SEQUENCE LISTING

<110> Regeneron Pharmaceuticals, Inc.

<120> Chimeric Antigen Receptors with BCMA
Specificity and Uses Thereof

<130> 10455WO01

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ccaggcaagg ggctggagtg ggtggcagtt atattacatg atggaagtag taactactat 180
gcagagtccg tgaagggccg attcatcatc tccagagaca attccaagaa cacactgtat 240
ctgcaaatga acagcctgag agctgaggac acggctctat attactgtac gaaaaggtat 300
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35 40 45
Ala Val Ile Leu His Asp Gly Ser Ser Asn Tyr Tyr Ala Glu Ser Val
50 55 60
Lys Gly Arg Phe Ile 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 Leu Tyr Tyr Cys
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Gly Gln Gly Thr Leu Val Thr Val Ser Ser
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aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
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            20   25   30
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        35   40   45
His Ala Ala Ser Ser Leu Gln 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

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 20 25 30
Val Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

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        35                  40                  45
Ser Ala Ile Ile Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Lys Arg Ala Gly Asp Asn Trp Asn Trp Phe Asp Pro Trp Gly Gln
            100                 105                 110
Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<210> 21
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<400> 21
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<210> 22
<211> 8
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<400> 22
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<210> 23
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gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
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            20                  25                  30
Leu Ala Trp Tyr Gln Arg Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Ala Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Lys Ser Val Pro Phe
                85                  90                  95
Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
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<400> 29
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<210> 30
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<400> 30
Ala Ala Ser
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ccagggaagg gcctggagtg ggtctcaggt atcagttgga atagtggtaa catgggatat 180
gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgttc 240
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            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 Asn Met Gly Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Phe
65   70   75   80
Leu Gln Met His Ser Leu Arg Ala Glu Asp Thr Ala Phe Tyr Tyr Cys
                85   90   95
Ala Lys Val Arg Leu Thr Ala Phe Asp Phe Trp Gly Gln Gly Thr Leu
            100   105   110
Val Thr Val Ser Ser
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gggaaagccc ctaaactcct catctatact gcatccagtt tgcagaatgg agtcccatca 180
aggttcactg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
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gggaccaagc tggagatcaa a   321

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            20   25   30
Leu Asn Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Thr Ala Ser Ser Leu Gln Asn Gly Val Pro Ser Arg Phe Thr 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 Phe Val Ile Tyr Tyr Cys Gln Gln Ser Phe Ser Thr Pro Tyr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100   105

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ccagggaagg ggctggagtg ggtttcatac attagttcta gtggtagttc cataaagtac 180
gcagactctg tgaagggccg attcaccatc tccagggaca acgccaagaa ctcactgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gagagaggga 300

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            20   25   30
Tyr Ile 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 Ser Ile Lys 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 Gly Gly Asn Tyr Gly Met Asp Val Trp Gly Gln Gly Thr
            100   105   110
Thr Val Thr Val Ser Ser
        115

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gggaaagccc ctaagctcct gatctatgct gcaaccagct tgcaaagtgg ggtcccatca 180
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            20   25   30
Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Ala Ala Thr Ser Leu Gln 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 Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Pro
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100   105

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<210> 62
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<400> 62
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ccagggaagg ggctggagtg ggtggccaac atgaaccaag atggaagtga gaaatactat 180
gtggactctg tgaagggccg attcaccatc tccagagaca acgccaagag ctcactgtat 240
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Phe
            20   25   30
Trp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ala Asn Met 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 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 Asp Arg Glu Tyr Cys Ile Ser Thr Ser Cys Tyr Asp Asp Phe
            100   105   110
Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

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<400> 67
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<210> 70
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<400> 70
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gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcatagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc 300
caagggacac gactggagat taaa 324

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<223> synthetic

<400> 74
Asp Ile Gln 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 Ser Ile Ser Ser Tyr
            20   25   30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Ala Ala Ser Ser Leu His 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 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro
                85   90   95
Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100   105

<210> 75
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 75
cagagcatta gcagctat 18

<210> 76

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

<220>
<223> synthetic

<400> 76
Gln Ser Ile Ser Ser Tyr
 1   5

<210> 77
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 77
gctgcatcc   9

<210> 78
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 78
Ala Ala Ser
 1

<210> 79
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 79
caacagagtt acagtacccc tccgatcacc   30

<210> 80
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 80
Gln Gln Ser Tyr Ser Thr Pro Pro Ile Thr
 1   5   10

<210> 81
<211> 1404
<212> DNA
<213> Artificial Sequence

<220>
<223> BCMA 16711 (VL-VH) ScFv CAR-T
      (16711_VK_v2(human).(G4S)3 Linker.16711 VH.hCD8a
      hinge/TM.hCD137 (4-1BB).hCD3 zeta)

<400> 81
gacatccaga tgacccagtc tccatcctcc gtgtctgcat ctgtaggaga cagagtcacc 60
atcacttgtc gggcgagtcg gggaattagc agctggttag cctggtatca gcagaagcca 120
gggaaagccc ctaagctcct gatccatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg ctacttacta ttgtcaacag gctatcagtt tcccattcac tttcggccct 300
gggaccaaag tggatatcaa aggcggcggt ggatctggag gcggtggaag cggtggcggg 360
ggaagtcagg tgcagctggt ggagtcgggg ggaggcgtgg tccagcctgg gaggtccctg 420
agactctcct gtgcagcctc tggattcacc ttcagtacct atggcattca ctgggtccgc 480
caggctccag gcaaggggct ggagtgggtg gcagttatat tacatgatgg aagtagtaac 540
tactatgcag agtccgtgaa gggccgattc atcatctcca gagacaattc caagaacaca 600
ctgtatctgc aaatgaacag cctgagagct gaggacacgg ctctatatta ctgtacgaaa 660
aggtattcag aagcagctgg cccaaattgg ttcgacccct ggggccaggg aaccctggtc 720
accgtctcct caactaccac tcctgctccc cgccccccaa cacctgctcc aactattgca 780
tcccaaccac tctccctcag acccgaagct tgtcgccccg ccgccggagg tgctgttcac 840
actagaggac tcgattttgc ttgcgacatt tatatctggg ccccacttgc aggtacttgc 900
ggagtattgc tgctctcact tgttattact ctttattgca aacggggcag aaagaaactc 960
ctgtatatat tcaaacaacc atttatgaga ccagtacaaa ctactcaaga ggaagatggc 1020
tgtagctgcc gatttccaga agaagaagaa ggaggatgtg aactgagagt gaagttcagc 1080
aggagcgcag acgcccccgc gtacaagcag ggccagaacc agctctataa cgagctcaat 1140
ctaggacgaa gagaggagta cgatgttttg gacaagagac gtggccggga ccctgagatg 1200
gggggaaagc cgagaaggaa gaaccctcag gaaggcctgt acaatgaact gcagaaagat 1260
aagatggcgg aggcctacag tgagattggg atgaaaggcg agcgccggag gggcaagggg 1320
cacgatggcc tttaccaggg tctcagtaca gccaccaagg acacctacga cgcccttcac 1380
atgcaggccc tgcccctcg ctaa   1404

<210> 82
<211> 467
<212> PRT
<213> Artificial Sequence

<220>
<223> BCMA 16711 (VL-VH) ScFv CAR-T
      (16711_VK_v2(human).(G4S)3 Linker.16711 VH.hCD8a
      hinge/TM.hCD137 (4-1BB).hCD3 zeta)

<400> 82
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly

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

<210> 83
<211> 1398
<212> DNA
<213> Artificial Sequence

<220>
<223> BCMA 16716 (VL-VH) ScFv CAR-T
      (16716_VK(human).(G4S)3
      Linker.16716_VH(human).hCD8a hinge/TM.hCD137
      (4-1BB).hCD3 zeta)

<400> 83
gacatccaga tgacccagtc tccatcttcc gtgtctgcat ctttaggaga cagagtcacc 60
atcacttgtc gggcgagtca gggtattagc agctggttag cctggtatca gcggaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tggggcggat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttacta ttgtcaacag gctaaaagtg tcccattcac tttcggccct 300
gggaccaaag tggatatcaa aggcggcggt ggatctggag gcggtggaag cggtggcggg 360
ggaagtgagg tgcagctggt ggagtctggg ggaggcttgg tacagcctgg ggggtccctg 420
agactctcct gtgcagcctc tggattcacc tttagcagct atgtcatgag ttgggtccgc 480
caggctccag ggaagggact ggagtgggtc tcagctatta ttggtagtgg tggtagcaca 540
tattacgcag actccgtgaa gggccggttc accatctcca gagacaattc caagaacacg 600
ctgtatctgc aaatgaacag cctgagagcc gaggacacgg ccgtatatta ctgtgcgaaa 660
agagccgggg ataactggaa ctggttcgac ccctggggcc agggaaccct ggtcaccgtc 720
tcctcaacta ccactcctgc tccccgcccc ccaacacctg ctccaactat tgcatcccaa 780
ccactctccc tcagacccga agcttgtcgc cccgccgccg gaggtgctgt tcacactaga 840
ggactcgatt ttgcttgcga catttatatc tgggccccac ttgcaggtac ttgcggagta 900
ttgctgctct cacttgttat tactctttat tgcaaacggg gcagaaagaa actcctgtat 960
atattcaaac aaccatttat gagaccagta caaactactc aagaggaaga tggctgtagc 1020
tgccgatttc cagaagaaga agaaggagga tgtgaactga gagtgaagtt cagcaggagc 1080
gcagacgccc ccgcgtacaa gcagggccag aaccagctct ataacgagct caatctagga 1140
cgaagagagg agtacgatgt tttggacaag agacgtggcc gggaccctga gatgggggga 1200
aagccgagaa ggaagaaccc tcaggaaggc ctgtacaatg aactgcagaa agataagatg 1260
gcggaggcct acagtgagat tgggatgaaa ggcgagcgcc ggaggggcaa ggggcacgat 1320
ggcctttacc agggtctcag tacagccacc aaggacacct acgacgccct tcacatgcag 1380
gccctgcccc ctcgctaa   1398

<210> 84
<211> 465
<212> PRT
<213> Artificial Sequence

<220>
<223> BCMA 16716 (VL-VH) ScFv CAR-T
      (16716_VK(human).(G4S)3
      Linker.16716_VH(human).hCD8a hinge/TM.hCD137
      (4-1BB).hCD3 zeta)

<400> 84
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Leu Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
            20   25   30
Leu Ala Trp Tyr Gln Arg Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Ala Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Lys Ser Val Pro Phe
                85   90   95
Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Gly Gly Gly Gly Ser
            100   105   110
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu
        115   120   125
Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
    130   135   140
Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Val Met Ser Trp Val Arg
145   150   155   160
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Ile Gly Ser
                165   170   175
Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile
            180   185   190
Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu
        195   200   205
Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Arg Ala Gly Asp
    210   215   220
Asn Trp Asn Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val
225   230   235   240
Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
                245   250   255
Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
            260   265   270
Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
        275   280   285
Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
    290   295   300
Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr
305   310   315   320
Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
                325   330   335
Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
            340   345   350
Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln
        355   360   365
Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
    370   375   380
Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
385   390   395   400
Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
                405   410   415
Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
            420   425   430

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
435 440 445
Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
450 455 460
Arg
465

<210> 85
<211> 1389
<212> DNA
<213> Artificial Sequence

<220>
<223> BCMA 16732 (VL-VH) ScFv CAR-T
(16732_VK_v2(human).(G4S)3
Linker.16732_VH(human).hCD8a hinge/TM.hCD137
(4-1BB).hCD3 zeta)

<400> 85
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc ggacaagtca gagcattggc aactatttaa attggtttca gcagaaacca 120
gggaaagccc ctaaactcct catctatact gcatccagtt tgcagaatgg agtcccatca 180
aggttcactg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaggattttg taatttacta ctgtcaacag agtttcagta ccccgtatac ttttggccag 300
gggaccaagc tggagatcaa aggcggcggt ggatctggag gcggtggaag cggtggcggg 360
ggaagtgaag tgcagctggt ggagtctggg ggaggcttgg tacagcctgg caggtccctg 420
agactctcct gtgcagcctc tggattcacc tttgatgatt atgccatgca ctgggtccgg 480
caagctccag ggaagggcct ggagtgggtc tcaggtatca gttggaatag tggtaacatg 540
ggatatgcgg actctgtgaa gggccgattc accatctcca gagacaacgc caagaactcc 600
ctgttcctgc aaatgcacag tttgagagct gaggacacgg ccttttatta ctgtgcaaaa 660
gtccgtctaa ctgcctttga cttttggggc cagggaaccc tggtcaccgt ctcctcaact 720
accactcctg ctccccgccc cccaacacct gctccaacta ttgcatccca accactctcc 780
ctcagacccg aagcttgtcg ccccgccgcc ggaggtgctg ttcacactag aggactcgat 840
tttgcttgcg acatttatat ctgggcccca cttgcaggta cttgcggagt attgctgctc 900
tcacttgtta ttactcttta ttgcaaacgg ggcagaaaga aactcctgta tatattcaaa 960
caaccattta tgagaccagt acaaactact caagaggaag atggctgtag ctgccgattt 1020
ccagaagaag aagaaggagg atgtgaactg agagtgaagt tcagcaggag cgcagacgcc 1080
cccgcgtaca agcagggcca gaaccagctc tataacgagc tcaatctagg acgaagagag 1140
gagtacgatg ttttggacaa gagacgtggc cgggaccctg agatgggggg aaagccgaga 1200
aggaagaacc ctcaggaagg cctgtacaat gaactgcaga aagataagat ggcggaggcc 1260
tacagtgaga ttgggatgaa aggcgagcgc cggaggggca aggggcacga tggcctttac 1320
cagggtctca gtacagccac caaggacacc tacgacgccc ttcacatgca ggccctgccc 1380
cctcgctaa 1389

<210> 86
<211> 462
<212> PRT
<213> Artificial Sequence

<220>
<223> BCMA 16732 (VL-VH) ScFv CAR-T
(16732_VK_v2(human).(G4S)3
Linker.16732_VH(human).hCD8a hinge/TM.hCD137

(4-1BB).hCD3 zeta)

<400> 86
Asp Ile Gln 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 Thr Ser Gln Ser Ile Gly Asn Tyr
            20   25   30
Leu Asn Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Thr Ala Ser Ser Leu Gln Asn Gly Val Pro Ser Arg Phe Thr 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 Phe Val Ile Tyr Tyr Cys Gln Gln Ser Phe Ser Thr Pro Tyr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
            100   105   110
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu
        115   120   125
Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys
    130   135   140
Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His Trp Val Arg
145   150   155   160
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Ser Trp Asn
                165   170   175
Ser Gly Asn Met Gly Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile
            180   185   190
Ser Arg Asp Asn Ala Lys Asn Ser Leu Phe Leu Gln Met His Ser Leu
        195   200   205
Arg Ala Glu Asp Thr Ala Phe Tyr Tyr Cys Ala Lys Val Arg Leu Thr
    210   215   220
Ala Phe Asp Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr
225   230   235   240
Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
                245   250   255
Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
            260   265   270
Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
        275   280   285
Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
    290   295   300
Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys
305   310   315   320
Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys
                325   330   335
Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val
            340   345   350
Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn
        355   360   365
Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
    370   375   380
Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
385   390   395   400
Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys

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                405                 410                 415
Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
            420                 425                 430
Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
        435                 440                 445
Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
    450                 455                 460
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<210> 87
<211> 1392
<212> DNA
<213> Artificial Sequence

<220>
<223> BCMA 16747 (VL-VH) ScFv CAR-T
(16747_VK(human).(G4S)3
Linker.16747_VH(human).hCD8a hinge/TM.hCD137
(4-1BB).hCD3 zeta)

<400> 87
gacatccaga tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60
atcacttgtc gggcgagtca gggtattaac aactggttag tctggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcaaccagct tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtgggtc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttacta ttgtcaacag gctaacagtt tccctcccac ttttggccag 300
gggaccaagc tggagatcaa aggcggcggt ggatctggag gcggtggaag cggtggcggg 360
ggaagtcagg tgcagctggt ggagtctggg ggaggcttgg tcaagcctgg agggtccctg 420
agactctcct gtgcagcctc tggattcacc ttcagtgact actacatcag ctggatccgc 480
caggctccag ggaaggggct ggagtgggtt tcatacatta gttctagtgg tagttccata 540
aagtacgcag actctgtgaa gggccgattc accatctcca gggacaacgc caagaactca 600
ctgtatctgc aaatgaacag cctgagagcc gaggacacgg ccgtatatta ctgtgcgaga 660
gagggaggga actacggtat ggacgtctgg ggccaaggga ccacggtcac cgtctcctca 720
actaccactc ctgctccccg ccccccaaca cctgctccaa ctattgcatc ccaaccactc 780
tccctcagac ccgaagcttg tcgccccgcc gccggaggtg ctgttcacac tagaggactc 840
gattttgctt gcgacattta tatctgggcc ccacttgcag gtacttgcgg agtattgctg 900
ctctcacttg ttattactct ttattgcaaa cggggcagaa agaaactcct gtatatattc 960
aaacaaccat ttatgagacc agtacaaact actcaagagg aagatggctg tagctgccga 1020
tttccagaag aagaagaagg aggatgtgaa ctgagagtga agttcagcag gagcgcagac 1080
gcccccgcgt acaagcaggg ccagaaccag ctctataacg agctcaatct aggacgaaga 1140
gaggagtacg atgttttgga caagagacgt ggccgggacc ctgagatggg gggaaagccg 1200
agaaggaaga accctcagga aggcctgtac aatgaactgc agaaagataa gatggcggag 1260
gcctacagtg agattgggat gaaaggcgag cgccggaggg gcaaggggca cgatggcctt 1320
taccagggtc tcagtacagc caccaaggac acctacgacg cccttcacat gcaggccctg 1380
ccccctcgct aa 1392

<210> 88
<211> 463
<212> PRT
<213> Artificial Sequence

<220>
<223> BCMA 16747 (VL-VH) ScFv CAR-T
(16747_VK(human).(G4S)3
Linker.16747_VH(human).hCD8a hinge/TM.hCD137

(4-1BB).hCD3 zeta)

<400> 88

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

```
Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
            420                 425                 430
Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
        435                 440                 445
Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
    450                 455                 460
```

<210> 89
<211> 1431
<212> DNA
<213> Artificial Sequence

<220>
<223> BCMA 21581 (VL-VH) ScFv CAR-T
(21581 VK(human).(G4S)3 Linker.21581
VH(human).G4S Linker_v2.hCD8a hinge/TM.hCD137
(4-1BB).hCD3 zeta)

<400> 89
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcatagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc 300
caagggacac gactggagat taaaggcggc ggtggatctg gaggcggtgg aagcggtggc 360
gggggaagtg aggtgcagct ggtggagtct gggggaggct tggtccagcc tgggggtcc 420
ctgagactct cctgtgcagc ctctggattc acctttagta acttttggat gacctgggtc 480
cgccaggctc cagggaaggg gctggagtgg gtggccaaca tgaaccaaga tggaagtgag 540
aaatactatg tggactctgt gaagggccga ttcaccatct ccagagacaa cgccaagagc 600
tcactgtatc tgcaaatgaa cagcctgaga gccgaggaca cggctgtgta ttactgtgcg 660
agagatcggg aatattgtat tagtaccagc tgctatgatg actttgacta ctggggccag 720
ggaaccctgg tcaccgtctc ctcaggaggc ggaggcagca ctaccactcc tgctccccgc 780
cccccaacac ctgctccaac tattgcatcc caaccactct ccctcagacc cgaagcttgt 840
cgccccgccg ccggaggtgc tgttcacact agaggactcg attttgcttg cgacatttat 900
atctgggccc cacttgcagg tacttgcgga gtattgctgc tctcacttgt tattactctt 960
tattgcaaac ggggcagaaa gaaactcctg tatatattca aacaaccatt tatgagacca 1020
gtacaaacta ctcaagagga agatggctgt agctgccgat ttccagaaga agaagaagga 1080
ggatgtgaac tgagagtgaa gttcagcagg agcgcagacg cccccgcgta caagcagggc 1140
cagaaccagc tctataacga gctcaatcta ggacgaagag aggagtacga tgttttggac 1200
aagagacgtg gccgggaccc tgagatgggg ggaaagccga gaaggaagaa ccctcaggaa 1260
ggcctgtaca atgaactgca gaaagataag atggcggagg cctacagtga gattgggatg 1320
aaaggcgagc gccggagggg caaggggcac gatggccttt accagggtct cagtacagcc 1380
accaaggaca cctacgacgc ccttcacatg caggccctgc cccctcgcta a   1431

<210> 90
<211> 476
<212> PRT
<213> Artificial Sequence

<220>
<223> BCMA 21581 (VL-VH) ScFv CAR-T
(21581 VK(human).(G4S)3 Linker.21581
VH(human).G4S Linker_v2.hCD8a hinge/TM.hCD137
(4-1BB).hCD3 zeta)

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

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

<210> 91
<211> 1437
<212> DNA
<213> Artificial Sequence

<220>
<223> HLA-A2/HPV16E7(11-19) 17363 ScFv (VL-VH) CAR-T
(Irrelevant Control)
(17363_ULC-VK(1)(human).G4Sx3_4.17363_VH(human).
G4S_V2.hCD8a hinge/TM.hCD137 (4-1BB).hCD3 zeta)

<400> 91
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gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca acagaaacca 120
gggaaagccc ctaagctcct gatctatgct gtttccattt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcaactc tctgcaacct 240
gaagattttg caacttactc ctgtcaacag acttacagta cccctccgat caccttcggc 300
caagggacac gactggagat taaaggtgga ggcggtagtg gcggaggcgg aagtggtgga 360
ggaggctcag aggtgcagct gttggagtct gggggaggct tggtacaacc tgggggtcc 420
ctgagactct cctgtgcagc ctctggattc acctttagca gttatgccat gacctgggtc 480
cgccaggctc cagggatggg actggagtgg gtctcagtta ttagtggtag tggtagtgaa 540
acatactacg cagactccgt gaagggccgg ttcaccatct ccagagacaa ttccaaaaac 600
acactgtatc tgcaaatgaa cagcctgaga gccgaagaca cggccgtata ttactgtgtg 660
aaagattctt cgtataggag ctcgtcgagg gcctactact actacggaat ggacgtctgg 720
ggcctaggga ccacggtcac cgtctcctca ggaggtggtg gaagtactac cactcctgct 780
ccccgccccc caacacctgc tccaactatt gcatcccaac cactctccct cagacccgaa 840
gcttgtcgcc ccgccgccgg aggtgctgtt cacactagag gactcgattt tgcttgcgac 900
atttatatct gggccccact tgcaggtact tgcggagtat tgctgctctc acttgttatt 960
actctttatt gcaaacgggg cagaaagaaa ctcctgtata tattcaaaca accatttatg 1020
agaccagtac aaactactca agaggaagat ggctgtagct gccgatttcc agaagaagaa 1080
gaaggaggat gtgaactgag agtgaagttc agcaggagcg cagacgcccc cgcgtacaag 1140
cagggccaga accagctcta taacgagctc aatctaggac gaagagagga gtacgatgtt 1200
ttggacaaga gacgtggccg ggaccctgag atgggggggaa agccgagaag gaagaaccct 1260
caggaaggcc tgtacaatga actgcagaaa gataagatgg cggaggccta cagtgagatt 1320
gggatgaaag gcgagcgccg gaggggcaag gggcacgatg gcctttacca gggtctcagt 1380
acagccacca aggacaccta cgacgccctt cacatgcagg ccctgccccc tcgctaa    1437
```

<210> 92
<211> 478
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A2/HPV16E7(11-19) 17363 ScFv (VL-VH) CAR-T

(Irrelevant Control)
(17363_ULC-VK(1)(human).G4Sx3_4.17363_VH(human).
G4S_V2.hCD8a hinge/TM.hCD137 (4-1BB).hCD3 zeta)

<400> 92

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

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


<210> 93
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 93
Gly Gly Gly Gly Ser
 1               5


<210> 94
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 94
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1               5                  10


<210> 95
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 95
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1               5                  10                  15


<210> 96
<211> 18
<212> PRT
<213> Artificial Sequence
```

<220>
<223> linker

<400> 96
Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
 1   5   10   15
Lys Gly

<210> 97
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> hinge

<400> 97
Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
 1   5   10   15
Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
            20   25   30
Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
        35   40   45

<210> 98
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> TM domain

<400> 98
Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
 1   5   10   15
Ser Leu Val Ile Thr Leu Tyr Cys
            20

<210> 99
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-1BB

<400> 99
Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
 1   5   10   15
Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe

```
            20                  25                  30
Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
        35                  40


<210> 100
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> cd3-Zeta

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


<210> 101
<211> 184
<212> PRT
<213> Artificial Sequence

<220>
<223> human BCMA (TNFRSF17) Protein NP_001183.2

<400> 101
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
```