cagcacatac 240
 tatgccgatt ccgtgaaggg ccggttcacc atcagcagag acaacgcca gaagacagt 300
 tacctgcaga tgatctccct gaagcctgag gataccgcag catactattg cgcagcagga 360
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<210> 203
 <211> 1869
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> BCMaX3 269A37946 GSI5015 CAR

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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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<210> 205

<211> 1815

<212> DNA
 <213> Artificial Sequence

<220>

<223> CD38x3 38A37717 GSI5017 CAR

<400> 205

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agacaggccc ctgggaaaca gagagagctg gtggcagaaa tcacctctag tggaaactacc 960
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gacgcccccg cgtaccagca gggccagaac cagctctata acgagctcaa tctaggacga 1560
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ccgagaagga agaaccctca ggaaggcctg tacaatgaac tgcagaaaga taagatggcg 1680
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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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

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Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Val	Asp	Lys	Ser	Lys		
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Asn	Thr	Ile	Tyr	Leu	Gln	Met	Asn	Ala	Leu	Lys	Pro	Glu	Asp	Thr	Ala		
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Val	Tyr	Tyr	Cys	Asn	Ala	Val	Ser	Ser	Asn	Arg	Asp	Pro	Asp	Tyr	Trp		
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Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Pro	Val	Gln	Leu	Val	Glu		
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Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala	Gly	Asp	Ser	Leu	Arg	Leu	Ser	Cys		
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Ala	Ala	Ser	Gly	Arg	Thr	Phe	Gly	Ile	Gly	Thr	Met	Gly	Trp	Phe	Arg		
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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						
Ser	Arg	Asp	Asn	Ala	Lys	Leu	Thr	Val	Asp	Leu	Gln	Met	Asp	Ser	Leu		
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Lys	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Asp	Arg	Leu	Ser		
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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		
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Pro	Pro	Pro	Tyr	Leu	Asp	Asn	Glu	Lys	Ser	Asn	Gly	Thr	Ile	Ile	His		
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Val	Lys	Gly	Lys	His	Leu	Cys	Pro	Ser	Pro	Leu	Phe	Pro	Gly	Pro	Ser		
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Lys	Pro	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	Cys	Tyr		
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Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Phe	Trp	Val	Arg	Ser	Lys		
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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	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		
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Gln	Ala	Leu	Pro	Pro	Arg												
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<210> 207

<211> 489

<212> PRT

<213> Artificial Sequence

<220>

<223> CD38xBCMA 38A37717 269A37346 GSI5001 CAR

<400> 207

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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
	130					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	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	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									
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<210> 208

<211> 494

<212> PRT

<213> Artificial Sequence

<220>

<223> CD38xBCMA 38A37717 269A37346 GSI5002 CAR

<400> 208

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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	
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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			
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 <211> 500
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD38xBCMA 38A37717 269A37346 GSI5003 CAR

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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	
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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		
			180					185					190				
Ala	Pro	Gly	Lys	Glu	Arg	Glu	Gly	Val	Ile	Cys	Ile	Ser	Arg	Ser	Asp		
		195					200					205					
Gly	Ser	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser		
	210					215					220						
Arg	Asp	Asn	Ala	Lys	Lys	Thr	Val	Tyr	Leu	Gln	Met	Ile	Ser	Leu	Lys		
225					230					235					240		
Pro	Glu	Asp	Thr	Ala	Ala	Tyr	Tyr	Cys	Ala	Ala	Gly	Ala	Asp	Cys	Ser		
			245					250						255			
Gly	Tyr	Leu	Arg	Asp	Tyr	Glu	Phe	Arg	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	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		
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Leu	Pro	Pro	Arg														
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 <213> Artificial Sequence

<220>
 <223> CD38xBCMA 38A37717 269A37346 GSI5004 CAR

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 His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
 20 25 30

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		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	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
	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	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					390					395					400
Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu
				405					410					415	
Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp
			420					425					430		
Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys
		435					440					445			
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
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 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	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	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	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	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Glu
145					150					155					160
Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala	Gly	Gly	Ser
				165					170					175	
Leu	Arg	Leu	Ser	Cys	Ile	Ala	Thr	Gly	Lys	Val	Phe	Ser	Ile	Tyr	Asp
			180					185					190		
Met	Gly	Trp	Tyr	Arg	Gln	Ala	Pro	Gly	Lys	Gln	Arg	Glu	Leu	Val	Ala
		195				200						205			
Glu	Ile	Thr	Ser	Ser	Gly	Thr	Thr	His	Tyr	Asp	Asp	Phe	Val	Ser	Gly
	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	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					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	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	
				165					170					175		
Gly	Leu	Val	Gln	Ala	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ile	Ala	Thr	
			180					185					190			
Gly	Lys	Val	Phe	Ser	Ile	Tyr	Asp	Met	Gly	Trp	Tyr	Arg	Gln	Ala	Pro	
		195					200					205				
Gly	Lys	Gln	Arg	Glu	Leu	Val	Ala	Glu	Ile	Thr	Ser	Ser	Gly	Thr	Thr	
		210				215					220					
His	Tyr	Asp	Asp	Phe	Val	Ser	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	
225					230					235					240	
Ala	Lys	Asn	Thr	Val	Tyr	Leu	Gln	Met	Asn	Thr	Leu	Lys	Ala	Glu	Asp	
				245					250					255		
Thr	Ala	Val	Tyr	Cys	Arg	Ala	Asn	His	Val	Phe	Gly	Gly	Ser	Tyr		
			260				265					270				
Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Thr	Ser	Thr	Ser	Thr	
		275					280					285				
Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	

290		295		300
Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly				
305		310		320
Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp				
		325		335
Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile				
		340		350
Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys				
		355		365
Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys				
		370		380
Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val				
385		390		400
Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn				
		405		415
Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val				
		420		430
Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg				
		435		445
Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys				
		450		460
Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg				
465		470		480
Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys				
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Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg				
		500		510

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

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

<400> 216
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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 Ser Gly Gly Gly Gly Gly Ser
145 150 155 160

Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly		
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			180					185					190				
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Tyr	Asp	Met	Gly	Trp	Tyr	Arg	Gln	Ala	Pro	Gly	Lys	Gln	Arg	Glu	Leu		
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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		
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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		
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Val	Thr	Val	Ser	Ser	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro		
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Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly		
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Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln		
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Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala		
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Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu		
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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		
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Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met		
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<210> 217

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

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

<400> 217

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taccgccagg ctccagggaa gcagcgcgcg ttcgtcgcac ctattactgt tctgtgtata 240
acaaactatg cagactccgt gaagggccga ttcaccatth ctgtagacaa gtccaaaaaac 300
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<210> 218

<211> 1470

<212> DNA

<213> Artificial Sequence

<220>

<223> CD38xBCMA 38A37717 269A37346 GSI5001 CAR

<400> 218

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ctgtcctgca tcgccaccgg caaggtgttc tccatctacg acatgggctg gtatcggcag 180
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gtgtttggag gaagctactg gggacaggga acccagggtg cagtgtctag cggaggagga 420
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aaagataaga tggcggaggc ctacagttag attgggatga aaggcgagcg ccggaggggc 1380

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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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ctgtcctgca	tcgccaccgg	caaggtgttc	tccatctacg	acatgggctg	gtatcggcag	180
gccccaggca	agcagagaga	gctggtggcc	gagatcacaa	gctccggcac	cacacactac	240
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gagcgccgga	ggggcaaggg	gcacgatggc	ctttaccagg	gtctcagtac	agccaccaag	1440
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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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cccagggaca	ccgcagcata	ctattgcgca	gcaggagcag	attgtagcgg	gtatctgcgg	780
gattatgagt	ttagaggaca	ggggacacag	gtcacagtca	gttccactag	taccacgacg	840
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gagattggga	tgaagggcga	gcgccggagg	ggcaaggggc	acgatggcct	ttaccagggt	1440
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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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gagcgccgga	ggggcaaggg	gcacgatggc	ctttaccagg	gtctcagtac	agccaccaag	1440
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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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<210> 227

<211> 1557

<212> DNA
 <213> Artificial Sequence

<220>

<223> BCMAxCD38 269A37346 38A37717 GSI5010 CAR

<400> 227

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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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taa
663

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<210> 229

<211> 23

<212> DNA
 <213> Artificial Sequence

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 <223> upstream primer CALL001

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 <210> 230
 <211> 23
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 <213> Artificial Sequence

 <220>
 <223> downstream primer CALLOO2

 <400> 230
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 <210> 231
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 <220>
 <223> upstream primer BACK-1

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 <210> 232
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 <223> downstream primer BACK-2

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<220>
 <223> EcoRI restriction site

 <400> 234
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 <223> HpaI restriction site

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 <210> 237
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 <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
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 <210> 239
 <211> 2307
 <212> DNA
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 <220>
 <223> tandem BCMA, CD38 269A37346 38A37717 GSI5013 CAR

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

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<220>
<223> CD19 VHH FR1

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<400> 240
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Pro Leu Arg Leu Ser Cys Ala Ala Ser Gly Asn Ile Phe Ser
20           25           30

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<210> 241
<211> 14

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<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 VHH FR2

<400> 241
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<210> 242
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 VHH FR3

<400> 242
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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
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1 5 10

<210> 244
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> CD20 VHH FR1

<400> 244
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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

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<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								
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	
						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	
						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	
1				5					10					15		
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	
						55					60					
Glu	Arg	Glu	Phe	Val	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		
		355					360					365					

Arg

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

<220>
 <223> CD19 CAR

<400> 250
 atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60
 ccgcaggtaa agctggagga gtctggggga gaattggtgc agcctggggg gcctctgaga 120
 ctctcctgtg cagcctcggg aaacatcttc agtatcaatc gcatgggctg gtaccgccag 180
 gctccaggga agcagcgcg 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 atggaaccat tatccatgtg 480
 aaagggaac acctttgtcc aagtccccta tttcccggac cttctaagcc cttttgggtg 540
 ctggtggtgg ttggtggagt cctggcttgc tatagcttgc tagtaacagt ggcctttatt 600
 attttctggg tgaggagtaa gaggagcagg ctctgcaca gtgactacat gaacatgact 660
 ccccgccgcc ccgggcccac ccgcaagcat taccagccct atgccccacc acgcgacttc 720

gcagcctatc	gctccagagt	gaagttcagc	aggagcgcag	acgccccccg	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

<400> 251						
atggccttac	cagtgaccgc	cttgctcctg	ccgctggcct	tgctgctcca	cgccgccagg	60
ccgccggtgc	agctgggtga	gtctggggga	ggcttggtgc	aggctgggga	ttctctgaga	120
ctctcctgtg	ctgcctctgg	acgcaccttc	ggtattggtg	ccatgggctg	gttccgcca	180
cctccaggga	aggagcgtga	atgtgtagca	gctattaggt	ggagtactgg	tggcactcgc	240
tatgcagact	ccgtgaaggg	ccgattcacc	atctcccag	acaacgcca	gctcacggtg	300
gatctgcaaa	tggacagcct	gaaacctgaa	gacacggccg	tttattactg	tgacagcagat	360
agactgtccc	ttgatttaag	tggtcgttac	cactacaacc	ccgccgtgta	tgactattgg	420
ggccaggggg	cccaggtcac	cgtctcctca	attgaagtta	tgtatcctcc	tccttaccta	480
gacaatgaga	agagcaatgg	aaccattatc	catgtgaaag	ggaaacacct	ttgtccaagt	540
cccctatttc	ccggaccttc	taagcccttt	tgggtgctgg	tggtgggttg	tgagtcctg	600
gcttgctata	gcttgctagt	aacagtggcc	tttattatct	tctgggtgag	gagtaagagg	660
agcaggctcc	tgacacagtga	ctacatgaac	atgactcccc	gccgccccgg	gccaccgcc	720
aagcattacc	agccctatgc	cccaccacgc	gacttcgcag	cctatcgctc	cagagtgaag	780
ttcagcagga	gcgcagacgc	ccccgcgtac	cagcaggggc	agaaccagct	ctataacgag	840
ctcaatctag	gacgaagaga	ggagtacgat	gttttgga	agagacgtgg	ccgggaccct	900
gagatggggg	gaaagccgag	aaggaagaac	cctcaggaag	gcctgtacaa	tgaactgcag	960
aaagataaga	tggcgagggc	ctacagtga	attgggatga	aaggcgagcg	ccggaggggc	1020
aaggggcacg	atggccttta	ccagggtctc	agtacagcca	ccaaggacac	ctacgacgcc	1080
cttcacatgc	aggccctgcc	ccctcgctga	taa			1113

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

<220>
 <223> 137P2F primer

<400> 252			
gtccttctcc	tgctactggg	tat	23

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

<220>
 <223> 137P2R primer

<400> 253			
tcttcttctt	ctggaaatcg	gca	23

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

<220>
 <223> Linker sequence 3

<400> 254
 ggcggcgcca gcggcgccgg cagcgccggc ggcagcgcg gcggcagc 48

<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	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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 gtgcagcctg ggggttctct gaggtctcc tgtgaagcct ctggattcac tttggattat 180
 tatgccatag gctggttccg ccaggcccca ggaaggagc gcgagggggg catatgtatt 240
 agtagaagtg atggtagcac atactatgca gactccgtga agggccgatt caccatctcc 300
 agagacaacg ccaagaaaac ggtgtatctg caaatgatga gcctgaaacc tgaggacacg 360
 gccgcttatt actgtgcagc aggggccgat tgttcggggg acctacgaga ttatgagttc 420

cgggggcagg	ggacccaggt	caccgtctcc	tcaactagta	ccacgacgcc	agcgccgcga	480
ccaccaaacac	cgggcgccac	catcgcgtcg	cagcccctgt	ccctgcgccc	agaggcgtgc	540
cggccagcgg	cggggggcgc	agtgcacacg	agggggctgg	acttcgcctg	tgatatctac	600
atctggggcg	ccttgccggg	gacttggtgg	gtccttctcc	tgctactggg	tatcacctt	660
tactgcaaac	ggggcagaaa	gaaactcctg	tatatattca	aacaaccatt	tatgagacca	720
gtacaaacta	ctcaagagga	agatggctgt	agctgccgat	ttccagaaga	agaagaagga	780
ggatgtgaac	tgagagtga	gttcagcagg	agcgacagcg	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	accaggggtct	cagtacagcc	1080
accaaggaca	cctacgacgc	ccttcacatg	caggccctgc	cccctcgcta	a	1131

<210> 262

<211> 1122

<212> DNA

<213> Artificial Sequence

<220>

<223> GSI5019 CAR 269A37353

<400> 262

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ccggttaacc	gcacgcgtcg	catgcatcag	gtaaagctgg	aggagtcttg	gggaggcttg	120
gtgcaggctg	ggcgttctct	gagactctcc	tgtgcagcct	ctgaacacac	cttcagtagc	180
catgtcatgg	gctgggttccg	ccaggctcca	gggaaggagc	gtgagtctgt	tgcagttatt	240
ggctggagag	atattagcac	aagctatgca	gactccgtga	agggccgatt	caccatctcc	300
agagacaacg	ccaagaagac	gctgtatctg	caaatagaata	gcctgaaacc	tgaggacacg	360
gccgtttact	actgtgcagc	acgtcggatc	gacgcagctg	actttgattc	ctggggggcag	420
gggacccagg	tcaccgtctc	ctcgactagt	accacgacgc	cagcgccgcg	accaccaaca	480
ccggcgccca	ccatcgcgtc	gcagcccctg	tccctgcgcc	cagaggcggtg	ccggccagcg	540
gcggggggcg	cagtgacacac	gagggggctg	gacttcgcct	gtgatatcta	catctggggc	600
cccttgggcg	ggacttggtg	ggtccttctc	ctgtcactgg	ttatcacccct	ttactgcaaa	660
cggggcagaa	agaaactcct	gtatatattc	aaacaacccat	ttatgagacc	agtacaaact	720
actcaagagg	aagatggctg	tagctgccga	tttccagaag	aagaagaagg	aggatgtgaa	780
ctgagagtga	agttcagcag	gagcgcagac	gccccgcgct	accagcaggg	ccagaaccag	840
ctctataacg	agctcaatct	aggacgaaga	gaggagtacg	atgtttttgga	caagagacgt	900
ggccgggacc	ctgagatggg	gggaaagccg	agaaggaaga	accctcagga	aggcctgtac	960
aatgaactgc	agaaagataa	gatggcggag	gcctacagtg	agattgggat	gaaaggcgag	1020
cgccggaggg	gcaaggggca	cgatggcctt	taccagggtc	tcagtacagc	caccaaggac	1080
acctacgacg	cccttcacat	gcaggccctg	ccccctcgct	aa		1122

<210> 263

<211> 1119

<212> DNA

<213> Artificial Sequence

<220>

<223> GSI5020 CAR 269A37917

<400> 263

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ccggttaacc	gcacgcgtcg	catgcatgag	gtgcagctgg	tggagtcttg	gggaggcttg	120
gtgcaggctg	gggggtctct	gagactctcc	tgtgcagcct	ctggacgcac	cttcacccatg	180
gggtggttcc	gtcaggctcc	agggaaggag	cgtgagtttg	tagcagctat	tagtttgagt	240
cctactttag	catattatgc	agagtcctgt	aagggccgat	tcaccatcag	ccgagacaac	300
gccaaagaaca	cggtggtttt	gcaaataaac	agcctgaaac	ctgaggacac	ggccctttat	360
tactgtgcag	cagaccggaa	atcagtaaatg	tctatttcggc	ccgactactg	gggccagggg	420

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accaggtca ccgctctctc aactagtacc acgacgccag cgccgcgacc accaacaccg 480
gcgcccacca tcgcgtcgca gcccttgccc ctgcgcccag aggcgtgccg gccagcgggc 540
gggggcgag tgcacacgag ggggctggac ttgcctgtg atatctacat ctgggcgccc 600
ttggccggga cttgtggggg cttctctctg tctactggta tcacccttta ctgcaaaccg 660
ggcagaaaga aactcctgta tatattcaaa caaccattta tgagaccagt acaaactact 720
caagaggaag atggctgtag ctgccgattt ccagaagaag aagaaggagg atgtgaactg 780
agagtgaagt tcagcaggag cgcagacgcc cccgcgtacc agcagggcca gaaccagctc 840
tataacgagc tcaatctagg acgaagagag gactacgatg ttttgacaa gagacgtggc 900
cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 960
gaactgcaga aagataagat ggcgagggcc tacagtgaga ttgggatgaa aggcgagcgc 1020
cggaggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc 1080
tacgacgccc ttcacatgca ggccctgccc cctcgctaa 1119

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<210> 264
 <211> 1110
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> GSI5012 CAR 38A37717

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<400> 264
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ccggttaacg aggtgcagct ggtggaaagc ggggggggac tgggtgcaggc aggcgggtca 120
ctgagactgt catgtatcgc aactgggaag gtgttttagca tctacgacat gggctgggtat 180
aggcaggcac caggaaagca gagggagctg gtggccgaga tcaccagctc cggcaccaca 240
cactacgacg atttcgtgtc tggccggttt accatcagca gagacaacgc caagaatata 300
gtgtatctgc agatgaacac cctgaaggcc gaggatacag ccgtgtacta ttgccgggct 360
aatcacgtct tcggcggtct ctactggggg cagggaactc aggtcactgt gtcattccacg 420
cgtcgcatgc atactagtag cacgacgcc ggcgcgac caccaacacc ggcgcccacc 480
atcgcgctgc agccccctgt cctgcgcccc gaggcgtgcc ggccagcggc ggggggcgca 540
gtgcacacga gggggctgga cttgcctgt gatattctaca tctgggcgcc cttggccggg 600
acttgtgggg tccttctcct gtcactggtt atcacccttt actgcaaacg gggcagaaag 660
aaactcctgt atatattcaa acaaccattt atgagaccag taaaactac 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 cctcaggaag gcctgtacaa tgaactgcag 960
aaagataaga tggcgagggc ctacagttag attgggatga aaggcgagcg ccggaggggc 1020
aaggggcacg atggccttta ccagggtctc agtacagcca ccaaggacac ctacgacgcc 1080
cttcacatgc aggcctgccc cctcgctaa 1110

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<210> 265
 <211> 488
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> GSI5021 CAR

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<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

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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 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	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
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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	
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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	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	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					380					
Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	
385					390					395					400	
Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	
			405						410					415		
Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	
		420						425					430			
Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	
		435				440						445				
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> 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	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
	450					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

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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					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	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> 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

atggctctgc	ccgtcaccgc	tctgctgctg	cctctggctc	tgctgctgca	cgctgctcgc	60
cctcagggtca	aactggaaga	atctggcgga	ggcctgggtgc	aggcaggacg	gagcctgcgc	120
ctgagctgcg	cagcatccga	gcacaccttc	agctcccacg	tgatgggctg	gtttcggcag	180
gccccaggca	aggagagaga	gagcgtggcc	gtgatcggct	ggagggacat	ctccacatct	240
tacgccgatt	ccgtgaaggg	ccggttcacc	atcagccggg	acaacgccaa	gaagacactg	300
tatctgcaga	tgaacagcct	gaagcccagag	gacaccgccg	tgtactattg	cgcagcaagg	360
agaatcgacg	cagcagactt	tgattccttg	ggccagggca	cccagggtgac	agtgtctagc	420
ggaggaggag	gatctgaggt	gcagctgggtg	gagagcggag	gcggcctggg	gcaggccgga	480
ggctctctga	ggctgagctg	tgcagcatcc	ggaagaacct	tcacaatggg	ctggttttagg	540
caggcaccag	gaaaggagag	ggagttcgtg	gcagcaatca	gcctgtcccc	taccttggcc	600
tactatgccg	agagcgtgaa	gggcagggtt	accatctccc	gcgataacgc	caagaataca	660
gtgggtgctgc	agatgaactc	cctgaaacct	gaggacacag	ccctgtacta	ttgtgccgcc	720
gatcggaaga	gcgtgatgag	cattagacca	gactattggg	ggcaggggaa	acaggtgacc	780
gtgagcagca	ctagtaccac	gacgccagcg	ccgcgaccac	caacaccggc	gccaccatc	840
gcgtcgcagc	ccctgtccct	gcgccagag	gcgtgccggc	cagcggcggg	gggcgcagtg	900
cacacgaggg	ggctggactt	cgctgtgat	atctacatct	gggcgcctt	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	cgctgaccag	cagggccaga	accagctcta	taacgagctc	1200
aatctaggac	gaagagagga	gtacgatgtt	ttggacaaga	gacgtggccg	ggaccctgag	1260
atgggggggaa	agccgagaag	gaagaacctt	caggaaggcc	tgtacaatga	actgcagaaa	1320
gataagatgg	cggaggccta	cagtgaagtt	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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 cctcagggtca aactggaaga aagtggggga ggcctggtgc aggcaggacg gagcctgcgc 120
 ctgagctgcg cagcatccga gcacaccttc agctcccacg tgatgggctg gtttcggcag 180
 gccccaggca aggagagaga gtccgtggcc gtgatcggct ggagggacat ctccacatct 240
 tacgccgatt ctgtgaaggc ccggttcacc atcagcagag acaacgccaa gaagacactg 300
 tatctgcaga tgaatagcct gaagcccagc gacaccgccg tgtactattg cgcagcaagg 360
 agaatcgacg cagcagactt tgattcctgg ggccagggca cccagggtgac 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 gggcagggtt 660
 accatctctc gcgataacgc caagaatata gtggtgctgc agatgaacag cctgaaacct 720
 gaggacacag ccctgtacta ttgtgccgcc gatcgggaaga gcgtgatgag cattagacct 780
 gattattggg gacagggcac acagggtgaca gtgagtagca ctagtaccac gacgccagcg 840
 ccgcgaccac caacaccggc gccaccatc gcgtcgcagc ccctgtccct gcgcccagag 900
 gcgtgccggc cagcggcggg ggccgagtg cacacgaggg ggctggactt cgcctgtgat 960
 atctacatct gggcgccctt ggccgggact tgtgggggtcc ttctcctgtc actggttatc 1020
 accctttact gcaaaccggg 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 gaagaacct 1320
 caggaaggcc tgtacaatga actgcagaaa gataagatgg cggaggccta cagtgaatt 1380
 gggatgaaag gcgagcgccg gaggggcaag gggcacgatg gcctttacca ggtctcagt 1440
 acagccacca aggacaccta cgacgccctt cacatgcagg ccctgcccc cgcgctaa 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 gtgatcggct ggagggacat ctccacatct 240
 tacgccgatt ccgtgaaggc ccggttcacc atcagccggg acaacgccaa gaagacactg 300
 tatctgcaga tgaacagcct gaagcccagc gacaccgccg tgtactattg cgcagcaagg 360
 agaatcgacg cagcagactt tgatagctgg ggccagggca cccagggtgac agtgtctagc 420
 ggaggaggag gatctggagg aggaggaagc ggaggaggag gaagcggcg cggcggtct 480
 ggcgcgggcg gcagcgaggt gcagctggtg gagagcgggc gcggcctggt gcaggccggc 540
 ggctctctga ggctgagctg tgcagcatcc ggaagaacct tcacaatggg ctggtttagg 600
 caggcaccag gaaaggagag ggagttcgtg gcagcaatca gcctgtcccc taccctggcc 660
 tactatgccg agagcgtgaa gggcagggtt accatctccc gcgataacgc caagaatata 720
 gtggtgttac aaatgaacag cctgaaacct gaggacacag ccctgtacta ttgtgccgcc 780

gatcgggaaga	gcgtgatgag	cattagaccc	gattattggg	ggcagggggac	acaggtgacc	840
gtgagcagca	ctagtaccac	gacgccagcg	ccgcgaccac	caacaccggc	gcccaccatc	900
gcgtcgcagc	ccctgtccct	gcgcccagag	gcgtgccggc	cagcggcggg	gggcgagtg	960
cacacgaggg	ggctggactt	cgctgtgat	atctacatct	gggcgcctt	ggccgggact	1020
tgtgggggtcc	ttctcctgtc	actggttatc	accctttact	gcaaacgggg	cagaaagaaa	1080
ctcctgtata	tattcaaaca	accatthtatg	agaccagtac	aaactactca	agaggaagat	1140
ggctgtagct	gccgatttcc	agaagaagaa	gaaggaggat	gtgaactgag	agtgaagttc	1200
agcaggagcg	cagacgcccc	cgctaccag	cagggccaga	accagctcta	taacgagctc	1260
aatctaggac	gaagagagga	gtacgatgtt	ttggacaaga	gacgtggccg	ggaccctgag	1320
atgggggggaa	agccgagaag	gaagaaccct	caggaaggcc	tgtacaatga	actgcagaaa	1380
gataagatgg	cggaggccta	cagtgaagatt	gggatgaaag	gcgagcgccg	gaggggcaag	1440
gggcacgatg	gcctttacca	gggtctcagt	acagccacca	aggacaccta	cgacgcctt	1500
cacatgcagg	ccctgcccc	tcgctaa				1527

<210> 274

<211> 1482

<212> DNA

<213> Artificial Sequence

<220>

<223> GSI5024 CAR

<400> 274

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agcgtgaagg	gcagggtttac	catctcccgc	gacaacgcc	agaatacagt	ggtgctgcag	300
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gccgtgtact	attgtgccgc	ccggcggatt	gacgccgcag	actttgactc	atgggggcag	780
ggaactcagg	tgaccgtgtc	ctcaactagt	accacgacgc	cagcgccgcg	accaccaaca	840
ccggcgccca	ccatcgcgtc	gcagccccctg	tccctgcgcc	cagaggcggtg	ccggccagcg	900
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cgccggaggg	gcaaggggca	cgatggcctt	taccagggtc	tcagtacagc	caccaaggac	1440
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<210> 275

<211> 1497

<212> DNA

<213> Artificial Sequence

<220>

<223> GSI5025 CAR

<400> 275

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<210> 276

<211> 1512

<212> DNA

<213> Artificial Sequence

<220>

<223> GSI5026 CAR

<400> 276

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atgaacagcc	tgaagccaga	ggacacagcc	ctgtactatt	gcgccgccga	tcggaagtct	360
gtgatgagca	tcagacccca	ttactggggc	cagggcaccc	aggtgacagt	gagctccgga	420
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aaacaacat	ttatgagacc	agtacaaact	actcaagagg	aagatggctg	tagctgccga	1140
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gcccccgct	accagcagg	ccagaaccag	ctctataacg	agctcaatct	aggacgaaga	1260
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gcctacagtg agattgggat gaaaggcgag cgccggaggg gcaaggggca cgatggcctt 1440
taccagggtc tcagtacagc caccaaggac acctacgacg cccttcacat gcaggccttg 1500
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<210> 277
<211> 768
<212> PRT
<213> Artificial Sequence
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<220>
<223> tandem BCMA, CD38 269A37346 38A37717 GSI5013 CARs
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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
225          230          235          240
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
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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Glu	Glu	Asn	Pro	Gly	Pro	Gly	Ser	Met	Ala	Leu	Pro	Val	Thr	Ala	Leu		
385					390					395					400		
Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu	His	Ala	Ala	Arg	Pro	Val	Asn	Arg		
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Thr	Arg	Arg	Met	His	Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu		
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Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Glu	Ala	Ser	Gly	Phe		
		435					440					445					
Thr	Leu	Asp	Tyr	Tyr	Ala	Ile	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys		
	450					455					460						
Glu	Arg	Glu	Gly	Val	Ile	Cys	Ile	Ser	Arg	Ser	Asp	Gly	Ser	Thr	Tyr		
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Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala		
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Lys	Lys	Thr	Val	Tyr	Leu	Gln	Met	Ile	Ser	Leu	Lys	Pro	Glu	Asp	Thr		
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Ala	Ala	Tyr	Tyr	Cys	Ala	Ala	Gly	Ala	Asp	Cys	Ser	Gly	Tyr	Leu	Arg		
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Asp	Tyr	Glu	Phe	Arg	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Thr		
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Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile		
545					550					555					560		
Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala		
				565					570					575			
Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr		
			580					585					590				
Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu		
	595					600					605						
Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile		
	610					615					620						
Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp		
625					630					635					640		
Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu		
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Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr		
	675					680						685					
Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys		
	690					695				700							
Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys		
705					710					715					720		
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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					