

SEQUENCE LISTING

<110> Juno Therapeutics, Inc.
SATHER, Blythe D.

<120> CHIMERIC ANTIGEN RECEPTORS SPECIFIC FOR
B-CELL MATURATION ANTIGEN AND ENCODING
POLYNUCLEOTIDES

<130> 735042004340

<140> Not Yet Assigned

<141> Concurrently Herewith

<150> US 62/580,431

<151> 2017-11-01

<150> US 62/596,772

<151> 2017-12-08

<160> 620

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-44, -45, -46, -51 CDR-H1 (aa) Kabat numbering

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Asp Tyr Ala Met Ser

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Asp Tyr Tyr Met Ser
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(aa) Kabat numbering

<400> 3

Asp Tyr Ala Met His
1 5

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<400> 4

Phe Ile Arg Ser Lys Ala Tyr Gly Gly Thr Thr Glu Tyr Ala Ala Ser
1 5 10 15
Val Lys Gly

<210> 5

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(aa) Kabat numbering

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

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(aa) Kabat numbering

<400> 6
Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val Lys
1 5 10 15
Gly

<210> 7
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-44, -45, -46, -51 and VH-2 CDR-H3 (aa)

<400> 7

Trp Ser Ala Pro Thr Asp Tyr
1 5

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Val Asp Gly Pro Pro Ser Ser Asp Ile
1 5

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Val Asp Gly Asp Tyr Val Asp Asp Tyr
1 5

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Val Asp Gly Pro Pro Ser Phe Asp Ile
1 5

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Asp Leu Gly Pro Asp Tyr Asp Pro Asp Ala Phe Asp Ile
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numbering

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Gly Phe Thr Phe Gly Asp Tyr
1 5

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Gly Phe Thr Phe Ser Asp Tyr
1 5

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Gly Phe Pro Phe Ser Asp Tyr
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Gly Phe Thr Phe Asp Asp Tyr
1 5

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Arg Ser Lys Ala Tyr Gly Gly Thr
1 5

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Chothia numbering

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

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(aa) Chothia numbering

<400> 18
Ser Trp Asn Ser Gly Ser
1 5

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-44, -45, -46, -51 CDR-H1 (aa) AbM numbering

<400> 19

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

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-49 CDR-H1 (aa) AbM numbering

<400> 20

Gly Phe Thr Phe Ser Asp Tyr Tyr Met Ser
1 5 10

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Gly Phe Pro Phe Ser Asp Tyr Tyr Met Ser
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Gly Phe Thr Phe Asp Asp Tyr Ala Met His
1 5 10

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<400> 23

Phe Ile Arg Ser Lys Ala Tyr Gly Gly Thr Thr Glu
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(aa) AbM numbering

<400> 24

Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr
1 5 10

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Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly
1 5 10

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<400> 26
Lys Ser Ser Gln Ser Val Leu Ser Thr Ser Asn Asn Lys Asn Tyr Leu
1 5 10 15
Ala

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Arg Ala Ser Gln Ser Ile Lys Thr Asn Leu Ala
1 5 10

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<223> BCMA-3, -46 CDR-L1 (aa)

<400> 28
Lys Ser Ser Gln Ser Val Leu His Ser Ser Asn Asn Lys Asn Tyr Leu
1 5 10 15
Ala

<210> 29
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<400> 29
Arg Ala Ser Gln Asp Ile Arg Asn Ser Leu Ala
1 5 10

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Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu

1	5	10	15
Ala			

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Arg Ala Ser Gln Ser Ile Ser Asn Ser Leu Ala		
1	5	10

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<400> 32		
Arg Ala Ser Gln Asp Ile Gly Asp Tyr Leu Ala		
1	5	10

<210> 33
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<400> 33

Gly Ala Asn Asn Ile Gly Ser Lys Ser Val His
1 5 10

<210> 34

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Gly Gly Asn Asn Ile Glu Arg Lys Asn Val His
1 5 10

<210> 35

<211> 13

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<223> BCMA-11 CDR-L1 (aa)

<400> 35

Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Ala Val Asn
1 5 10

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Ser Gly Ser Arg Ser Asn Ile Gly Asn Asn Tyr Val Ser

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14

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 Ala Ala Ser Arg Leu Glu Ser
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 <400> 41
 Ala Ala Ser Asn Val Glu Asp
 1 5

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 Val Ala Ser Thr Leu Gln Ser
 1 5

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Asp Asp Asp Asp Arg Pro Ser
1 5

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<400> 44
Asp Asp Ser Asp Arg Ala Ser
1 5

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<400> 45
Asn Ser His Gln Arg Pro Ser
1 5

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<400> 46
Asp Asn Ala Lys Arg Pro Ser
1 5

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<400> 47
Gln Gln Tyr Phe Ser Ser Pro Tyr Thr
1 5

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<223> BCMA-2 CDR-L3 (aa)

<400> 48
Gln Gln Tyr Gly Ser Ser Pro Thr
1 5

<210> 49

<211> 9
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Gln Gln Tyr Tyr Thr Thr Pro Leu Thr
1 5

<210> 50
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Gln Gln Tyr Tyr Ser Leu Pro Leu Ser
1 5

<210> 51
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<400> 51
Gln Gln Tyr Tyr Ser Thr Pro Trp Thr
1 5

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<400> 52
Gln Gln Ser His Met Tyr Pro Pro Thr
1 5

<210> 53
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<400> 53
Gln Gln Tyr His Ser His Pro Trp Thr
1 5

<210> 54
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<400> 54
Gln Gln Tyr Tyr Ser Thr Pro Tyr Thr
1 5

<210> 55
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<223> BCMA-9 CDR-L3 (aa)

<400> 55

His	Val	Trp	Asp	Arg	Ser	Arg	Asp	His	Tyr	Val
1				5					10	

<210> 56

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<223> BCMA-10 CDR-L3 (aa)

<400> 56

Gln	Ala	Trp	Asp	Ser	Ser	Ser	Thr	Leu	Tyr	Val
1				5					10	

<210> 57

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<223> BCMA-11 CDR-L3 (aa)

<400> 57

Ala	Ala	Trp	Asp	Asp	Ser	Leu	Arg	Gly	Tyr	Val
1				5					10	

<210> 58

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<223> BCMA-12, -32, -48 CDR-L3 (aa)

<400> 58

Gln Val Trp Asp Ser Ser Ser Asp His Trp Val
1 5 10

<210> 59

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<223> BCMA-1, -3, -4, -5, -6, -7, -8, -45, -46 VH FR1
(aa)

<400> 59

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

<210> 60

<211> 30

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<223> BCMA-2, -12, -22, -23, -26, -40, -48 VH FR1 (aa)

<400> 60

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

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

<210> 62
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<223> BCMA-10 VH FR1 (aa)

<400> 62
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ser
20 25 30

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<400> 63
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Arg

<223> BCMA-11 VH FR2 (aa)

<400> 66

Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
1 5 10

<210> 67

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-44, -45, -46, -51 VH FR3 (aa)

<400> 67

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

<210> 68

<211> 32

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-41, -48, -49 VH FR3 (aa)

<400> 68

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

<210> 69

<211> 32

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<223> BCMA-9, -11, -17, -24, -28, -29, -30, -33, -34,
-35, -36, -38, -39 VH FR3 (aa)

<400> 69

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

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-38, -40, -41, -42, -44, -45, -46, -51 VH FR4 (aa)

<400> 70

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

<210> 71

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-34, -39, -48, -49, -50 VH FR4 (aa)

<400> 71

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

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<223> BCMA-1 VL FR1 (aa)

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

<210> 73
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<400> 73
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15
Glu Thr Ala Thr Leu Ser Cys
20

<210> 74
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<400> 74

Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Asp	Ser	Leu	Val	Val	Ser	Leu	Gly
1				5				10						15	
Glu	Arg	Ala	Thr	Ile	Asn	Cys									
			20												

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 <223> BCMA-4 VL FR1 (aa)

Ala	Ile	Arg	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Leu	Gly
1				5				10						15	
Asp	Arg	Val	Thr	Ile	Thr	Cys									
			20												

<210> 76
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<220>
 <223> BCMA-5, -8, -24 VL FR1 (aa)

Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Asp	Ser	Leu	Ala	Val	Ser	Leu	Gly
1				5				10						15	
Glu	Arg	Ala	Thr	Ile	Asn	Cys									
			20												

<210> 77
 <211> 23
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>

<223> BCMA-6 VL FR1 (aa)

<400> 77

Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Val	Ser	Val	Gly
1				5				10					15		
Glu	Arg	Val	Thr	Ile	Thr	Cys									
			20												

<210> 78

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-7 VL FR1 (aa)

<400> 78

Val	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10					15		
Asp	Arg	Val	Thr	Ile	Thr	Cys									
			20												

<210> 79

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-9 VL FR1 (aa)

<400> 79

Ser	Tyr	Glu	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Val	Ala	Pro	Gly	Gln
1				5				10					15		
Thr	Ala	Arg	Val	Thr	Cys										
			20												

<210> 80

<211> 22

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-10, -26 VL FR1 (aa)

<400> 80
Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15
Thr Ala Arg Ile Thr Cys
20

<210> 81
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-11 VL FR1 (aa)

<400> 81
Gln Leu Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15
Arg Val Thr Ile Ser Cys
20

<210> 82
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-12 VL FR1 (aa)

<400> 82
Gln Ser Ala Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln
1 5 10 15
Lys Val Thr Ile Ser Cys

<210> 83
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-1 VL FR2 (aa)

<400> 83
 Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Arg Leu Leu Leu Tyr
 1 5 10 15

<210> 84
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-2, -34 VL FR2 (aa)

<400> 84
 Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
 1 5 10 15

<210> 85
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-3, -5, -8, -24, -44, -46 VL FR2 (aa)

<400> 85
 Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
 1 5 10 15

<210> 86
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-4 VL FR2 (aa)

<400> 86
Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Lys Leu Leu Leu Ser
1 5 10 15

<210> 87
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-6 VL FR2 (aa)

<400> 87
Trp Tyr Lys Gln Arg Pro Gly Glu Ala Pro Lys Leu Leu Ile His
1 5 10 15

<210> 88
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-7 VL FR2 (aa)

<400> 88
Trp Phe Gln Gln Arg Pro Gly Lys Ala Pro Lys Ser Leu Ile Tyr
1 5 10 15

<210> 89
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-9, -26, -35 VL FR2 (aa)

<400> 89
Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Met Leu Val Val Tyr
1 5 10 15

<210> 90
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-10 VL FR2 (aa)

<400> 90
Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Pro Val Val Tyr
1 5 10 15

<210> 91
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-11 VL FR2 (aa)

<400> 91
Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Glu Val Leu Ile Tyr
1 5 10 15

<210> 92
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-12 VL FR2 (aa)

<400> 92
Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr
1 5 10 15

<210> 93
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-1, -3, -5, -8, -31, -44, -46 VL FR3 (aa)

<400> 93
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15
Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
20 25 30

<210> 94
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-2 VL FR3 (aa)

<400> 94
Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15
Leu Thr Ile Thr Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

20

25

30

<210> 95
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-4 VL FR3 (aa)

<400> 95
 Gly Val Pro Ser Arg Phe Ser Gly Thr Thr Ser Gly Ala Glu Tyr Ala
 1 5 10 15
 Leu Ser Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Ser Tyr Phe Cys
 20 25 30

<210> 96
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-6 VL FR3 (aa)

<400> 96
 Gly Val Pro Ser Arg Phe Ser Gly Arg Gly Ser Gly Thr Val Phe Thr
 1 5 10 15
 Leu Ala Ile Ser Asn Val Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
 20 25 30

<210> 97
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-7 VL FR3 (aa)

<400> 97

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

<210> 98

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-9, -26, -35 VL FR3 (aa)

<400> 98

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

<210> 99

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-10 VL FR3 (aa)

<400> 99

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

<210> 100

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-11 VL FR3 (aa)

<400> 100

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

<210> 101

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-12 VL FR3 (aa)

<400> 101

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

<210> 102

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-1 VL FR4 (aa)

<400> 102

Phe	Gly	His	Gly	Thr	Lys	Leu	Glu	Ile	Lys
1				5				10	

<210> 103

<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-2, -39 VL FR4 (aa)

<400> 103
Phe Gly Arg Gly Thr Lys Leu Glu Ile Lys
1 5 10

<210> 104
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-3, -4, -6, -30, -46 VL FR4 (aa)

<400> 104
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 105
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-5, -45 VL FR4 (aa)

<400> 105
Phe Gly Gln Gly Thr Lys Val Asp Ile Lys
1 5 10

<210> 106
<211> 10
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-7 VL FR4 (aa)

<400> 106

Phe	Gly	Pro	Gly	Thr	Lys	Val	Asp	Ile	Lys
1				5					10

<210> 107

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-8, -44 VL FR4 (aa)

<400> 107

Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys
1				5					10

<210> 108

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-9, -10, -11, -26, -40, -47 VL FR4 (aa)

<400> 108

Phe	Gly	Thr	Gly	Thr	Lys	Leu	Thr	Val	Leu
1				5					10

<210> 109

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-12, -14, -15, -16, -17, -18, -32, -33, -36,
-37, -38, -41, -48, -49, -50 VL FR4 (aa)

<400> 109

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
1 5 10

<210> 110

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-1, -3, -4, -5, -6, -7, -8, -45, -46 VH Chain
(aa)

<400> 110

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

<210> 111

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-2 VH Chain (aa)

<400> 111

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

<210> 112

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-9 VH Chain (aa)

<400> 112

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

Ala Arg Val Asp Gly Asp Tyr Val Asp Asp Tyr Trp Gly Gln Gly Thr
100 105 110
Leu Val Thr Val Ser Ser
115

<210> 113
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-10 VH Chain (aa)

<400> 113
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ser Asp Tyr
20 25 30
Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Lys Val Asp Gly Pro Pro Ser Phe Asp Ile Trp Gly Gln Gly Thr
100 105 110
Met Val Thr Val Ser Ser
115

<210> 114
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-11 VH Chain (aa)

<400> 114
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Arg

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

<210> 115

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-12, -26, -48 VH Chain (aa)

<400> 115

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

<210> 116

<211> 113

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-1 VL Chain (aa)

<400> 116
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ser Val Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Ile Ser Cys Lys Ser Ser Gln Ser Val Leu Ser Thr
20 25 30
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45
Pro Pro Arg Leu Leu Leu Tyr Trp Ala Ser Thr Arg Glu Ala Gly Val
50 55 60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95
Tyr Phe Ser Ser Pro Tyr Thr Phe Gly His Gly Thr Lys Leu Glu Ile
100 105 110
Lys

<210> 117
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-2 VL Chain (aa)

<400> 117
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15
Glu Thr Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Lys Thr Asn
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Ala Ala Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Glu Pro

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

<210> 118
 <211> 113
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-3, -46 VL Chain (aa)

<400> 118
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Val Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu His Ser
20 25 30
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95
Tyr Tyr Thr Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110
Lys

<210> 119
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-4 VL Chain (aa)

<400> 119

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

<210> 120

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-5 VL Chain (aa)

<400> 120

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

Lys

<210> 121

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-6 VL Chain (aa)

<400> 121

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

<210> 122

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-7 VL Chain (aa)

<400> 122

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

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 123
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-8 VL Chain (aa)

<400> 123
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95
Tyr Tyr Ser Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
100 105 110
Lys

<210> 124
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-9 VL Chain (aa)

<400> 124
Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15
Thr Ala Arg Val Thr Cys Gly Ala Asn Asn Ile Gly Ser Lys Ser Val

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

<210> 125

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-10 VL Chain (aa)

<400> 125

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

<210> 126

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-11 VL Chain (aa)

<400> 126

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

<210> 127

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-12 VL Chain (aa)

<400> 127

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

<210> 128

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

<220>
 <223> Synthetic

<220>
 <223> BCMA-1 scFv (aa)

<400> 128
 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Gly Asp Tyr
 20 25 30
 Ala Met Ser Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Gly Phe Ile Arg Ser Lys Ala Tyr Gly Gly Thr Thr Glu Tyr Ala Ala
 50 55 60
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
 65 70 75 80
 Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
 85 90 95
 Tyr Cys Ala Ala Trp Ser Ala Pro Thr Asp Tyr Trp Gly Gln Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 115 120 125
 Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu
 130 135 140
 Ser Val Ser Pro Gly Glu Arg Ala Thr Ile Ser Cys Lys Ser Ser Gln
 145 150 155 160
 Ser Val Leu Ser Thr Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln
 165 170 175
 Gln Lys Pro Gly Gln Pro Pro Arg Leu Leu Leu Tyr Trp Ala Ser Thr
 180 185 190
 Arg Glu Ala Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
 195 200 205
 Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val
 210 215 220
 Tyr Tyr Cys Gln Gln Tyr Phe Ser Ser Pro Tyr Thr Phe Gly His Gly
 225 230 235 240
 Thr Lys Leu Glu Ile Lys
 245

<210> 129
 <211> 239
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-2 scFv (aa)

<400> 129

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

<210> 130

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-3, 46 scFv (aa)

<400> 130

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

<210> 131

<211> 240

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-4 scFv (aa)

<400> 131

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

<210> 132

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-5 scFv (aa)

<400> 132

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

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

<210> 133

<211> 240

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-6 scFv (aa)

<400> 133

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

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

<210> 134

<211> 240

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-7 scFv (aa)

<400> 134

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

				100					105					110			
Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser		
				115					120					125			
Gly	Gly	Gly	Gly	Ser	Val	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu		
				130					135					140			
Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln		
145					150					155					160		
Asp	Ile	Gly	Asp	Tyr	Leu	Ala	Trp	Phe	Gln	Gln	Arg	Pro	Gly	Lys	Ala		
				165					170					175			
Pro	Lys	Ser	Leu	Ile	Tyr	Val	Ala	Ser	Thr	Leu	Gln	Ser	Gly	Val	Pro		
				180					185					190			
Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	His	Phe	Thr	Leu	Thr	Ile		
		195						200					205				
Asn	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr		
		210				215						220					
His	Ser	His	Pro	Trp	Thr	Phe	Gly	Pro	Gly	Thr	Lys	Val	Asp	Ile	Lys		
225					230					235					240		

<210> 135
 <211> 246
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-8 scFv (aa)

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

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

<210> 136

<211> 241

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-9 scFv (aa)

<400> 136

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

				165					170				175			
Met	Leu	Val	Val	Tyr	Asp	Asp	Asp	Asp	Arg	Pro	Ser	Gly	Ile	Pro	Glu	
			180					185					190			
Arg	Phe	Ser	Gly	Ser	Asn	Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Ser	
		195					200					205				
Gly	Val	Glu	Ala	Gly	Asp	Glu	Ala	Asp	Tyr	Phe	Cys	His	Val	Trp	Asp	
	210					215					220					
Arg	Ser	Arg	Asp	His	Tyr	Val	Phe	Gly	Thr	Gly	Thr	Lys	Leu	Thr	Val	
225					230					235					240	
Leu																

<210> 137

<211> 241

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-10 scFv (aa)

<400> 137

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

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

<210> 138
 <211> 247
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-11 scFv (aa)

<400> 138

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

210	215	220
Tyr Cys Ala Ala Trp Asp Asp Ser Leu Arg Gly Tyr Val Phe Gly Thr		
225	230	235
Gly Thr Lys Leu Thr Val Leu		240
245		

<210> 139
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-12 scFv (aa)

<400> 139

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

Thr Val Leu

<210> 140
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-13 CDR-H1 (aa) Kabat numbering

<400> 140
Ser Tyr Ala Met His
1 5

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

<220>
<223> Synthetic

<220>
<223> BCMA-14, -15 CDR-H1 (aa) Kabat numbering

<400> 141
Ser Tyr Gly Met His
1 5

<210> 142
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-16 CDR-H1 (aa) Kabat numbering

<400> 142
Ser Ser Ala Met Gln

1 5

<210> 143
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-18 CDR-H1 (aa) Kabat numbering

<400> 143
Ser Tyr Trp Met Ser
1 5

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

<220>
<223> Synthetic

<220>
<223> BCMA-19 CDR-H1 (aa) Kabat numbering

<400> 144
Ser Tyr Tyr Met His
1 5

<210> 145
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-13, -14, -15 CDR-H2 (aa) Kabat numbering

<400> 145
Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 146

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-16 CDR-H2 (aa) Kabat numbering

<400> 146

Trp	Ile	Val	Val	Gly	Ser	Gly	Asn	Thr	Asn	Tyr	Ala	Gln	Lys	Phe	Gln
1				5				10						15	
Glu															

<210> 147

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-18 CDR-H2 (aa) Kabat numbering

<400> 147

His	Ile	Asn	Gln	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val	Lys
1				5				10						15	
Gly															

<210> 148

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-19 CDR-H2 (aa) Kabat numbering

<400> 148

Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15
Gly

<210> 149

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-13, -14 CDR-H3 (aa)

<400> 149

Leu Pro Gly Arg Asp Gly Tyr Pro Gly Ala Phe Asp Tyr
1 5 10

<210> 150

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-15 CDR-H3 (aa)

<400> 150

Asp Gln Tyr Ser Ser Ser Ala Gln Arg Ala Asp Phe Asp Tyr
1 5 10

<210> 151

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-16 CDR-H3 (aa)

<400> 151

Ala Pro Tyr Tyr Asp Ile Leu Thr Gly Tyr Tyr Leu
1 5 10

<210> 152

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-17, -33 CDR-H3 (aa)

<400> 152

Glu Ala Asp Ser Ser Ala Asp Tyr
1 5

<210> 153

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-18 CDR-H3 (aa)

<400> 153

Trp Leu Ala Val Thr Asn
1 5

<210> 154

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-19 CDR-H3 (aa)

<400> 154

Asp Gly Gly Asp Val
1 5

<210> 155

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-20, -27 CDR-H3 (aa)

<400> 155

Gly Gly Leu Gly Ile Thr Pro Tyr Tyr Phe Asp Tyr
1 5 10

<210> 156

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-21 CDR-H3 (aa)

<400> 156

Val Asp Gly Gly Tyr Thr Glu Asp Tyr
1 5

<210> 157

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-22, -23, -40 CDR-H3 (aa)

<400> 157

Val Asp Gly Asp Tyr Thr Glu Asp Tyr

1 5

<210> 158

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-13, -14, -15, -18 CDR-H1 (aa) Chothia
numbering

<400> 158

Gly Phe Thr Phe Ser Ser Tyr

1 5

<210> 159

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-16 CDR-H1 (aa) Chothia numbering

<400> 159

Gly Phe Thr Phe Thr Ser Ser

1 5

<210> 160

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-19 CDR-H1 (aa) Chothia numbering

<400> 160

Gly Tyr Thr Phe Thr Ser Tyr

1 5

<210> 161

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-13, -14, -15 CDR-H2 (aa) Chothia numbering

<400> 161

Ser Tyr Asp Gly Ser Asn

1 5

<210> 162

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-16 CDR-H2 (aa) Chothia numbering

<400> 162

Val Val Gly Ser Gly Asn

1 5

<210> 163

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-18 CDR-H2 (aa) Chothia numbering

<400> 163

Asn Gln Asp Gly Ser Glu
1 5

<210> 164

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-19 CDR-H2 (aa) Chothia numbering

<400> 164

Asn Pro Asn Ser Gly Gly
1 5

<210> 165

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-13 CDR-H1 (aa) AbM numbering

<400> 165

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

<210> 166

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-14, -15 CDR-H1 (aa) AbM numbering

<400> 166

Gly Phe Thr Phe Ser Ser Tyr Gly Met His
1 5 10

<210> 167

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-16 CDR-H1 (aa) AbM numbering

<400> 167

Gly Phe Thr Phe Thr Ser Ser Ala Met Gln
1 5 10

<210> 168

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-18 CDR-H1 (aa) AbM numbering

<400> 168

Gly Phe Thr Phe Ser Ser Tyr Trp Met Ser
1 5 10

<210> 169

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-19 CDR-H1 (aa) AbM numbering

<400> 169

Gly Tyr Thr Phe Thr Ser Tyr Tyr Met His

1 5 10

<210> 170
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-13, -14, -15 CDR-H2 (aa) AbM numbering

<400> 170
Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr
1 5 10

<210> 171
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-16 CDR-H2 (aa) AbM numbering

<400> 171
Trp Ile Val Val Gly Ser Gly Asn Thr Asn
1 5 10

<210> 172
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-18 CDR-H2 (aa) AbM numbering

<400> 172
His Ile Asn Gln Asp Gly Ser Glu Lys Tyr
1 5 10

<210> 173
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-19 CDR-H2 (aa) AbM numbering

<400> 173
Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn
1 5 10

<210> 174
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-13, -14, -15, -16, -18, -21 CDR-L1 (aa)

<400> 174
Gly Ser Gly Ser Asn Ile Gly Ser Asn Asp Val Ser
1 5 10

<210> 175
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-17, -33 CDR-L1 (aa)

<400> 175
Gly Gly Asn Asn Ile Gly Phe Lys Gly Val Gln
1 5 10

<210> 176
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-19 CDR-L1 (aa)

<400> 176
Thr Gly Thr Ser Ser Asp Val Gly Asp Tyr Asn Tyr Val Ala
1 5 10

<210> 177
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-20, -27 CDR-L1 (aa)

<400> 177
Ser Gly Gly Lys Thr Val Asn
1 5

<210> 178
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-22, -23 CDR-L1 (aa)

<400> 178
Thr Gly Ser Ser Ser Asp Val Gly Lys Tyr Asn Leu Val Ser
1 5 10

<210> 179
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-13, -14, -15, -16, -18, -21 CDR-L2 (aa)

<400> 179
Trp Asn Asp Gln Arg Pro Ser
1 5

<210> 180
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-17, -32, -33 CDR-L2 (aa)

<400> 180
Asp Asp Ser Asp Arg Pro Ser
1 5

<210> 181
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-19 CDR-L2 (aa)

<400> 181
Glu Val Ile Asn Arg Pro Ser
1 5

<210> 182

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

<220>
<223> Synthetic

<220>
<223> BCMA-20, -27 CDR-L2 (aa)

<400> 182
Ser Asn Asp Gln Arg Pro Ser
1 5

<210> 183
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-22, -23, -40 CDR-L2 (aa)

<400> 183
Asp Val Asn Lys Arg Pro Ser
1 5

<210> 184
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-13 CDR-L3 (aa)

<400> 184
Ala Ala Trp Asp Asp Ser Leu Gly Gly Ser Trp Val
1 5 10

<210> 185
<211> 12

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-14 CDR-L3 (aa)

<400> 185
Ala Ala Trp Asp Asp Arg Leu Asn Gly Phe Trp Val
1 5 10

<210> 186
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-15 CDR-L3 (aa)

<400> 186
Ala Ala Trp Asp Asp Ser Leu Ser Gly Trp Val
1 5 10

<210> 187
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-16 CDR-L3 (aa)

<400> 187
Ala Ser Trp Asp Asp Ser Leu Ser Gly Trp Val
1 5 10

<210> 188
<211> 11
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-17, -33 CDR-L3 (aa)

<400> 188

Gln	Val	Trp	Asp	Ser	Ala	Ser	Asp	His	Trp	Val
1				5					10	

<210> 189

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-18 CDR-L3 (aa)

<400> 189

Ala	Ala	Trp	Asp	Asp	Ser	Leu	Asn	Gly	Trp	Val
1				5					10	

<210> 190

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-19 CDR-L3 (aa)

<400> 190

Ile	Ser	Tyr	Ser	Arg	Gly	Ser	Thr	Pro	Tyr	Val
1				5					10	

<210> 191

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-20, -27 CDR-L3 (aa)

<400> 191

Gly	Ser	Trp	Asp	Asp	Ser	Leu	Asn	Ala	Trp	Val
1				5					10	

<210> 192

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-21 CDR-L3 (aa)

<400> 192

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

<210> 193

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-22, -40 CDR-L3 (aa)

<400> 193

Cys	Ser	Tyr	Gly	Gly	Ser	Arg	Ser	Tyr	Val
1				5					10

<210> 194

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-23 CDR-L3 (aa)

<400> 194

Ser	Ser	Tyr	Gly	Gly	Ser	Arg	Ser	Tyr	Val
1				5					10

<210> 195

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-13 VH FR1 (aa)

<400> 195

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

<210> 196

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-14 VH FR1 (aa)

<400> 196

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

<210> 197

<211> 30

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-15, -47 VH FR1 (aa)

<400> 197
Gln Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

<210> 198
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-16 VH FR1 (aa)

<400> 198
Glu Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Thr
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe Thr
20 25 30

<210> 199
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-17, -33, -36, -38, -41 VH FR1 (aa)

<400> 199
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser

20

25

30

<210> 200

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-18 VH FR1 (aa)

<400> 200

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

<210> 201

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-19 VH FR1 (aa)

<400> 201

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

<210> 202

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-20 VH FR1 (aa)

<400> 202

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

<210> 203

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-21 VH FR1 (aa)

<400> 203

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

<210> 204

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-13, -14, -15 VH FR2 (aa)

<400> 204

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

<210> 205

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-16 VH FR2 (aa)

<400> 205

Trp Val Arg Gln Ala Arg Gly Gln Arg Leu Glu Trp Ile Gly
1 5 10

<210> 206

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-17 VH FR2 (aa)

<400> 206

Trp Ile Arg Leu Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
1 5 10

<210> 207

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-18 VH FR2 (aa)

<400> 207

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

<210> 208

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-19 VH FR2 (aa)

<400> 208

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
1 5 10

<210> 209

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-20, -27, -28, -29, -30, -34, -39 VH FR2 (aa)

<400> 209

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

<210> 210

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-13 VH FR3 (aa)

<400> 210

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

<210> 211

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-14 VH FR3 (aa)

<400> 211

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

<210> 212

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-15 VH FR3 (aa)

<400> 212

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

<210> 213

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-16 VH FR3 (aa)

<400> 213

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

<210> 214

<211> 32

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-18 VH FR3 (aa)

<400> 214
Arg Phe Thr Ile Ser Arg Asp Asn Ala Glu Ser Ser Leu Tyr Leu Gln
1 5 10 15
Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 215
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-19 VH FR3 (aa)

<400> 215
Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu
1 5 10 15
Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 216
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-20, -27 VH FR3 (aa)

<400> 216
Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
1 5 10 15
Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Lys

<210> 217
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-13 VH FR4 (aa)

<400> 217
 Arg Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 1 5 10

<210> 218
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-14 VH FR4 (aa)

<400> 218
 Arg Gly Pro Gly Thr Leu Val Thr Val Ser Ser
 1 5 10

<210> 219
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-17, -33 VH FR4 (aa)

<400> 219
 Trp Gly Gln Gly Thr Leu Val Asn Val Ser Ser
 1 5 10

<210> 220
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-19 VH FR4 (aa)

<400> 220
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
1 5 10

<210> 221
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-13, -14 VL FR1 (aa)

<400> 221
Gln Ala Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15
Arg Val Thr Ile Ser Cys
20

<210> 222
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-15, -18, -21 VL FR1 (aa)

<400> 222
Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln

1	5	10	15
Arg	Val Thr	Ile Ser	Cys
	20		

<210> 223
 <211> 22
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-16 VL FR1 (aa)

<400> 223															
Gln	Ser	Ala	Leu	Thr	Gln	Pro	Pro	Ser	Ala	Ser	Gly	Thr	Pro	Gly	Gln
1				5				10						15	
Arg	Val	Thr	Ile	Ser	Cys										
			20												

<210> 224
 <211> 22
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-17, -33 VL FR1 (aa)

<400> 224															
Gln	Pro	Val	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Val	Ala	Pro	Gly	Lys
1				5				10						15	
Thr	Ala	Met	Ile	Thr	Cys										
			20												

<210> 225
 <211> 22
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>

<223> BCMA-19 VL FR1 (aa)

<400> 225

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

<210> 226

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-20, -27 VL FR1 (aa)

<400> 226

Gln	Pro	Val	Leu	Thr	Gln	Pro	Pro	Ser	Ala	Ser	Gly	Thr	Pro	Gly	Gln
1				5					10					15	
Arg	Val	Thr	Ile	Ser	Cys										
			20												

<210> 227

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-22, -23, -40 VL FR1 (aa)

<400> 227

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

<210> 228

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-13, -14, -15, -16, -18, -21 VL FR2 (aa)

<400> 228

Trp	Tyr	Gln	Gln	Ile	Pro	Gly	Thr	Ala	Pro	Lys	Leu	Leu	Ile	Tyr
1				5					10					15

<210> 229

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-17, -33 VL FR2 (aa)

<400> 229

Trp	Tyr	Gln	Gln	Lys	Thr	Gly	Gln	Ala	Pro	Val	Leu	Val	Val	Tyr
1				5					10					15

<210> 230

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-19 VL FR2 (aa)

<400> 230

Trp	Tyr	Gln	Gln	His	Pro	Gly	Lys	Asp	Pro	Lys	Leu	Met	Ile	Phe
1				5					10					15

<210> 231

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-20, -27 VL FR2 (aa)

<400> 231

Trp	Phe	Arg	Gln	Val	Pro	Gly	Thr	Ala	Pro	Gln	Leu	Leu	Ile	Tyr
1				5					10					15

<210> 232

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-22, -23, -40 VL FR2 (aa)

<400> 232

Trp	Tyr	Gln	Gln	Pro	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Ile	Ile	Tyr
1				5					10					15

<210> 233

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-13 VL FR3 (aa)

<400> 233

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

<210> 234

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-14 VL FR3 (aa)

<400> 234

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

<210> 235

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-15 VL FR3 (aa)

<400> 235

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

<210> 236

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-16 VL FR3 (aa)

<400> 236

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

<210> 237
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-17, -33 VL FR3 (aa)

<400> 237
Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr
1 5 10 15
Leu Thr Ile Ser Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys
20 25 30

<210> 238
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-18 VL FR3 (aa)

<400> 238
Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser
1 5 10 15
Leu Ala Ile Ser Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Cys
20 25 30

<210> 239
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-19 VL FR3 (aa)

<400> 239

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

<210> 240

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-20, -27 VL FR3 (aa)

<400> 240

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

<210> 241

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-21 VL FR3 (aa)

<400> 241

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

<210> 242

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-22, -23, -40 VL FR3 (aa)

<400> 242

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

<210> 243

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-13 VL FR4 (aa)

<400> 243

Phe	Gly	Gly	Gly	Thr	Lys	Val	Thr	Val	Leu
1				5					10

<210> 244

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-19 VL FR4 (aa)

<400> 244

Ile	Gly	Thr	Gly	Thr	Lys	Val	Thr	Val	Leu
1				5					10

<210> 245

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-20, -27 VL FR4 (aa)

<400> 245

Phe	Gly	Gly	Glu	Thr	Lys	Leu	Thr	Val	Leu
1				5					10

<210> 246

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-21, -22, -23 VL FR4 (aa)

<400> 246

Phe	Gly	Thr	Gly	Thr	Lys	Val	Thr	Val	Leu
1				5					10

<210> 247

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-13 VH Chain (aa)

<400> 247

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

Leu	Gln	Met	Asn	Ser	Leu	Lys	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Thr	Leu	Pro	Gly	Arg	Asp	Gly	Tyr	Pro	Gly	Ala	Phe	Asp	Tyr	Arg
			100					105					110		
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser						
		115					120								

<210> 248
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-14 VH Chain (aa)

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

<210> 249
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-15 VH Chain (aa)

<400> 249

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

<210> 250

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-16 VH Chain (aa)

<400> 250

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

<210> 251
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-17 VH Chain (aa)

<400> 251
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30
Tyr Met Ser Trp Ile Arg Leu Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Glu Ala Asp Ser Ser Ala Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110
Val Asn Val Ser Ser
115

<210> 252
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-18 VH Chain (aa)

<400> 252
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
Trp Met Ser Trp His Arg Gln Ala Pro Gly Lys Gly Pro Glu Trp Val
35 40 45
Ala His Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val

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

<210> 253
 <211> 114
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-19 VH Chain (aa)

<400> 253															
Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala
1				5					10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr
			20					25					30		
Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
		35					40					45			
Gly	Trp	Ile	Asn	Pro	Asn	Ser	Gly	Gly	Thr	Asn	Tyr	Ala	Gln	Lys	Phe
	50				55					60					
Gln	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	Ser	Ile	Ser	Thr	Ala	Tyr
65				70					75						80
Met	Glu	Leu	Ser	Arg	Leu	Arg	Ser	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85					90					95		
Ala	Arg	Asp	Gly	Gly	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val
			100					105					110		
Ser	Ser														

<210> 254
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>

<223> BCMA-20 VH Chain (aa)

<400> 254

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

<210> 255

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-21 VH Chain (aa)

<400> 255

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

115

<210> 256
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-22, -23, -40 VH Chain (aa)

<400> 256
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30
Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Lys Val Asp Gly Asp Tyr Thr Glu Asp Tyr Trp Gly Gln Gly Thr
100 105 110
Leu Val Thr Val Ser Ser
115

<210> 257
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-13 VL Chain (aa)

<400> 257
Gln Ala Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15
Arg Val Thr Ile Ser Cys Ser Gly Ser Gly Ser Asn Ile Gly Ser Asn
20 25 30

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

<210> 258

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-14 VL Chain (aa)

<400> 258

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

<210> 259

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-15 VL Chain (aa)

<400> 259

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

<210> 260

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-16 VL Chain (aa)

<400> 260

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

<210> 261

<211> 108

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-17, -33 VL Chain (aa)

<400> 261
Gln Pro Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Lys
1 5 10 15
Thr Ala Met Ile Thr Cys Gly Gly Asn Asn Ile Gly Phe Lys Gly Val
20 25 30
Gln Trp Tyr Gln Gln Lys Thr Gly Gln Ala Pro Val Leu Val Val Tyr
35 40 45
Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80
Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ala Ser Asp His
85 90 95
Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 262
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-18 VL Chain (aa)

<400> 262
Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15
Arg Val Thr Ile Ser Cys Ser Gly Ser Gly Ser Asn Ile Gly Ser Asn
20 25 30
Asp Val Ser Trp Tyr Gln Gln Ile Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45
Ile Tyr Trp Asn Asp Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu

				85					90					95
Asn	Gly	Trp	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	
			100					105					110	

<210> 263
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-19 VL Chain (aa)

<400> 263															
Gln	Ala	Val	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser	Pro	Gly	Gln
1				5					10				15		
Ser	Ile	Thr	Ile	Ser	Cys	Thr	Gly	Thr	Ser	Ser	Asp	Val	Gly	Asp	Tyr
			20					25				30			
Asn	Tyr	Val	Ala	Trp	Tyr	Gln	Gln	His	Pro	Gly	Lys	Asp	Pro	Lys	Leu
		35				40					45				
Met	Ile	Phe	Glu	Val	Ile	Asn	Arg	Pro	Ser	Gly	Val	Ser	Asp	Arg	Phe
	50					55				60					
Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Asp	Ile	Ser	Gly	Leu
65					70				75					80	
Gln	Pro	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Ile	Ser	Tyr	Ser	Arg	Gly
				85				90					95		
Ser	Thr	Pro	Tyr	Val	Ile	Gly	Thr	Gly	Thr	Lys	Val	Thr	Val	Leu	
			100					105					110		

<210> 264
 <211> 104
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-20, -27 VL Chain (aa)

<400> 264															
Gln	Pro	Val	Leu	Thr	Gln	Pro	Pro	Ser	Ala	Ser	Gly	Thr	Pro	Gly	Gln
1				5					10				15		
Arg	Val	Thr	Ile	Ser	Cys	Ser	Gly	Gly	Lys	Thr	Val	Asn	Trp	Phe	Arg
			20					25					30		

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

<210> 265
 <211> 110
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-21 VL Chain (aa)

<400> 265
 Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
 1 5 10 15
 Arg Val Thr Ile Ser Cys Ser Gly Ser Gly Ser Asn Ile Gly Ser Asn
 20 25 30
 Asp Val Ser Trp Tyr Gln Gln Ile Pro Gly Thr Ala Pro Lys Leu Leu
 35 40 45
 Ile Tyr Trp Asn Asp Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
 50 55 60
 Gly Ser Lys Ser Gly Ile Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
 65 70 75 80
 Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
 85 90 95
 Asn Gly Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
 100 105 110

<210> 266
 <211> 110
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>

<223> BCMA-22 VL Chain (aa)

<400> 266

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

<210> 267

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-23 VL Chain (aa)

<400> 267

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

<210> 268

<211> 248

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-13 scFv (aa)

<400> 268
Gln Met Gln Leu Val Gln Tyr Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Thr Leu Pro Gly Arg Asp Gly Tyr Pro Gly Ala Phe Asp Tyr Arg
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ala Val Leu Thr Gln Pro
130 135 140
Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser
145 150 155 160
Gly Ser Gly Ser Asn Ile Gly Ser Asn Asp Val Ser Trp Tyr Gln Gln
165 170 175
Ile Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Trp Asn Asp Gln Arg
180 185 190
Pro Ser Gly Val Pro Asp Arg Phe Ser Ala Ser Lys Ser Gly Thr Ser
195 200 205
Ala Ser Leu Ala Ile Ser Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr
210 215 220
Tyr Cys Ala Ala Trp Asp Asp Ser Leu Gly Gly Ser Trp Val Phe Gly
225 230 235 240
Gly Gly Thr Lys Val Thr Val Leu
245

<210> 269
<211> 248
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-14 scFv (aa)

<400> 269

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

<210> 270

<211> 248

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-15 scFv (aa)

<400> 270

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

<210> 271

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-16 scFv (aa)

<400> 271

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

<210> 272

<211> 240

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-17 scFv (aa)

<400> 272

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

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

<210> 273
 <211> 240
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-18 scFv (aa)

<400> 273
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Trp Met Ser Trp His Arg Gln Ala Pro Gly Lys Gly Pro Glu Trp Val
 35 40 45
 Ala His Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val

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

<210> 274

<211> 240

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-19 scFv (aa)

<400> 274

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

Ala	Arg	Asp	Gly	Gly	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val
			100					105					110		
Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly
		115					120					125			
Ser	Gln	Ala	Val	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser	Pro	Gly
		130				135					140				
Gln	Ser	Ile	Thr	Ile	Ser	Cys	Thr	Gly	Thr	Ser	Ser	Asp	Val	Gly	Asp
145					150					155				160	
Tyr	Asn	Tyr	Val	Ala	Trp	Tyr	Gln	Gln	His	Pro	Gly	Lys	Asp	Pro	Lys
			165					170					175		
Leu	Met	Ile	Phe	Glu	Val	Ile	Asn	Arg	Pro	Ser	Gly	Val	Ser	Asp	Arg
			180				185					190			
Phe	Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Asp	Ile	Ser	Gly
		195				200					205				
Leu	Gln	Pro	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Ile	Ser	Tyr	Ser	Arg
	210				215					220					
Gly	Ser	Thr	Pro	Tyr	Val	Ile	Gly	Thr	Gly	Thr	Lys	Val	Thr	Val	Leu
225					230					235					240

<210> 275

<211> 240

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-20 scFv (aa)

<400> 275

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

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

<210> 276

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-21 scFv (aa)

<400> 276

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

Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Asn	Asp	Gln	Arg	Pro	Ser	Gly	Val
			180					185					190		
Pro	Asp	Arg	Phe	Ser	Gly	Ser	Lys	Ser	Gly	Ile	Ser	Ala	Ser	Leu	Ala
		195					200					205			
Ile	Ser	Gly	Leu	Arg	Ser	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Ala	Ala
	210					215					220				
Trp	Asp	Asp	Ser	Leu	Asn	Gly	Tyr	Val	Phe	Gly	Thr	Gly	Thr	Lys	Val
225					230					235					240
Thr	Val	Leu													

<210> 277

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-22 scFv (aa)

<400> 277

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

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

<210> 278
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-23 scFv (aa)

<400> 278

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

Ser	Tyr	Gly	Gly	Ser	Arg	Ser	Tyr	Val	Phe	Gly	Thr	Gly	Thr	Lys	Val
225					230					235					240
Thr	Val	Leu													

<210> 279
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> VH-3 CDR-H3 (aa)

Val	Asp	Gly	Asp	Asp	Ala	Phe	Asp	Ile
1				5				

<210> 280
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> VH-4 CDR-H3 (aa)

Asp	Pro	Leu	Ser	Trp	Asp	Ser	Ser	Gly	Lys	Gly	Pro	Arg
1				5					10			

<210> 281
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> VH-5 CDR-H3 (aa)

<400> 281
Glu Asn Tyr Asp Phe Trp Ser Trp Arg Tyr Tyr Tyr Asp Met Asp Val
1 5 10 15

<210> 282
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> VH-6 CDR-H3 (aa)

<400> 282
Val Asp Gly Pro Pro Ser Tyr Asp Ile
1 5

<210> 283
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> VH-7 CDR-H3 (aa)

<400> 283
Gly Asp Trp Asp Asp Ala Phe Asp Ile
1 5

<210> 284
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> VH-9 CDR-H3 (aa)

<400> 284

Val Asp Gly Asp Tyr Glu Asp Tyr
1 5

<210> 285
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> VH-10 CDR-H3 (aa)

<400> 285
Asp Val Pro Ser Ser Gly Asp Asp Ala Phe Asp Ile
1 5 10

<210> 286
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> VH-11 CDR-H3 (aa)

<400> 286
Val Asp Gly Asp Asp Val Phe Asp Ile
1 5

<210> 287
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> VH-12 CDR-H3 (aa)

<400> 287
Val Asp Gly Asp Ala Phe Asp Ile

1 5

<210> 288
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-C1 VH CDR-H1 (aa)

<400> 288
Asp Tyr Ser Ile Asn
1 5

<210> 289
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-C2 VH CDR-H1 (aa)

<400> 289
Asn Phe Gly Met Asn
1 5

<210> 290
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-C1 VH CDR-H2 (aa)

<400> 290
Trp Ile Asn Thr Glu Thr Arg Glu Pro Ala Tyr Ala Tyr Asp Phe Arg
1 5 10 15

Gly

<210> 291

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-C2 VH CDR-H2 (aa)

<400> 291

Trp Ile Asn Thr Tyr Thr Gly Glu Ser Tyr Phe Ala Asp Asp Phe Lys

1

5

10

15

Gly

<210> 292

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-C1 VH CDR-H3 (aa)

<400> 292

Asp Tyr Ser Tyr Ala Met Asp Tyr

1

5

<210> 293

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-C2 VH CDR-H3 (aa)

<400> 293
Gly Glu Ile Tyr Tyr Gly Tyr Asp Gly Gly Phe Ala Tyr
1 5 10

<210> 294
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-C1 VH CDR-H1 (aa) Chothia numbering

<400> 294
Gly Tyr Thr Phe Thr Asp Tyr
1 5

<210> 295
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-C2 VH CDR-H1 (aa) Chothia numbering

<400> 295
Gly Tyr Thr Phe Thr Asn Phe
1 5

<210> 296
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-C1 VH CDR-H2 (aa) Chothia numbering

<400> 296

Asn Thr Glu Thr Arg Glu
1 5

<210> 297
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-C2 VH CDR-H2 (aa) Chothia numbering

<400> 297
Asn Thr Tyr Thr Gly Glu
1 5

<210> 298
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-C1 VH CDR-H1 (aa) AbM numbering

<400> 298
Gly Tyr Thr Phe Thr Asp Tyr Ser Ile Asn
1 5 10

<210> 299
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-C2 VH CDR-H1 (aa) AbM numbering

<400> 299
Gly Tyr Thr Phe Thr Asn Phe Gly Met Asn

1 5 10

<210> 300
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-C1 VH CDR-H2 (aa) AbM numbering

<400> 300
Trp Ile Asn Thr Glu Thr Arg Glu Pro Ala
1 5 10

<210> 301
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-C2 VH CDR-H2 (aa) AbM numbering

<400> 301
Trp Ile Asn Thr Tyr Thr Gly Glu Ser Tyr
1 5 10

<210> 302
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-C1 VL CDR-L1 (aa)

<400> 302
Arg Ala Ser Glu Ser Val Thr Ile Leu Gly Ser His Leu Ile His
1 5 10 15

<210> 303
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-C2 VL CDR-L1 (aa)

<400> 303
Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ser
1 5 10

<210> 304
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-C1 VL CDR-L2 (aa)

<400> 304
Leu Ala Ser Asn Val Gln Thr
1 5

<210> 305
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-C2 VL CDR-L2 (aa)

<400> 305
Ser Ala Ser Tyr Arg Tyr Thr
1 5

<210> 306
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-C1 VL CDR-L3 (aa)

<400> 306
Leu Gln Ser Arg Thr Ile Pro Arg Thr
1 5

<210> 307
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-C2 VL CDR-L3 (aa)

<400> 307
Gln Gln His Tyr Ser Thr Pro Trp Thr
1 5

<210> 308
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-C1 VH FR1 (aa)

<400> 308
Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
1 5 10 15
Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
20 25 30

<210> 309
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-C2 VH FR1 (aa)

<400> 309
Gln Ile Gln Leu Val Gln Ser Gly Pro Asp Leu Lys Lys Pro Gly Glu
1 5 10 15
Thr Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
20 25 30

<210> 310
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-C1 VH FR2 (aa)

<400> 310
Trp Val Lys Arg Ala Pro Gly Lys Gly Leu Lys Trp Met Gly
1 5 10

<210> 311
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-C2 VH FR2 (aa)

<400> 311
Trp Val Lys Gln Ala Pro Gly Lys Gly Phe Lys Trp Met Ala

1 5 10

<210> 312
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-C1 VH FR3 (aa)

<400> 312
Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr Leu Gln
1 5 10 15
Ile Asn Asn Leu Lys Tyr Glu Asp Thr Ala Thr Tyr Phe Cys Ala Leu
20 25 30

<210> 313
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-C2 VH FR3 (aa)

<400> 313
Arg Phe Ala Phe Ser Val Glu Thr Ser Ala Thr Thr Ala Tyr Leu Gln
1 5 10 15
Ile Asn Asn Leu Lys Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg
20 25 30

<210> 314
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-C1 VH FR4 (aa)

<400> 314
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
1 5 10

<210> 315
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-C2 VH FR4 (aa)

<400> 315
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
1 5 10

<210> 316
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-C1 VL FR1 (aa)

<400> 316
Asp Ile Val Leu Thr Gln Ser Pro Pro Ser Leu Ala Met Ser Leu Gly
1 5 10 15
Lys Arg Ala Thr Ile Ser Cys
20

<210> 317
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>

<223> BCMA-C2 VL FR1 (aa)

<400> 317

Asp	Val	Val	Met	Thr	Gln	Ser	His	Arg	Phe	Met	Ser	Thr	Ser	Val	Gly
1				5				10						15	
Asp	Arg	Val	Ser	Ile	Thr	Cys									
			20												

<210> 318

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-C1 VL FR2 (aa)

<400> 318

Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Pro	Pro	Thr	Leu	Leu	Ile	Gln
1				5				10						15

<210> 319

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-C2 VL FR2 (aa)

<400> 319

Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Phe
1				5				10						15

<210> 320

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-C1 VL FR3 (aa)

<400> 320

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

<210> 321

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-C2 VL FR3 (aa)

<400> 321

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

<210> 322

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-C1 VL FR4 (aa)

<400> 322

Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys
1				5				10	

<210> 323

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-C2 VL FR4 (aa)

<400> 323

Phe Gly Gly Gly Thr Lys Leu Asp Ile Lys
1 5 10

<210> 324

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-C1 VH Chain (aa)

<400> 324

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

<210> 325

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-C2 VH Chain (aa)

<400> 325

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

<210> 326

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-C1 VL Chain (aa)

<400> 326

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

<210> 327
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-C2 VL Chain (aa)

<400> 327
 Asp Val Val Met Thr Gln Ser His Arg Phe Met Ser Thr Ser Val Gly
 1 5 10 15
 Asp Arg Val Ser Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala
 20 25 30
 Val Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
 35 40 45
 Phe Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
 50 55 60
 Ser Gly Ser Gly Ala Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala
 65 70 75 80
 Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His Tyr Ser Thr Pro Trp
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Leu Asp Ile Lys
 100 105

<210> 328
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-C1 VL-VH scFv (aa)

<400> 328
 Asp Ile Val Leu Thr Gln Ser Pro Pro Ser Leu Ala Met Ser Leu Gly
 1 5 10 15
 Lys Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Thr Ile Leu
 20 25 30
 Gly Ser His Leu Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45
 Thr Leu Leu Ile Gln Leu Ala Ser Asn Val Gln Thr Gly Val Pro Ala
 50 55 60

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

<210> 329

<211> 244

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-C2 VH-VL scFv (aa)

<400> 329

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

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

<210> 330

<211> 738

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-1 scFv (nt)

<400> 330

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caggtgcagc tgggtgcagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60
tcctgtacag cttctggatt cacctttggt gattatgcta tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtaggtttc attagaagca aagcttatgg tgggacaaca 180
gaatacgccg cgtctgtgaa aggtagattc accatctcaa gagatgattc caaaagcatc 240
gcctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtatta ctgtgcggcc 300
tggagtgcgc cgactgacta ctggggccag ggaaccctgg tcaccgtctc ctcaggtgga 360
ggcgggttcag gcgagggtgg ctctggcggt ggcggatcgg atattgtgat gaccagtcct 420
ccagactccc tgtctgtgtc tccgggagag agggccacca tcagctgcaa gtccagccag 480
agtgttttat ccacctcaa caataagaac tatttagctt ggtatcagca gaaaccagga 540
cagcccccta ggctgtcctt ttactgggca tctaccggg aggccggggt ccctgaccga 600
ttcagtggca gcggtcttgg gacagatttc actctacca tcagcagcct gcaggctgaa 660
gatgtggcgg ttattacttg tcaacaatat ttcagttctc cgtacacttt tggccacggg 720
accaagctgg aaatcaaaa

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<210> 331
 <211> 717
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-2 scFv (nt)

<400> 331
 gaggtgcagc tgggtggagtc tggggggaggc ttggtcaagc ctggagggtc cctgagactc 60
 tcctgtgcag cctctggatt caccttcagt gactactaca tgagctggat ccgccaggct 120
 ccagggaagg ggctggagtg ggtttcatac attagtagta gtggtagtac catatactac 180
 gcagactctg tgaagggccg attcaccatc tccagggaca acgccaagaa ctactgtat 240
 ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gaaagtggat 300
 ggccctcctt cttctgatat ctggggccaa gggacaatgg tcaccgtctc ctgaggtgga 360
 ggcggttcag gcggagggtg ctctggcggg ggcggatcgg aaatagtgtat gacgcagtct 420
 ccagccaccc tgtctgtgtc tccaggggaa acagccaccc tctcctgcag ggccagtcag 480
 agtattaaga ccaacttggc ctggtaccag cagaaacctg gccaggctcc caggctcctc 540
 atctatgctg catccaccag ggccactggc atcccagaca gattcagtgg cagtgggtct 600
 gggacagact tcactctcac catcaccaga ctggagcctg aagattttgc agtgtattac 660
 tgtcagcaat atggtagctc acccactttt ggccggggga ccaagctgga aatcaaa 717

<210> 332
 <211> 738
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-3 scFv (nt)

<400> 332
 caggtgcagc tgggtgcagtc tggggggaggc ttggtacagc cagggcggtc cctgagactc 60
 tcctgtacag cttctggatt caccttttgt gattatgcta tgagctgggt ccgccaggct 120
 ccagggaagg ggctggagtg ggtaggtttc attagaagca aagcttatgg tgggacaaca 180
 gaatacgccg cgtctgtgaa aggagattc accatctcaa gagatgattc caaaagcatc 240
 gcctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtatta ctgtgcggcc 300
 tggagtgtcc cgactgacta ctggggccag ggaaccctgg tcaccgtctc ctgaggtgga 360
 ggcggttcag gcggagggtg ctctggcggg ggcggatcgg atattgtgat gaccagtcct 420
 ccagactccc tggttgtgtc tctgggcgag agggccacca tcaactgcaa gtccagccag 480
 agtgttttac acagctccaa caataagaat tacttagctt ggtaccagca gaaaccagga 540
 cagcctccta agctgtctat ttactgggca tctaccggg aatccggggc ccctgaccgg 600
 ttcagtggca gcgggtcttg gacagatttc actctacca tcagcagcct gcaggctgaa 660
 gatgtggcag tttattactg tcagcagtat tatactactc cgctcacttt cggcggaggg 720

accaaggtgg aaatcaaa

738

<210> 333

<211> 720

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-4 scFv (nt)

<400> 333

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tcctgtacag cttctggatt cacctttggt gattatgcta tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtaggtttc attagaagca aagcttatgg tgggacaaca 180
gaatacgccg cgtctgtgaa aggagattc accatctcaa gagatgattc caaaagcatc 240
gcctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtatta ctgtgcggcc 300
tggagtgtccc cgactgacta ctggggccag ggaaccctgg tcaccgtctc ctcagggtgga 360
ggcggttcag gcgagggtgg ctctggcggg ggcggatcgg ccatccggat gacccagtct 420
ccatcctccc tgtccgcgtc tctgggggac agagtcacca tcaattgccg ggcgagtcag 480
gacattagga attctttggc ctggtatcag cagaggccag ggaaagcccc taaactcctg 540
ctttctgctg catccagatt ggaaagtggg gtcccttcta gggttcagtgg cactacttct 600
ggggcggagt atgctctcag catcagcagc ctgcagcctg aagatgtcgc atcttatttc 660
tgtcagcagt attatagtct ccctctctcc ttcggcggag ggaccaaggt ggaaatcaaa 720
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<210> 334

<211> 738

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-5 scFv (nt)

<400> 334

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tcctgtacag cttctggatt cacctttggt gattatgcta tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtaggtttc attagaagca aagcttatgg tgggacaaca 180
gaatacgccg cgtctgtgaa aggagattc accatctcaa gagatgattc caaaagcatc 240
gcctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtatta ctgtgcggcc 300
tggagtgtccc cgactgacta ctggggccag ggaaccctgg tcaccgtctc ctcagggtgga 360
ggcggttcag gcgagggtgg ctctggcggg ggcggatcgg acatcgtgat gacccagtct 420
ccagactccc tggctgtgtc tctgggcgag agggccacca tcaactgcaa gtccagccag 480
agtgttttat acagctccaa caataagaac tacttagctt ggtaccagca gaaaccagga 540
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cagcctccta agctgctcat ttactgggca tctacccggg aatccgggggt ccctgaccga 600
ttcagtggca gcggttctgg gacagatttc actctcacca tcagcagcct gcaggctgaa 660
gatgtggcag tttattactg tcagcaatat tatagtactc cgtggacggt cggccaaggg 720
accaaggtgg atatcaaaa                                     738

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<210> 335

<211> 720

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-6 scFv (nt)

<400> 335

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caggtgcagc tgggtgcagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60
tcctgtacag cttctggatt cacctttggg gattatgcta tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtaggtttc attagaagca aagcttatgg tgggacaaca 180
gaatacgccg cgtctgtgaa aggcagattc accatctcaa gagatgattc caaaagcatc 240
gcctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtatta ctgtgcggcc 300
tggagtgtcc cgactgacta ctggggccag ggaaccctgg tcaccgtctc ctcaggtgga 360
ggcggttcag gcgagggtgg ctctggcggg ggcggtatcg atattgtgat gaccagtcct 420
ccatcgtccc tgtctgtgtc tgtaggagag agagtcacca tcacttgtcg ggcgagtcag 480
tctataagta attccttagc ctggtataaa cagagaccgg gagaagcccc taaactcctg 540
atacatgctg catccaatgt ggaagatggg gtcccttcga gggttcagcg caggggatct 600
gggacagttt tactctcgc catcagcaat gtacagcctg aagatttcgc aacttactac 660
tgtcagcaga gtcacatgta ccctccgact ttcggcgggg ggaccaaggt ggaaatcaaa 720

```

<210> 336

<211> 720

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-7 scFv (nt)

<400> 336

```

caggtgcagc tgggtgcagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60
tcctgtacag cttctggatt cacctttggg gattatgcta tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtaggtttc attagaagca aagcttatgg tgggacaaca 180
gaatacgccg cgtctgtgaa aggcagattc accatctcaa gagatgattc caaaagcatc 240
gcctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtatta ctgtgcggcc 300
tggagtgtcc cgactgacta ctggggccag ggaaccctgg tcaccgtctc ctcaggtgga 360

```

```

ggcggttcag gcgagggtgg ctctggcggt ggcggatcgg tcatccagtt gacccagtct 420
ccctcctcac tgtctgcatc tgtagggggac agagtcacca tcacttgctg ggcgagtcag 480
gacattggcg attatttagc ctggttttcag cagagaccag ggaaagcccc taagtccctg 540
atctatgttg cgtccacttt gcagagtggg gtcccatcaa ggttcagcgg cagtggatct 600
gggacacact tcactctcac catcaacagc ctgcagcctg aagattttgc aacttattac 660
tgccaacagt atcatagtca cccgtggacg ttcggcccag ggaccaaggt ggatatcaaa 720

```

<210> 337

<211> 738

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-8 scFv (nt)

<400> 337

```

cagggtccagc tgggtgcagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60
tcctgtacag cttctggatt cacctttggt gattatgcta tgagctggtt ccgccaggct 120
ccagggaagg ggctggagtg ggtaggtttc attagaagca aagcttatgg tgggacaaca 180
gaatacgccg cgtctgtgaa aggagattc accatctcaa gagatgattc caaaagcatc 240
gcctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtatta ctgtgcggcc 300
tggagtgtccc cgactgacta ctggggccag ggaaccctgg tcaccgtctc ctcagggtgga 360
ggcggttcag gcgagggtgg ctctggcggt ggcggatcgg atattgtgat gacccagtct 420
ccagactccc tggctgtgtc tctgggcgag agggccacca tcaactgcaa gtccagccag 480
agtgttttat acagctcaa caataagaac tacttagctt ggtaccagca gaaaccagga 540
cagctccta agctgtcat ttactgggca tctaccggg aatccggggt ccctgaccga 600
ttcagtggca gcgggtctgg gacagatttc actctacca tcagcagcct gcaggctgaa 660
gatgtggcag tttattactg tcagcaatat tatagtactc cgtacacttt tggccagggg 720
accaagctgg aaatcaaa 738

```

<210> 338

<211> 723

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-9 scFv (nt)

<400> 338

```

gaagtgcagc tgggtgcagtc tgggggaggc ttggtcaagc ctggagggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt gactactaca tgagctggat ccgccaggct 120
ccagggaagg ggctggagtg ggtttcatac attagtagta gtggtagtac catatactac 180

```

```

gcagactctg tgaagggccg attcaccatc tccagggaca acgccaagaa ctactgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagagtggac 300
ggtgactacg tcgatgacta ctggggccag ggaaccctgg tcaccgtctc ctcaggtgga 360
ggcggttcag gcgagggtgg ctctggcggg ggccggatcgt cctatgagct gactcagccg 420
ccctcgggtgt ctgtggcccc aggacagacg gccagggtta cctgtggggc aaataatatt 480
ggaagcaaaa gtgtccactg gtaccagcag aagccaggcc aggcccccat gctggtcgtc 540
tatgatgatg acgaccggcc ctccgggatc cctgagcgat tctctggctc caactctggg 600
aacacggcca ccctgaccat cagcgggggtc gaggccgggg atgaggccga ctacttctgt 660
cacgtgtggg atagaagtcg tgatcattat gtcttcggaa ctgggaccaa gctgaccgtc 720
cta 723

```

<210> 339
 <211> 723
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-10 scFv (nt)

```

<400> 339
gaagtgcagc tgggtgcagtc tgggggaggc ttggtcaagc ctggagggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt gactactaca tgagctggat ccgccaggct 120
ccagggaagg ggctggagtg ggtttcatac attagtagta gtggtagtac catatactac 180
gcagactctg tgaagggccg attcaccatc tccagggaca acgccaagaa ctactgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagagtggac 300
ggtgactacg tcgatgacta ctggggccag ggaaccctgg tcaccgtctc ctcaggtgga 360
ggcggttcag gcgagggtgg ctctggcggg ggccggatcgt cctatgagct gactcagccg 420
ccctcgggtgt ctgtggcccc aggacagacg gccagggtta cctgtggggc aaataatatt 480
ggaagcaaaa gtgtccactg gtaccagcag aagccaggcc aggcccccat gctggtcgtc 540
tatgatgatg acgaccggcc ctccgggatc cctgagcgat tctctggctc caactctggg 600
aacacggcca ccctgaccat cagcgggggtc gaggccgggg atgaggccga ctacttctgt 660
cacgtgtggg atagaagtcg tgatcattat gtcttcggaa ctgggaccaa gctgaccgtc 720
cta 723

```

<210> 340
 <211> 741
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-11 scFv (nt)

<400> 340

```

cagggtgcagc tgggtacagtc tggggggaggc ttggtacagc ctggcagggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccggcgagct 120
ccagggaagg gccttgagtg ggtctcagggt attagttaga atagtggtag cataggctat 180
gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaatga acagtctgag agctgaggac acggccgtgt attactgtgc gagagatctg 300
gggcccgaact acgatcccga tgcttttgat atctggggcc aagggaacaat ggtcaccgtt 360
tcctcagggtg gaggcgggtt aggcggagggt ggctctggcg gtggcggatc gcagcttggtg 420
ctgactcagc caccctcagc gtctgggacc cccgggcaga gggtcacat ctcttggttct 480
ggaagcagct ccaacatcgg aagtaatgct gtaaactgggt accagcagct cccaggaacg 540
gccccgaag tcctcatcta taatagtcac cagcggccct caggggtccc tgaccgattc 600
tctggctcca agtctggcac ctcagcctcc ctggccatca atgggctcca gtctgaggac 660
gaggctgatt attactgtgc agcatgggat gacagcctga gaggttacgt cttcggaact 720
gggaccaagc tcaccgtcct a 741

```

<210> 341

<211> 729

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-12 scFv (nt)

<400> 341

```

gagggtgcagc tgggtggagtc tggggggaggc ttggtcaagc ctggagggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt gactactaca tgagctggat ccgccaggct 120
ccagggaagg ggcttgagtg ggtttcatac attagtagta gtggtagtac catatactac 180
gcagactctg tgaagggccg attcaccatc tccagggaca acgccaagaa ctactgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gaaagtggat 300
ggccctcctt cttttgatat ctggggccaa gggacaatgg tcaccgtctc ctcagggtga 360
ggcgggttcag gcggagggtg ctctggcggt ggcggatcgc agtctgccct gacgcagccg 420
ccctcagtggt ctgcggcccc aggacagaag gtcaccatct cctgctctgg aagccgctcc 480
aacattggga ataattatgt atcctggtac caacagctcc caggaacagc ccccaaactc 540
ctcatattatg acaatgctaa gcgaccctca ggaattcctg accgattctc tggctccaag 600
tctggcacgt cagccaccct ggacatcgcc ggactccaga ctggggatga ggccgactat 660
tactgtcagg tgtgggtag tagtagtgat cattgggtat tcggcggagg gaccaagctc 720
accgtccta 729

```

<210> 342

<211> 744

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-13 scFv (nt)

<400> 342

```
cagatgcagc tgggtgcagta tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt agctatgcta tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactac 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgaa agctgaggac acggctgtgt attactgtgc taccctaccc 300
ggtagagatg gctaccccg agcctttgac tacaggggcc agggaaaccct ggtcaccgtc 360
tcctcagggtg gaggcggttc aggcggagggt ggctctggcg gtggcggatc gcaggctgtg 420
ctgactcagc caccctcagc gtctgggacc cccgggcaga gggtcacccat ctcttgttct 480
ggaagcggct ccaacatcgg aagtaatgat gtctcctgggt atcagcagat cccaggaacg 540
gcccccaaac tcctcatcta ctggaatgat cagcgccct caggggtccc tgaccgattc 600
tctgcctcca agtctggcac ctcagcctcc ctggccatca gtgggctccg gtccgaggat 660
gaggctgatt attactgtgc agcatgggat gacagcctgg gtggttcttg ggtgttcggc 720
ggagggacca aggtcaccgt ccta 744
```

<210> 343

<211> 744

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-14 scFv (nt)

<400> 343

```
gaggtgcagc tgttgagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactac 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc taccctaccc 300
ggtagagatg gctaccccg agcctttgac tacaggggcc cgggaaccct ggtcaccgtc 360
tcctcagggtg gaggcggttc aggcggagggt ggctctggcg gtggcggatc gcaggctgtg 420
ctgactcagc caccctcagc gtctgggacc cccgggcaga gggtcacccat ctcttgttct 480
ggaagcggct ccaacatcgg aagtaatgat gtctcctgggt atcagcagat cccaggaacg 540
gcccccaaac tcctcatcta ctggaatgat cagcgccct caggggtccc tgaccgattc 600
tctggctcca agtctggcgc ctcagcctct ctggccatca gtgggctcca gtctgaggat 660
gaggctgatt attattgtgc agcatgggat gacaggttga acggtttttg ggtgttcggc 720
ggagggacca agctcaccgt ccta 744
```

<210> 344

<211> 744

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-15 scFv (nt)

<400> 344

```
cagggtgcagc tgttggagtc tgggggaggc ctggtcaagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gaaagatcag 300
tatagcagta gcgcacaaag ggccgacttt gactactggg gccagggaac cctggtcacc 360
gtctcctcag gtggaggcgg ttcaggcgga ggtggttctg gcggtggcgg atcgcagtct 420
gtgctgacgc agccaccctc agcgtctggg acccccgggc agagggtcac catctcttgt 480
tctggaagcg gctccaacat cggaagtaat gatgtctcct ggtatcagca gatcccagga 540
acggcccca aactcctcat ctactggaat gatcagcggc cctcagggggt ccctgaccgg 600
ttctcaggct ccaagtctgg cacctcagcc tccctgggtca tcagtgggct ccggtccgag 660
gatgaggctg attattactg tgcagcatgg gatgacagcc tgagtgggtg ggtgttcggc 720
ggagggacca agctgaccgt ccta 744
```

<210> 345

<211> 738

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-16 scFv (nt)

<400> 345

```
gagggtccagc tgggtacagtc tgggcctgag gtgaagaagc ctgggacctc agtgaaggtc 60
tcctgcaagg cttctggatt cacctttact agctctgcta tgcagtgggt gcgacaggct 120
cgtggacaac gccttgagtg gataggatgg atcgtcgttg gcagtggtaa cacaactac 180
gcacagaagt tccaggaaag agtcaccatt accagggaaca tgtccacaag cacagcctac 240
atggagctga gcagcctgag atccgaggac acggccgtgt attactgtgc ggcagctccg 300
tattacgata ttttgactgg ttattattta tggggccagg gaacgctggg caccgtctcc 360
tcagggtggag gcggttctgg cggagggtggc tctggcggtg gcggatcgca gtctgccctg 420
actcagccac cctcagcgtc tgggaccccc gggcagaggg tcaccatctc ttgttctgga 480
agcggctcca acatcggaag taatgatgtc tcctgggtatc agcagatccc aggaacggcc 540
cccaaactcc tcattacttg gaatgatcag cggccctcag gggtcctga ccgattctct 600
ggctccaagt ctggcacctc agcctccctg gccatcagtg ggctccagtc tgaggatgag 660
gctgattatt actgtgcatc atgggatgac agcctgagtg gttgggtgtt cggcggaggg 720
accaagctga ccgtccta 738
```

<210> 346

<211> 720

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-17 scFv (nt)

<400> 346

```
caggttcagc tgggtgcagtc tgggggaggc ttggtcaagc ctggagggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt gactactaca tgagctggat ccgcctggct 120
ccagggaagg ggctggagtg ggtttcatac attagtagta gtggtagtac catatactac 180
gcagactctg tgaagggccg attcaccatc tccagggaca acgccaagaa ctactgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagagaggcc 300
gatagtagcg ctgactactg gggccaggga accctgggtca acgtctcctc aggtggaggc 360
ggttcaggcg gaggtggctc tggcgggtggc ggatcgagc ctgtgctgac tcagccaccc 420
tcggtgtcag tggccccagg aaagacggcc atgattacct gtgggggaaa caacattgga 480
tttaaagggtg tgcagtggta ccagcagaag acaggccagg cccctgtgct ggctgtctat 540
gatgatagcg accggccctc agggatccct gagcgattct ctggctccaa ctctgggaac 600
acggccaccc tgaccatcag cagggtcgaa gccggggatg aggccgatta ttactgtcag 660
gtgtgggata gtgctagtga tcattgggtg ttcggcggag ggaccaagct gaccgtccta 720
```

<210> 347

<211> 720

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-18 scFv (nt)

<400> 347

```
gaggtgcagc tgttggagtc tgggggaggc ttggtccagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt cacgtttagt agctattgga tgagctggca ccgccaggct 120
ccagggaagg ggccggagtg ggtggccac ataaaccaag acggaagtga gaagtactat 180
gtggactctg tgaagggccg attcaccatc tccagagaca acgccgagag ttactgtat 240
ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gaggtggctg 300
gcggttacta actggggcca gggaaccctg gtcaccgtct cctcagggtg aggcggttca 360
ggcggagggtg gctctggcgg tggcggatcg cagtctgtgt tgactcagcc accctcagcg 420
tctgggaccc ccgggcagag ggtcaccatc tcttgttctg gaagcggctc caacatcgga 480
agtaatgatg tctcctggta tcagcagatc ccagggacgg cccccaact cctcatctac 540
tggaatgatc agcggccctc aggggtccct gaccgattct ctggctccaa gtctggcacc 600
tcagcctccc tggccatcag tgggctccgg tccgaggatg aggctgatta ttactgtgca 660
gcatgggatg acagcctgaa tggttgggtg ttcggcggag ggaccaagct gaccgtccta 720
```

<210> 348
 <211> 720
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-19 scFv (nt)

<400> 348
 cagggtccagc tgggtacagtc tgggggctgag gtgaagaagc ctggggcctc agtgaaggctc 60
 tcctgcaagg cttctggata cacccttcacc agctactata tgcactgggt gcgacaggcc 120
 cctggacaag ggcttgagtg gatgggatgg atcaacccta acagtgggtg cacaactat 180
 gcacagaagt ttcagggcag gggtcaccatg accagggaca cgtccatcag cacagcctac 240
 atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gagagatgg 300
 ggggacgtct gggggccaagg gaccacgggtc accgtctcct cagggtggagg cggttcaggc 360
 ggagggtggct ctggcgggtg cggatcgcag gctgtgctga ctcagcctgc ctccgtgtct 420
 ggggtctcctg gacagtcgat caccatctcc tgcactggaa ccagcagtga cgttgggtgat 480
 tataactatg tcgcctggta tcaacaacac ccaggcaaag accccaaact catgattttt 540
 gaggtcatta atcggccctc aggggtttct gatcgcttct ctggctcaa gtctggcaac 600
 acggcctccc tggacatctc tgggctccag cctgaggacg aggctgatta ttactgcatc 660
 tcatattcac gaggcagcac tccttatgtc atcggaactg ggaccaaggt gaccgtccta 720

<210> 349
 <211> 720
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-20 scFv (nt)

<400> 349
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggcaggctc cctgagactc 60
 tcctgtgcag cctctggatt cacccttgat gattatgcca tgcactgggt ccggcaagct 120
 ccagggaagg gcctggagtg ggtctcaggc attagttaga atagtggtag cataggctat 180
 gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
 ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgc aaaggggggc 300
 ctaggaataa ccccatacta ctttgactac tggggccagg gaaccctggc caccgtctcc 360
 tcagggtggag gcggttcagg cggagggtggc tctggcgggt gcggatcgca gcctgtgctg 420
 actcagccac cctcagcgtc tgggaccccc gggcagaggg tcaccatctc ttgttcggga 480
 ggcaagactg taaactgggt ccggcagggtc ccagggaacgg cccccaaact cctcatctat 540
 agtaatgatc agcggccctc aggggtccct gaccgattct ctggctcaa gtctggctcc 600
 tcagcctccc tggacatcag tgggctccag tctgaggatg aggcttatta ttactgtgga 660

tcatgggatg acagcctcaa tgcttgggtg ttcggcggag agaccaagct gaccgtccta 720

<210> 350

<211> 729

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-21 scFv (nt)

<400> 350

gaagtgcagc	tggtggagtc	tgggggaggc	ttggtcaagc	ctggagggtc	cctgaaactc	60
tcctgtgcag	cctctggatt	caccttcagt	gactactaca	tgagctggat	ccgccaggct	120
ccagggaagg	ggctggagtg	ggtttcatac	attagtagta	gtggtagtac	catatactac	180
gcagactctg	tgaagggccg	attcaccatc	tccagggaca	acgccaagaa	ctcactgtat	240
ctgcaaatga	acagcctgag	agccgaggac	acggccgtgt	attactgtgc	gaaagtagac	300
ggaggctaca	cagaggacta	ctggggccag	ggaaccctgg	tcaccgtctc	ctcagggtgga	360
ggcggttcag	gcggagggtg	ctctggcggt	ggcggatcgc	agtctgtgct	gactcagcca	420
ccctcagcgt	ctgggacccc	cgggcagagg	gtcaccatct	cttgttctgg	aagcggctcc	480
aacatcggaa	gtaatgatgt	ctcctggtat	cagcagatcc	caggaacggc	ccccaaactc	540
ctcatctact	ggaatgatca	gcggccctca	ggggtccctg	accggttctc	aggctccaag	600
tctggcatct	cagcctccct	ggccatcagc	gggctccggt	ccgaggatga	ggctgattat	660
tactgtgcag	catgggatga	cagcctgaat	ggttatgtct	tcggaactgg	gaccaaggtc	720
accgtccta						729

<210> 351

<211> 729

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-22 scFv (nt)

<400> 351

gaagtgcagc	tggtggagtc	tgggggaggc	ttggtcaagc	ctggagggtc	cctgagactc	60
tcctgtgcag	cctctggatt	caccttcagt	gactactaca	tgagctggat	ccgccaggct	120
ccagggaagg	ggctggagtg	ggtttcatac	attagtagta	gtggtagtac	catatactac	180
gcagactctg	tgaagggccg	attcaccatc	tccagggaca	acgccaagaa	ctcactgtat	240
ctgcaaatga	acagcctgag	agccgaggac	acggccgtgt	attactgtgc	gaaagtagac	300
ggagactaca	cagaggacta	ctggggccag	ggaaccctgg	tcaccgtctc	ctcagggtgga	360
ggcggttcag	gcggagggtg	ctctggcggt	ggcggatcgc	agtctgccct	gactcagcct	420
gcctccgtgt	ctgggtctcc	tggacagtcg	atcactatct	cctgcactgg	aagcagcagt	480

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gatgttggca aatataatct tgtctcctgg taccaacagc cccaggcaa agcccccaag 540
ctcataatTT atgacgtcaa taagcggccc tcaggggttt ctaatcgctt ctctggctcc 600
aagtctggca acacggccac cctgacaatc tctgggctcc aggggtgacga cgaggctgat 660
tattattgtt gctcatatgg aggtagtagg tcttatgtct tcggaactgg gaccaagggtg 720
accgtccta 729

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<210> 352

<211> 729

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-23 scFv (nt)

<400> 352

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tcctgtgcag cctctggatt caccttcagt gactactaca tgagctggat ccgccaggct 120
ccagggaagg ggctggagtg ggtttcatac attagtagta gtggtagtac catatactac 180
gcagactctg tgaagggccg attcaccatc tccagggaca acgccaagaa ctactgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gaaagtagac 300
ggagactaca cagaggacta ctggggccag ggaaccctgg tcaccgtctc ctcagggtga 360
ggcggttcag gcgagggtgg ctctggcggt ggcggatcgc agtctgccct gactcagcct 420
gcctccgtgt ctgggtctcc tggacagtcg atcactatct cctgcactgg aagcagcagt 480
gatgttggca aatataatct tgtctcctgg taccaacagc cccaggcaa agcccccaag 540
ctcataatTT atgacgtcaa taagcggccc tcaggggttt ctaatcgctt ctctggctcc 600
aagtctggca acacggccac cctgacaatc tctgggctcc aggggtgacga cgaggctgat 660
tattattgta gctcatatgg aggtagtagg tcttatgtct tcggaactgg gaccaagggtg 720
accgtccta 729

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<210> 353

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> Consensus CDR-H1

<220>

<221> VARIANT

<222> 1

<223> Xaa = d or s

<220>

<221> VARIANT
<222> 2
<223> Xaa = y or s

<220>
<221> VARIANT
<222> 3
<223> Xaa = a, g, w or y

<220>
<221> VARIANT
<222> 5
<223> Xaa = h, q or s

<400> 353
Xaa Xaa Xaa Met Xaa
1 5

<210> 354
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<223> Consensus CDR-H2

<220>
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<222> 1
<223> Xaa = F, G, H, V, W or Y

<220>
<221> VARIANT
<222> 2
<223> Xaa = N, R, S or V

<220>
<221> VARIANT
<222> 3
<223> Xaa = P, Q, S, V, W or Y

<220>
<221> VARIANT
<222> 4
<223> Xaa = K or null

<220>
 <221> VARIANT
 <222> 5
 <223> Xaa = A or null

<220>
 <221> VARIANT
 <222> 6
 <223> Xaa = D, G, N, S, or Y

<220>
 <221> VARIANT
 <222> 7
 <223> Xaa = G or S

<220>
 <221> VARIANT
 <222> 8
 <223> Xaa = G or S

<220>
 <221> VARIANT
 <222> 9
 <223> Xaa = E, G, N, T or S

<220>
 <221> VARIANT
 <222> 10
 <223> Xaa = I, K, or T

<220>
 <221> VARIANT
 <222> 11
 <223> Xaa = E, G, N or Y

<220>
 <221> VARIANT
 <222> 12
 <223> Xaa = A or V

<220>
 <221> VARIANT
 <222> 13
 <223> Xaa = A, D or Q

<220>
 <221> VARIANT
 <222> 14

<223> Xaa = K or S

<220>

<221> VARIANT

<222> 15

<223> Xaa = F or V

<220>

<221> VARIANT

<222> 16

<223> Xaa = K or Q

<400> 354

Xaa Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Xaa Xaa
1 5 10 15
Xaa Xaa Xaa

<210> 355

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> Consensus CDR-H3

<220>

<221> VARIANT

<222> 1

<223> Xaa = A, D, E, G, L, V or W

<220>

<221> VARIANT

<222> 2

<223> Xaa = A, D, G, L, P, Q or S

<220>

<221> VARIANT

<222> 3

<223> Xaa = A, D, G, L or Y

<220>

<221> VARIANT

<222> 4

<223> Xaa = D, G, P, R, S, V, Y or null

<220>
 <221> VARIANT
 <222> 5
 <223> Xaa = D, I, P, S, T, Y or null

<220>
 <221> VARIANT
 <222> 6
 <223> Xaa = A, G, I, S, T, V, Y or null

<220>
 <221> VARIANT
 <222> 7
 <223> Xaa = A, D, E, F, L, P, S, Y or null

<220>
 <221> VARIANT
 <222> 8
 <223> Xaa = P, Q, T, Y or null

<220>
 <221> VARIANT
 <222> 9
 <223> Xaa = D, G, R, Y or null

<220>
 <221> VARIANT
 <222> 10
 <223> Xaa = A, F, Y or null

<220>
 <221> VARIANT
 <222> 11
 <223> Xaa = D, F or null

<220>
 <221> VARIANT
 <222> 12
 <223> Xaa = F or null

<220>
 <221> VARIANT
 <222> 13
 <223> Xaa = D, T or Y

<220>
 <221> VARIANT
 <222> 14

<223> Xaa = I, L, N, V or Y

<400> 355

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

<210> 356

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> Consensus CDR-L1

<220>

<221> VARIANT

<222> 1

<223> Xaa = G, K, R, S or T

<220>

<221> VARIANT

<222> 2

<223> Xaa = A, G or S

<220>

<221> VARIANT

<222> 3

<223> Xaa = G, N, S or T

<220>

<221> VARIANT

<222> 4

<223> Xaa = G, K, N, Q, R or S

<220>

<221> VARIANT

<222> 5

<223> Xaa = S or null

<220>

<221> VARIANT

<222> 6

<223> Xaa = D, N, V or null

<220>

<221> VARIANT
<222> 7
<223> Xaa = L, V or null

<220>
<221> VARIANT
<222> 8
<223> Xaa = H, S, Y or null

<220>
<221> VARIANT
<222> 9
<223> Xaa = S, T or null

<220>
<221> VARIANT
<222> 10
<223> Xaa = S or null

<220>
<221> VARIANT
<222> 11
<223> Xaa = D, G, I, N, S or null

<220>
<221> VARIANT
<222> 12
<223> Xaa = D, E, G, K, I, N or null

<220>
<221> VARIANT
<222> 13
<223> Xaa = F, G, K, N, R, S, Y or null

<220>
<221> VARIANT
<222> 14
<223> Xaa = D, K, N, T or null

<220>
<221> VARIANT
<222> 15
<223> Xaa = A, D, G, L, N, S, T or Y

<220>
<221> VARIANT
<222> 16
<223> Xaa = L or V

<400> 356
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15
Xaa

<210> 357
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> Consensus CDR-L2

<220>
<221> VARIANT
<222> 1
<223> Xaa = A, D, E, N, S, V or W

<220>
<221> VARIANT
<222> 2
<223> Xaa = A, D, N, S or V

<220>
<221> VARIANT
<222> 3
<223> Xaa = A, D, H, I, N or S

<220>
<221> VARIANT
<222> 4
<223> Xaa = D, K, N, Q, R or T

<220>
<221> VARIANT
<222> 5
<223> Xaa = L, R or V

<220>
<221> VARIANT
<222> 6
<223> Xaa = A, E, P or Q

<220>

<221> VARIANT
<222> 7
<223> Xaa = A, D, S or T

<400> 357
Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 358
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> Consensus CDR-L3

<220>
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<222> 1
<223> Xaa = A, C, G, H, I, Q or S

<220>
<221> VARIANT
<222> 2
<223> Xaa = A, Q, S or V

<220>
<221> VARIANT
<222> 3
<223> Xaa = S, W or Y

<220>
<221> VARIANT
<222> 4
<223> Xaa = D, F, G, H or Y

<220>
<221> VARIANT
<222> 5
<223> Xaa = D, G, M, R, S or T

<220>
<221> VARIANT
<222> 6
<223> Xaa = A, G, H, L, R, S, T or Y

<220>
<221> VARIANT
<222> 7
<223> Xaa = L, P, R, S or null

<220>
<221> VARIANT
<222> 8
<223> Xaa = D, G, N, R, S, T or null

<220>
<221> VARIANT
<222> 9
<223> Xaa = A, G, H, L, P or null

<220>
<221> VARIANT
<222> 10
<223> Xaa = F, S or null

<220>
<221> VARIANT
<222> 11
<223> Xaa = L, P, W or Y

<220>
<221> VARIANT
<222> 12
<223> Xaa = S, T or V

<400> 358
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

<210> 359
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> 4GS linker (aa)

<400> 359
Gly Gly Gly Gly Ser

1

5

<210> 360

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> 3GS linker (aa)

<400> 360

Gly Gly Gly Ser

1

<210> 361

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> (4GS)3 linker (aa)

<400> 361

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

1

5

10

15

<210> 362

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> Linker (aa)

<400> 362

Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr

1

5

10

15

Lys Gly

<210> 363
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> Spacer (IgG4hinge) (aa)

<400> 363
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
1 5 10

<210> 364
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> Spacer (IgG4hinge) (nt)

<400> 364
gaatctaagt acggaccgcc ctgccccctt tgccct 36

<210> 365
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> Hinge-CH3 spacer (aa)

<400> 365
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Gly Gln Pro Arg
1 5 10 15
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys

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

<210> 366

<211> 229

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> Hinge-CH2-CH3 spacer (aa)

<400> 366

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

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
180 185 190
Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
210 215 220
Leu Ser Leu Gly Lys
225

<210> 367
<211> 184
<212> PRT
<213> Homo sapiens

<220>
<223> Synthetic

<220>
<223> Human BCMA; GenBank No. BAB60895.1

<400> 367
Met Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser
1 5 10 15
Leu Leu His Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr
20 25 30
Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser
35 40 45
Val Lys Gly Thr Asn Ala Ile Leu Trp Thr Cys Leu Gly Leu Ser Leu
50 55 60
Ile Ile Ser Leu Ala Val Phe Val Leu Met Phe Leu Leu Arg Lys Ile
65 70 75 80
Ser Ser Glu Pro Leu Lys Asp Glu Phe Lys Asn Thr Gly Ser Gly Leu
85 90 95
Leu Gly Met Ala Asn Ile Asp Leu Glu Lys Ser Arg Thr Gly Asp Glu
100 105 110
Ile Ile Leu Pro Arg Gly Leu Glu Tyr Thr Val Glu Glu Cys Thr Cys
115 120 125
Glu Asp Cys Ile Lys Ser Lys Pro Lys Val Asp Ser Asp His Cys Phe
130 135 140
Pro Leu Pro Ala Met Glu Glu Gly Ala Thr Ile Leu Val Thr Thr Lys
145 150 155 160
Thr Asn Asp Tyr Cys Lys Ser Leu Pro Ala Ala Leu Ser Ala Thr Glu
165 170 175
Ile Glu Lys Ser Ile Ser Ala Arg
180

<210> 368

<211> 184
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Human BCMA; NCBI No. NP_001183.2

<400> 368
 Met Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser
 1 5 10 15
 Leu Leu His Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr
 20 25 30
 Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser
 35 40 45
 Val Lys Gly Thr Asn Ala Ile Leu Trp Thr Cys Leu Gly Leu Ser Leu
 50 55 60
 Ile Ile Ser Leu Ala Val Phe Val Leu Met Phe Leu Leu Arg Lys Ile
 65 70 75 80
 Asn Ser Glu Pro Leu Lys Asp Glu Phe Lys Asn Thr Gly Ser Gly Leu
 85 90 95
 Leu Gly Met Ala Asn Ile Asp Leu Glu Lys Ser Arg Thr Gly Asp Glu
 100 105 110
 Ile Ile Leu Pro Arg Gly Leu Glu Tyr Thr Val Glu Glu Cys Thr Cys
 115 120 125
 Glu Asp Cys Ile Lys Ser Lys Pro Lys Val Asp Ser Asp His Cys Phe
 130 135 140
 Pro Leu Pro Ala Met Glu Glu Gly Ala Thr Ile Leu Val Thr Thr Lys
 145 150 155 160
 Thr Asn Asp Tyr Cys Lys Ser Leu Pro Ala Ala Leu Ser Ala Thr Glu
 165 170 175
 Ile Glu Lys Ser Ile Ser Ala Arg
 180

<210> 369
 <211> 135
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Human BCMA Variant; GenBank No. ABN42510.1

<400> 369
 Met Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser
 1 5 10 15
 Leu Leu His Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr
 20 25 30
 Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Arg Ser Gly Leu Leu
 35 40 45

Gly	Met	Ala	Asn	Ile	Asp	Leu	Glu	Lys	Ser	Arg	Thr	Gly	Asp	Glu	Ile
50						55					60				
Ile	Leu	Pro	Arg	Gly	Leu	Glu	Tyr	Thr	Val	Glu	Glu	Cys	Thr	Cys	Glu
65					70					75					80
Asp	Cys	Ile	Lys	Ser	Lys	Pro	Lys	Val	Asp	Ser	Asp	His	Cys	Phe	Pro
				85					90					95	
Leu	Pro	Ala	Met	Glu	Glu	Gly	Ala	Thr	Ile	Leu	Val	Thr	Thr	Lys	Thr
			100					105					110		
Asn	Asp	Tyr	Cys	Lys	Ser	Leu	Pro	Ala	Ala	Leu	Ser	Ala	Thr	Glu	Ile
		115					120					125			
Glu	Lys	Ser	Ile	Ser	Ala	Arg									
	130					135									

<210> 370

<211> 185

<212> PRT

<213> Mus musculus

<220>

<223> Mouse BCMA; NCBI No. NP_035738.1

<400> 370

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

<210> 371
 <211> 183
 <212> PRT
 <213> Macaca fascicular

<220>
 <223> Cynomolgus BCMA; GenBank No. EHH60172.1

<400> 371
 Met Leu Gln Met Ala Arg Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser
 1 5 10 15
 Leu Leu His Asp Cys Lys Pro Cys Gln Leu Arg Cys Ser Ser Thr Pro
 20 25 30
 Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Met Thr Asn Ser Val
 35 40 45
 Lys Gly Met Asn Ala Ile Leu Trp Thr Cys Leu Gly Leu Ser Leu Ile
 50 55 60
 Ile Ser Leu Ala Val Phe Val Leu Thr Phe Leu Leu Arg Lys Met Ser
 65 70 75 80
 Ser Glu Pro Leu Lys Asp Glu Phe Lys Asn Thr Gly Ser Gly Leu Leu
 85 90 95
 Gly Met Ala Asn Ile Asp Leu Glu Lys Gly Arg Thr Gly Asp Glu Ile
 100 105 110
 Val Leu Pro Arg Gly Leu Glu Tyr Thr Val Glu Glu Cys Thr Cys Glu
 115 120 125
 Asp Cys Ile Lys Asn Lys Pro Lys Val Asp Ser Asp His Cys Phe Pro
 130 135 140
 Leu Pro Ala Met Glu Glu Gly Ala Thr Ile Leu Val Thr Thr Lys Thr
 145 150 155 160
 Asn Asp Tyr Cys Asn Ser Leu Ser Ala Ala Leu Ser Val Thr Glu Ile
 165 170 175
 Glu Lys Ser Ile Ser Ala Arg
 180

<210> 372
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-28 CDR-H2 (aa) Kabat numbering

<220>
 <221> VARIANT
 <222> 10

<223> Xaa = any amino acid

<400> 372

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

<210> 373

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-33 CDR-H2 (aa) Kabat numbering

<400> 373

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

<210> 374

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-41 CDR-H2 Kabat numbering

<400> 374

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

<210> 375

<211> 7

<212> PRT

<213> Homo sapiens

<220>

<223> human BCMA epitope (residues 21-27)

<400> 375

Cys Ile Pro Cys Gln Leu Arg

1

5

<210> 376

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-24, -28, -29, -39 CDR-H3 (aa)

<400> 376

Asp Leu Gly Pro Pro Tyr Gly Asp Asp Ala Phe Asp Ile

1

5

10

<210> 377

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-30 CDR-H3 (aa)

<400> 377

Asp Leu Asp Pro Asp Asp Ala Phe Asp Ile

1

5

10

<210> 378

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-35 CDR-H3 (aa)

<400> 378

Val Asp Gly Asp Tyr Asp Asp Tyr
1 5

<210> 379

<211> 10

<212> PRT

<213> Homo sapiens

<220>

<223> human BCMA epitope (residues 30-39)

<400> 379

Ser Asn Thr Pro Pro Leu Thr Cys Gln Arg
1 5 10

<210> 380

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-25 CDR-L1 (aa)

<400> 380

Arg Ala Ser Gln Gly Ile Ser Asn Tyr Leu Ala
1 5 10

<210> 381

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-28 CDR-L1 (aa)

<400> 381

Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp
1 5 10 15

<210> 382

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-29 CDR-L1 (aa)

<400> 382

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

<210> 383

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-30 CDR-L1 (aa)

<400> 383

Arg Ala Ser Gln Pro Ile Arg Ser Asn Leu Ala
1 5 10

<210> 384

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-31 CDR-L1 (aa)

<400> 384

Lys Ser Ser Gln Ser Val Leu Asn Ser Ser Asn Asn Lys Asn Tyr Val

1	5	10	15
Ala			

<210> 385
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-32 CDR-L1 (aa)

<400> 385
Gly Gly Asn Asn Ile Gly Ser Lys Gly Val His
1 5 10

<210> 386
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-34 CDR-L1 (aa)

<400> 386
Arg Ala Ser Gln Ser Ile Ser Asn Tyr Leu Ala
1 5 10

<210> 387
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-36 CDR-L1 (aa)

<400> 387

Gly Ser Ser Thr Gly Pro Val Thr Ser Ala His Ser Pro Ser
1 5 10

<210> 388

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-37, -38 CDR-L1 (aa)

<400> 388

Gly Ser Ser Thr Gly Ala Val Thr Asn Gly His Ser Pro Tyr
1 5 10

<210> 389

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-39 CDR-L1 (aa)

<220>

<221> VARIANT

<222> 11

<223> Xaa = any amino acid

<400> 389

Arg Ala Ser Gln Gly Ile Arg Tyr Glu Leu Xaa
1 5 10

<210> 390

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-40 CDR-L1 (aa)

<400> 390

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

<210> 391

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-41 CDR-L1 (aa)

<400> 391

Ser Gly Ser Ser Ser Asn Ile Gly Gly Asn Ser Val Asp
1 5 10

<210> 392

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-42 CDR-L1 (aa)

<400> 392

Arg Ala Ser Gln Gly Ile Gly Asn Gly Leu Ala
1 5 10

<210> 393

<211> 7

<212> PRT

<213> Homo sapiens

<220>

<223> human BCMA epitope (residues 44-50)

<400> 393

Ser Val Thr Asn Ser Val Lys
1 5

<210> 394
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-44 CDR-L1 (aa)

<400> 394
Lys Ser Ser Gln Asn Leu Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu
1 5 10 15
Ala

<210> 395
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-45 CDR-L1 (aa)

<400> 395
Arg Ala Ser Gln Gly Ile Gly Arg Ser Leu Ala
1 5 10

<210> 396
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-47, -48 CDR-L1 (aa)

<400> 396
Gly Gly Asn Asn Ile Gly Ser Lys Ser Val His
1 5 10

<210> 397
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-49 CDR-L1 (aa)

<400> 397
Gly Gly Asp Gln Ile Gly Arg Lys Ser Val His
1 5 10

<210> 398
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-51 CDR-L1 (aa)

<400> 398
Arg Ala Ser Gln Asn Ile Gly Asp Trp Leu Ala
1 5 10

<210> 399
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-24 CDR-L2 (aa)

<400> 399

Trp Gly Ser Thr Arg Glu Ser
1 5

<210> 400

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-25 CDR-L2 (aa)

<400> 400

Ser Ala Ser Thr Leu Gln Ser
1 5

<210> 401

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-28 CDR-L2 (aa)

<400> 401

Leu Gly Ser Asn Arg Ala Ser
1 5

<210> 402

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-29 CDR-L2 (aa)

<400> 402

Glu Val Ser Lys Arg Pro Ser

1 5

<210> 403
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-30 CDR-L2 (aa)

<400> 403
Ser Ala Ser Thr Arg Ala Thr
1 5

<210> 404
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-34 CDR-L2 (aa)

<400> 404
Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 405
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-36 CDR-L2 (aa)

<400> 405
Glu Thr Thr Asn Arg His Ser
1 5

<210> 406
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-37 CDR-L2 (aa)

<400> 406
Asp Thr Thr Asn Arg His Ser
1 5

<210> 407
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-38 CDR-L2 (aa)

<400> 407
Asp Thr Asn Asn Arg His Ser
1 5

<210> 408
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-39 CDR-L2 (aa)

<400> 408
Ala Ala Ser Thr Leu Gln Ser
1 5

<210> 409
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-41 CDR-L2 (aa)

<400> 409
Ala Asn Asp Arg Arg Pro Ser
1 5

<210> 410
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<223> human BCMA epitope (residues 8-15)

<400> 410
Cys Ser Gln Asn Glu Tyr Phe
1 5

<210> 411
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-45 CDR-L2 (aa)

<400> 411
Asp Ala Ser Ser Leu Arg Ser
1 5

<210> 412
<211> 7
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-47, -48 CDR-L2 (aa)

<400> 412

Tyr Asp Thr Asp Arg Pro Ser
1 5

<210> 413

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-49 CDR-L2 (aa)

<400> 413

Tyr Asp Ser Asp Arg Pro Ser
1 5

<210> 414

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-51 CDR-L2 (aa)

<400> 414

Gly Ala Ser Ile Leu Glu Ser
1 5

<210> 415

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-24 CDR-L3 (aa)

<400> 415

Gln Gln Tyr Ile Ser Leu Pro Trp Thr
1 5

<210> 416

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-25 CDR-L3 (aa)

<400> 416

Gln Gln Ser Tyr Thr Ser Arg Gln Thr
1 5

<210> 417

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-28 CDR-L3 (aa)

<400> 417

Met Gln Ala Leu Gln Thr Pro Pro Trp Thr
1 5 10

<210> 418

<211> 12

<212> PRT

<213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-29 CDR-L3 (aa)

<400> 418
 Cys Ser Tyr Ala Gly Ser Ser Thr Ser Arg Asp Val
 1 5 10

<210> 419
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-30 CDR-L3 (aa)

<400> 419
 Arg His Tyr Ala Pro Leu Thr
 1 5

<210> 420
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-34 CDR-L3 (aa)

<400> 420
 Gln Gln Arg Ser Asn Trp Pro Pro Tyr Thr
 1 5 10

<210> 421
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-26, -35 CDR-L3 (aa)

<400> 421

His	Leu	Trp	Asp	Arg	Ser	Arg	Asp	His	Tyr	Val
1				5					10	

<210> 422

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-36 CDR-L3 (aa)

<400> 422

Leu	Leu	Ser	Ser	Gly	Asp	Ala	Arg	Met	Val
1				5					10

<210> 423

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-37 CDR-L3 (aa)

<400> 423

Ser	Leu	Ser	His	Ala	Gly	Asp	Arg	Val	Phe
1				5					10

<210> 424

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-38 CDR-L3 (aa)

<400> 424

Leu Leu Ser Tyr Ser Asp Ala Arg Leu Ala
1 5 10

<210> 425

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-39 CDR-L3 (aa)

<400> 425

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 426

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-41 CDR-L3 (aa)

<400> 426

Glu Ser Trp Asp Asp Ala Leu Asn Gly His Val
1 5 10

<210> 427

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-42 CDR-L3 (aa)

<400> 427

Gln Gln Tyr Val Glu Asp Ala Leu Thr
1 5

<210> 428

<211> 11

<212> PRT

<213> Homo sapiens

<220>

<223> human BCMA epitope (residues 17-27)

<400> 428

Leu Leu His Ala Cys Ile Pro Cys Gln Leu Arg
1 5 10

<210> 429

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-44 CDR-L3 (aa)

<400> 429

Gln Gln Tyr Tyr Ser Ser Pro Tyr Thr
1 5

<210> 430

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-45 CDR-L3 (aa)

<400> 430

Gln Gln Leu Asn Gly Tyr Pro Trp Thr
1 5

<210> 431
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-47 CDR-L3 (aa)

<400> 431
Gln Leu Trp Asp Ser Asp Ser Asp Asp Phe Ala
1 5 10

<210> 432
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-49 CDR-L3 (aa)

<400> 432
Gln Val Trp Asp Ser Ser Thr Gly Gln Tyr Val Val
1 5 10

<210> 433
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-51 CDR-L3 (aa)

<400> 433
Gln Lys Tyr Asp Gly Ala Pro Pro Trp Thr

1 5 10

<210> 434
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-27 VH FR1 (aa)

<400> 434
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Asp
20 25 30

<210> 435
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-30 VH FR1 (aa)

<400> 435
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly
20 25 30

<210> 436
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-25, -31, -44, -51 VH FR1 (aa)

<400> 436

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

<210> 437

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-32, -49 VH FR1 (aa)

<400> 437

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

<210> 438

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-34 VH FR1 (aa)

<400> 438

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

<210> 439

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-42 VH FR1 (aa)

<400> 439

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

<210> 440

<211> 746

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-52 scFv (nt)

<400> 440

tcctatgagc	tgactcagcc	accctcagcg	tctgggaccc	ccgggcagag	ggtcaccatg	60
tcttgttctg	gaaccagctc	caacatcgga	agtcactctg	taaactggta	ccagcagctc	120
ccaggaacgg	cccccaaact	cctcatctat	actaataatc	agcggccctc	aggggtccct	180
gaccgattct	ctggctccaa	gtctggcacc	tcagcctccc	tggccatcag	tggcctccag	240
tctgaggatg	aggctgatta	ttactgtgca	gcatgggatg	gcagcctgaa	tggctctgga	300
ttcggcggag	ggaccaagct	gaccgtccta	ggttctagag	gtggtgggtg	tagcggcggc	360
ggcggctctg	gtggtgggtg	atccctcgag	atggccgagg	tgcagctggt	gcagtctgga	420
gcagagggtga	aaaagcccgg	ggagtctctg	aagatctcct	gtaagggttc	tggatacagc	480
tttaccagct	actggatcgg	ctgggtgcgc	cagatgcccg	ggaaaggcct	ggagtggatg	540
gggatcatct	atcctgggtga	ctctgatacc	agatacagcc	cgtccttcca	aggccacgtc	600
accatctcag	ctgacaagtc	catcagcact	gcctacctgc	agtggagcag	cctgaaggcc	660
tcggacaccg	ccatgtatta	ctgtgcgcgc	tactctgggt	ctttcgataa	ctgggggtcaa	720
ggtactctgg	tgaccgtctc	ctcagc				746

<210> 441

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-37 VH FR3 (aa)

<400> 441

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

<210> 442

<211> 248

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-52 scFv (aa)

<400> 442

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

Met Tyr Tyr Cys Ala Arg Tyr Ser Gly Ser Phe Asp Asn Trp Gly Gln
 225 230 235 240
 Gly Thr Leu Val Thr Val Ser Ser
 245

<210> 443
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-47 VH FR3 (aa)

<400> 443
 Asp Ser Pro Ser Pro Gly Thr Thr Pro Lys Asn Ser Leu Tyr Leu Gln
 1 5 10 15
 Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys
 20 25 30

<210> 444
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-28 VH FR4 (aa)

<400> 444
 Gly Gly Gln Gly Thr Met Val Thr Val Ser Ser
 1 5 10

<210> 445
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>

<223> BCMA-47 VH FR4 (aa)

<400> 445

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

<210> 446

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-25 VL FR1 (aa)

<400> 446

Asp Ile Gln Met Thr Gln Ser Pro Ala Phe Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Val Thr Cys
20

<210> 447

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-28 VL FR1 (aa)

<400> 447

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15
Glu Pro Ala Ser Ile Ser Cys
20

<210> 448

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-29 VL FR1 (aa)

<400> 448

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

<210> 449

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-30 VL FR1 (aa)

<400> 449

Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Val	Ser	Pro	Gly
1				5					10					15	
Glu	Arg	Ala	Thr	Leu	Ser	Cys									
			20												

<210> 450

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-31 VL FR1 (aa)

<400> 450

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

<210> 451

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

<220>
<223> Synthetic

<220>
<223> BCMA-32 VL FR1 (aa)

<400> 451
Gln Thr Val Val Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15
Thr Ala Arg Ile Thr Cys
20

<210> 452
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-34 VL FR1 (aa)

<400> 452
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Asp Arg Ala Thr Leu Ser Cys
20

<210> 453
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-35 VL FR1 (aa)

<400> 453
Asn Phe Met Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15

Thr Ala Arg Ile Thr Cys
20

<210> 454
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-36 VL FR1 (aa)

<400> 454
Gln Ser Val Leu Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Glu
1 5 10 15
Thr Val Thr Leu Thr Cys
20

<210> 455
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-37 VL FR1 (aa)

<400> 455
Gln Leu Val Leu Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
1 5 10 15
Thr Val Thr Leu Thr Cys
20

<210> 456
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>

<223> BCMA-38 VL FR1 (aa)

<400> 456

Gln Ala Val Leu Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
1 5 10 15
Thr Val Thr Leu Thr Cys
20

<210> 457

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-39 VL FR1 (aa)

<220>

<221> VARIANT

<222> 4

<223> Xaa = any amino acid

<400> 457

Asp Ile Gln Xaa Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys
20

<210> 458

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-41 VL FR1 (aa)

<400> 458

Gln Pro Val Leu Thr Gln Pro Pro Ser Val Ser Gly Thr Pro Gly Gln
1 5 10 15
Arg Val Thr Ile Pro Cys
20

<210> 459
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-42 VL FR1 (aa)

<400> 459
Asp Ile Gln Met Thr Gln Ser Pro Ser Leu Val Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys
20

<210> 460
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-55 scFv (nt)
(0/SSE)

<400> 460
cagtctgccc tgacacagcc tgccagcggt agtgctagtc ccggacagtc tatcgccatc 60
agctgtaccg gcaccagctc tgacgttggc tggatatcagc agcaccctgg caaggcccct 120
aagctgatga tctacgagga cagcaagagg cccagcggcg tgtccaatag attcagcggc 180
agcaagagcg gcaacaccgc cagcctgaca attagcggac tgcaggccga ggacgaggcc 240
gattactact gcagcagcaa caccgggtcc agcacactgg tttttggcgg aggcaccaag 300
ctgacagtgc tgggatctag aggtggcgga ggatctggcg gcggaggaag cggaggcggc 360
ggatctcttg aaatggctga agtgcagctg gtgcagtctg gcgccgagat gaagaaacct 420
ggcgccctctc tgaagctgag ctgcaaggcc agcggctaca ctttcacga ctactacgtg 480
tactggatgc ggcaggcccc tggacaggga ctcgaatcta tgggctggat caacccaat 540
agcggcggca ccaattacgc ccagaaattc cagggcagag tgaccatgac cagagacacc 600
agcatcagca ccgcctacat ggaactgagc cggctgagat ccgacgacac cgccatgtac 660
tactgcgcca gatctcagcg cgacggctac atggattatt ggggccaggg aaccctggtc 720
accgtgtcca gc 732

<210> 461
<211> 23

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-44 VL FR1 (aa)

<400> 461
Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Ile Asn Cys
20

<210> 462
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-45 VL FR1 (aa)

<400> 462
Ala Ile Arg Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys
20

<210> 463
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-47 VL FR1 (aa)

<400> 463
Gln Ala Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Lys
1 5 10 15
Thr Ala Thr Ile Thr Cys

<210> 464
 <211> 22
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-48 VL FR1 (aa)

<400> 464
 Gln Pro Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Lys
 1 5 10 15
 Thr Ala Thr Ile Thr Cys
 20

<210> 465
 <211> 22
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-49 VL FR1 (aa)

<400> 465
 Leu Pro Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Lys
 1 5 10 15
 Thr Ala Arg Ile Thr Cys
 20

<210> 466
 <211> 23
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-51 VL FR1 (aa)

<400> 466

Ala	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Thr	Leu	Ser	Ala	Ser	Val	Gly
1				5					10					15	
Asp	Arg	Val	Ala	Ile	Thr	Cys									
			20												

<210> 467

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-25 VL FR2 (aa)

<400> 467

Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Asn	Ala	Pro	Arg	Leu	Leu	Ile	Tyr
1				5					10					15

<210> 468

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-28 VL FR2 (aa)

<400> 468

Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr
1				5					10					15

<210> 469

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-29 VL FR2 (aa)

<400> 469

Trp	Tyr	Gln	Gln	His	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Met	Ile	Tyr
1				5				10						15

<210> 470

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-30 VL FR2 (aa)

<400> 470

Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Lys	Leu	Leu	Ile	Tyr
1				5				10						15

<210> 471

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-31 VL FR2 (aa)

<400> 471

Trp	Tyr	Lys	Gln	Lys	Pro	Gly	Gln	Pro	Pro	Lys	Leu	Val	Ile	Ser
1				5				10						15

<210> 472

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-32 VL FR2 (aa)

<400> 472

Trp	Tyr	Arg	Gln	Arg	Pro	Gly	Gln	Ala	Pro	Glu	Val	Val	Ile	Tyr
1				5					10					15

<210> 473

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-36 VL FR2 (aa)

<400> 473

Trp	Phe	Gln	Lys	Lys	Pro	Gly	Gln	Ala	Pro	Thr	Thr	Leu	Ile	Tyr
1				5					10					15

<210> 474

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-37, -38 VL FR2 (aa)

<400> 474

Trp	Phe	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Thr	Leu	Ile	Tyr
1				5					10					15

<210> 475

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-39 VL FR2 (aa)

<400> 475

Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr
1				5				10						15

<210> 476

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-41 VL FR2 (aa)

<400> 476

Trp	Phe	Gln	Glu	Val	Pro	Gly	Thr	Ala	Pro	Lys	Leu	Leu	Ile	Tyr
1				5				10						15

<210> 477

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-42 VL FR2 (aa)

<400> 477

Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Leu	Phe
1				5				10						15

<210> 478

<211> 244

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-55 scFv (aa)

<400> 478

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

<210> 479

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-45 VL FR2 (aa)

<400> 479

Trp	Tyr	Lys	Gln	Lys	Pro	Gly	Gly	Val	Pro	Gln	Leu	Leu	Ile	His
1				5					10					15

<210> 480
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-47, -48 VL FR2 (aa)

<400> 480
Trp Tyr Gln Arg Lys Pro Gly Gln Gly Pro Val Val Val Ile Gln
1 5 10 15

<210> 481
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-49 VL FR2 (aa)

<400> 481
Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Met Ser
1 5 10 15

<210> 482
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-51 VL FR2 (aa)

<400> 482
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Phe
1 5 10 15

<210> 483
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-24 VL FR3 (aa)

<400> 483
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15
Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Ile Tyr His Cys
20 25 30

<210> 484
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-25 VL FR3 (aa)

<400> 484
Gly Val Pro Ser Arg Phe Arg Gly Thr Gly Tyr Gly Thr Glu Phe Ser
1 5 10 15
Leu Thr Ile Asp Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
20 25 30

<210> 485
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-28 VL FR3 (aa)

<400> 485
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

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

<210> 486
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-29 VL FR3 (aa)

<400> 486
Gly Val Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser
1 5 10 15
Pro Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
20 25 30

<210> 487
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-30 VL FR3 (aa)

<400> 487
Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15
Leu Thr Ile Ser Arg Leu Glu His Glu Asp Phe Ala Val Tyr Tyr Arg
20 25 30

<210> 488
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>

<223> BCMA-32 VL FR3 (aa)

<400> 488

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

<210> 489

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-34 VL FR3 (aa)

<400> 489

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

<210> 490

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-36 VL FR3 (aa)

<400> 490

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

<210> 491

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-37 VL FR3 (aa)

<400> 491

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

<210> 492

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-38 VL FR3 (aa)

<400> 492

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

<210> 493

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-39 VL FR3 (aa)

<400> 493

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

<210> 494
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-41 VL FR3 (aa)

<400> 494
Gly Val Pro Asp Arg Phe Ser Gly Thr Lys Ser Gly Thr Ser Ala Ser
1 5 10 15
Leu Ala Ile Arg Gly Leu Gln Ser Asp Asp Ala His Tyr Tyr Cys
20 25 30

<210> 495
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-42 VL FR3 (aa)

<400> 495
Gly Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Tyr Thr
1 5 10 15
Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys
20 25 30

<210> 496
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-52 CDR-H1 (aa)

<400> 496

Gly Tyr Ser Phe Thr Ser Tyr Trp
1 5

<210> 497

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-45 VL FR3 (aa)

<400> 497

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

<210> 498

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-47 VL FR3 (aa)

<400> 498

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

<210> 499

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-48 VL FR3 (aa)

<400> 499

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

<210> 500

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-49 VL FR3 (aa)

<400> 500

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

<210> 501

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-51 VL FR3 (aa)

<400> 501

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

<210> 502

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-25 VL FR4 (aa)

<400> 502

Phe	Gly	Pro	Gly	Thr	Arg	Leu	Asp	Ile	Lys
1				5					10

<210> 503

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-29 VL FR4 (aa)

<220>

<221> VARIANT

<222> 3

<223> Xaa = any amino acid

<400> 503

Phe	Gly	Xaa	Gly	Thr	Lys	Leu	Thr	Val	Leu
1				5					10

<210> 504

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-31, -34 VL FR4 (aa)

<400> 504

Phe	Gly	Gln	Gly	Thr	Lys	Leu	Asp	Ile	Lys
1				5					10

<210> 505
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-35 VL FR4 (aa)

<400> 505
Phe Gly Thr Gly Thr Lys Leu Asp Ile Lys
1 5 10

<210> 506
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-42 VL FR4 (aa)

<400> 506
Phe Gly Gly Gly Thr Lys Val Asp Ile Lys
1 5 10

<210> 507
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-52 CDR-H2 (aa)

<400> 507
Ile Tyr Pro Gly Asp Ser Asp Thr
1 5

<210> 508
 <211> 10
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <220>
 <223> BCMA-24, -28, -51 VL FR4 (aa)

 <400> 508
 Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 1 5 10

<210> 509
 <211> 10
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <220>
 <223> BCMA-30 CDR-H1 (aa) AbM numbering

 <400> 509
 Gly Phe Thr Phe Gly Asp Tyr Ala Met His
 1 5 10

<210> 510
 <211> 10
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <220>
 <223> BCMA-28 CDR-H2 (aa) AbM numbering

 <220>
 <221> VARIANT
 <222> 10
 <223> Xaa = any amino acid

 <400> 510

Gly Ile Ser Trp Asn Ser Gly Ser Ile Xaa
1 5 10

<210> 511
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-33 CDR-H2 (aa) AbM numbering

<400> 511
Tyr Ile Ser Gly Ser Gly Ser Thr Ile Tyr
1 5 10

<210> 512
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-41 CDR-H2 AbM numbering

<400> 512
Tyr Ile Ser Ser Ser Gly Asn Thr Ile Tyr
1 5 10

<210> 513
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-52 CDR-H3 (aa)

<400> 513
Ala Arg Tyr Ser Gly Ser Phe Asp Asn

1 5

<210> 514
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-28 CDR-H2 (aa) Chothia numbering

<400> 514
Ser Trp Asn Ser Gly
1 5

<210> 515
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-33 CDR-H2 (aa) Chothia numbering

<400> 515
Ser Gly Ser Gly Ser Thr
1 5

<210> 516
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-41 CDR-H2 Chothia numbering

<400> 516
Ser Ser Ser Gly Asn Thr
1 5

<210> 517
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-52 CDR-L1 (aa)

<400> 517
 Ser Ser Asn Ile Gly Ser His Ser
 1 5

<210> 518
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-24 VH chain (aa)

<400> 518
 Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
 20 25 30
 Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Leu Gly Pro Pro Tyr Gly Asp Asp Ala Phe Asp Ile Trp
 100 105 110
 Gly Gln Gly Thr Met Val Thr Val Ser Ser
 115 120

<210> 519

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

<220>
<223> Synthetic

<220>
<223> BCMA-25, -31, -44, -51 VH chain (aa)

<400> 519
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Gly Asp Tyr
20 25 30
Ala Met Ser Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Gly Phe Ile Arg Ser Lys Ala Tyr Gly Gly Thr Thr Glu Tyr Ala Ala
50 55 60
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
65 70 75 80
Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95
Tyr Cys Ala Ala Trp Ser Ala Pro Thr Asp Tyr Trp Gly Gln Gly Thr
100 105 110
Leu Val Thr Val Ser Ser
115

<210> 520
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-27 VH chain (aa)

<400> 520
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95
 Ala Lys Gly Gly Leu Gly Ile Thr Pro Tyr Tyr Phe Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 521
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-28 VH chain (aa)

<220>
 <221> VARIANT
 <222> 59
 <223> Xaa = any amino acid

<400> 521
 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Xaa Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Leu Gly Pro Pro Tyr Gly Asp Asp Ala Phe Asp Ile Gly
 100 105 110
 Gly Gln Gly Thr Met Val Thr Val Ser Ser
 115 120

<210> 522
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-29, -39 VH chain (aa)

<400> 522

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

<210> 523

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-30 VH chain (aa)

<400> 523

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

				85						90					95			
Ala	Arg	Asp	Leu	Asp	Pro	Asp	Asp	Ala	Phe	Asp	Ile	Trp	Gly	Gln	Gly			
			100					105					110					
Thr	Met	Val	Thr	Val	Ser	Ser												
			115															

<210> 524
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-32, -49 VH chain (aa)

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

<210> 525
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-33 VH chain (aa)

<400> 525

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

<210> 526

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-34 VH chain (aa)

<400> 526

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

<210> 527

<211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-35 VH chain (aa)

<400> 527
 Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
 20 25 30
 Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Val Asp Gly Asp Tyr Asp Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110
 Val Thr Val Ser Ser
 115

<210> 528
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-36, 38 VH chain (aa)

<400> 528
 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
 20 25 30
 Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr
65					70					75					80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85					90						95	
Ala	Arg	Val	Asp	Gly	Asp	Tyr	Val	Asp	Asp	Tyr	Trp	Gly	Gln	Gly	Thr
			100					105					110		
Leu	Val	Thr	Val	Ser	Ser										
			115												

<210> 529
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-37 VH chain (aa)

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

<210> 530
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>

<223> BCMA-41 VH chain (aa)

<400> 530

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

<210> 531

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-42 VH chain (aa)

<400> 531

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

<210> 532
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-52 CDR-L2 (aa)

<400> 532
Thr Asn Asn
1

<210> 533
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-47 VH chain (aa)

<400> 533
Gln Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30
Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Asp Ser Pro Ser Pro Gly Thr Thr Pro Lys Asn Ser Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Lys Val Asp Gly Pro Pro Ser Phe Asp Ile Trp Arg Gln Gly Thr
100 105 110
Met Val Thr Val Ser Ser
115

<210> 534

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

<220>
<223> Synthetic

<220>
<223> BCMA-24 VL chain (aa)

<400> 534
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45
Pro Pro Lys Leu Leu Ile Tyr Trp Gly Ser Thr Arg Glu Ser Gly Val
50 55 60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Ile Tyr His Cys Gln Gln
85 90 95
Tyr Ile Ser Leu Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110
Lys

<210> 535
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-25 VL chain (aa)

<400> 535
Asp Ile Gln Met Thr Gln Ser Pro Ala Phe Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Val Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Asn Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Ser Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Arg Gly
50 55 60

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

<210> 536
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-26 VL chain (aa)

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

<210> 537
 <211> 113
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-28 VL chain (aa)

<400> 537
 Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Ser Val Thr Pro Gly

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

Lys

<210> 538
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-29 VL chain (aa)

<220>
 <221> VARIANT
 <222> 105
 <223> Xaa = any amino acid

<400> 538

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

<210> 539
 <211> 105
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-30 VL chain (aa)

<400> 539
 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Pro Ile Arg Ser Asn
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ser Ala Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu His
 65 70 75 80
 Glu Asp Phe Ala Val Tyr Tyr Arg Arg His Tyr Ala Pro Leu Thr Phe
 85 90 95
 Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 540
 <211> 113
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-31 VL chain (aa)

<400> 540
 Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 Glu Arg Ala Thr Ile Ser Cys Lys Ser Ser Gln Ser Val Leu Asn Ser
 20 25 30
 Ser Asn Asn Lys Asn Tyr Val Ala Trp Tyr Lys Gln Lys Pro Gly Gln
 35 40 45
 Pro Pro Lys Leu Val Ile Ser Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr
65					70					75					80
Ile	Ser	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys	Gln	Gln
				85					90					95	
Tyr	Tyr	Ser	Thr	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Asp	Ile
			100					105					110		
Lys															

<210> 541
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-32 VL chain (aa)

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

<210> 542
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-34 VL chain (aa)

<400> 542

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

<210> 543

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-35 VL chain (aa)

<400> 543

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

<210> 544

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-36 VL chain (aa)

<400> 544

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

<210> 545

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-37 VL chain (aa)

<400> 545

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

100

105

110

<210> 546

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-38 VL chain (aa)

<400> 546

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

<210> 547

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-39 VL chain (aa)

<220>

<221> VARIANT

<222> 4

<223> Xaa = any amino acid

<220>

<221> VARIANT

<222> 34

<223> Xaa = any amino acid

<400> 547

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

<210> 548

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-40 VL chain (aa)

<400> 548

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

<210> 549

<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-41 VL chain (aa)

<400> 549
Gln Pro Val Leu Thr Gln Pro Pro Ser Val Ser Gly Thr Pro Gly Gln
1 5 10 15
Arg Val Thr Ile Pro Cys Ser Gly Ser Ser Ser Asn Ile Gly Gly Asn
20 25 30
Ser Val Asp Trp Phe Gln Glu Val Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45
Ile Tyr Ala Asn Asp Arg Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60
Gly Thr Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Arg Gly Leu Gln
65 70 75 80
Ser Asp Asp Asp Ala His Tyr Tyr Cys Glu Ser Trp Asp Asp Ala Leu
85 90 95
Asn Gly His Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 550
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-42 VL chain (aa)

<400> 550
Asp Ile Gln Met Thr Gln Ser Pro Ser Leu Val Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Gly Asn Gly
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Leu
35 40 45
Phe Ala Ala Ser Arg Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Arg Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Val Glu Asp Ala Leu
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys
 100 105

<210> 551
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-52 CDR-L3 (aa)

<400> 551
 Ala Ala Trp Asp Gly Ser Leu Asn Gly Leu Val
 1 5 10

<210> 552
 <211> 113
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-44 VL chain (aa)

<400> 552
 Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Asn Leu Leu Tyr Ser
 20 25 30
 Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45
 Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60
 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80
 Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
 85 90 95
 Tyr Tyr Ser Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
 100 105 110
 Lys

<210> 553
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-45 VL chain (aa)

<400> 553
 Ala Ile Arg Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Gly Arg Ser
 20 25 30
 Leu Ala Trp Tyr Lys Gln Lys Pro Gly Gly Val Pro Gln Leu Leu Ile
 35 40 45
 His Asp Ala Ser Ser Leu Arg Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Gly Val Gln Ser
 65 70 75 80
 Glu Asp Ser Ala Thr Tyr His Cys Gln Gln Leu Asn Gly Tyr Pro Trp
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys
 100 105

<210> 554
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-47 VL chain (aa)

<400> 554
 Gln Ala Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Lys
 1 5 10 15
 Thr Ala Thr Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val
 20 25 30
 His Trp Tyr Gln Arg Lys Pro Gly Gln Gly Pro Val Val Val Ile Gln
 35 40 45

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

<210> 555
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-48 VL chain (aa)

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

<210> 556
 <211> 109
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-49 VL chain (aa)

<400> 556

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

<210> 557

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-51 VL chain (aa)

<400> 557

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

<210> 558

<211> 250

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-24 scFv sequence (aa)

<220>

<221> VARIANT

<222> 204

<223> Xaa = any amino acid

<400> 558

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

<210> 559

<211> 240

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-25 scFv sequence (aa)

<400> 559

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

<210> 560
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>

<223> BCMA-26 scFv sequence (aa)

<400> 560

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1           5           10           15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
 20           25           30
Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35           40           45
Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
 50           55           60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65           70           75           80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85           90           95
Ala Lys Val Asp Gly Pro Pro Ser Phe Asp Ile Trp Gly Gln Gly Thr
100           105           110
Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115           120           125
Gly Gly Gly Gly Ser Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser
130           135           140
Val Ala Pro Gly Gln Thr Ala Arg Ile Thr Cys Gly Ala Asn Asn Ile
145           150           155           160
Gly Ser Lys Ser Val His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
165           170           175
Met Leu Val Val Tyr Asp Asp Asp Asp Arg Pro Ser Gly Ile Pro Glu
180           185           190
Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser
195           200           205
Gly Val Glu Ala Gly Asp Glu Ala Asp Tyr Phe Cys His Leu Trp Asp
210           215           220
Arg Ser Arg Asp His Tyr Val Phe Gly Thr Gly Thr Lys Leu Thr Val
225           230           235           240
Leu
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<210> 561

<211> 240

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-27 scFv sequence (aa)

<400> 561

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

<210> 562

<211> 250

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-28 scFv sequence (aa)

<220>

<221> VARIANT

<222> 59

<223> Xaa = any amino acid

<400> 562

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

<210> 563

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-29 scFv sequence (aa)

<220>

<221> VARIANT
 <222> 242
 <223> Xaa = any amino acid

<400> 563

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

<210> 564
 <211> 239
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-30 scFv sequence (aa)

<400> 564

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

<210> 565

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-31 scFv sequence (aa)

<400> 565

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

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

<210> 566

<211> 241

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-32 scFv sequence (aa)

<400> 566

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

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

<210> 567
 <211> 240
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-33 scFv sequence (aa)

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

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

<210> 568

<211> 245

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-34 scFv sequence (aa)

<400> 568

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

Gly	Gln	Gly	Thr	Met	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly
		115					120					125			
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Ile	Val	Met	Thr	Gln	Ser
	130					135					140				
Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly	Asp	Arg	Ala	Thr	Leu	Ser	Cys
145					150					155					160
Arg	Ala	Ser	Gln	Ser	Ile	Ser	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys
			165					170					175		
Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	Tyr	Asp	Ala	Ser	Asn	Arg	Ala
		180						185					190		
Thr	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe
	195						200					205			
Thr	Leu	Thr	Ile	Ser	Ser	Leu	Glu	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr
	210					215					220				
Cys	Gln	Gln	Arg	Ser	Asn	Trp	Pro	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr
225					230					235					240
Lys	Leu	Asp	Ile	Lys											
				245											

<210> 569

<211> 240

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-35 scFv sequence (aa)

<400> 569

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

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

<210> 570

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-36 scFv sequence (aa)

<400> 570

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

Gln	Ala	Pro	Thr	Thr	Leu	Ile	Tyr	Glu	Thr	Thr	Asn	Arg	His	Ser	Trp
			180					185					190		
Thr	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Leu	Leu	Gly	Gly	Lys	Ala	Ala	Leu
		195				200						205			
Thr	Leu	Ser	Gly	Ala	Gln	Pro	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Leu
	210				215						220				
Leu	Ser	Ser	Gly	Asp	Ala	Arg	Met	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu
225					230					235					240
Thr	Val	Leu													

<210> 571

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-37 scFv sequence (aa)

<400> 571

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

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

<210> 572
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-38 scFv sequence (aa)

<400> 572

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

Leu Ser Tyr Ser Asp Ala Arg Leu Ala Phe Gly Gly Gly Thr Lys Leu
 225 230 235 240
 Thr Val Leu

<210> 573
 <211> 244
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-39 scFv sequence (aa)

<220>
 <221> VARIANT
 <222> 141
 <223> Xaa = any amino acid

<400> 573
 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Leu Gly Pro Pro Tyr Gly Asp Asp Ala Phe Asp Ile Trp
 100 105 110
 Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
 115 120 125
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Xaa Thr Gln Ser
 130 135 140
 Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
 145 150 155 160
 Arg Ala Ser Gln Gly Ile Arg Tyr Glu Leu Xaa Trp Tyr Gln Gln Lys
 165 170 175
 Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln
 180 185 190
 Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
 195 200 205

Ala	Leu	Thr	Ile	Arg	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr
210						215					220				
Cys	Leu	Gln	His	Asn	Ser	Tyr	Pro	Leu	Thr	Phe	Gly	Arg	Gly	Thr	Lys
225					230					235					240
Leu	Glu	Ile	Lys												

<210> 574
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-40 scFv sequence (aa)

<400> 574

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

225	230	235	240
Thr Val Leu			

<210> 575
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-41 scFv sequence (aa)

<400> 575
 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
 20 25 30
 Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Tyr Ile Ser Ser Ser Gly Asn Thr Ile Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Val Asp Gly Asp Tyr Val Asp Asp Tyr Trp Gly Gln Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 115 120 125
 Gly Gly Gly Gly Ser Gln Pro Val Leu Thr Gln Pro Pro Ser Val Ser
 130 135 140
 Gly Thr Pro Gly Gln Arg Val Thr Ile Pro Cys Ser Gly Ser Ser Ser
 145 150 155 160
 Asn Ile Gly Gly Asn Ser Val Asp Trp Phe Gln Glu Val Pro Gly Thr
 165 170 175
 Ala Pro Lys Leu Leu Ile Tyr Ala Asn Asp Arg Arg Pro Ser Gly Val
 180 185 190
 Pro Asp Arg Phe Ser Gly Thr Lys Ser Gly Thr Ser Ala Ser Leu Ala
 195 200 205
 Ile Arg Gly Leu Gln Ser Asp Asp Asp Ala His Tyr Tyr Cys Glu Ser
 210 215 220
 Trp Asp Asp Ala Leu Asn Gly His Val Phe Gly Gly Gly Thr Lys Leu
 225 230 235 240
 Thr Val Leu

<210> 576
 <211> 240
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-42 scFv sequence (aa)

<400> 576
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Gly Asp Tyr
 20 25 30
 Ala Met Ser Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Gly Phe Ile Arg Ser Lys Ala Tyr Gly Gly Thr Thr Glu Tyr Ala Ala
 50 55 60
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile
 65 70 75 80
 Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
 85 90 95
 Tyr Cys Ala Ala Trp Ser Ala Pro Thr Asp Tyr Trp Gly Gln Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 115 120 125
 Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Leu Val
 130 135 140
 Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
 145 150 155 160
 Gly Ile Gly Asn Gly Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala
 165 170 175
 Pro Lys Leu Leu Leu Phe Ala Ala Ser Arg Leu Glu Ser Gly Val Pro
 180 185 190
 Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Tyr Thr Leu Thr Ile
 195 200 205
 Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr
 210 215 220
 Val Glu Asp Ala Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys
 225 230 235 240

<210> 577
 <211> 116
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-52 VH (aa)

<400> 577

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

<210> 578

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-44 scFv sequence (aa)

<400> 578

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

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

<210> 579

<211> 240

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-45 scFv sequence (aa)

<400> 579

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

				100					105					110			
Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser		
		115						120					125				
Gly	Gly	Gly	Gly	Ser	Ala	Ile	Arg	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu		
		130				135						140					
Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln		
145					150					155					160		
Gly	Ile	Gly	Arg	Ser	Leu	Ala	Trp	Tyr	Lys	Gln	Lys	Pro	Gly	Gly	Val		
				165				170						175			
Pro	Gln	Leu	Leu	Ile	His	Asp	Ala	Ser	Ser	Leu	Arg	Ser	Gly	Val	Pro		
			180					185					190				
Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile		
		195					200					205					
Ser	Gly	Val	Gln	Ser	Glu	Asp	Ser	Ala	Thr	Tyr	His	Cys	Gln	Gln	Leu		
	210					215					220						
Asn	Gly	Tyr	Pro	Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Asp	Ile	Lys		
225					230					235					240		

<210> 580

<211> 241

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-47 scFv sequence (aa)

<400> 580

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

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

<210> 581

<211> 241

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-48 scFv sequence (aa)

<400> 581

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

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

<210> 582

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-49 scFv sequence (aa)

<400> 582

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

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

<210> 583
 <211> 241
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-51 scFv sequence (aa)

<400> 583

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

210	215	220
Asp Gly Ala Pro Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile		
225	230	235
Lys		240

<210> 584
 <211> 729
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-41 scFv sequence (nt)

<400> 584
 caggtgcagc tgggtgcaatc tgggggaggc ttgggtcaagc ctggagggtc cctgagactc 60
 tcctgtgcag cctctggatt caccttcagt gactactaca tgagctggat ccgccaggct 120
 ccagggaagg ggctggagtg ggtttcatac attagtagta gtggtataac catatactac 180
 gcagactctg taaagggccg attcaccatc tccagggaca acgcaaaaaa ctcactgtat 240
 ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gaaagtggac 300
 ggtgactacg tcgatgacta ctggggccag ggaaccctgg tcaccgtctc ctcagggtgga 360
 ggcgggttcag gcggagggtg ctctggcggt ggcggatcgc agcctgtgct gactcagcca 420
 ccctcagtgt ctgggacccc cgggcagagg gtcaccatcc cttgttctgg aagcagctcc 480
 aacatcgag gtaactctgt agactgggtc caggagggtc cagggacggc ccccaaactc 540
 ctcatctacg ctaatgatcg gcggccctcg ggtgtccctg accgcttctc tggcaccaag 600
 tcgggcacct cagcctccct ggccatcagg gggctccagt ctgacgatga cgctcattat 660
 tactgtgaat cctgggacga tgccctgaac ggtcacgtgt tcggcggagg gaccaagctg 720
 accgtccta 729

<210> 585
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-C1 VH-VL scFv (aa)

<400> 585
 Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
 1 5 10 15
 Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30

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

<210> 586

<211> 244

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-C2 VL-VH scFv (aa)

<400> 586

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

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

<210> 587
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-52 VL (aa)

<400> 587															
Ser	Tyr	Glu	Leu	Thr	Gln	Pro	Pro	Ser	Ala	Ser	Gly	Thr	Pro	Gly	Gln
1				5				10					15		
Arg	Val	Thr	Met	Ser	Cys	Ser	Gly	Thr	Ser	Ser	Asn	Ile	Gly	Ser	His
			20				25					30			
Ser	Val	Asn	Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Thr	Ala	Pro	Lys	Leu	Leu
		35				40					45				
Ile	Tyr	Thr	Asn	Asn	Gln	Arg	Pro	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser
	50				55				60						
Gly	Ser	Lys	Ser	Gly	Thr	Ser	Ala	Ser	Leu	Ala	Ile	Ser	Gly	Leu	Gln
65				70						75					80

Ser	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Ala	Ala	Trp	Asp	Gly	Ser	Leu
				85					90					95	
Asn	Gly	Leu	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	
			100					105					110		

<210> 588
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-55 CDR-H1 (aa)

<400> 588
 Gly Tyr Thr Phe Ile Asp Tyr Tyr
 1 5

<210> 589
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-55 CDR-H2 (aa)

<400> 589
 Ile Asn Pro Asn Ser Gly Gly Thr
 1 5

<210> 590
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-55 CDR-H3 (aa)

<400> 590
Ala Arg Ser Gln Arg Asp Gly Tyr Met Asp Tyr
1 5 10

<210> 591
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-55 CDR-L1 (aa)

<400> 591
Ile Ser Cys Thr Gly Thr Ser Ser Asp
1 5

<210> 592
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-55 CDR-L2 (aa)

<400> 592
Glu Asp Ser
1

<210> 593
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA-55 CDR-L3 (aa)

<400> 593

Ser Ser Asn Thr Arg Ser Ser Thr Leu Val
 1 5 10

<210> 594
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-55 VH (aa)

<400> 594
 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Met Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Leu Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ile Asp Tyr
 20 25 30
 Tyr Val Tyr Trp Met Arg Gln Ala Pro Gly Gln Gly Leu Glu Ser Met
 35 40 45
 Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Ala Arg Ser Gln Arg Asp Gly Tyr Met Asp Tyr Trp Gly Gln Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ser
 115

<210> 595
 <211> 105
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> BCMA-55 VL (aa)

<400> 595
 Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Ala Ser Pro Gly Gln
 1 5 10 15
 Ser Ile Ala Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Trp Tyr

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

<210> 596
 <211> 24
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> T2A

<400> 596
 Leu Glu Gly Gly Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp
 1 5 10 15
 Val Glu Glu Asn Pro Gly Pro Arg
 20

<210> 597
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> T2A

<400> 597
 Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
 1 5 10 15
 Gly Pro

<210> 598
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> P2A

<400> 598
Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
1 5 10 15
Glu Glu Asn Pro Gly Pro
20

<210> 599
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> P2A

<400> 599
Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn
1 5 10 15
Pro Gly Pro

<210> 600
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> E2A

<400> 600
Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly Asp Val Glu Ser

1	5	10	15
Asn Pro Gly Pro			
20			

<210> 601
 <211> 22
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> F2A

<400> 601
 Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val
 1 5 10 15
 Glu Ser Asn Pro Gly Pro
 20

<210> 602
 <211> 357
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <223> EGFRt

<400> 602
 Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
 1 5 10 15
 Ala Phe Leu Leu Ile Pro Arg Lys Val Cys Asn Gly Ile Gly Ile Gly
 20 25 30
 Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe
 35 40 45
 Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala
 50 55 60
 Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu
 65 70 75 80
 Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile
 85 90 95
 Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu
 100 105 110

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

<210> 603

<211> 335

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> EGFRT

<400> 603

Arg	Lys	Val	Cys	Asn	Gly	Ile	Gly	Ile	Gly	Glu	Phe	Lys	Asp	Ser	Leu
1				5					10					15	
Ser	Ile	Asn	Ala	Thr	Asn	Ile	Lys	His	Phe	Lys	Asn	Cys	Thr	Ser	Ile

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

<210> 604

<211> 720

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-25 scFv sequence (nt)

<400> 604

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gaggtgcagc tgggtgcagag cggaggaggc ctgggtgcagc ctggcagggtc cctg'gc'cctg 60
tcttgcaccg ccagcggcctt cacatttggc gactatgcc'a tgtcctgggtt caggcaggca 120
ccaggcaagg gcctggagtg ggtgggcttt atccgctcta aggcctacgg cggcaccaca 180
gagtatgccg ccagcgtgaa gggccgggtt accatcagcc gggacgactc taagagcatc 240
gcctacctgc agatgaactc tctgaagacc gaggacacag ccgtgtacta ttgcgcagca 300
tggagcgccc caaccgatta ttggggccag ggcaccctgg tgacagt'gag ctccggcggc 360
ggcggctctg gaggaggagg aagcggagga ggaggatccg acatccagat gacacagtcc 420
cctgcctttc tgtccgcctc tgtgggcgat aggg'tgaccg tgacatgtcg cgcctcccag 480
ggcatctcta actacctggc ctggtatcag cagaagccc'g gcaatgcccc tcggctgctg 540
atctacagcg cctccaccct gcagagcgga gtgccctccc gg'ttcagagg aaccggctat 600
ggcacagagt tttctctgac catcgacagc ctgcagccag aggatttcgc cacatactat 660
tgtcagcagt cttacaccag ccggcagaca tttggccccg gcacaagact ggatatcaag 720
```

<210> 605

<211> 723

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-26 scFv sequence (nt)

<400> 605

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gaggtgcagc tgg'tggagtc cggaggaggc ctgg'tgaagc caggaggctc tctgaggctg 60
agctgcgcag cctccggcctt caccttttct gactactata tgagctggat caggcaggca 120
ccaggcaagg gcctggagtg ggtgtcttac atcagctcct ctggcagcac aatctactat 180
gccgactccg tgaagggcag gttcaccatc tctcgcgata acgccaagaa tagcctgtat 240
ctgcagatga actccctgcg ggccgaggat acagccgtgt actattgcgc caaggtggac 300
ggccccctt cctttgatat ctggggccag ggcacaatgg tgaccgtgag ctccggagga 360
ggaggatccg gcggaggagg ctctggcggc ggcggctcta gctatgtgct gaccagcca 420
ccatccgtgt ctgtggcacc tggacagaca gcaaggatca cctgtggagc aaacaatatc 480
ggcagcaagt ccgtgcactg gtaccagcag aagcctggcc aggccccaat gctgg'tgg'tg 540
tatgacgatg acgatcggcc cagcggcatc cctgagagat tttctggcag caactccggc 600
aataaccgcca cactgaccat ctctggagtg gaggcaggcg acgaggcaga ttacttctgt 660
cacctgtggg accggagcag agatcactac gtgttcggca caggcaccaa gctgaccgtg 720
ctg 723
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<210> 606

<211> 744

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-52 scFv sequence (nt)

<400> 606

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tcctatgagc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcacccatg 60
tcttgttctg gaaccagctc caacatcgga agtcactctg taaactggta ccagcagctc 120
ccaggaacgg cccccaact cctcatctat actaataatc agcggccctc aggggtccct 180
gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tggcctccag 240
tctgaggatg aggctgatta ttactgtgca gcatgggatg gcagcctgaa tggctctggta 300
ttcggcggag ggaccaagct gaccgtccta gggtctagag gtgggtggagg tagcggcggc 360
ggcggctctg gtgggtggagg atccctcgag atggccgagg tgcagctggg gcagtctgga 420
gcagagggtga aaaagcccgg ggagtctctg aagatctcct gtaagggttc tggatacagc 480
tttaccagct actggatcgg ctgggtgcgc cagatgcccg ggaaaggcct ggagtggatg 540
gggatcatct atcctgggtga ctctgatacc agatacagcc cgtccttcca aggccacgtc 600
accatctcag ctgacaagtc catcagcact gcctacctgc agtggagcag cctgaaggcc 660
tcggacaccg ccatgtatta ctgtgcgcgc tactctgggt ctttcgataa ctgggggtcaa 720
gggtactctgg tgaccgtctc ctca 744
```

<210> 607

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA-55 scFv sequence (nt)

<400> 607

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caatctgccc tgactcagcc tgcctccgtg tctgcgtctc ctggacagtc gatcgccatc 60
tcctgcactg gaaccagcag tgacgttggg ttggatcaac agcaccagc caaagcccc 120
aaactcatga tttatgagga cagtaagcgg ccctcagggg tttctaatac cttctctggc 180
tccaagtctg gcaacacggc ctccctgacc atctctgggc tccaggctga ggacgaggct 240
gattattact gcagctcaaa tacaagaagc agcactttgg tgttcggcgg agggaccaag 300
ctgaccgtcc taggttctag aggtgggtgg ggtagcggcg gcggcggctc tgggtgggtg 360
ggatccctcg agatggccga agtgcagctg gtgcagctct gggctgagat gaagaagcct 420
ggggcctcac tgaagctctc ctgcaaggct tctggataca ctttcacga ctactatgta 480
tactggatgc gacaggcccc tggacaaggg cttgagtcca tgggatggat caaccctaac 540
agtgggtggc caaactatgc acagaagttt cagggcaggg tcaccatgac cagggaacag 600
tccatcagca cagcctacat ggagctgagc aggtgagat ctgacgacac cgccatgtat 660
tactgtgcgc gctcccagcg tgacgggttac atggattact ggggtcaagg tactctgggt 720
accgtctcct ca 732
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<210> 608

<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA epitope

<400> 608
Ser Asn Thr Pro Pro Leu Thr Cys Gln Arg
1 5 10

<210> 609
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA epitope

<400> 609
Cys Ile Pro Cys Gln Leu Arg
1 5

<210> 610
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<223> BCMA epitope

<400> 610
Ser Val Thr Asn Ser Val Lys
1 5

<210> 611
<211> 7
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA epitope

<400> 611

Cys Ser Gln Asn Glu Tyr Phe
1 5

<210> 612

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA epitope

<400> 612

Leu Leu His Ala Cys Ile Pro Cys Gln Leu Arg
1 5 10

<210> 613

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA epitope

<400> 613

Gln Asn Glu Tyr Phe
1 5

<210> 614

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA epitope

<400> 614

Cys Ile Pro Cys Gln Leu

1

5

<210> 615

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA epitope

<400> 615

Cys Gln Arg Tyr Cys

1

5

<210> 616

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA epitope

<400> 616

Met Leu Met Ala Gly

1

5

<210> 617

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA epitope

<400> 617

Gln Asn Glu Tyr Phe Asp Ser Leu Leu
1 5

<210> 618

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA epitope

<400> 618

Tyr Phe Asp Ser Leu
1 5

<210> 619

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA epitope

<400> 619

Gln Leu Arg Cys Ser Ser Asn Thr Pro Pro Leu
1 5 10

<210> 620

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<223> BCMA epitope

<400> 620

Tyr Phe Asp Ser Leu Leu
1 5