

ANTIGEN BINDING POLYPEPTIDES

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims the benefit under 35 U.S. C. § 119(e) of U.S. Provisional Application No. 63/540,332, filed September 25, 2023, and U.S. Provisional Application No. 63/618,880, filed January 8, 2024, and each of which is incorporated by reference herein in its entirety.

STATEMENT REGARDING SEQUENCE LISTING

The Sequence Listing associated with this application is provided in XML format in lieu of a paper copy and is hereby incorporated by reference into the specification. The name of the XML file containing the Sequence Listing is KELO-011-WO1_ST26.xml. The XML file is 1176 KB, was created on September 20, 2024, and is being submitted electronically via Patent Center, concurrent with the filing of the specification.

Technical Field

The present disclosure relates to antigen binding polypeptides. More particularly, the disclosure relates to polypeptides comprising antibodies or antigen binding fragments thereof, nucleic acids encoding the polypeptides, and vectors for expressing the same.

Description of the Related Art

B cell maturation antigen (BCMA) is a member of the tumor necrosis factor receptor superfamily and is also known as tumor necrosis factor receptor superfamily member 17 (TNFRSF17). BCMA is normally expressed in mature B lymphocytes and plasma cells. BCMA expression is also detected in various lymphomas and multiple myelomas. Multiple myeloma is an incurable plasma cell malignancy that originates in the bone marrow.

Multiple myeloma is the second most prevalent hematological malignancy after non-lymphoma. In 2020, an estimated 176,404 people world-wide were diagnosed with multiple myeloma and about 117,077 patients succumbed to the disease. In 2023, an estimated 35,730

people in the United States alone will be diagnosed with multiple myeloma and an estimated 12,590 multiple myeloma patients will pass from the disease or associated complications. The 5-year relative survival rate for multiple myeloma in the United States is only about 58%

Multiple myeloma may initially be treated with an autologous stem cell transplantation (ASCT) and/or various drug combinations (*e.g.*, proteasome inhibitors including bortezomib, carfilzomib, ixazomib; immunomodulatory drugs (IMiDs) including pomalidomide, lenalidomide, thalidomide; and corticosteroids like dexamethasone) but patients eventually relapse with the disease becoming refractory to treatment. Subsequent lines of treatment include monoclonal antibodies, bispecific antibodies, *e.g.*, BiTEs, antibody-drug conjugates, and finally chimeric antigen receptor T cell therapy.

Autologous *ex vivo* chimeric antigen receptor (CAR) T cell therapy is emerging as a late line treatment for multiple myeloma patients. Although promising, these *ex vivo* CAR T cell therapies have yet to realize their potential because drug product manufacturing timelines are long and costly, because access to the therapies is limited to a few treatment centers with specialized expertise necessary to provide the therapies, because these therapies are associated with high rates of cytokine release syndrome, and because most patients eventually relapse and succumb to the disease. There remains a significant unmet need for multiple myeloma patients for more affordable, more accessible, and more efficacious therapies.

BRIEF SUMMARY

The present disclosure generally relates, in part, antibodies and antigen binding fragments thereof directed against B cell maturation antigen (BCMA), polypeptides comprising an anti-BCMA antibody or antigen binding fragment thereof, bispecific antibodies comprising an anti-BCMA antibody or antigen binding fragment thereof and an anti-CD3 antibody, immunoconjugates comprising an anti-BCMA antibody drug linked to a cytotoxic agent, and anti-BCMA chimeric antigen receptors, polynucleotides encoding the polypeptides, vectors for expressing the polynucleotides, and compositions comprising the foregoing.

In various embodiments, the disclosure contemplates, in part, an antibody or antigen binding fragment thereof comprising: (a) a heavy chain variable region (VH) comprising a CDRH1, a CDRH2, and a CDRH3 of an antibody or antigen binding fragment thereof set

forth in Table 1; a polypeptide linker; and a light chain variable region (VL) comprising a CDRL1, a CDRL2, and a CDRL3 of an antibody or antigen binding fragment thereof set forth in Table 1; or (b) a VHH domain comprising a CDRH1, a CDRH2, and a CDRH3 of an antibody or antigen binding fragment thereof set forth in Table 1.

- 5 In particular embodiments: (a) the VH comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 12, 13, and 14 and the VL comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 16, 17, and 18; (b) the VH comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 22, 23, and 24 and
- 10 the VL comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 26, 27, and 28; (c) the VH comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 32, 33, and 34 and the VL comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 36, 37, and 38; (d) the VH comprises a CDRH1, a CDRH2, and a
- 15 CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 42, 43, and 44 and the VL comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 46, 47, and 48; (e) the VH comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 52, 53, and 54 and the VL comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 56, 57, and 58; (f) the VH comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 62, 63, and 64 and the VL comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 66, 67, and 68; (g) the VH comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 72, 73, and 74 and
- 25 the VL comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 76, 77, and 78; (h) the VH comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 82, 83, and 84 and the VL comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 86, 87, and 88; (i) the VH comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 92, 93, and 94 and the VL comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 96, 97, and 98; (j) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 102,

103, and 104; (k) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 106, 107, and 108; (l) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 110, 111, and 112; (m) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 114, 115, and 116; (n) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 118, 119, and 120; (o) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 122, 123, and 124; (p) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 126, 127, and 128; (q) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 130, 131, and 132; (r) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 134, 135, and 136; (s) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 138, 139, and 140; or (t) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 142, 143, and 144. In a particular embodiment, the VH comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 62, 63, and 64 and the VL comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 66, 67, and 68.

In some embodiments: (a) the VH comprises the amino acid sequence set forth in SEQ ID NO: 11 and the VL comprises the amino acid sequence set forth in SEQ ID NO: 15; (b) the VH comprises the amino acid sequence set forth in SEQ ID NO: 21 and the VL comprises the amino acid sequence set forth in SEQ ID NO: 25; (c) the VH comprises the amino acid sequence set forth in SEQ ID NO: 31 and the VL comprises the amino acid sequence set forth in SEQ ID NO: 35; (d) the VH comprises the amino acid sequence set forth in SEQ ID NO: 41 and the VL comprises the amino acid sequence set forth in SEQ ID NO: 45; (e) the VH comprises the amino acid sequence set forth in SEQ ID NO: 51 and the VL comprises the amino acid sequence set forth in SEQ ID NO: 55; (f) the VH comprises the amino acid sequence set forth in SEQ ID NO: 61 and the VL comprises the amino acid sequence set forth in SEQ ID NO: 65; (g) the VH comprises the amino acid sequence set forth in SEQ ID NO: 71 and the VL comprises the amino acid sequence set forth in SEQ ID

NO: 75; (h) the VH comprises the amino acid sequence set forth in SEQ ID NO: 81 and the VL comprises the amino acid sequence set forth in SEQ ID NO: 85; (i) the VH comprises the amino acid sequence set forth in SEQ ID NO: 91 and the VL comprises the amino acid sequence set forth in SEQ ID NO: 95; or (a) the VHH domain comprises the amino acid sequence set forth in any one of SEQ ID NOs: 101, 105, 109, 113, 117, 121, 125, 129, 133, 137, and 141. In particular embodiments, the VH comprises the amino acid sequence set forth in SEQ ID NO: 61 and the VL comprises the amino acid sequence set forth in SEQ ID NO: 65.

In certain embodiments, the polypeptide linker is selected from the group consisting of: TGEKP (SEQ ID NO: 2); (GGGS)_n wherein n = 1, 2, 3, 4 or 5 (SEQ ID NOs: 3, and 976-979); EGKSSGSGSESKVD (SEQ ID NO: 4); KESGSVSSEQLAQFRSLD (SEQ ID NO: 5); LRQRDGERP (SEQ ID NO: 6); LRQKDGGGSRP (SEQ ID NO: 7); LRQKD(GGGS)₂ERP (SEQ ID NO: 8), GEGTSTGSGGSGGSGGAD (SEQ ID NO: 9), and GSTSGSGKPGSGEGSTKG (SEQ ID NO: 10).

In particular embodiments, the antibody or antigen binding fragment thereof comprises the amino acid sequence set forth in any one of SEQ ID NOs: 19, 20, 29, 30, 39, 40, 49, 50, 59, 60, 69, 70, 79, 80, 89, 90, 99, 100, 101, 105, 109, 113, 117, 121, 125, 129, 133, 137, and 141, preferably, SEQ ID NO: 69 or 70.

In various embodiments, the disclosure contemplates, in part, a bispecific antibody comprising the antibody or antigen binding fragment thereof contemplated herein.

In some embodiments, the bispecific antibody further comprises an anti-CD3 antibody that binds CD3 δ , CD3 ϵ , CD3 γ , or CD3 ζ .

In various embodiments, the disclosure contemplates, in part, an antibody conjugate comprising the antibody or antigen binding fragment thereof contemplated herein.

In certain embodiments, the antigen or antigen binding fragment thereof is conjugated to a cytotoxic agent.

In particular embodiments: (a) the cytotoxic agent is a toxin selected from the group consisting of: saporin, diphtheria toxin, pseudomonas exotoxin A, Ricin A chain derivatives, a small molecule toxin, and combinations thereof; (b) the cytotoxic agent is a radioisotope selected from the group consisting of: ¹³¹I, ⁹⁰Y, ¹⁷⁷Lu, ¹⁸⁸Re, ⁶⁷Cu, ²¹³Bi, ²¹¹At, and ²²⁷Ac; (c) the cytotoxic agent is an RNA polymerase II inhibitor and/or RNA polymerase III inhibitor selected from the group consisting of: an amatoin, α -amanitin, β -amanitin, γ -amanitin, ϵ -amanitin, amanin, amaninamide, amanullin, amanullinic acid and any functional

fragments, derivatives or analogs thereof; or (d) the cytotoxic agent is a DNA-damaging agent selected from the group consisting of: an antitubulin agent, a DNA crosslinking agent, a DNA alkylating agent and a mitotic disrupting agent.

In various embodiments, the disclosure contemplates, in part, a chimeric antigen
5 receptor (CAR) comprising the antibody or antigen binding fragment thereof contemplated herein; a spacer domain; a transmembrane domain, and one or more intracellular signaling domains.

In some embodiments, the spacer domain comprises a hinge domain or fragment thereof selected from the group consisting of: a CD4 hinge, a CD8 β hinge, a CD8 α hinge, a
10 CD28 hinge, a CD134 hinge, a CD137 hinge, a CD152 hinge, a CD278 hinge, an IgG1 hinge, an IgG2 hinge, an IgG3 hinge, and an IgG4 hinge.

In particular embodiments, the spacer domain comprises an amino acid sequence set forth in any one of SEQ ID NOs: 145, 146, 147, 148, 149, and 150 or an amino acid sequence at least 95% identical thereto.

15 In some embodiments, the transmembrane domain is isolated or derived from a polypeptide selected from the group consisting of an alpha, beta, gamma, or delta chain of the T-cell receptor, CD3 δ , CD3 ϵ , CD3 γ , CD3 ζ , CD4, CD5, CD8 α , CD9, CD16, CD22, CD27, CD28, CD33, CD37, CD45, CD64, CD80, CD86, CD134, CD137, CD152, CD154, CD278, amnionless (AMN), and programmed cell death 1 (PDCD1).

20 In particular embodiments, the transmembrane domain comprises an amino acid sequence set forth in any one of SEQ ID NOs: 151, 152, 153, 154, 155, 156, and 157 or an amino acid sequence at least 95% identical thereto.

In certain embodiments, the one or more intracellular signaling domains comprises a primary signaling domain isolated or derived from a polypeptide selected from the group
25 consisting of FcR γ , FcR β , CD3 γ , CD3 δ , CD3 ϵ , CD3 ζ , CD22, CD79a, CD79b, and CD66d.

In some embodiments, the one or more intracellular signaling domains comprises a primary signaling domain isolated from CD3 ζ .

In certain embodiments, the primary signaling domain comprises an amino acid sequence set forth in SEQ ID NO: 158 or an amino acid sequence at least 95% identical
30 thereto.

In particular embodiments, the one or more intracellular signaling domains comprises a costimulatory signaling domain isolated or derived from a polypeptide selected from the group consisting of TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9, TLR10,

CARD11, CD2, CD7, CD27, CD28, CD30, CD40, ICAM, CD83, CD94, CD134 (OX40), CD137 (4-1BB), CD278 (ICOS), DAP10, LAT, SLP76, TRAT1, TNFR2, TNFRS14, TNFRS18, TNFRS25, and ZAP70.

In some embodiments, the one or more intracellular signaling domains comprises a
5 costimulatory signaling domain comprising an amino acid sequence set forth in any one of
SEQ ID NOs: 159, 160, 161, 162, 163, and 164 or an amino acid sequence at least 95%
identical thereto.

In various embodiments, the disclosure contemplates, in part, a CAR comprising an
antibody or antigen binding fragment thereof comprises the amino acid sequence set forth in
10 any one of SEQ ID NOs: 39, 59, 70, 90, 101, or 117; a spacer domain comprising the amino
acid sequence set forth in any one of SEQ ID NOs: 145, 146, and 148 or an amino acid
sequence at least 95% identical thereto; a transmembrane domain comprising the amino acid
sequence set forth in SEQ ID NOs: 151 or 153; one or more intracellular signaling domains
comprising a costimulatory signaling domain comprising an amino acid sequence set forth
15 in any one of SEQ ID NOs: 159, 160, and 162 or an amino acid sequence at least 95%
identical thereto and further comprising a primary signaling domain comprising an amino
acid sequence set forth in SEQ ID NO: 158 or an amino acid sequence at least 95% identical
thereto.

In various embodiments, the disclosure contemplates, in part, a CAR comprising the
20 amino acid sequence set forth in any one of SEQ ID NOs: 165-860.

In various embodiments, the disclosure contemplates, in part, a CAR comprising the
amino acid sequence set forth in any one of SEQ ID NOs: 261, 262, 263, 264, 265, 266, 267,
268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, and 283.

In various embodiments, the disclosure contemplates, in part, a CAR comprising the
25 amino acid sequence set forth in any one of SEQ ID NOs: 357, 358, 359, 360, 361, 362, 363,
364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, and 380.

In various embodiments, the disclosure contemplates, in part, a CAR comprising the
amino acid sequence set forth in any one of SEQ ID NOs: 429, 430, 431, 432, 433, 434, 435,
436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, and 452. In
30 particular embodiments, a CAR comprising the amino acid sequence set forth in SEQ ID
NO: 429 or an amino acid sequence 95% identical thereto.

In various embodiments, the disclosure contemplates, in part, a CAR comprising the amino acid sequence set forth in any one of SEQ ID NOs: 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, and 548.

In various embodiments, the disclosure contemplates, in part, a CAR comprising the amino acid sequence set forth in any one of SEQ ID NOs: 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, and 620.

In various embodiments, the disclosure contemplates, in part, a CAR comprising the amino acid sequence set forth in any one of SEQ ID NOs: 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, and 716.

In some embodiments, the CAR further comprises a signal peptide.

In particular embodiments, the signal peptide comprises an amino acid sequence set forth in any one of SEQ ID NOs: 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, and 873.

In particular embodiments, a polynucleotide encoding a CAR, comprises a polynucleotide sequence set forth in any one of SEQ ID NOs: 905-924.

In particular embodiments, a polynucleotide encoding a signal peptide and a CAR comprises a polynucleotide sequence set forth in any one of SEQ ID NOs: 925-944.

In various embodiments, the disclosure contemplates, in part, a polynucleotide encoding an antibody or antigen binding fragment thereof, a bispecific antibody, an antibody conjugate, or a CAR contemplated herein.

In various embodiments, the disclosure contemplates, in part, a polynucleotide encoding or comprising a promoter operably linked to a polynucleotide set forth in any one of SEQ ID NOs: 905-944.

In certain embodiments, the promoter comprises the polynucleotide sequence set forth in any one of SEQ ID NOs: 948, 949, 950, 951, 952, and 953, preferably SEQ ID NO: 949.

In particular embodiments, the polynucleotide further comprises a post-transcriptional response element.

In some embodiments, the post-transcriptional response element comprises the polynucleotide sequence set forth in any one of SEQ ID NOs: 945, 946, and 947.

In various embodiments, the disclosure contemplates, in part, a DNA comprising the polynucleotide sequence set forth in any one of SEQ ID NOs: 945, 946, and 947.

In various embodiments, the disclosure contemplates, in part, an RNA encoded by the polynucleotide sequence set forth in any one of SEQ ID NOs: 945, 946, and 947.

In various embodiments, the disclosure contemplates, in part, a vector comprising the polynucleotide sequence set forth in any one of SEQ ID NOs: 945, 946, and 947.

5 In various embodiments, the disclosure contemplates, in part, a vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 950 operably linked to a polynucleotide encoding a signal peptide and a chimeric antigen receptor comprising an anti-BCMA antibody or antigen binding fragment thereof comprising an amino acid set forth in any one of SEQ ID NOs: 11-144, and optionally comprising a polynucleotide comprising
10 a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

In various embodiments, the disclosure contemplates, in part, a vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 950 operably linked to a polynucleotide encoding a signal peptide and a chimeric antigen receptor comprising an anti-BCMA antibody or antigen binding fragment thereof comprising an amino acid set forth
15 in any one of SEQ ID NOs: 20, 30, 39, 50, 59, 70, 80, 90, 100, 101, 105, 109, 113, 117, 121, 125, 129, 133, 137, and 141, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

In various embodiments, the disclosure contemplates, in part, a vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 950 operably linked
20 to a polynucleotide encoding a signal peptide and a chimeric antigen receptor comprising an amino acid set forth in any one of SEQ ID NOs: 165-860, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

In various embodiments, the disclosure contemplates, in part, a vector encoding or
25 comprising a promoter comprising a sequence set forth in SEQ ID NO: 950 operably linked to a polynucleotide encoding a signal peptide and a chimeric antigen receptor comprising an amino acid set forth in any one of SEQ ID NOs: 189, 237, 261, 333, 357, 429, 477, 525, 573, 597, 621, 645, 669, 693, 717, 741, 765, 789, 813, and 837, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of
30 SEQ ID NOs: 945-947.

In various embodiments, the disclosure contemplates, in part, a vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 950 operably linked to a polynucleotide comprising a polynucleotide sequence set forth in SEQ ID NO: 904 and

a polynucleotide sequence set forth in any one of SEQ ID NOs: 905-924, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

5 In particular embodiments, a vector encoding or comprising a promoter comprises a sequence set forth in SEQ ID NO: 950 operably linked to a polynucleotide comprising a polynucleotide sequence set forth in any one of SEQ ID NOs: 925-944, and optionally comprises a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

10 In various embodiments, the disclosure contemplates, in part, a vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 949 operably linked to a polynucleotide encoding a signal peptide and a chimeric antigen receptor comprising an anti-BCMA antibody or antigen binding fragment thereof comprising an amino acid set forth in any one of SEQ ID NOs: 11-144, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

15 In various embodiments, the disclosure contemplates, in part, a vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 949 operably linked to a polynucleotide encoding a signal peptide and a chimeric antigen receptor comprising an anti-BCMA antibody or antigen binding fragment thereof comprising an amino acid set forth in any one of SEQ ID NOs: 20, 30, 39, 50, 59, 70, 80, 90, 100, 101, 105, 109, 113, 117, 121,
20 125, 129, 133, 137, and 141, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

In various embodiments, the disclosure contemplates, in part, a vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 949 operably linked to a polynucleotide encoding a signal peptide and a chimeric antigen receptor comprising an
25 amino acid set forth in any one of SEQ ID NOs: 165-860, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

In various embodiments, the disclosure contemplates, in part, a vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 949 operably linked
30 to a polynucleotide encoding a signal peptide and a chimeric antigen receptor comprising an amino acid set forth in any one of SEQ ID NOs: 189, 237, 261, 333, 357, 429, 477, 525, 573, 597, 621, 645, 669, 693, 717, 741, 765, 789, 813, and 837, preferably SEQ ID NO: 429 and

optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

In various embodiments, the disclosure contemplates, in part, a vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 949 operably linked
5 to a polynucleotide comprising a polynucleotide sequence set forth in SEQ ID NO: 904 and a polynucleotide sequence set forth in any one of SEQ ID NOs: 905-924, preferably SEQ ID NO: 910 and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

In certain embodiments, a vector encoding or comprising a promoter comprises a
10 sequence set forth in SEQ ID NO: 949 operably linked to a polynucleotide comprising a polynucleotide sequence set forth in any one of SEQ ID NOs: 925-944, preferably SEQ ID NO: 930 and optionally comprises a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

In certain embodiments, the vector is an expression vector.

15 In particular embodiments, the vector is a transfer plasmid or viral vector.

In some embodiments, the vector is a plasmid.

In particular embodiments, the vector is a viral vector selected from the group consisting of an adenoviral (Ad) vector, an adeno-associated virus (AAV) vector, a herpes simplex virus (HSV) vector, a parvovirus vector, a rhabdovirus vector, a vesiculovirus vector,
20 a paramyxovirus vector, a morbillivirus vector, a henipavirus vector, an alphavirus vector, a flavivirus vector, a retroviral vector, and a lentiviral vector (LVV).

In certain embodiments, the lentiviral vector is engineered or derived from the genome of a lentivirus selected from the group consisting of: HIV (HIV type 1 or HIV type 2); visna-maedi virus (VMV); caprine arthritis-encephalitis virus (CAEV); equine infectious
25 anemia virus (EIAV); feline immunodeficiency virus (FIV); bovine immune deficiency virus (BIV); and simian immunodeficiency virus (SIV).

In various embodiments, the disclosure contemplates, in part, a lentiviral vector comprising: a 5' long terminal repeat (LTR) comprising R and U5 regions; a Psi (Ψ) packaging signal; a cPPT/FLAP; an export element; a polynucleotide encoding or
30 comprising a promoter operably linked to a polynucleotide sequence set forth in SEQ ID NO: 904 and a polynucleotide sequence set forth in any one of SEQ ID NOs: 905-924 preferably SEQ ID NO: 910; optionally a WPRE; a 3' LTR comprising U3 and R regions; a polyadenylation signal and a poly(A) tail.

In various embodiments, the disclosure contemplates, in part, a lentiviral vector comprising: a 5' long terminal repeat (LTR) comprising R and U5 regions; a Psi (Ψ) packaging signal; a cPPT/FLAP; an export element; a polynucleotide encoding or comprising a promoter operably linked to a polynucleotide sequence set forth in any one of
 5 SEQ ID NOs: 925-944 preferably SEQ ID NO: 930; optionally a WPRE; a 3' LTR comprising U3 and R regions; a polyadenylation signal and a poly(A) tail.

In various embodiments, the disclosure contemplates, in part, an RNA comprising: a 5' long terminal repeat (LTR) comprising R and U5 regions; a Psi (Ψ) packaging signal; a cPPT/FLAP; an export element; a polynucleotide encoding a promoter operably linked to a
 10 polynucleotide sequence set forth in SEQ ID NO: 904 and a polynucleotide sequence set forth in any one of SEQ ID NOs: 905-924 preferably SEQ ID NO: 910; optionally a WPRE; a 3' LTR comprising U3 and R regions; a polyadenylation signal and optionally a poly(A) tail.

In various embodiments, the disclosure contemplates, in part, an RNA comprising: a
 15 5' long terminal repeat (LTR) comprising R and U5 regions; a Psi (Ψ) packaging signal; a cPPT/FLAP; an export element; a polynucleotide encoding a promoter operably linked to a polynucleotide sequence set forth in any one of SEQ ID NOs: 925-944 preferably SEQ ID NO: 930; optionally a WPRE; a 3' LTR comprising U3 and R regions; a polyadenylation signal and optionally a poly(A) tail.

20 In various embodiments, the disclosure contemplates, in part, a recombinant lentivirus comprising one or more copies of a lentiviral vector or an RNA contemplated herein.

In various embodiments, the disclosure contemplates, in part, a composition comprising an antibody or antigen binding fragment thereof, a bispecific antibody, an
 25 antibody conjugate, a CAR, a polynucleotide, a vector, an RNA, or a recombinant lentivirus contemplated herein.

BRIEF DESCRIPTION OF SEVERAL VIEWS OF THE DRAWINGS

Figure 1 is a cartoon of a vector encoding a promoter operably linked to a polynucleotide encoding an anti-BCMA CAR and an optional post-transcriptional response
 30 element (PRE) operably linked to the 3' prime end of the polynucleotide encoding the anti-BCMA CAR.

Figure 2A shows Jurkat cell titer of recombinant lentiviruses comprising a viral envelope expressing a mutated vesicular stomatitis Indiana virus envelope glycoprotein G (VSIV-G) and a non-viral membrane-bound tropism polypeptide that binds CD3 and a lentiviral vector encoding an MNDU3 promoter operably linked to a polynucleotide
5 encoding a CD8 α signal peptide and an anti-BCMA CAR and a WPRE operably linked to the 3' prime end of the polynucleotide encoding the anti-BCMA CAR (18 anti-BCMA CARs were evaluated).

Figure 2B shows anti-BCMA CAR expression on PBMCs transduced with recombinant lentiviral particles comprising a viral envelope expressing a mutated VSIV-G and a non-viral membrane-bound tropism polypeptide that binds CD3 and a lentiviral vector
10 encoding an MNDU3 promoter operably linked to a polynucleotide encoding a CD8 α signal peptide and an anti-BCMA CAR and a WPRE operably linked to the 3' prime end of the polynucleotide encoding the anti-BCMA CAR (18 anti-BCMA CARs were evaluated).

Figure 2C shows the vector copy number (VCN) in PBMCs transduced with recombinant lentiviral particles comprising a viral envelope expressing a mutated VSIV-G and a non-viral membrane-bound tropism polypeptide that binds CD3 and a lentiviral vector
15 encoding an MNDU3 promoter operably linked to a polynucleotide encoding a CD8 α signal peptide and an anti-BCMA CAR and a WPRE operably linked to the 3' prime end of the polynucleotide encoding the anti-BCMA CAR (18 anti-BCMA CARs were evaluated).

Figure 2D shows the anti-BCMA CAR activity measured as the amount of IFN γ produced in a co-culture assay. PBMCs transduced with recombinant lentiviral particles comprising a viral envelope expressing a mutated VSIV-G and a non-viral membrane-bound tropism polypeptide that binds CD3 and a lentiviral vector encoding an MNDU3 promoter
20 operably linked to a polynucleotide encoding a CD8 α signal peptide and an anti-BCMA CAR and a WPRE operably linked to the 3' prime end of the polynucleotide encoding the anti-BCMA CAR (18 anti-BCMA CARs were evaluated) were co-cultured with Daudi cells (low BCMA expression) or RPMI-8226 cells (high BCMA expression) for 24 hours. After 24 hours, IFN γ levels in co-culture supernatant were measured and plotted as a function of % anti-BCMA CAR positive cells in the co-culture.

Figure 3A shows Jurkat cell functional titer of recombinant lentivirus comprising a viral envelope expressing a mutated VSIV-G and a non-viral membrane-bound tropism polypeptide that binds CD3 and a lentiviral vector encoding either an MNDU3 promoter, an
30 SFFV promoter, or an EF1 α promoter operably linked to a polynucleotide encoding a CD8 α

signal peptide and an anti-BCMA CAR (6 anti-BCMA CARs were evaluated) and either no PRE or a wild-type or mutated WPRE operably linked to the 3' prime end of the polynucleotide encoding the anti-BCMA CAR.

Figure 3B shows the VCN in transduced PBMCs as a function of the percentage of PBMCs expressing an anti-BCMA CAR. Human PBMCs were transduced with a recombinant lentivirus comprising a viral envelope expressing a mutated VSIV-G and a non-viral membrane-bound tropism polypeptide that binds CD3 and a lentiviral vector encoding either an MNDU3 promoter, an SFFV promoter, or an EF1 α promoter operably linked to a polynucleotide encoding a CD8 α signal peptide and an anti-BCMA CAR (6 anti-BCMA CARs were evaluated) and either no PRE or a wild-type or mutated WPRE operably linked to the 3' prime end of the polynucleotide encoding the anti-BCMA CAR.

Figure 3C shows the amount of IFN γ secreted from PBMCs expressing an anti-BCMA CAR co-cultured with RPMI-8226 cells (BCMA expressing cells) for 24 hours as a function of the percentage of CAR-expressing cells in the co-culture.

Figure 3D shows the amount of IL-2 secreted from PBMCs expressing an anti-BCMA CAR co-cultured with RPMI-8226 cells (BCMA expressing cells) for 24 hours as a function of the percentage of CAR-expressing cells in the co-culture.

Figure 3E shows the amount of IFN γ secreted from PBMCs expressing an anti-BCMA CAR in the absence of target cells. Human PBMCs were transduced with a recombinant lentivirus comprising a viral envelope expressing a mutated VSIV-G and a non-viral membrane-bound tropism polypeptide that binds CD3 and a lentiviral vector comprising one of the following lentiviral vector architectures, MNDU3 promoter and wild-type WPRE, MNDU3 promoter and a mutated WPRE, SFFV promoter and a mutated WPRE, and EF1 α promoter and no WPRE and encoding an anti-BCMA CAR (6 anti-BCMA CARs were evaluated).

Figure 3F shows the levels of off-target transduction in BCMA expressing cells (RPMI-8226 and KMS-11) of recombinant lentiviruses comprising a viral envelope expressing a mutated VSIV-G and a non-viral membrane-bound tropism polypeptide that binds CD3 and a lentiviral vector comprising one of the following lentiviral vector architectures, MNDU3 promoter and wild-type WPRE, MNDU3 promoter and a mutated WPRE, SFFV promoter and a mutated WPRE, and EF1 α promoter and no WPRE and encoding an anti-BCMA CAR (6 anti-BCMA CARs were evaluated). Transduction was

normalized to VCN in cells transduced with a recombinant lentivirus encoding GFP in place of an anti-BCMA CAR.

Figure 4A shows the results from an *in vivo* Daudi mouse model. Mice were administered a recombinant lentivirus comprising a viral envelope expressing a mutated VSIV-G and a non-viral membrane-bound tropism polypeptide that binds CD3 and a lentiviral vector encoding either an MNDU3 promoter operably linked to a polynucleotide encoding a CD8 α signal peptide and an anti-BCMA CAR (4 anti-BCMA CARs were evaluated) and a wild-type WPRE operably linked to the 3' prime end of the polynucleotide encoding the anti-BCMA CAR; *ex vivo* CAR T cells, or vehicle.

Figure 4B shows the results from an *in vivo* Daudi mouse model. Mice were administered a recombinant lentivirus comprising a viral envelope expressing a mutated VSIV-G and a non-viral membrane-bound tropism polypeptide that binds CD3 and a lentiviral vector comprising one of the following lentiviral vector architectures, MNDU3 promoter and wild-type WPRE, MNDU3 promoter and a mutated WPRE, SFFV promoter and a mutated WPRE, and EF1 α promoter and no WPRE and encoding an anti-BCMA CAR (5 anti-BCMA CARs were evaluated); *ex vivo* CAR T cells, or vehicle.

Figure 4C shows the results from an *in vivo* Daudi mouse model. Mice were administered a recombinant lentivirus comprising a viral envelope expressing a mutated VSIV-G and a non-viral membrane-bound tropism polypeptide that binds CD3 and a lentiviral vector comprising one of the following lentiviral vector architectures, MNDU3 promoter and a mutated WPRE, SFFV promoter and a mutated WPRE, and EF1 α promoter and no WPRE and encoding an anti-BCMA CAR (4 anti-BCMA CARs were evaluated); *ex vivo* CAR T cells, or vehicle.

Figure 4D shows the results from an *in vivo* RPMI-8226 mouse model. Mice were administered a recombinant lentivirus comprising a viral envelope expressing a mutated VSIV-G and a non-viral membrane-bound tropism polypeptide that binds CD3 and a lentiviral vector comprising one of the following lentiviral vector architectures, MNDU3 promoter and a mutated WPRE, or EF1 α promoter and no WPRE and encoding an anti-BCMA CAR (2 anti-BCMA CARs were evaluated); *ex vivo* CAR T cells, or vehicle.

Figure 4E shows the results from an *in vivo* RPMI-8226 mouse model. Mice were administered three doses (1.25×10^7 IU, 5.0×10^7 IU, or 1.25×10^8 IU) of a recombinant lentivirus comprising a viral envelope expressing a mutated VSIV-G and a non-viral membrane-bound tropism polypeptide that binds CD3 and a lentiviral vector comprising an

EF1 α promoter operably linked to a polynucleotide encoding an anti-BCMA CAR without a PRE; *ex vivo* CAR T cells, or vehicle.

Figure 4F shows the results from an *in vivo* RPMI-8226 mouse model. Mice were administered two doses (5.0×10^7 IU or 1.25×10^8 IU) of a recombinant lentivirus comprising a viral envelope expressing a mutated VSIV-G and a non-viral membrane-bound tropism polypeptide that binds CD3 and a lentiviral vector comprising an EF1 α promoter operably linked to a polynucleotide encoding an anti-BCMA CAR without a PRE; *ex vivo* CAR T cells, or vehicle.

Figure 4G shows the results from an *in vivo* Daudi mouse model. Mice were administered a recombinant lentivirus comprising a viral envelope expressing a mutated VSIV-G and a non-viral membrane-bound tropism polypeptide that binds CD3 and a lentiviral vector encoding an anti-BCMA CAR and comprising one of the following lentiviral vector architectures, MNDU3 promoter and a mutated WPRE or MNDU3 promoter and a mutated WPRE (at 1.25×10^8 IU) or an EF1 α promoter and no WPRE (5.6×10^7 IU); *ex vivo* CAR T cells, or vehicle.

Figure 5A shows the results from a Daudi mouse model interrogated with *in vivo* lentivirus. Mice were administered vehicle control or recombinant lentivirus comprising a viral envelope expressing a mutated VSIV-G and a non-viral membrane-bound tropism polypeptide that binds CD3 and a lentiviral vector encoding one of three anti-BCMA CARs or a GFP control.

Figure 5B shows the results from a Daudi mouse model interrogated with *ex vivo* manufactured CAR T cells. Mice were administered vehicle control, untransduced PBMCs, or PBMCs transduced with a recombinant lentivirus comprising a viral envelope expressing a mutated VSIV-G and a non-viral membrane-bound tropism polypeptide that binds CD3 and a lentiviral vector and encoding one of three anti-BCMA CARs.

BRIEF DESCRIPTION OF THE SEQUENCE IDENTIFIERS

SEQ ID NO: 1 sets forth an amino acid sequence of a B cell maturation antigen (BCMA) polypeptide.

SEQ ID NOs: 2-10 and 976-979 set forth amino acid sequences of polypeptide linkers.

SEQ ID NOs: 11-144 set forth amino acid sequences of antibodies.

SEQ ID NOs: 145-150 set forth amino acid sequences of spacer domains.

SEQ ID NOs: 151-157 set forth amino acid sequences of transmembrane domains.

SEQ ID NOs: 158-164 set forth amino acid sequences of intracellular signaling domains.

5 SEQ ID NOs: 165-860 set forth amino acid sequences of chimeric antigen receptors (CARs).

SEQ ID NOs: 861-873 set forth amino acid sequences of signal peptides.

SEQ ID NOs: 874-893 set forth nucleic acid sequences encoding antibodies.

SEQ ID NOs: 894-897 set forth nucleic acid sequences encoding spacer domains.

10 SEQ ID NOs: 898-899 set forth nucleic acid sequences encoding transmembrane domains.

SEQ ID NOs: 900-903 set forth nucleic acid sequences encoding intracellular signaling domains.

SEQ ID NO: 904 sets forth a nucleic acid sequence encoding a signal peptide.

15 SEQ ID NOs: 905-924 set forth nucleic acid sequences encoding chimeric antigen receptors (CARs) without a signal peptide.

SEQ ID NOs: 925-944 set forth nucleic acid sequences encoding CARs comprising a signal peptide.

20 SEQ ID NOs: 945-947 set forth nucleic acid sequences of post-transcriptional response elements.

SEQ ID NOs: 948-953 set forth nucleic acid sequences of promoters.

SEQ ID NOs: 954-955 set forth amino acid sequences of anti-BCMA CARs.

SEQ ID NOs: 956-975 set forth amino acid sequences of viral self-cleaving peptides.

25 In the foregoing sequences, X, if present, refers to any amino acid, a specified group of amino acids or the absence of an amino acid.

DETAILED DESCRIPTION

A. OVERVIEW

Chimeric antigen receptors (CARs) are used to redirect immune effector cells to target cells. Typically, immune effector cells are harvested from a patient, modified *ex vivo*

with a vector to express a CAR, and then infused back into the patient where the CAR expressing immune effector cells seek out and destroy target cells, *e.g.*, cancer cells.

Thoughtful vector design and consideration of CAR architecture both contribute to an effective CAR-based therapy. Vector design considerations include but are not limited to selection of the type of vector, *e.g.*, viral or non-viral; promoter selection; selection of post-transcriptional regulatory elements; and the like. CARs comprise several components including but not limited to a target antigen binding moiety, *e.g.*, a ligand, antibody or antigen binding fragment thereof; a spacer domain that positions the target binding domain the appropriate distance from the immune effector cell surface; a transmembrane domain that anchors the CAR to the immune effector cell; and one or more intracellular signaling domains that transduce extracellular signals to intracellular cell signaling cascades that provide for durable and effective immune responses. Too much CAR expression or activity could result in tonic signaling (activation of immune effector cells in the absence of target cells) and too little CAR expression or activity may result in ineffective recognition and destruction of target cells.

Recently, *ex vivo* CAR T cell therapies that target B cell maturation antigen (BCMA) have been used to treat relapsed and refractory multiple myeloma. Although many multiple myeloma patients that have been treated with *ex vivo* anti-BCMA CAR T cell therapies experience partial or complete remissions, most relapse and succumb to the disease. There is a significant unmet need for a durable, one-time, and potentially curative treatment for multiple myeloma.

The present disclosure offers solutions to foregoing challenges and others that exist in the field of treating multiple myeloma using anti-BCMA binding proteins.

The present disclosure generally relates to, in part, anti-BCMA binding proteins comprising an antibody or antigen binding fragment thereof directed against BCMA. In particular embodiments, an anti-BCMA binding protein is an anti-BCMA antibody or antigen binding fragment thereof; a polypeptide comprising an anti-BCMA antibody or antigen binding fragment thereof; a bispecific antibody comprising an anti-BCMA antibody or antigen binding fragment thereof and an anti-CD3 antibody; an immunoconjugate comprising an anti-BCMA antibody drug linked to a cytotoxic agent; or an anti-BCMA chimeric antigen receptor.

The present disclosure also relates, in part, polynucleotides encoding the polypeptides, vectors for expressing the polynucleotides, and compositions comprising the foregoing.

In particular embodiments, a chimeric antigen receptor comprises one or more anti-BCMA antibodies or antigen binding fragments thereof. The anti-BCMA CARs provide several advantages compared to existing anti-BCMA CARs including but not limited to decreased immunogenicity because the CAR components are derived from human proteins; improved cytokine profile including increased expression of interferon gamma (IFN γ) and interleukin 2 (IL-2) in the presence of BCMA expressing target cells; low or absent tonic signaling (antigen independent signaling), and increased efficacy in mouse models when compared to existing CARs.

Techniques for recombinant (*i.e.*, engineered) DNA, peptide and oligonucleotide synthesis, immunoassays, tissue culture, transformation (*e.g.*, electroporation, lipofection), enzymatic reactions, purification and related techniques and procedures may be generally performed as described in various general and more specific references in microbiology, molecular biology, biochemistry, molecular genetics, cell biology, virology and immunology as cited and discussed throughout the present specification. *See, e.g.*, Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, 4th ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.; *Current Protocols in Molecular Biology* (John Wiley and Sons, updated July 2008); *Short Protocols in Molecular Biology: A Compendium of Methods from Current Protocols in Molecular Biology*, Greene Pub. Associates and Wiley-Interscience (2002); Glover, *DNA Cloning: A Practical Approach*, vol. I & II (IRL Press, Oxford Univ. Press USA, 1985); *Current Protocols in Immunology* (Edited by: John E. Coligan, Ada M. Kruisbeek, David H. Margulies, Ethan M. Shevach, Warren Strober 2001 John Wiley & Sons, NY, NY); *Real-Time PCR: Current Technology and Applications*, Edited by Julie Logan, Kirstin Edwards and Nick Saunders, 2009, Caister Academic Press, Norfolk, UK; Anand, *Techniques for the Analysis of Complex Genomes*, (Academic Press, New York, 1992); Guthrie and Fink, *Guide to Yeast Genetics and Molecular Biology* (Academic Press, New York, 1991); *Oligonucleotide Synthesis* (N. Gait, Ed., 1984); *Nucleic Acid the Hybridization* (B. Hames & S. Higgins, Eds., 1985); *Transcription and Translation* (B. Hames & S. Higgins, Eds., 1984); *Animal Cell Culture* (R. Freshney, Ed., 1986); Perbal, *A Practical Guide to Molecular Cloning* (1984); *Next-Generation Genome Sequencing* (Janitz, 2008 Wiley-VCH); *PCR Protocols* (Methods in Molecular Biology) (Park, Ed., 3rd Edition,

2010 Humana Press); *Immobilized Cells and Enzymes* (IRL Press, 1986); the treatise, *Methods in Enzymology* (Academic Press, Inc., N.Y.); *Gene Transfer Vectors for Mammalian Cells* (J. H. Miller and M. P. Calos eds., 1987, Cold Spring Harbor Laboratory); Harlow and Lane, *Antibodies*, (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1998); *Immunochemical Methods in Cell and Molecular Biology* (Mayer and Walker, eds., Academic Press, London, 1987); *Handbook of Experimental Immunology*, Volumes I-IV (D. M. Weir and CC Blackwell, eds., 1986); Roitt, *Essential Immunology*, 6th Edition, (Blackwell Scientific Publications, Oxford, 1988); *Current Protocols in Immunology* (Q. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach and W. Strober, eds., 1991); *Annual Review of Immunology*; as well as monographs in journals such as *Advances in Immunology*.

B. DEFINITIONS

Prior to setting forth this disclosure in more detail, it may be helpful to an understanding thereof to provide definitions of certain terms to be used herein.

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by those of ordinary skill in the art to which the invention belongs. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of particular embodiments, preferred embodiments of compositions, methods and materials are described herein. For the purposes of the present disclosure, the following terms are defined below.

The articles “a,” “an,” and “the” are used herein to refer to one or to more than one (*i.e.*, to at least one, or to one or more) of the grammatical object of the article. By way of example, “an element” means one element or one or more elements.

The use of the alternative (*e.g.*, “or”) should be understood to mean either one, both, or any combination of the recited alternatives.

The term “and/or” should be understood to mean either one of, or both of, the alternatives.

As used herein, the term “about” or “approximately” refers to a quantity, level, value, number, frequency, percentage, dimension, size, amount, weight or length that varies by as much as 15%, 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2% or 1% to a reference quantity, level, value, number, frequency, percentage, dimension, size, amount, weight or length. In one embodiment, the term “about” or “approximately” refers a range of quantity, level, value,

number, frequency, percentage, dimension, size, amount, weight or length $\pm 15\%$, $\pm 10\%$, $\pm 9\%$, $\pm 8\%$, $\pm 7\%$, $\pm 6\%$, $\pm 5\%$, $\pm 4\%$, $\pm 3\%$, $\pm 2\%$, or $\pm 1\%$ of a reference quantity, level, value, number, frequency, percentage, dimension, size, amount, weight or length.

In one embodiment, a range, *e.g.*, 1 to 5, about 1 to 5, or about 1 to about 5, refers to each numerical value encompassed by the range. For example, in one non-limiting and merely illustrative embodiment, the range “1 to 5” is equivalent to the expression 1, 2, 3, 4, 5; or 1.0, 1.5, 2.0, 2.5, 3.0, 3.5, 4.0, 4.5, or 5.0; or 1.0, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2.0, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3.0, 3.1, 3.2, 3.3, 3.4, 3.5, 3.6, 3.7, 3.8, 3.9, 4.0, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, or 5.0.

As used herein, the term “substantially” refers to a quantity, level, value, number, frequency, percentage, dimension, size, amount, weight or length that is 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or higher compared to a reference quantity, level, value, number, frequency, percentage, dimension, size, amount, weight or length. In one embodiment, “substantially the same” refers to a quantity, level, value, number, frequency, percentage, dimension, size, amount, weight or length that produces an effect, *e.g.*, a physiological effect, that is approximately the same as a reference quantity, level, value, number, frequency, percentage, dimension, size, amount, weight or length.

Throughout this specification, unless the context requires otherwise, the words “comprise”, “comprises” and “comprising” will be understood to imply the inclusion of a stated step or element or group of steps or elements but not the exclusion of any other step or element or group of steps or elements. By “consisting of” is meant including, and limited to, whatever follows the phrase “consisting of.” Thus, the phrase “consisting of” indicates that the listed elements are required or mandatory and that no other elements may be present. The phrase “consisting essentially of” means including any elements listed after the phrase and other elements that do not interfere with or contribute to the activity or action specified in the disclosure for the listed elements. Thus, the phrase “consisting essentially of” indicates that the listed elements are required or mandatory but that no other elements are present that materially affect the activity or action of the listed elements.

Reference throughout this specification to “one embodiment,” “an embodiment,” “a particular embodiment,” “a related embodiment,” “a certain embodiment,” “an additional embodiment,” or “a further embodiment” or combinations thereof means that a particular feature, structure or characteristic described in connection with the embodiment is included in at least one embodiment. Thus, the appearances of the foregoing phrases in various places

throughout this specification are not necessarily all referring to the same embodiment. Furthermore, the particular features, structures, or characteristics may be combined in any suitable manner in one or more embodiments. It is also understood that the positive recitation of a feature in one embodiment, serves as a basis for excluding the feature in a particular
5 embodiment.

The terms, “binding domain,” “extracellular binding domain,” and “extracellular antigen binding domain” are used interchangeably and refers to a domain that enables a chimeric antigen receptor (CAR) to specifically bind to a target antigen. The binding domain may be derived either from a natural, synthetic, semi-synthetic, or recombinant source.

10 A “spacer domain” refers to a polypeptide domain or sequence of amino acids in a chimeric antigen receptor that plays a role in positioning the antigen binding domain away from the immune effector cell surface to enable proper cell/cell contact, antigen binding and activation. In particular embodiments, a spacer domain may also be referred to, and is synonymous with, a hinge domain. A spacer domain is placed between a binding domain
15 and a transmembrane domain (TM). A spacer domain may be derived either from a natural, synthetic, semi-synthetic, or recombinant source. A spacer domain may be altered by substituting one or more cysteine and/or proline residues in a naturally occurring immunoglobulin hinge domain with one or more other amino acid residues (*e.g.*, one or more serine residues).

20 A “transmembrane domain” or “TM domain” refers to a hydrophobic portion of a chimeric antigen receptor polypeptide that anchors the polypeptide to the plasma membrane of the cell. The TM domain may be derived either from a natural, synthetic, semi-synthetic, or recombinant source.

An “intracellular signaling domain” refers to a polypeptide domain that participates
25 in transducing the message of effective binding of a target antigen by a chimeric antigen receptor expressed on an immune effector cell to the immune effector cell’s interior to elicit one or more effector functions (an “effector function” refers to a specialized function of an immune effector cell), *e.g.*, activation, cytokine production, proliferation and cytotoxic activity, including the release of cytotoxic factors, or other cellular responses elicited with
30 antigen binding to the receptor expressed on the immune effector cell. “Intracellular signaling domains” include a polypeptide domain or functional fragment thereof, which transduces an effector function signal and that directs a cell to perform a specialized function.

The term intracellular signaling domain is meant to include any truncated portion of an intracellular signaling domain sufficient to transduce effector function signal.

T cell activation can be said to be mediated by two distinct classes of intracellular signaling domains: primary signaling domains that initiate antigen-dependent primary activation through the TCR (*e.g.*, a TCR/CD3 complex) and costimulatory signaling domains that act in an antigen-independent manner to provide a secondary or costimulatory signal.

A “primary signaling domain” refers to a signaling domain that regulates the primary activation of a TCR complex either in a stimulatory way, or in an inhibitory way. Primary signaling domains that act in a stimulatory manner may contain one or more signaling motifs which are known as immunoreceptor tyrosine-based activation motifs or ITAMs.

A “costimulatory signaling domain” or “costimulatory signaling domain” refers to an intracellular signaling domain of a costimulatory molecule. Costimulatory molecules are cell surface molecules other than antigen receptors or Fc receptors that provide a second signal required for efficient activation and function of T lymphocytes upon binding to antigen.

“Linker,” “peptide linker,” and “polypeptide linker” are used interchangeably and refer to a plurality of amino acid residues between various polypeptide domains added for appropriate spacing, conformation, and function. A polypeptide linker sequence may be employed to separate any two or more polypeptide components by a distance sufficient to ensure that each polypeptide folds into its appropriate secondary and tertiary structures so as to allow the polypeptide domains to exert their desired functions. Linkers include a “variable domain linking sequence,” an amino acid sequence that connects two or more domains of an antibody or antigen binding fragments thereof and provides a spacer function compatible with interaction of the two sub-binding domains so that the resulting polypeptide retains a specific binding affinity to the same target molecule as an antibody that comprises the same light and/or heavy chain variable domains. A linker may be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 or more amino acids long. Illustrative examples of linkers include, but are not limited to the following amino acid sequences: TGEKP (SEQ ID NO: 2); (GGGS)_n wherein n = 1, 2, 3, 4 or 5 (SEQ ID NOs: 3, and 976-979); EGKSSGSGSESKVD (SEQ ID NO: 4); KESGSVSSEQLAQFRSLD (SEQ ID NO: 5); LRQRDGERP (SEQ ID NO: 6); LRQKDGGGSRP (SEQ ID NO: 7);

LRQKD(GGGS)₂ERP (SEQ ID NO: 8), GEGTSTGSGGSGGSGGAD (SEQ ID NO: 9), and GSTSGSGKPGSGEGSTKG (SEQ ID NO: 10).

Additional definitions are set forth throughout this disclosure.

C. ANTIBODIES

5 B cell maturation antigen (BCMA) is a member of the tumor necrosis factor receptor superfamily 17 (TNFRSF17) and is highly expressed on the plasma cells of multiple myeloma (MM) patients. The restricted expression of BCMA makes it a suitable therapeutic target for treating multiple myeloma. The present disclosure contemplates antibodies and antigen binding fragments thereof that bind BCMA. An “antibody” refers to a polypeptide
10 or antigen binding fragment thereof that comprises at least a light chain immunoglobulin variable region and/or a heavy chain immunoglobulin variable region, which specifically recognizes and binds one or more epitopes of a BCMA polypeptide, *e.g.*, SEQ ID NO: 1 (MLQMAGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNA ILWTCLGLSLIISLAVFVLMFLLRKINSEPLKDEFKNTGSGLLGMANIDLEKSRTGD
15 EIILPRGLEYTVEECTCEDCIKSKPKVDSDFHCFPLPAMEEGATILVTTKTNDYCKSL PAALSATEIEKSISAR).

An antibody or antigen binding fragment thereof “specifically binds” a BCMA polypeptide if it binds with an affinity or $K_a \geq 10^5 \text{ M}^{-1}$, while not significantly binding other components present in a test sample. An antibody or antigen binding fragment thereof may
20 be classified as “high affinity” or “low affinity.” “High affinity” antibodies or antigen binding fragments thereof refer to antibodies that bind BCMA with a K_a of at least 10^7 M^{-1} , at least 10^8 M^{-1} , at least 10^9 M^{-1} , at least 10^{10} M^{-1} , at least 10^{11} M^{-1} , at least 10^{12} M^{-1} , or at least 10^{13} M^{-1} . “Low affinity” antibodies or antigen binding fragments thereof refer to antibodies that bind BCMA with a K_a of up to 10^7 M^{-1} , up to 10^6 M^{-1} , up to 10^5 M^{-1} .
25 Alternatively, affinity may be defined as an equilibrium dissociation constant (K_d) of a particular binding interaction with units of M (*e.g.*, 10^{-5} M to 10^{-13} M).

Antibodies include polyclonal and monoclonal antibodies and antigen binding fragments thereof; camelid antibodies, and human antibodies, and antigen binding fragments thereof; and chimeric antibodies, an antibody that comprises variable regions from a non-
30 human species and human constant regions, heteroconjugate antibodies, and humanized antibodies, an antibody that comprises complementarity determining regions (CDRs) from a

non-human species and human framework and constant regions, and antigen binding fragments thereof.

Chimeric, humanized, and human antibodies comprise two heavy chains and two light chains. Each heavy chain consists of a variable region (VH) and three constant regions (CH1, CH2, CH3), while each light chain consists of a variable region (VL) and a constant region (CL). Mammalian immunoglobulin heavy chains are classified as immunoglobulin (Ig)A, IgD, IgE, IgG, and IgM. Mammalian immunoglobulin light chains are classified as λ or κ .

Light and heavy chain variable regions contain a “framework” region interrupted by three hypervariable regions, also called “complementarity-determining regions” or “CDRs.”

The sequences of the framework regions of different light or heavy chains are relatively conserved within a species, such as humans. The framework regions serve to position and align the CDRs in three-dimensional space to bind to an epitope. The CDRs of each chain are numbered sequentially starting from the N-terminus and are also typically identified by the chain in which the particular CDR is located. Heavy chain CDRs are referred to as CDRH1, CDRH2, and CDRH3, and light chain CDRs are referred to as CDRL1, CDRL2, and CDRL3. Although CDRs vary from antibody to antibody, the limited number of amino acid positions within the CDRs directly involved in antigen binding are called specificity determining residues (SDRs).

CDRs can be defined or identified by conventional methods, such as by sequence according to Wu and Kabat, *J Exp Med.* 132(2):211-50 (1970) and Kabat and Wu, *Ann New York Acad Sci.* 190:382–93 (1971), or by structure according to Chothia and Lesk, *J Mol Biol.* 196(4): 901-917 (1987) and Chothia *et al.*, *Nature.* 342:877–83(1989). Other boundaries defining CDRs overlapping with the Kabat CDRs have been described by Padlan *et al.*, *FASEB J.* 9:133–9 (1995) and MacCallum *et al.*, *J Mol Biol.* 262:732–745 (1996). Additional methods of determining CDRs include the Gelfand numbering system described in Gelfand and Kister, *PNAS USA.* 92:10884–8(1995), Gelfand *et al.*, *Protein Eng.* 11:1015–25 (1998), and Gelfand *et al.*, *PNAS USA.* 93:3675–8 (1996); the Honneger number system described in Honneger and Plückthun, *J Mol Biol.* 309:657–70 (2001); the AbM numbering system described by Abhinandan and Martin, *Mol Immunol.* 45:3832–9 (2008); and the IMGT numbering system described in Giudicelli *et al.*, *Nucleic Acids Res.* 25:206–11 (1997), Lefranc, *Immunol Today* 18:509 (1997), and Lefranc *et al.*, *Dev Comp Immunol.* 27:55–77

(2003). Proprietary and publicly programs that identify CDRs are available, *e.g.*, abYsis (abysis.org/abysis/) and IMGT/V-QUEST (imgt.org/IMGT_vquest).

“VL” or “V_L” refers to the variable region of an immunoglobulin light chain or antigen binding fragment thereof. “VH” or “V_H” refer to the variable region of an immunoglobulin heavy chain or antigen binding fragment thereof.

An “antigen binding fragment” or “antigen binding portion” refers to one or more fragments of an antibody that retain the ability to specifically bind to an antigen. An “isolated antibody or antigen binding fragment thereof” refers to an antibody or antigen binding fragment thereof that has been separated from its natural environment and/or that is derived from a natural, synthetic, semi-synthetic, or recombinant source. Illustrative examples of antigen binding fragments contemplated in particular embodiments herein include, but are not limited to, a Llama Ig, a Fab' fragment, a F(ab')₂ fragment, a bispecific Fab dimer (Fab₂), a trispecific Fab trimer (Fab₃), an Fv, a single chain Fv protein (“scFv”), a bis-scFv, (scFv)₂, a minibody, a diabody, a triabody, a tetrabody, a disulfide stabilized Fv protein (“dsFv”), and a single-domain antibody (sdAb or nanobody, *e.g.*, a camelid VHH) other portions of full length antibodies sufficient for antigen binding, and combinations thereof.

A “heavy chain antibody” or “hcAb” refers to an antibody that contains two heavy chain variable domains and no light chains. A “camelid antibody” or “camelid Ig” refers to an hcAb isolated from a Camel, Alpaca, or Llama that consists of a homodimer of a heavy chain variable domain (VHH) and CH₂ and CH₃ constant domains. A “single domain antibody,” “sdAb,” or “nanobody” as used herein refers to an antibody fragment that contains the smallest known antigen binding unit of the variable region of a heavy chain antibody, *e.g.*, a camelid VHH. A “humanized VHH” refers to a single domain non-human VHH that has undergone humanization to reduce potential immunogenicity of the antibody in human recipients.

A “single-chain Fv” or “scFv” antibody fragment comprises the VH and VL domains of an antibody, wherein these domains are present in a single polypeptide chain and in either orientation (*e.g.*, VL-VH or VH-VL). Generally, the scFv polypeptide further comprises a polypeptide linker between the VH and VL domains which enables the scFv to form the desired structure for antigen binding.

In particular embodiments, an anti-BCMA antibody or antigen binding fragment thereof comprises a heavy chain variable region (VH) comprising a CDRH₁, a CDRH₂, and a CDRH₃ of an antibody or antigen binding fragment thereof set forth in Table 1; a

polypeptide linker; and a light chain variable region (VL) comprising a CDRL1, a CDRL2, and a CDRL3 of an antibody or antigen binding fragment thereof set forth in Table 1.

In particular embodiments, an anti-BCMA antibody or antigen binding fragment thereof comprises in either orientation (*e.g.*, VL-linker-VH or VH-linker-VL): a VH that
 5 comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 12, 13, and 14, a polypeptide linker, and a VL that comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 16, 17, and 18; a VH that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 22, 23, and 24, a polypeptide linker, and a VL that
 10 comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 26, 27, and 28; a VH that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 32, 33, and 34, a polypeptide linker, and a VL that comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 36, 37, and 38; a VH that comprises a CDRH1, a
 15 CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 42, 43, and 44, a polypeptide linker, and a VL that comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 46, 47, and 48; a VH that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 52, 53, and 54, a polypeptide linker, and a VL that comprises a CDRL1,
 20 a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 56, 57, and 58; a VH that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 62, 63, and 64, a polypeptide linker, and a VL that comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 66, 67, and 68; a VH that comprises a CDRH1, a CDRH2, and a CDRH3
 25 comprising the amino acid sequences set forth in SEQ ID NOs: 72, 73, and 74, a polypeptide linker, and a VL that comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 76, 77, and 78; a VH that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 82, 83, and 84, a polypeptide linker, and a VL that comprises a CDRL1, a CDRL2, and a CDRL3
 30 comprising the amino acid sequences set forth in SEQ ID NOs: 86, 87, and 88; and a VH that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 92, 93, and 94, a polypeptide linker, and a VL that comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 96,

97, and 98. In particular embodiments, the polypeptide linker is selected from the group consisting of: (GGGGS)_n wherein n = 1, 2, 3, 4 or 5; GEGTSTGSGGSGGSGGAD, GSTSGSGKPGSGEGSTKG and variants thereof comprising an amino acid sequence at least 90% identical thereto.

5 In particular embodiments, an anti-BCMA antibody or antigen binding fragment thereof comprises in either orientation (*e.g.*, VL-linker-VH or VH-linker-VL): a VH that comprises the amino acid sequence set forth in SEQ ID NO: 11; a polypeptide linker; and a VL that comprises the amino acid sequence set forth in SEQ ID NO: 15; wherein the polypeptide linker is selected from the group consisting of: (GGGGS)_n wherein n = 1, 2, 3,
10 4 or 5, GEGTSTGSGGSGGSGGAD, GSTSGSGKPGSGEGSTKG and variants thereof comprising an amino acid sequence 95% identical thereto.

In particular embodiments, an anti-BCMA antibody or antigen binding fragment thereof comprises in either orientation (*e.g.*, VL-linker-VH or VH-linker-VL): a VH that comprises the amino acid sequence set forth in SEQ ID NO: 21; a polypeptide linker; and a
15 VL that comprises the amino acid sequence set forth in SEQ ID NO: 25; wherein the polypeptide linker is selected from the group consisting of: (GGGGS)_n wherein n = 1, 2, 3, 4 or 5, GEGTSTGSGGSGGSGGAD, GSTSGSGKPGSGEGSTKG and variants thereof comprising an amino acid sequence 95% identical thereto.

In particular embodiments, an anti-BCMA antibody or antigen binding fragment
20 thereof comprises in either orientation (*e.g.*, VL-linker-VH or VH-linker-VL): a VH that comprises the amino acid sequence set forth in SEQ ID NO: 31; a polypeptide linker; and a VL that comprises the amino acid sequence set forth in SEQ ID NO: 35; wherein the polypeptide linker is selected from the group consisting of: (GGGGS)_n wherein n = 1, 2, 3, 4 or 5, GEGTSTGSGGSGGSGGAD, GSTSGSGKPGSGEGSTKG and variants thereof
25 comprising an amino acid sequence 95% identical thereto.

In particular embodiments, an anti-BCMA antibody or antigen binding fragment thereof comprises in either orientation (*e.g.*, VL-linker-VH or VH-linker-VL): a VH that comprises the amino acid sequence set forth in SEQ ID NO: 41; a polypeptide linker; and a
VL that comprises the amino acid sequence set forth in SEQ ID NO: 45; wherein the
30 polypeptide linker is selected from the group consisting of: (GGGGS)_n wherein n = 1, 2, 3, 4 or 5, GEGTSTGSGGSGGSGGAD, GSTSGSGKPGSGEGSTKG and variants thereof comprising an amino acid sequence 95% identical thereto.

In particular embodiments, an anti-BCMA antibody or antigen binding fragment thereof comprises in either orientation (*e.g.*, VL-linker-VH or VH-linker-VL): a VH that comprises the amino acid sequence set forth in SEQ ID NO: 51; a polypeptide linker; and a VL that comprises the amino acid sequence set forth in SEQ ID NO: 55; wherein the polypeptide linker is selected from the group consisting of: (GGGGS)_n wherein n = 1, 2, 3, 4 or 5, GEGTSTGSGGSGGSGGAD, GSTSGSGKPGSGEGSTKG and variants thereof comprising an amino acid sequence 95% identical thereto.

In particular embodiments, an anti-BCMA antibody or antigen binding fragment thereof comprises in either orientation (*e.g.*, VL-linker-VH or VH-linker-VL): a VH that comprises the amino acid sequence set forth in SEQ ID NO: 61; a polypeptide linker; and a VL that comprises the amino acid sequence set forth in SEQ ID NO: 65; wherein the polypeptide linker is selected from the group consisting of: (GGGGS)_n wherein n = 1, 2, 3, 4 or 5, GEGTSTGSGGSGGSGGAD, GSTSGSGKPGSGEGSTKG and variants thereof comprising an amino acid sequence 95% identical thereto.

In particular embodiments, an anti-BCMA antibody or antigen binding fragment thereof comprises in either orientation (*e.g.*, VL-linker-VH or VH-linker-VL): a VH that comprises the amino acid sequence set forth in SEQ ID NO: 71; a polypeptide linker; and a VL that comprises the amino acid sequence set forth in SEQ ID NO: 75; wherein the polypeptide linker is selected from the group consisting of: (GGGGS)_n wherein n = 1, 2, 3, 4 or 5, GEGTSTGSGGSGGSGGAD, GSTSGSGKPGSGEGSTKG and variants thereof comprising an amino acid sequence 95% identical thereto.

In particular embodiments, an anti-BCMA antibody or antigen binding fragment thereof comprises in either orientation (*e.g.*, VL-linker-VH or VH-linker-VL): a VH that comprises the amino acid sequence set forth in SEQ ID NO: 81; a polypeptide linker; and a VL that comprises the amino acid sequence set forth in SEQ ID NO: 85; wherein the polypeptide linker is selected from the group consisting of: (GGGGS)_n wherein n = 1, 2, 3, 4 or 5, GEGTSTGSGGSGGSGGAD, GSTSGSGKPGSGEGSTKG and variants thereof comprising an amino acid sequence 95% identical thereto.

In particular embodiments, an anti-BCMA antibody or antigen binding fragment thereof comprises in either orientation (*e.g.*, VL-linker-VH or VH-linker-VL): a VH that comprises the amino acid sequence set forth in SEQ ID NO: 91; a polypeptide linker; and a VL that comprises the amino acid sequence set forth in SEQ ID NO: 95; wherein the polypeptide linker is selected from the group consisting of: (GGGGS)_n wherein n = 1, 2, 3,

4 or 5, GEGTSTGSGGSGGSGGAD, GSTSGSGKPGSGEGSTKG and variants thereof comprising an amino acid sequence 95% identical thereto.

In particular embodiments, an anti-BCMA antibody or antigen binding fragment thereof comprises the amino acid sequence set forth in any one of SEQ ID NOs: 19, 20, 29, 30, 39, 40, 49, 50, 59, 60, 69, 70, 79, 80, 89, 90, 99, and 100 or an amino acid sequence with at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identity thereto.

In particular embodiments, an anti-BCMA antibody or antigen binding fragment thereof comprises a VHH domain comprising a CDRH1, a CDRH2, and a CDRH3 of an antibody or antigen binding fragment thereof set forth in Table 1.

In particular embodiments, an anti-BCMA antibody or antigen binding fragment thereof comprises: a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 102, 103, and 104; a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 106, 107, and 108; a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 110, 111, and 112; a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 114, 115, and 116; a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 118, 119, and 120; a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 122, 123, and 124; a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 126, 127, and 128; a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 130, 131, and 132; a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 134, 135, and 136; a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 138, 139, and 140; or a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 142, 143, and 144.

In particular embodiments, an anti-BCMA antibody or antigen binding fragment thereof comprises a VHH that comprises the amino acid sequence set forth in any one of SEQ ID NOs: 101, 105, 109, 113, 117, 121, 125, 129, 133, 137, and 141 or an amino acid sequence

with at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identity thereto.

Table 1

AB ID	SEQ ID NO	ID	AMINO ACID SEQUENCE
BCMA.1	11	VH	QITLKESGPTLVKPTQTLLTCTFSGFSLSTSGVGVGWIRQPPG KALEWLALIIYWNDEKRYSPSLKSRLTITKDTSKNQVVLMTNMD PVDTA VYYCARDEYGGFDIWGQGTMTVTVSS
	12	CDRH1	TSGVGVG
	13	CDRH2	LIYWNDEKRYSPSLKS
	14	CDRH3	DEYGGFDI
	15	VL	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAP RLIIYDASN RATGIPARFSGSGSGTDFTLTISLLEPEDFAVYYC QQRVVYPITFGGGTKVEIK
	16	CDRL1	RASQSVSSYLA
	17	CDRL2	DASN RAT
	18	CDRL3	QQRVVYPIT
	19	scFv	QITLKESGPTLVKPTQTLLTCTFSGFSLSTSGVGVGWIRQPPG KALEWLALIIYWNDEKRYSPSLKSRLTITKDTSKNQVVLMTNMD PVDTA VYYCARDEYGGFDIWGQGTMTVTVSSGGGGSGGGSGGGG SGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQ KPGQAPRLIIYDASN RATGIPARFSGSGSGTDFTLTISLLEPED FAVYYCQQRVVYPITFGGGTKVEIK
	20	scFv	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAP RLIIYDASN RATGIPARFSGSGSGTDFTLTISLLEPEDFAVYYC QQRVVYPITFGGGTKVEIKGGGGSGGGSGGGSGGGSGGGG QITLKESGPTLVKPTQTLLTCTFSGFSLSTSGVGVGWIRQPPG KALEWLALIIYWNDEKRYSPSLKSRLTITKDTSKNQVVLMTNMD PVDTA VYYCARDEYGGFDIWGQGTMTVTVSS
BCMA.2	21	VH	QITLKESGPTLVKPTQTLLTCTFSGFSLSTSGVGVGWIRQPPG KALEWLALIIYWNDDKRYSPSLKSRLTITKDTSKNQVVLMTNMD PVDTA VYYCARDEYGGFDIWGQGTMTVTVSS
	22	CDRH1	TSGVGVG
	23	CDRH2	LIYWNDDKRYSPSLKS
	24	CDRH3	DEYGGFDI
	25	VL	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAP RLIIYDASN RATGIPARFSGSGSGTDFTLTISLLEPEDFAVYYC QQRFDYPIITFGGGTKVEIK
	26	CDRL1	RASQSVSSYLA
	27	CDRL2	DASN RAT
	28	CDRL3	QQRFDYPIIT
	29	scFv	QITLKESGPTLVKPTQTLLTCTFSGFSLSTSGVGVGWIRQPPG KALEWLALIIYWNDDKRYSPSLKSRLTITKDTSKNQVVLMTNMD PVDTA VYYCARDEYGGFDIWGQGTMTVTVSSGGGGSGGGSGGGG SGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQ KPGQAPRLIIYDASN RATGIPARFSGSGSGTDFTLTISLLEPED FAVYYCQQRFDYPIITFGGGTKVEIK
	30	scFv	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAP RLIIYDASN RATGIPARFSGSGSGTDFTLTISLLEPEDFAVYYC QQRFDYPIITFGGGTKVEIKGGGGSGGGSGGGSGGGSGGGG QITLKESGPTLVKPTQTLLTCTFSGFSLSTSGVGVGWIRQPPG KALEWLALIIYWNDDKRYSPSLKSRLTITKDTSKNQVVLMTNMD PVDTA VYYCARDEYGGFDIWGQGTMTVTVSS
BCMA.3	31	VH	QVQLVESGGGVVQPGRLSLRSCAASGFTFSSYGMHWVRQAPGKG LEWVAVISYEGSNKYADSVKGRFTISRDN SKNTLYLQMNSLR

			EDTAVYYCARELGDMVWGQGT TTVTVSS
	32	CDRH1	SYGMH
	33	CDRH2	VISYEGSNKYYADSVKG
	34	CDRH3	ELGDGMDV
	35	VL	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAP RLLIYDASNRA TGIPARFSGSGSGTDFTLTISSELEPEDFAVYYC QQRVDLWTFGGG TKVEIK
	36	CDRL1	RASQSVSSYLA
	37	CDRL2	DASNRA T
	38	CDRL3	QQRVDLWT
	39	scFv-ok	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKG LEWVAVISYEGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCARELGDMVWGQGT TTVTVSSGGGGSGGGSGGGGS GGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQK PGQAPRLLIYDASNRA TGIPARFSGSGSGTDFTLTISSELEPEDF AVYYCQQRVDLWTFGGG TKVEIK
	40	scFv	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAP RLLIYDASNRA TGIPARFSGSGSGTDFTLTISSELEPEDFAVYYC QQRVDLWTFGGG TKVEIKGGGGSGGGSGGGSGGGSGVQLVE SGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAV ISYEGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVY YCARELGDMVWGQGT TTVTVSS
BCMA . 4	41	VH	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKG LEWVSYISSSGSTIYYADSVKGRFTISRDN AKNSLYLQMNSLRA EDTAVYYCARDQGNYGVDVWGQGT TTVTVSS
	42	CDRH1	DYYMS
	43	CDRH2	YISSSGSTIYYADSVKG
	44	CDRH3	DQGNYGVDV
	45	VL	DIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAP KLLIYDASSLESGVPSRFSGSGSGTEFTLTISSLQPD DFATYYC QQVSSLPPTFGGG TKVEIK
	46	CDRL1	RASQSISSWLA
	47	CDRL2	DASSLES
	48	CDRL3	QQVSSLPPT
	49	scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKG LEWVSYISSSGSTIYYADSVKGRFTISRDN AKNSLYLQMNSLRA EDTAVYYCARDQGNYGVDVWGQGT TTVTVSSGGGGSGGGSGGGG SGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQ KPGKAPKLLIYDASSLESGVPSRFSGSGSGTEFTLTISSLQPD D FATYYCQQVSSLPPTFGGG TKVEIK
	50	scFv	DIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAP KLLIYDASSLESGVPSRFSGSGSGTEFTLTISSLQPD DFATYYC QQVSSLPPTFGGG TKVEIKGGGGSGGGSGGGSGGGSGVQLV ESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVS YISSSGSTIYYADSVKGRFTISRDN AKNSLYLQMNSLRAEDTAV YYCARDQGNYGVDVWGQGT TTVTVSS
BCMA . 5	51	VH	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKG LEWVSYISSSGSTIYYADSVKGRFTISRDN AKNSLYLQMNSLRA EDTAVYYCARDQGNYGVDVWGQGT TTVTVSS
	52	CDRH1	DYYMS
	53	CDRH2	YISSSGSTIYYADSVKG
	54	CDRH3	DQGNYGVDV
	55	VL	DIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAP KLLIYEASSLESGVPSRFSGSGSGTEFTLTISSLQPD DFATYYC QQSDSHPITFGGG TKVEIK
	56	CDRL1	RASQSISSWLA
	57	CDRL2	EASSLES
	58	CDRL3	QQSDSHPIT

	59	scFv-ok	QVQLVESGGGLVQPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKG LEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRA EDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGSGGGG SGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQ KPGKAPKLLIYEASSLESQVPSRFSGSGSGTEFTLTISLQPD FATYYCQQSDSHPITFGGGTKVEIK
	60	scFv	DIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAP KLLIYEASSLESQVPSRFSGSGSGTEFTLTISLQPDDEFATYYC QQSDSHPITFGGGTKVEIKGGGGSGGGSGGGSGGGGQVQLV ESGGGLVQPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKLEWVS YISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAV YYCARDQGNYGVDVWGQGTITVTVSS
BCMA . 6	61	VH	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKG LEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRA EDTAVYYCARDQGNYGVDVWGQGTITVTVSS
	62	CDRH1	DYYMS
	63	CDRH2	YISSSGSTIYYADSVKG
	64	CDRH3	DQGNYGVDV
	65	VL	DIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAP KLLIYEASSLESQVPSRFSGSGSGTEFTLTISLQPDDEFATYYC QQANSHPIITFGGGTKVEIK
	66	CDRL1	RASQSISSWLA
	67	CDRL2	EASSLES
	68	CDRL3	QQANSHPIIT
	69	scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKG LEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRA EDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGSGGGG SGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQ KPGKAPKLLIYEASSLESQVPSRFSGSGSGTEFTLTISLQPD FATYYCQQANSHPIITFGGGTKVEIK
	70	scFv-ok	DIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAP KLLIYEASSLESQVPSRFSGSGSGTEFTLTISLQPDDEFATYYC QQANSHPIITFGGGTKVEIKGGGGSGGGSGGGSGGGGSEVQLV ESGGGLVQPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKLEWVS YISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAV YYCARDQGNYGVDVWGQGTITVTVSS
BCMA . 7	71	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKG LEWVSAISGGSTIYYADSVKGRFTISRDNKNTLYLQMNSLRA EDTAVYYCARPGDGYEGVYFDYWGQGTITVTVSS
	72	CDRH1	NYAMS
	73	CDRH2	AISGGSGSTIYYADSVKG
	74	CDRH3	PGDGYEGVYFDY
	75	VL	DIQMTQSPSSLSASVGDRTITCRASQSISSYLNWYQQKPGKAP KLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYC QQAHSPIITFGGGTKVEIK
	76	CDRL1	RASQSISSYLN
	77	CDRL2	AASSLQS
	78	CDRL3	QQAHSPIIT
	79	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKG LEWVSAISGGSGSTIYYADSVKGRFTISRDNKNTLYLQMNSLRA EDTAVYYCARPGDGYEGVYFDYWGQGTITVTVSSGGGGSGGGG GGGGSGGGGSDIQMTQSPSSLSASVGDRTITCRASQSISSYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISL QPEDFATYYCQQAHSPIITFGGGTKVEIK
	80	scFv	DIQMTQSPSSLSASVGDRTITCRASQSISSYLNWYQQKPGKAP KLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYC QQAHSPIITFGGGTKVEIKGGGGSGGGSGGGSGGGGSEVQLL ESGGGLVQPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKLEWVS AISGGSGSTIYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAV

			YYCARPGDGYEGVYFDYWGQGTTLVTVSS
BCMA . 8	81	VH	QITLKESGPTLVKPTQTTLTLCTFSGFSLSTSGVGVGWIRQPPG KALEWLALIIYWNDEKRYSPSLKSRLTITKDTSKNQVLTMTNMD PVDTA VYYCAREGSHDYKSSNWFDPPWGQGTTLVTVSS
	82	CDRH1	TSGVGVG
	83	CDRH2	LIYWNDEKRYSPSLKS
	84	CDRH3	EGSHDYKSSNWFDPP
	85	VL	DIQMTQSPSSLSASVGDRTITCQASQDIANYLNWYQKPGKAP KLLIYDASNLETGVP SRFSGSGSGTDFTF TISSLQPEDIATYYC QQHFNLP LTFGGG TKVEIK
	86	CDRL1	QASQDIANYLN
	87	CDRL2	DASNLET
	88	CDRL3	QQHFNLP LTF
	89	scFv	QITLKESGPTLVKPTQTTLTLCTFSGFSLSTSGVGVGWIRQPPG KALEWLALIIYWNDEKRYSPSLKSRLTITKDTSKNQVLTMTNMD PVDTA VYYCAREGSHDYKSSNWFDPPWGQGTTLVTVSSGGGGSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRTITCQASQDIANY LNWYQKPGKAPKLLIYDASNLETGVP SRFSGSGSGTDFTF TIS SLQPEDIATYYCQQHFNLP LTFGGG TKVEIK
	90	scFv-ok	DIQMTQSPSSLSASVGDRTITCQASQDIANYLNWYQKPGKAP KLLIYDASNLETGVP SRFSGSGSGTDFTF TISSLQPEDIATYYC QQHFNLP LTFGGG TKVEIKGGGGSGGGGSGGGGSGGGGSGITLK ESGPTLVKPTQTTLTLCTFSGFSLSTSGVGVGWIRQPPGKALEW LALIIYWNDEKRYSPSLKSRLTITKDTSKNQVLTMTNMDPVDTA VYYCAREGSHDYKSSNWFDPPWGQGTTLVTVSS
BCMA . 9	91	VH	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKG LEWVSSISSSSSYIYYADSVKGRFTISRDNAKNSLYLQMNSLRA EDTA VYYCARAGDTYSAADYYMDVWGKGT TTVTVSS
	92	CDRH1	YSMN
	93	CDRH2	SISSSSSYIYYADSVKG
	94	CDRH3	AGDTYSAADYYMDV
	95	VL	DIVMTQSPSLPVP TPGEPASISCRSSQSLLSNGYNYLDWYLQK PGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDV GVYYCMQALGLITFGGG TKVEIK
	96	CDRL1	RSSQSLLSNGYNYLD
	97	CDRL2	LGSNRAS
	98	CDRL3	MQALGLIT
	99	scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKG LEWVSSISSSSSYIYYADSVKGRFTISRDNAKNSLYLQMNSLRA EDTA VYYCARAGDTYSAADYYMDVWGKGT TTVTVSSGGGGSGGG GSGGGGSGGGGSDIVMTQSPSLPVP TPGEPASISCRSSQSLLS NGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDF TLKISRVEAEDVGVYYCMQALGLITFGGG TKVEIK
	100	scFv	DIVMTQSPSLPVP TPGEPASISCRSSQSLLSNGYNYLDWYLQK PGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDV GVYYCMQALGLITFGGG TKVEIKGGGGSGGGGSGGGGSGGGGSE VQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGL EWVSSISSSSSYIYYADSVKGRFTISRDNAKNSLYLQMNSLRAE DTA VYYCARAGDTYSAADYYMDVWGKGT TTVTVSS
BCMA . 10	101	VHH-ok	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKE RELVS AISGSGEVTYIYADSVKGRFTISRDNKNTLYLQMNSLRA EDTA VYYCQRLVEAKRHWGQGTQVTVSS
	102	CDRH1	SEAMS
	103	CDRH2	AISGSGEVTYIYADSVKG
	104	CDRH3	LVEAKRH
BCMA . 11	105	VHH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSEAMSWVRQAPGKE RELVS VITSEGSTYIYADSVKGRFTISRDNKNTLYLQMNSLRAE DTA VYYCAHIEWETRLNWGQGTQVTVSS

	106	CDRH1	SEAMS
	107	CDRH2	VITSEGSTYYADSVKG
	108	CDRH3	IEWETRLN
BCMA.12	109	VHH	EVQLLESGGGLVQPGGSLRLSCAASGFTTFDEYTMHWFRQAPGKE REFVSAISGGGSETYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCAAGGEEAGVGYWGQGTQVTVSS
	110	CDRH1	EYTMH
	111	CDRH2	AISGGGSETYYADSVKG
	112	CDRH3	GGEEAGVGY
BCMA.13	113	VHH	EVQLLESGGGLVQPGGSLRLSCAASGFTTFEDYAMSWFRQAPGKE REGVSAISGKGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSS
	114	CDRH1	DYAMS
	115	CDRH2	AISGKGSTYYADSVKG
	116	CDRH3	LDEEAGAEGGY
BCMA.14	117	VHH-ok	EVQLLESGGGLVQPGGSLRLSCAASGFTTFDRYAMSWFRQAPGKE REGVSAISTSGDSTYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSS
	118	CDRH1	RYAMS
	119	CDRH2	AISTSGDSTYYADSVKG
	120	CDRH3	LDEEAGAEGGY
BCMA.15	121	VHH	EVQLLESGGGLVQPGGSLRLSCAASGFTTFASDAMSWYRQAPGKE RELVSAISGGGSETYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSS
	122	CDRH1	SDAMS
	123	CDRH2	AISGGGSETYYADSVKG
	124	CDRH3	HDSGEAYLAFDY
BCMA.16	125	VHH	EVQLLESGGGLVQPGGSLRLSCAASGFTTFDSYTMWSYRQAPGKE RELVSAISGHGDSTYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCTRISITTEWLAGDYWGQGTQVTVSS
	126	CDRH1	SYTMS
	127	CDRH2	AISGHGDSTYYADSVKG
	128	CDRH3	ISITTEWLAGDY
BCMA.17	129	VHH	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWFRQAPGKE REFVSFISGSGDSTYYADSVKGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSS
	130	CDRH1	SYAMS
	131	CDRH2	FISGSGDSTYYADSVKG
	132	CDRH3	WPYDFEEPSEPGVY
BCMA.18	133	VHH	EVQLLESGGGLVQPGGSLRLSCAASGFTTFDYDMSWYRQAPGKE RELVSVIHSGGSETYYADSVKGRFTISRDN SKNTLYLQMNSLRAE DTAVYYCAPGYSDLSFDYYNFDYWGQGTQVTVSS
	134	CDRH1	DYDMS
	135	CDRH2	VIHSGGSETYYADSVKG
	136	CDRH3	GYSDLSFDYYNFDY
BCMA.19	137	VHH	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYAMHWFRQAPGKE RVLVSSIDSGGSETYYADSVKGRFTISRDN SKNTLYLQMNSLRAE DTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSS
	138	CDRH1	DYAMH
	139	CDRH2	SIDSGGSETYYADSVKG
	140	CDRH3	GFKGDHPHPKDAFDI
BCMA.20	141	VHH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMWSYRQAPGKE RELVSAISGSGDHTYYADSVRGRFTISRDN SKNTLYLQMNSLRA EDTAVYYCNALEGGPTTAIQGGPDYWGQGTQVTVSS
	142	CDRH1	SEGMS
	143	CDRH2	AISGSGDHTYYADSVRG
	144	CDRH3	LEGGPTTAIQGGPDY

In particular embodiments, an anti-BCMA antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in Table 1 is conjugated to a cytotoxic agent. In some embodiments, a cytotoxic agent is selected from the group consisting of: a toxin, a radioisotope, an RNA polymerase II inhibitor and/or RNA polymerase III inhibitor, and a DNA-damaging agent.

In particular embodiments, an anti-BCMA antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in Table 1 is conjugated to a cytotoxic agent that comprises a toxin. Illustrative examples of toxins contemplated in particular embodiments include but are not limited to saporin, diphtheria toxin, pseudomonas exotoxin A, Ricin A chain derivatives, a small molecule toxin, and combinations thereof.

In particular embodiments, an anti-BCMA antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in Table 1 is conjugated to a cytotoxic agent that comprises a radioisotope. Illustrative examples of radioisotopes contemplated in particular embodiments include but are not limited to ^{131}I , ^{90}Y , ^{177}Lu , ^{188}Re , ^{67}Cu , ^{213}Bi , ^{211}At , and ^{227}Ac .

In particular embodiments, an anti-BCMA antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in Table 1 is conjugated to a cytotoxic agent that comprises an RNA polymerase II and/or III inhibitor. Illustrative examples of RNA polymerase II and/or III inhibitors contemplated in particular embodiments include but are not limited to an amanitin, including without limitation, α -amanitin, β -amanitin, γ -amanitin, ϵ -amanitin, amanin, amaninamide, amanullin, amanullinic acid and any functional fragments, derivatives or analogs thereof.

In particular embodiments, an anti-BCMA antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in Table 1 is conjugated to a cytotoxic agent that comprises a DNA-damaging agent. Illustrative examples of DNA-damaging agents contemplated in particular embodiments include but are not limited to an antitubulin agent, a DNA crosslinking agent, a DNA alkylating agent and a mitotic disrupting agent.

D. CHIMERIC ANTIGEN RECEPTORS

Chimeric antigen receptors (CARs) are fusion polypeptides that exploit antibody-based specificity for a desired antigen (*e.g.*, BCMA) to redirect immune effector cell specificity, thereby triggering proliferation, cytokine production, phagocytosis or production of molecules that can mediate cell death of the target antigen expressing cell in a major

histocompatibility (MHC) independent manner. As used herein, the term “chimeric” refers to a molecule that is composed of two or more polypeptides, or polynucleotides, of different origins.

The present disclosure contemplates improved anti-BCMA CARs that are suitable for *in vivo* modification, or *ex vivo* manufacture, of immune effector cells to redirect cytotoxicity toward BCMA-expressing cells (*e.g.*, B cells). In various embodiments, a CAR comprises a binding domain comprising one or more antibodies or antigen binding fragments thereof that binds to BCMA, a spacer domain, a transmembrane domain, and one or more intracellular signaling domains. In particular embodiments, a CAR comprises an antibody or antigen binding fragment thereof that binds to BCMA, a spacer domain, a transmembrane domain, and a primary signaling domain. In particular embodiments, a CAR comprises an antibody or antigen binding fragment thereof that binds to BCMA, a spacer domain, a transmembrane domain, one or more costimulatory signaling domains, and a primary signaling domain.

Illustrative examples of chimeric antigen receptor polypeptides are set forth in SEQ ID NOs: 165-860 and illustrative examples of polynucleotides encoding chimeric antigen receptor polypeptides are set forth in SEQ ID NOs: 905-944.

I. BINDING DOMAINS

In particular embodiments, a CAR comprises an extracellular antigen binding domain that comprises an antibody or antigen binding fragment thereof that specifically binds to a human BCMA polypeptide. The term “binding domain” or “extracellular antigen binding domain” are used interchangeably and refer to one or more antibodies or antigen binding fragments thereof that bind BCMA. The binding domain may be derived either from a natural, synthetic, semi-synthetic, or recombinant source.

In particular embodiments, a CAR comprises a binding domain that comprises one or more single chain variable fragments (scFv) and/or VHH domains that bind BCMA. In particular embodiments, a CAR comprises a binding domain that comprises one or more scFvs that bind BCMA. In particular embodiments, a CAR comprises a binding domain that comprises one or more VHH domains that bind BCMA.

In particular embodiments, a CAR comprises an anti-BCMA antibody or antigen binding fragment thereof comprising a heavy chain variable region (VH) that comprises a CDRH1, a CDRH2, and a CDRH3 of an antibody or antigen binding fragment thereof set

forth in Table 1; a polypeptide linker; and a light chain variable region (VL) that comprises a CDRL1, a CDRL2, and a CDRL3 of an antibody or antigen binding fragment thereof set forth in Table 1; a spacer domain; a transmembrane domain; a costimulatory signaling domain; and a primary signaling domain.

5 In particular embodiments, a CAR comprises an anti-BCMA antibody or antigen binding fragment thereof in either orientation (*e.g.*, VL-linker-VH or VH-linker-VL) comprising a VH that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 12, 13, and 14; a polypeptide linker; and a VL that comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth
10 in SEQ ID NOs: 16, 17, and 18; a spacer domain; a transmembrane domain; a costimulatory signaling domain; and a primary signaling domain. In particular embodiments, a CAR comprises an anti-BCMA antibody or antigen binding fragment thereof in either orientation (*e.g.*, VL-linker-VH or VH-linker-VL) comprising a VH that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 22,
15 23, and 24, a polypeptide linker, and a VL that comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 26, 27, and 28; a spacer domain; a transmembrane domain; a costimulatory signaling domain; and a primary signaling domain. In particular embodiments, a CAR comprises an anti-BCMA antibody or antigen binding fragment thereof in either orientation (*e.g.*, VL-linker-VH or VH-linker-VL)
20 comprising a VH that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 32, 33, and 34, a polypeptide linker, and a VL that comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 36, 37, and 38; a spacer domain; a transmembrane domain; a costimulatory signaling domain; and a primary signaling domain. In particular embodiments, a CAR
25 comprises an anti-BCMA antibody or antigen binding fragment thereof in either orientation (*e.g.*, VL-linker-VH or VH-linker-VL) comprising a VH that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 42, 43, and 44, a polypeptide linker, and a VL that comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 46, 47, and 48; a spacer
30 domain; a transmembrane domain; a costimulatory signaling domain; and a primary signaling domain. In particular embodiments, a CAR comprises an anti-BCMA antibody or antigen binding fragment thereof in either orientation (*e.g.*, VL-linker-VH or VH-linker-VL) comprising a VH that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino

acid sequences set forth in SEQ ID NOs: 52, 53, and 54, a polypeptide linker, and a VL that comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 56, 57, and 58; a spacer domain; a transmembrane domain; a costimulatory signaling domain; and a primary signaling domain. In particular preferred embodiments, a

5 CAR comprises an anti-BCMA antibody or antigen binding fragment thereof in either orientation (*e.g.*, VL-linker-VH or VH-linker-VL) comprising a VH that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 62, 63, and 64, a polypeptide linker, and a VL that comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 66, 67, and 68; a

10 spacer domain; a transmembrane domain; a costimulatory signaling domain; and a primary signaling domain. In particular embodiments, a CAR comprises an anti-BCMA antibody or antigen binding fragment thereof in either orientation (*e.g.*, VL-linker-VH or VH-linker-VL) comprising a VH that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 72, 73, and 74, a polypeptide linker, and a VL that

15 comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 76, 77, and 78; a spacer domain; a transmembrane domain; a costimulatory signaling domain; and a primary signaling domain. In particular embodiments, a CAR comprises an anti-BCMA antibody or antigen binding fragment thereof in either orientation (*e.g.*, VL-linker-VH or VH-linker-VL) comprising a VH that comprises a CDRH1, a

20 CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 82, 83, and 84, a polypeptide linker, and a VL that comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 86, 87, and 88; a spacer domain; a transmembrane domain; a costimulatory signaling domain; and a primary signaling domain. In particular embodiments, a CAR comprises an anti-BCMA antibody or

25 antigen binding fragment thereof in either orientation (*e.g.*, VL-linker-VH or VH-linker-VL) comprising a VH that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 92, 93, and 94, a polypeptide linker, and a VL that comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 96, 97, and 98; a spacer domain; a transmembrane domain; a costimulatory

30 signaling domain; and a primary signaling domain. In particular embodiments, the polypeptide linker is selected from the group consisting of: (GGGGS)_n wherein n = 1, 2, 3, 4 or 5; GEGTSTGSGGSGGSGGAD, GSTSGSGKPGSGEGSTKG and variants thereof comprising an amino acid sequence at least 90% identical thereto.

In particular embodiments, a CAR comprises an anti-BCMA antibody or antigen binding fragment thereof in either orientation (*e.g.*, VL-linker-VH or VH-linker-VL) comprising a VH that comprises the amino acid sequence set forth in SEQ ID NO: 11; a polypeptide linker selected from the group consisting of: (GGGGS)_n wherein n = 1, 2, 3, 4 or 5, GEGTSTGSGGSGGSGGAD, GSTSGSGKPGSGEGSTKG and variants thereof comprising an amino acid sequence 95% identical thereto; a VL that comprises the amino acid sequence set forth in SEQ ID NO: 15; a spacer domain; a transmembrane domain; a costimulatory signaling domain; and a primary signaling domain.

In particular embodiments, a CAR comprises an anti-BCMA antibody or antigen binding fragment thereof in either orientation (*e.g.*, VL-linker-VH or VH-linker-VL) comprising a VH that comprises the amino acid sequence set forth in SEQ ID NO: 21; a polypeptide linker selected from the group consisting of: (GGGGS)_n wherein n = 1, 2, 3, 4 or 5, GEGTSTGSGGSGGSGGAD, GSTSGSGKPGSGEGSTKG and variants thereof comprising an amino acid sequence 95% identical thereto; and a VL that comprises the amino acid sequence set forth in SEQ ID NO: 25; a spacer domain; a transmembrane domain; a costimulatory signaling domain; and a primary signaling domain.

In particular embodiments, a CAR comprises an anti-BCMA antibody or antigen binding fragment thereof in either orientation (*e.g.*, VL-linker-VH or VH-linker-VL) comprising a VH that comprises the amino acid sequence set forth in SEQ ID NO: 31; a polypeptide linker selected from the group consisting of: (GGGGS)_n wherein n = 1, 2, 3, 4 or 5, GEGTSTGSGGSGGSGGAD, GSTSGSGKPGSGEGSTKG and variants thereof comprising an amino acid sequence 95% identical thereto; and a VL that comprises the amino acid sequence set forth in SEQ ID NO: 35; a spacer domain; a transmembrane domain; a costimulatory signaling domain; and a primary signaling domain.

In particular embodiments, a CAR comprises an anti-BCMA antibody or antigen binding fragment thereof in either orientation (*e.g.*, VL-linker-VH or VH-linker-VL) comprising a VH that comprises the amino acid sequence set forth in SEQ ID NO: 41; a polypeptide linker selected from the group consisting of: (GGGGS)_n wherein n = 1, 2, 3, 4 or 5, GEGTSTGSGGSGGSGGAD, GSTSGSGKPGSGEGSTKG and variants thereof comprising an amino acid sequence 95% identical thereto; and a VL that comprises the amino acid sequence set forth in SEQ ID NO: 45; a spacer domain; a transmembrane domain; a costimulatory signaling domain; and a primary signaling domain.

In particular embodiments, a CAR comprises an anti-BCMA antibody or antigen binding fragment thereof in either orientation (*e.g.*, VL-linker-VH or VH-linker-VL) comprising a VH that comprises the amino acid sequence set forth in SEQ ID NO: 51; a polypeptide linker selected from the group consisting of: (GGGGS)_n wherein n = 1, 2, 3, 4 or 5, GEGTSTGSGGSGGSGGAD, GSTSGSGKPGSGEGSTKG and variants thereof comprising an amino acid sequence 95% identical thereto; and a VL that comprises the amino acid sequence set forth in SEQ ID NO: 55; a spacer domain; a transmembrane domain; a costimulatory signaling domain; and a primary signaling domain.

In particular embodiments, a CAR comprises an anti-BCMA antibody or antigen binding fragment thereof in either orientation (*e.g.*, VL-linker-VH or VH-linker-VL) comprising a VH that comprises the amino acid sequence set forth in SEQ ID NO: 61; a polypeptide linker selected from the group consisting of: (GGGGS)_n wherein n = 1, 2, 3, 4 or 5, GEGTSTGSGGSGGSGGAD, GSTSGSGKPGSGEGSTKG and variants thereof comprising an amino acid sequence 95% identical thereto; and a VL that comprises the amino acid sequence set forth in SEQ ID NO: 65; a spacer domain; a transmembrane domain; a costimulatory signaling domain; and a primary signaling domain.

In particular embodiments, a CAR comprises an anti-BCMA antibody or antigen binding fragment thereof in either orientation (*e.g.*, VL-linker-VH or VH-linker-VL) comprising a VH that comprises the amino acid sequence set forth in SEQ ID NO: 71; a polypeptide linker selected from the group consisting of: (GGGGS)_n wherein n = 1, 2, 3, 4 or 5, GEGTSTGSGGSGGSGGAD, GSTSGSGKPGSGEGSTKG and variants thereof comprising an amino acid sequence 95% identical thereto; and a VL that comprises the amino acid sequence set forth in SEQ ID NO: 75; a spacer domain; a transmembrane domain; a costimulatory signaling domain; and a primary signaling domain.

In particular embodiments, a CAR comprises an anti-BCMA antibody or antigen binding fragment thereof in either orientation (*e.g.*, VL-linker-VH or VH-linker-VL) comprising a VH that comprises the amino acid sequence set forth in SEQ ID NO: 81; a polypeptide linker selected from the group consisting of: (GGGGS)_n wherein n = 1, 2, 3, 4 or 5, GEGTSTGSGGSGGSGGAD, GSTSGSGKPGSGEGSTKG and variants thereof comprising an amino acid sequence 95% identical thereto; and a VL that comprises the amino acid sequence set forth in SEQ ID NO: 85; a spacer domain; a transmembrane domain; a costimulatory signaling domain; and a primary signaling domain.

In particular embodiments, a CAR comprises an anti-BCMA antibody or antigen binding fragment thereof in either orientation (*e.g.*, VL-linker-VH or VH-linker-VL) comprising a VH that comprises the amino acid sequence set forth in SEQ ID NO: 91; a polypeptide linker selected from the group consisting of: (GGGGS)_n wherein n = 1, 2, 3, 4
 5 or 5, GEGTSTGSGGSGGSGGAD, GSTSGSGKPGSGEGSTKG and variants thereof comprising an amino acid sequence 95% identical thereto; and a VL that comprises the amino acid sequence set forth in SEQ ID NO: 95; a spacer domain; a transmembrane domain; a costimulatory signaling domain; and a primary signaling domain.

In particular embodiments, a CAR comprises an anti-BCMA antibody or antigen
 10 binding fragment thereof comprises the amino acid sequence set forth in any one of SEQ ID NOs: 19, 20, 29, 30, 39, 40, 49, 50, 59, 60, 69, 70, 79, 80, 89, 90, 99, and 100 or an amino acid sequence with at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identity thereto; a spacer domain; a transmembrane domain; a costimulatory signaling domain; and a primary
 15 signaling domain.

In particular embodiments, a CAR comprises one or more VHH domains that bind BCMA comprising a CDRH1, a CDRH2, and a CDRH3 of an antibody or antigen binding fragment thereof set forth in Table 1; a spacer domain; a transmembrane domain; a costimulatory signaling domain; and a primary signaling domain. In particular embodiments,
 20 a CAR comprises a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 102, 103, and 104; a spacer domain; a transmembrane domain; a costimulatory signaling domain; and a primary signaling domain. In particular embodiments, a CAR comprises a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 106, 107, and 108; a spacer domain; a transmembrane domain; a
 25 costimulatory signaling domain; and a primary signaling domain. In particular embodiments, a CAR comprises a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 110, 111, and 112; a spacer domain; a transmembrane domain; a costimulatory signaling domain; and a primary
 30 signaling domain. In particular embodiments, a CAR comprises a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 114, 115, and 116; a spacer domain; a transmembrane domain; a costimulatory signaling domain; and a primary signaling domain. In particular embodiments,

a CAR comprises a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 118, 119, and 120; a spacer domain; a transmembrane domain; a costimulatory signaling domain; and a primary signaling domain. In particular embodiments, a CAR comprises a VHH domain that

5 comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 122, 123, and 124; a spacer domain; a transmembrane domain; a costimulatory signaling domain; and a primary signaling domain. In particular embodiments, a CAR comprises a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 126, 127, and 128; a spacer

10 domain; a transmembrane domain; a costimulatory signaling domain; and a primary signaling domain. In particular embodiments, a CAR comprises a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 130, 131, and 132; a spacer domain; a transmembrane domain; a costimulatory signaling domain; and a primary signaling domain. In particular embodiments,

15 a CAR comprises a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 134, 135, and 136; a spacer domain; a transmembrane domain; a costimulatory signaling domain; and a primary signaling domain. In particular embodiments, a CAR comprises a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 138, 139, and 140; a spacer domain; a transmembrane domain; a costimulatory signaling domain; and a primary signaling domain. In particular embodiments,

20 a CAR comprises a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 142, 143, and 144 a spacer domain; a transmembrane domain; a costimulatory signaling domain; and a primary signaling domain. In particular embodiments, a CAR comprises one or more VHH domains set forth in SEQ ID NOs: 101, 105, 109, 113, 117, 121, 125, 129, 133, 137, and 141 or an amino acid sequence with at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identity thereto; a spacer domain; a transmembrane domain; a costimulatory signaling domain; and a

25 primary signaling domain.

30

2. SPACER DOMAIN

Chimeric antigen receptors contemplated herein comprise a spacer domain. A spacer domain is disposed between the extracellular antigen binding domain and the transmembrane domain of a CAR. A spacer domain plays a role in positioning the extracellular antigen binding domain away from the effector cell surface to enable proper cell/cell contact, antigen binding and activation. A spacer domain may be derived from a hinge domain or stalk domain of a naturally occurring polypeptide or from a synthetic, semi-synthetic, or recombinant source.

In particular embodiments, a CAR comprises a spacer domain comprising a hinge and/or stalk domain isolated from CD4, CD7, CD8 α , CD8 β , CD28, CD134, CD137, CD152, and CD278, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity thereto. In particular embodiments, a CAR comprises a spacer domain comprising a naturally occurring immunoglobulin hinge region isolated from IgG1, IgG2, IgG3, or IgG4, optionally in combination with one or more heavy chain constant regions, *e.g.*, CH2 and/or CH3.

In particular embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in Table 1; a spacer domain selected from the group consisting of: a CD4 hinge, a CD8 β hinge, a CD8 α hinge, a CD28 hinge, a CD134 hinge, a CD137 hinge, a CD152 hinge, a CD278 hinge, an IgG1 hinge, an IgG2 hinge, an IgG3 hinge, and an IgG4 hinge; a transmembrane domain; one or more costimulatory signaling domains; and a primary signaling domain.

In particular embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in Table 1; a spacer domain comprising an amino acid sequence set forth in Table 2; a transmembrane domain; one or more costimulatory signaling domains; and a primary signaling domain.

Table 2

SEQ ID NO:	AMINO ACID SEQUENCE
145	TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACD
146	IEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLPFGPSKP
147	SGQVLLESNIKVLPTWSTPVQP
148	ESKYGPPCPPCP
149	ESKYGPPCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFQSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLGLK
150	LEPKSCDKTHTCPPCP

In particular embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in Table 1; a spacer domain comprising an amino acid sequence set forth in any one of SEQ ID NOs: 145, 146, 147, 148, 149, and 150; a transmembrane domain; one or more costimulatory signaling domains; and
5 a primary signaling domain.

3. *TRANSMEMBRANE DOMAIN*

Chimeric antigen receptors contemplated herein comprise a transmembrane domain. The transmembrane domain is a hydrophobic domain that fuses the extracellular and intracellular portions of the CAR and anchors the CAR to the plasma membrane of the
10 immune effector cell. The transmembrane domain may be derived either from a natural, synthetic, semi-synthetic, or recombinant source. In particular embodiments, the CAR further comprises a short oligo- or polypeptide linker, preferably between 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acids in length disposed between the transmembrane domain and the intracellular domains of the CAR.

In particular embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in Table 1; a spacer domain; a transmembrane domain isolated or derived from a polypeptide selected from the group consisting of an alpha, beta, gamma, or delta chain of the T-cell receptor, CD3δ, CD3ε, CD3γ, CD3ζ, CD4, CD5, CD8α, CD9, CD16, CD22, CD27, CD28, CD33, CD37, CD45,
20 CD64, CD80, CD86, CD134, CD137, CD152, CD154, CD278, amnionless (AMN), and programmed cell death 1 (PDCD1); one or more costimulatory signaling domains; and a primary signaling domain.

In particular embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in Table 1; a spacer domain; a
25 transmembrane domain comprising an amino acid sequence set forth in Table 3; one or more costimulatory signaling domains; and a primary signaling domain.

Table 3

SEQ ID NO:	AMINO ACID SEQUENCE
151	IYIWAPLAGTCGVLLLSLVITLYC
152	IISFFLALTSTALLFLLFFLTFRFSVV
153	FWVLVVVGVLACYSLLVTVAFIIFWV
154	VAAILGLGLVLGLLGPLAILL
155	WLPIGCAAFVVVCILGCILICWL
156	VMSVATIVVDICITGGLLLVYYWS
157	MALIVLGGVAGLLFFIGLGIFF

In particular embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in Table 1; a spacer domain; a transmembrane domain comprising an amino acid sequence set forth in any one of SEQ ID NOs: 151, 152, 153, 154, 155, 156, and 157; one or more costimulatory signaling domains; and a primary signaling domain.

4. INTRACELLULAR SIGNALING DOMAIN

Chimeric antigen receptors contemplated herein comprise one or more intracellular signaling domains that function to transduce a signal of extracellular antigen recognition to the interior of the immune effector cell and elicit one or more effector cell functions including but not limited to activation, cytokine production, proliferation and cytotoxic activity. T cell activation is mediated by two distinct classes of intracellular signaling domains: primary signaling domains that initiate antigen-dependent primary activation through the TCR (*e.g.*, a TCR/CD3 complex) and costimulatory signaling domains that act in an antigen-independent manner to provide a secondary or costimulatory signal. The intracellular primary signaling and costimulatory signaling domains may be linked in any order in tandem to the carboxyl terminus of the transmembrane domain.

In particular embodiments a CAR comprises one or more intracellular signaling domains that comprise one or more costimulatory signaling domains and a primary signaling domain.

A primary signaling domain regulates primary activation of the TCR complex either in a stimulatory way, or in an inhibitory way. Primary signaling domains that act in a stimulatory manner may contain signaling motifs which are known as immunoreceptor tyrosine-based activation motifs or ITAMs. Primary signaling domains comprising one or more ITAMs may be obtained, isolated, or derived from FcR γ , FcR β , CD3 γ , CD3 δ , CD3 ϵ , CD3 ζ , CD22, CD79a, CD79b, and CD66d. In particular embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in Table 1; a spacer domain; a transmembrane domain; a primary signaling domain isolated from a polypeptide selected from the group consisting of FcR γ , FcR β , CD3 γ , CD3 δ , CD3 ϵ , CD3 ζ , CD22, CD79a, CD79b, and CD66d; and optionally, one or more co-stimulatory signaling domains.

A costimulatory signaling domain provides a second signal required for efficient activation and function of immune effector cells upon binding to antigen. Costimulatory

signaling domains may be obtained, isolated, or derived from costimulatory molecules selected from the group consisting of: TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9, TLR10, CARD11, CD2, CD7, CD27, CD28, CD30, CD40, ICAM, CD83, CD94, CD134 (OX40), CD137 (4-1BB), CD278 (ICOS), DAP10, LAT, SLP76, TRAT1, 5 TNFR2, TNFRS14, TNFRS18, TNFRS25, and ZAP70.

In particular embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in Table 1; a spacer domain; a transmembrane domain; a primary signaling domain isolated from a polypeptide selected from the group consisting of FcR γ , FcR β , CD3 γ , CD3 δ , CD3 ϵ , CD3 ζ , CD22, CD79a, 10 CD79b, and CD66d; and optionally, one or more costimulatory signaling domains isolated from a costimulatory molecule selected from the group consisting of: TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9, TLR10, CARD11, CD2, CD7, CD27, CD28, CD30, CD40, ICAM, CD83, CD94, CD134 (OX40), CD137 (4-1BB), CD278 (ICOS), DAP10, LAT, SLP76, TRAT1, TNFR2, TNFRS14, TNFRS18, TNFRS25, and ZAP70.

15 In particular embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in Table 1; a spacer domain; a transmembrane domain; a primary signaling domain and one or more costimulatory signaling domains comprising an amino acid sequence set forth in Table 4.

Table 4

SEQ ID NO:	DOMAIN	AMINO ACID SEQUENCE
158	PRIMARY	RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGKPPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
159	COSTIM	KRGRKLLYIFKQPFMRPVQTTQEEDGCSCRFPPEEEGGGCEL
160	COSTIM	RSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRS
161	COSTIM	ALYLLRRDQRLPPDAHKKPPGGGSFRTPIQEEQADAHSTLAKI
162	COSTIM	TKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTL
163	COSTIM	QRRKYRSNKGESPVPAEPCHYSCPREEGSTIPIQEDYRKPEPACSP
164	COSTIM	KKKPLCLQREAKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQFQAPGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQVPFSSKEECAFRSQLETPETLLGSTEEKPLPLGVDPDAGMKPS

20 In particular embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in Table 1; a spacer domain; a transmembrane domain; one or more costimulatory domains comprising an amino acid sequence set forth in any one of SEQ ID NOs: 159, 160, 161, 162, 163, and 164 or an amino acid sequence at least 95% identical thereto; and a primary signaling domain comprising an

amino acid sequence set forth in SEQ ID NO: 158 or an amino acid sequence at least 95% identical thereto.

E. ILLUSTRATIVE CHIMERIC ANTIGEN RECEPTORS

In particular embodiments, a CAR comprises an antibody or antigen binding
 5 fragment thereof comprising an amino acid sequence set forth in Table 1; a spacer domain
 comprising a hinge domain or fragment thereof selected from the group consisting of a CD4
 hinge, a CD8 β hinge, a CD8 α hinge, a CD28 hinge, a CD134 hinge, a CD137 hinge, a CD152
 hinge, a CD278 hinge, an IgG1 hinge, an IgG2 hinge, an IgG3 hinge, and an IgG4 hinge; a
 transmembrane domain isolated or derived from a polypeptide selected from the group
 10 consisting of an alpha, beta, gamma, or delta chain of the T-cell receptor, CD3 δ , CD3 ϵ ,
 CD3 γ , CD3 ζ , CD4, CD5, CD8 α , CD9, CD16, CD22, CD27, CD28, CD33, CD37, CD45,
 CD64, CD80, CD86, CD134, CD137, CD152, CD154, CD278, AMN, and PDCD1; one or
 more costimulatory signaling domains isolated from a costimulatory molecule selected from
 the group consisting of: TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9,
 15 TLR10, CARD11, CD2, CD7, CD27, CD28, CD30, CD40, ICAM, CD83, CD94, CD134
 (OX40), CD137 (4-1BB), CD278 (ICOS), DAP10, LAT, SLP76, TRAT1, TNFR2,
 TNFRS14, TNFRS18, TNFRS25, and ZAP70; and a primary signaling domain isolated from
 CD3 ζ , CD22, CD79a, CD79b, or CD66d.

In particular embodiments, a CAR comprises an antibody or antigen binding
 20 fragment thereof comprising an amino acid sequence set forth in Table 1; a spacer domain
 comprising a hinge domain or fragment thereof selected from the group consisting of a
 CD8 α hinge, a CD28 hinge, an IgG1 hinge, and an IgG4 hinge; a CD8 α or CD28
 transmembrane domain; a CD134, CD137, or CD278 costimulatory domain; and a CD3 ζ
 primary signaling domain.

In particular embodiments, a CAR comprises an antibody or antigen binding
 25 fragment thereof comprising an amino acid sequence set forth in SEQ ID NO: 19 or SEQ ID
 NO: 20; a spacer domain comprising an amino acid sequence set forth in SEQ ID NO: 145,
 SEQ ID NO: 146, SEQ ID NO: 148, or SEQ ID NO: 150; a transmembrane domain
 comprising an amino acid sequence set forth in SEQ ID NO: 151 or SEQ ID NO: 153; a
 30 costimulatory domain comprising an amino acid sequence set forth in SEQ ID NO: 159, SEQ
 ID NO: 160, or SEQ ID NO: 162; and a primary signaling domain comprising an amino acid
 sequence set forth in SEQ ID NO: 158. In particular embodiments, a CAR comprises an

amino acid sequence set forth in any one of SEQ ID NOs: 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, and 188. In particular embodiments, a CAR comprises an amino acid sequence set forth in any one of SEQ ID NOs: 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 5 204, 205, 206, 207, 208, 209, 210, 211, and 212.

SEQ ID NO.	AMINO ACID SEQUENCE
165	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYICARDEYGGFDIWGQGTMTVTVSSGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQOKPGQAPRLLIYDASNRTG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKLLYIF KQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKD TYDALHMQALPPR
166	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYICARDEYGGFDIWGQGTMTVTVSSGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQOKPGQAPRLLIYDASNRTG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKSRLLHSD YMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDT YDALHMQALPPR
167	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYICARDEYGGFDIWGQGTMTVTVSSGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQOKPGQAPRLLIYDASNRTG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKYSVSHD PNGEYMFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHM QALPPR
168	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYICARDEYGGFDIWGQGTMTVTVSSGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQOKPGQAPRLLIYDASNRTG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLVACYSLLVTVAFIIFWVKRGRKLL YIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTA TKDTYDALHMQALPPR
169	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYICARDEYGGFDIWGQGTMTVTVSSGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQOKPGQAPRLLIYDASNRTG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLVACYSLLVTVAFIIFWVRSKRSL HSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTAT KDTYDALHMQALPPR
170	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYICARDEYGGFDIWGQGTMTVTVSSGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQOKPGQAPRLLIYDASNRTG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLVACYSLLVTVAFIIFWVTKKKYSSS VHDPNGEYMFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDA LHMQALPPR

171	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYCARDEYGGFDIWGQGTMTVTVSSGGGGSGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSRASQSVSSYLAWYQOKPGQAPRLLIYDASNRTG IPARFSGSGSGTDFTLTIISSLEPEDFAVYVCQORVVYPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMR PVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQOGQONQLYNELNLGRREEYDVLDKRRG RDPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALH MQALPPR
172	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYCARDEYGGFDIWGQGTMTVTVSSGGGGSGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSRASQSVSSYLAWYQOKPGQAPRLLIYDASNRTG IPARFSGSGSGTDFTLTIISSLEPEDFAVYVCQORVVYPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMT RRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQOGQONQLYNELNLGRREEYDVLDKRRGR RDPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALH MQALPPR
173	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYCARDEYGGFDIWGQGTMTVTVSSGGGGSGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSRASQSVSSYLAWYQOKPGQAPRLLIYDASNRTG IPARFSGSGSGTDFTLTIISSLEPEDFAVYVCQORVVYPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYM FMRVNTAKKSRLTDVTLRVKFSRSADAPAYQOGQONQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
174	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYCARDEYGGFDIWGQGTMTVTVSSGGGGSGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSRASQSVSSYLAWYQOKPGQAPRLLIYDASNRTG IPARFSGSGSGTDFTLTIISSLEPEDFAVYVCQORVVYPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYM FMRVNTAKKSRLTDVTLRVKFSRSADAPAYQOGQONQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
175	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYCARDEYGGFDIWGQGTMTVTVSSGGGGSGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSRASQSVSSYLAWYQOKPGQAPRLLIYDASNRTG IPARFSGSGSGTDFTLTIISSLEPEDFAVYVCQORVVYPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYM FMRVNTAKKSRLTDVTLRVKFSRSADAPAYQOGQONQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
176	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYCARDEYGGFDIWGQGTMTVTVSSGGGGSGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSRASQSVSSYLAWYQOKPGQAPRLLIYDASNRTG IPARFSGSGSGTDFTLTIISSLEPEDFAVYVCQORVVYPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYM FMRVNTAKKSRLTDVTLRVKFSRSADAPAYQOGQONQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
177	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYCARDEYGGFDIWGQGTMTVTVSSGGGGSGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSRASQSVSSYLAWYQOKPGQAPRLLIYDASNRTG IPARFSGSGSGTDFTLTIISSLEPEDFAVYVCQORVVYPITFGGGTKVEIKIESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRV KFSRSADAPAYQOGQONQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
178	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYCARDEYGGFDIWGQGTMTVTVSSGGGGSGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSRASQSVSSYLAWYQOKPGQAPRLLIYDASNRTG IPARFSGSGSGTDFTLTIISSLEPEDFAVYVCQORVVYPITFGGGTKVEIKIESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVK

	F SRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
179	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWQGTMVTVSSGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSRASQSVSSYLAWYQQKPGQAPRLIIYDASNRTG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKESKYGPPCPPCFWV WAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSAD APAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI GMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
180	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWQGTMVTVSSGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSRASQSVSSYLAWYQQKPGQAPRLIIYDASNRTG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKESKYGPPCPPCFWV LVVVGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEDGCSCRFPEEEEGGCE LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
181	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWQGTMVTVSSGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSRASQSVSSYLAWYQQKPGQAPRLIIYDASNRTG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKESKYGPPCPPCFWV LVVVGVLACYSLLVTVAFIIFWVRSKRSLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRS RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
182	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWQGTMVTVSSGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSRASQSVSSYLAWYQQKPGQAPRLIIYDASNRTG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKESKYGPPCPPCFWV LVVVGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSR SADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQKDKMAEAY SEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
183	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWQGTMVTVSSGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSRASQSVSSYLAWYQQKPGQAPRLIIYDASNRTG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKLEPKSCDKTHTCPC PIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
184	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWQGTMVTVSSGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSRASQSVSSYLAWYQQKPGQAPRLIIYDASNRTG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKLEPKSCDKTHTCPC PIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEDGCSCRFPEEEEGGC SRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
185	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWQGTMVTVSSGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSRASQSVSSYLAWYQQKPGQAPRLIIYDASNRTG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKLEPKSCDKTHTCPC PIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFS RSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQKDKMAEA YSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
186	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWQGTMVTVSSGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSRASQSVSSYLAWYQQKPGQAPRLIIYDASNRTG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKLEPKSCDKTHTCPC PFWVLVVVGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEDGCSCRFPEEE GGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
187	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL

	KSRLTITKDTSKNQVVLMTNMDPVD TAVVYCARDEYGGFDIWGQGTMTVTVSSGGGGSGGGSGG GGSGGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASN RATG IPARFSGSGSGTDFTLTISSELEPEDFAVYYCQQRVVYPITFGGGTKVEIKLEPKSCDKTHTCPPC PFWVLVVGVLACYSLLVTVAFIIFWVRSKRSLHSDYMNMTPRRPGPTRKHYQPYAPPRDFA AYRSRVKFSRSADAPAYQQGNQLYNELNLRREEYDVL DKRRGRDP EMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
188	QITLKESGPTLVKPTQTTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLAL IYWNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVD TAVVYCARDEYGGFDIWGQGTMTVTVSSGGGGSGGGSGG GGSGGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASN RATG IPARFSGSGSGTDFTLTISSELEPEDFAVYYCQQRVVYPITFGGGTKVEIKLEPKSCDKTHTCPPC PFWVLVVGVLACYSLLVTVAFIIFWVTKKYSVSDPNGEYMFMRVNTAKKSRLTDVTLRV KF SRSADAPAYQQGNQLYNELNLRREEYDVL DKRRGRDP EMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
189	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASN RATGIPARFSGS GSGTDFTLTISSELEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGGSGGGSGGGSGGGSGQIT LKESGPTLVKPTQTTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLAL IYWNDEKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVVYCARDEYGGFDIWGQGTMTVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKLLYIF KQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGNQLYNELNLRREEYDV LDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKD TYDALHMQALPPR
190	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASN RATGIPARFSGS GSGTDFTLTISSELEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGGSGGGSGGGSGGGSGQIT LKESGPTLVKPTQTTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLAL IYWNDEKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVVYCARDEYGGFDIWGQGTMTVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKLLYIF YMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGNQLYNELNLRREEYDVL DKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDT YDALHMQALPPR
191	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASN RATGIPARFSGS GSGTDFTLTISSELEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGGSGGGSGGGSGGGSGQIT LKESGPTLVKPTQTTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLAL IYWNDEKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVVYCARDEYGGFDIWGQGTMTVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKYSVSDPN NGEYMFMRVNTAKKSRLTDVTLRVKF SRSADAPAYQQGNQLYNELNLRREEYDVL DKRRGR DP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDALH MQALPPR
192	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASN RATGIPARFSGS GSGTDFTLTISSELEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGGSGGGSGGGSGGGSGQIT LKESGPTLVKPTQTTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLAL IYWNDEKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVVYCARDEYGGFDIWGQGTMTVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGVLACYSLLVTVAFIIFWVTKRGRKLL YIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGNQLYNELNLRREE YDVL DKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK GHDGLYQGLSTA TKDTYDALHMQALPPR
193	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASN RATGIPARFSGS GSGTDFTLTISSELEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGGSGGGSGGGSGGGSGQIT LKESGPTLVKPTQTTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLAL IYWNDEKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVVYCARDEYGGFDIWGQGTMTVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGVLACYSLLVTVAFIIFWVRSKRSLH SDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGNQLYNELNLRREEY DVL DKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK GHDGLYQGLSTAT KDTYDALHMQALPPR
194	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASN RATGIPARFSGS GSGTDFTLTISSELEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGGSGGGSGGGSGGGSGQIT LKESGPTLVKPTQTTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLAL IYWNDEKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVVYCARDEYGGFDIWGQGTMTVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGVLACYSLLVTVAFIIFWVTKKYSVSD PNGEYMFMRVNTAKKSRLTDVTLRVKF SRSADAPAYQQGNQLYNELNLRREEYDVL DKR

	RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
195	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISLSEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGITLKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWYNDKRYSPSLKSRLTITKDTSKNQVVLMTNMDPVDTAVYYCARDEYGGFDIWGQGTMTVTVSSIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGDCSCRFPEEEEGGCELVRVKSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
196	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISLSEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGITLKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWYNDKRYSPSLKSRLTITKDTSKNQVVLMTNMDPVDTAVYYCARDEYGGFDIWGQGTMTVTVSSIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGDCSCRFPEEEEGGCELVRVKSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
197	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISLSEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGITLKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWYNDKRYSPSLKSRLTITKDTSKNQVVLMTNMDPVDTAVYYCARDEYGGFDIWGQGTMTVTVSSIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKKYYSSSVHDPNGEYMFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
198	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISLSEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGITLKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWYNDKRYSPSLKSRLTITKDTSKNQVVLMTNMDPVDTAVYYCARDEYGGFDIWGQGTMTVTVSSIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKKYYSSSVHDPNGEYMFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
199	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISLSEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGITLKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWYNDKRYSPSLKSRLTITKDTSKNQVVLMTNMDPVDTAVYYCARDEYGGFDIWGQGTMTVTVSSIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGDCSCRFPEEEEGGCELVRVKSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
200	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISLSEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGITLKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWYNDKRYSPSLKSRLTITKDTSKNQVVLMTNMDPVDTAVYYCARDEYGGFDIWGQGTMTVTVSSIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGDCSCRFPEEEEGGCELVRVKSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
201	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISLSEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGITLKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWYNDKRYSPSLKSRLTITKDTSKNQVVLMTNMDPVDTAVYYCARDEYGGFDIWGQGTMTVTVSSIESKYGPPCPPCIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGDCSCRFPEEEEGGCELVRVKSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
202	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISLSEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGITLKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWYNDKRYSPSLKSR

	LTITKDTSKNQVVLMTNMDPVDTAVYYCARDEYGGFDIWGQGTMTVTSSESKEYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVK FSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQDKDMA EAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
203	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSELEDFAVYYCQQRVVYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWYNDKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVDTAVYYCARDEYGGFDIWGQGTMTVTSSESKEYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSAD APAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQDKDMAEAYSEI GMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
204	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSELEDFAVYYCQQRVVYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWYNDKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVDTAVYYCARDEYGGFDIWGQGTMTVTSSESKEYGPPCPPCFWV LVVVGVLACYSLLVTVAFIIFWVKRGRKLLYIFKQPFMRPVQTTQEDGCSCRFPEEEEGGCE LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQK DMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
205	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSELEDFAVYYCQQRVVYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWYNDKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVDTAVYYCARDEYGGFDIWGQGTMTVTSSESKEYGPPCPPCFWV LVVVGVLACYSLLVTVAFIIFWVRSKRSLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRS RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQK DMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
206	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSELEDFAVYYCQQRVVYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWYNDKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVDTAVYYCARDEYGGFDIWGQGTMTVTSSESKEYGPPCPPCFWV LVVVGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFS SADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQDKDMAEAY SEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
207	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSELEDFAVYYCQQRVVYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWYNDKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVDTAVYYCARDEYGGFDIWGQGTMTVTSSESLEPKSCKDTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCRGRKLLYIFKQPFMRPVQTTQEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
208	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSELEDFAVYYCQQRVVYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWYNDKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVDTAVYYCARDEYGGFDIWGQGTMTVTSSESLEPKSCKDTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYR SRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
209	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSELEDFAVYYCQQRVVYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWYNDKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVDTAVYYCARDEYGGFDIWGQGTMTVTSSESLEPKSCKDTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFS RSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQDKDMAEA YSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
210	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSELEDFAVYYCQQRVVYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWYNDKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVDTAVYYCARDEYGGFDIWGQGTMTVTSSESLEPKSCKDTHTCPPC PFWVLVVVGVLACYSLLVTVAFIIFWVKRGRKLLYIFKQPFMRPVQTTQEDGCSCRFPEEEE GGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYN

	ELQDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
211	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVYPIITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGITLKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYWNDEKRYSPSLKSRLTITKDTSKNQVVLMTNMDPVDTAVYYCARDEYGGFDIWGQGTMTVTVSSLEPKSCDKTHTCPPCFWVLLVVGGLVACYSLLVTVAFIIFWVRSKRSLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
212	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVYPIITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGITLKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYWNDEKRYSPSLKSRLTITKDTSKNQVVLMTNMDPVDTAVYYCARDEYGGFDIWGQGTMTVTVSSLEPKSCDKTHTCPPCFWVLLVVGGLVACYSLLVTVAFIIFWVTKKYSVSDPNGEYMFMRVNTAKKSRSLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR

In particular embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in SEQ ID NO: 29 or SEQ ID NO: 30; a spacer domain comprising an amino acid sequence set forth in SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 148, or SEQ ID NO: 150; a transmembrane domain
5 comprising an amino acid sequence set forth in SEQ ID NO: 151 or SEQ ID NO: 153; a costimulatory domain comprising an amino acid sequence set forth in SEQ ID NO: 159, SEQ ID NO: 160, or SEQ ID NO: 162; and a primary signaling domain comprising an amino acid sequence set forth in SEQ ID NO: 158. In particular embodiments, a CAR comprises an amino acid sequence set forth in any one of SEQ ID NOs: 213, 214, 215, 216, 217, 218, 219,
10 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, and 236. In particular embodiments, a CAR comprises an amino acid sequence set forth in any one of SEQ ID NOs: 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, and 260.

SEQ ID NO.	AMINO ACID SEQUENCE
213	QITLKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYWNDDKRYSPSLKSRLTITKDTSKNQVVLMTNMDPVDTAVYYCARDEYGGFDIWGQGTMTVTVSSGGGSGGGGSGGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRFDYPIITFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
214	QITLKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYWNDDKRYSPSLKSRLTITKDTSKNQVVLMTNMDPVDTAVYYCARDEYGGFDIWGQGTMTVTVSSGGGSGGGGSGGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRFDYPIITFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
215	QITLKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYWNDDKRYSPSLKSRLTITKDTSKNQVVLMTNMDPVDTAVYYCARDEYGGFDIWGQGTMTVTVSSGGGSGGGGSGGGGG

	GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRTG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQORFDYPITFGGGTKVEIKTTTPAPRPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVTITLYCTKKKYSSSVHD PNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHM QALPPR
216	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYWNDDKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYYCARDEYGGFDIWGQGTMTVTVSSGGGGSGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRTG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQORFDYPITFGGGTKVEIKTTTPAPRPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLACYSLLVTVAFIIFWVKRGRKKLL YIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTA TKDTYDALHMQALPPR
217	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYWNDDKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYYCARDEYGGFDIWGQGTMTVTVSSGGGGSGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRTG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQORFDYPITFGGGTKVEIKTTTPAPRPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLACYSLLVTVAFIIFWVRSKRSRL HSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTAT KDTYDALHMQALPPR
218	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYWNDDKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYYCARDEYGGFDIWGQGTMTVTVSSGGGGSGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRTG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQORFDYPITFGGGTKVEIKTTTPAPRPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLACYSLLVTVAFIIFWVTKKKYSSS VHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDA LHMQALPPR
219	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYWNDDKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYYCARDEYGGFDIWGQGTMTVTVSSGGGGSGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRTG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQORFDYPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVTITLYCKRGRKKLLYIFKQPFMR PVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRG RDPPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALH MQALPPR
220	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYWNDDKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYYCARDEYGGFDIWGQGTMTVTVSSGGGGSGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRTG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQORFDYPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVTITLYCKRGRKKLLHSDYMNMT PRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHM QALPPR
221	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYWNDDKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYYCARDEYGGFDIWGQGTMTVTVSSGGGGSGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRTG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQORFDYPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVTITLYCTKKKYSSSVHDPNGEY MFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
222	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYWNDDKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYYCARDEYGGFDIWGQGTMTVTVSSGGGGSGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRTG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQORFDYPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVTITLYCTKKKYSSSVHDPNGEY MFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR

	RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
223	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYWNDDKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYCARDEYGGFDIWQOGTMVTVSSGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSRASQSVSSYLAWYQOKPGQAPRLIIYDASNRTG IPARFSGSGSGTDFTLTISSLEPEDFAVYQCQORFDYPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPFVVLVVGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMN MTPRRPGPTRKHYPYAPPRDFAAYRSRVKF SRSADAPAYQOGQONQLYNELNLGRREEYDVLDR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
224	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYWNDDKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYCARDEYGGFDIWQOGTMVTVSSGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSRASQSVSSYLAWYQOKPGQAPRLIIYDASNRTG IPARFSGSGSGTDFTLTISSLEPEDFAVYQCQORFDYPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPFVVLVVGVLACYSLLVTVAFIIFWVTKKYSVSDHPNG EYMFMRVNTAKKSRSLTDVTLRVKF SRSADAPAYQOGQONQLYNELNLGRREEYDVLDRGRDPE MGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQAL PPR
225	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYWNDDKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYCARDEYGGFDIWQOGTMVTVSSGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSRASQSVSSYLAWYQOKPGQAPRLIIYDASNRTG IPARFSGSGSGTDFTLTISSLEPEDFAVYQCQORFDYPITFGGGTKVEIKESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEDGCSCRFPEEEEGGCELRV KFSRSADAPAYQOGQONQLYNELNLGRREEYDVLDRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
226	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYWNDDKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYCARDEYGGFDIWQOGTMVTVSSGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSRASQSVSSYLAWYQOKPGQAPRLIIYDASNRTG IPARFSGSGSGTDFTLTISSLEPEDFAVYQCQORFDYPITFGGGTKVEIKESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEDGCSCRFPEEEEGGCELRV KFSRSADAPAYQOGQONQLYNELNLGRREEYDVLDRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
227	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYWNDDKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYCARDEYGGFDIWQOGTMVTVSSGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSRASQSVSSYLAWYQOKPGQAPRLIIYDASNRTG IPARFSGSGSGTDFTLTISSLEPEDFAVYQCQORFDYPITFGGGTKVEIKESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEDGCSCRFPEEEEGGCELRV KFSRSADAPAYQOGQONQLYNELNLGRREEYDVLDRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
228	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYWNDDKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYCARDEYGGFDIWQOGTMVTVSSGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSRASQSVSSYLAWYQOKPGQAPRLIIYDASNRTG IPARFSGSGSGTDFTLTISSLEPEDFAVYQCQORFDYPITFGGGTKVEIKESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEDGCSCRFPEEEEGGCELRV KFSRSADAPAYQOGQONQLYNELNLGRREEYDVLDRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
229	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYWNDDKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYCARDEYGGFDIWQOGTMVTVSSGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSRASQSVSSYLAWYQOKPGQAPRLIIYDASNRTG IPARFSGSGSGTDFTLTISSLEPEDFAVYQCQORFDYPITFGGGTKVEIKESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEDGCSCRFPEEEEGGCELRV KFSRSADAPAYQOGQONQLYNELNLGRREEYDVLDRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
230	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYWNDDKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYCARDEYGGFDIWQOGTMVTVSSGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSRASQSVSSYLAWYQOKPGQAPRLIIYDASNRTG IPARFSGSGSGTDFTLTISSLEPEDFAVYQCQORFDYPITFGGGTKVEIKESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEDGCSCRFPEEEEGGCELRV KFSRSADAPAYQOGQONQLYNELNLGRREEYDVLDRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

	SEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
231	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIYWND DKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWGQGTMTVTVSSGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLS CRASQSVSSYLAWYQQKPGQAPRLLIYDASN RATG IPARFSGSGSGTDFTLTIS SLEPEDFAVYYCQORFDYPITFGGGTKVEIKLEPKSCDKTHTC PPC PIYIWAPLAGTCGVLLLSLVITLYCKRGRKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
232	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIYWND DKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWGQGTMTVTVSSGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLS CRASQSVSSYLAWYQQKPGQAPRLLIYDASN RATG IPARFSGSGSGTDFTLTIS SLEPEDFAVYYCQORFDYPITFGGGTKVEIKLEPKSCDKTHTC PPC PIYIWAPLAGTCGVLLLSLVITLYCKRGRKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC SRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
233	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIYWND DKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWGQGTMTVTVSSGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLS CRASQSVSSYLAWYQQKPGQAPRLLIYDASN RATG IPARFSGSGSGTDFTLTIS SLEPEDFAVYYCQORFDYPITFGGGTKVEIKLEPKSCDKTHTC PPC PIYIWAPLAGTCGVLLLSLVITLYCKKYS SSVHDPNGEYMFRAVNTAKKSRLTDVTLRVKFS RSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEA YSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
234	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIYWND DKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWGQGTMTVTVSSGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLS CRASQSVSSYLAWYQQKPGQAPRLLIYDASN RATG IPARFSGSGSGTDFTLTIS SLEPEDFAVYYCQORFDYPITFGGGTKVEIKLEPKSCDKTHTC PPC PFWVLVVGGVLACYSLLVTVAFIIFWVKRGRKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEE GGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
235	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIYWND DKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWGQGTMTVTVSSGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLS CRASQSVSSYLAWYQQKPGQAPRLLIYDASN RATG IPARFSGSGSGTDFTLTIS SLEPEDFAVYYCQORFDYPITFGGGTKVEIKLEPKSCDKTHTC PPC PFWVLVVGGVLACYSLLVTVAFIIFWVRSKR S RLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFA AYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
236	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIYWND DKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWGQGTMTVTVSSGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLS CRASQSVSSYLAWYQQKPGQAPRLLIYDASN RATG IPARFSGSGSGTDFTLTIS SLEPEDFAVYYCQORFDYPITFGGGTKVEIKLEPKSCDKTHTC PPC PFWVLVVGGVLACYSLLVTVAFIIFWVTKKY S SSVHDPNGEYMFRAVNTAKKSRLTDVTLRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
237	EIVLTQSPATLSLSPGERATLS CRASQSVSSYLAWYQQKPGQAPRLLIYDASN RATGIPARFSGS SGTDFTLTIS SLEPEDFAVYYCQORFDYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIYWND DKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWGQGTMTVTVSSTTPAPRPPTPAPT ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKLLYIF KQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYD VL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR
238	EIVLTQSPATLSLSPGERATLS CRASQSVSSYLAWYQQKPGQAPRLLIYDASN RATGIPARFSGS SGTDFTLTIS SLEPEDFAVYYCQORFDYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIYWND DKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWGQGTMTVTVSSTTPAPRPPTPAPT ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKLLYIF YMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYD VL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR

239	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISLLEPEDFAVYYCQORFDYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWND DKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWGQGTMTVTSSTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHD PNGEYMFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGNQLYNELNLGRREYDVLDKRRGR DPEMGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
240	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISLLEPEDFAVYYCQORFDYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWND DKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWGQGTMTVTSSTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGVLACYSLLVTVAFIIFWVKRGRKKLL YIFKQPFMRPVQTTQEDGCSRFP EEEEGGCCELRVKFSRSADAPAYQQGNQLYNELNLGRREE YDVLDKRRGRDPEMGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA TKDTYDALHMQALPPR
241	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISLLEPEDFAVYYCQORFDYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWND DKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWGQGTMTVTSSTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGVLACYSLLVTVAFIIFWVRSKRSRLL HSDYMMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGNQLYNELNLGRREEY DVLDKRRGRDPEMGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT KDTYDALHMQALPPR
242	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISLLEPEDFAVYYCQORFDYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWND DKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWGQGTMTVTSSTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGVLACYSLLVTVAFIIFWVTKKYSSS VHDPNGEYMFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGNQLYNELNLGRREYDVLDKR RGRDPEMGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
243	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISLLEPEDFAVYYCQORFDYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWND DKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWGQGTMTVTSSEIVMYPPPYLDNEKS NGTIIHVKGKHLCPSP LFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMR PVQTTQEDGCSRFP EEEEGGCCELRVKFSRSADAPAYQQGNQLYNELNLGRREYDVLDKRRG RDPPEMGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH MQALPPR
244	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISLLEPEDFAVYYCQORFDYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWND DKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWGQGTMTVTSSEIVMYPPPYLDNEKS NGTIIHVKGKHLCPSP LFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMMTP RRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGNQLYNELNLGRREYDVLDKRRGR DPEMGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
245	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISLLEPEDFAVYYCQORFDYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWND DKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWGQGTMTVTSSEIVMYPPPYLDNEKS NGTIIHVKGKHLCPSP LFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYM FRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGNQLYNELNLGRREYDVLDKRRGRDPEMG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
246	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISLLEPEDFAVYYCQORFDYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWND DKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWGQGTMTVTSSEIVMYPPPYLDNEKS

	NGTIIHVKGKHLCPSPFLFPGPSKPFVWLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEDGDCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDRGRDRPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
247	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISLLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGITLKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWNDKRYSPSLKSLRTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWGQGTMTVTVSSIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPFVWLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDRGRDRPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
248	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISLLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGITLKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWNDKRYSPSLKSLRTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWGQGTMTVTVSSIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPFVWLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDRGRDRPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
249	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISLLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGITLKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWNDKRYSPSLKSLRTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWGQGTMTVTVSSIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPFVWLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDRGRDRPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
250	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISLLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGITLKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWNDKRYSPSLKSLRTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWGQGTMTVTVSSIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPFVWLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDRGRDRPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
251	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISLLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGITLKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWNDKRYSPSLKSLRTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWGQGTMTVTVSSIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPFVWLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDRGRDRPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
252	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISLLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGITLKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWNDKRYSPSLKSLRTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWGQGTMTVTVSSIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPFVWLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDRGRDRPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
253	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISLLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGITLKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWNDKRYSPSLKSLRTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWGQGTMTVTVSSIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPFVWLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDRGRDRPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
254	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISLLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGITLKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWNDKRYSPSLKSLRTITKDTSKNQVVLMTNMDPVD TAVYYCARDEYGGFDIWGQGTMTVTVSSIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPFVWLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDRGRDRPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

	LVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSR SADAPAYQQGQNLYNELNLRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAY SEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
255	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSELEDFAVYYCQQRFDYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWNDKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVDTAIVYCARDEYGGFDIWGQGTMTVTVSSLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQNLYNELNLRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
256	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSELEDFAVYYCQQRFDYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWNDKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVDTAIVYCARDEYGGFDIWGQGTMTVTVSSLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC SRVKFSRSADAPAYQQGQNLYNELNLRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
257	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSELEDFAVYYCQQRFDYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWNDKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVDTAIVYCARDEYGGFDIWGQGTMTVTVSSLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFS RSADAPAYQQGQNLYNELNLRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEA YSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
258	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSELEDFAVYYCQQRFDYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWNDKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVDTAIVYCARDEYGGFDIWGQGTMTVTVSSLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEE GGCLRVKFSRSADAPAYQQGQNLYNELNLRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
259	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSELEDFAVYYCQQRFDYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWNDKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVDTAIVYCARDEYGGFDIWGQGTMTVTVSSLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRGPTRKHYPYAPPRDFA AYRSRVKFSRSADAPAYQQGQNLYNELNLRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
260	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSELEDFAVYYCQQRFDYPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWNDKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVDTAIVYCARDEYGGFDIWGQGTMTVTVSSLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRV KFSRSADAPAYQQGQNLYNELNLRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR

In preferred embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in SEQ ID NO: 39; a spacer domain comprising an amino acid sequence set forth in SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 148, or SEQ ID NO: 150; a transmembrane domain comprising an amino acid sequence set forth in SEQ ID NO: 151 or SEQ ID NO: 153; a costimulatory domain comprising an amino acid sequence set forth in SEQ ID NO: 159, SEQ ID NO: 160, or SEQ ID NO: 162; and a primary signaling domain comprising an amino acid sequence set forth in SEQ ID NO: 158. In preferred embodiments, a CAR comprises an amino acid sequence set

forth in any one of SEQ ID NOs: 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, and 284.

SEQ ID NO.	AMINO ACID SEQUENCE
261	QVQLVESGGGVVQPGRSLRLSCAASGFTTFSSYGMHVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTITVTVSSGGGGSGGGSGGGSGGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGG TKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
262	QVQLVESGGGVVQPGRSLRLSCAASGFTTFSSYGMHVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTITVTVSSGGGGSGGGSGGGSGGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGG TKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
263	QVQLVESGGGVVQPGRSLRLSCAASGFTTFSSYGMHVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTITVTVSSGGGGSGGGSGGGSGGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGG TKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
264	QVQLVESGGGVVQPGRSLRLSCAASGFTTFSSYGMHVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTITVTVSSGGGGSGGGSGGGSGGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGG TKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLVACYSLLVTVAFIIFWVRSKRSLLSHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
265	QVQLVESGGGVVQPGRSLRLSCAASGFTTFSSYGMHVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTITVTVSSGGGGSGGGSGGGSGGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGG TKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLVACYSLLVTVAFIIFWVRSKRSLLSHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
266	QVQLVESGGGVVQPGRSLRLSCAASGFTTFSSYGMHVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTITVTVSSGGGGSGGGSGGGSGGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGG TKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLVACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
267	QVQLVESGGGVVQPGRSLRLSCAASGFTTFSSYGMHVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTITVTVSSGGGGSGGGSGGGSGGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGG TKVEIKIEVMYPPPYLDNEKSGTIIHVKGKHLCPSPLEFGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKLLYIFKQPFMRPV

	QTTQEEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRD PEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQ ALPPR
268	QVQLVESGGGVVQPGRSRLRLSCAASGFTTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGT'TVTVSSGGGGSGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI PARFSGSGSGTDFTLTITSSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKIEVMYPPPYLDNEKSNG TIIHVKGKHLCPSPLEFPGPSKPIYIWAFLAGTCGVLLLSLVITLYCRSKRSRLHSDYMNMTPRR PGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQA LPPR
269	QVQLVESGGGVVQPGRSRLRLSCAASGFTTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGT'TVTVSSGGGGSGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI PARFSGSGSGTDFTLTITSSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKIEVMYPPPYLDNEKSNG TIIHVKGKHLCPSPLEFPGPSKPIYIWAFLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMF RAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDP PEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
270	QVQLVESGGGVVQPGRSRLRLSCAASGFTTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGT'TVTVSSGGGGSGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI PARFSGSGSGTDFTLTITSSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKIEVMYPPPYLDNEKSNG TIIHVKGKHLCPSPLEFPGPSKPIYIWAFLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMF RAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDP PEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH MQALPPR
271	QVQLVESGGGVVQPGRSRLRLSCAASGFTTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGT'TVTVSSGGGGSGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI PARFSGSGSGTDFTLTITSSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKIEVMYPPPYLDNEKSNG TIIHVKGKHLCPSPLEFPGPSKPIYIWAFLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMF RAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDP PEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH MQALPPR
272	QVQLVESGGGVVQPGRSRLRLSCAASGFTTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGT'TVTVSSGGGGSGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI PARFSGSGSGTDFTLTITSSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKIEVMYPPPYLDNEKSNG TIIHVKGKHLCPSPLEFPGPSKPIYIWAFLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMF RAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDP PEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPP R
273	QVQLVESGGGVVQPGRSRLRLSCAASGFTTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGT'TVTVSSGGGGSGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI PARFSGSGSGTDFTLTITSSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKESKYGPCCPPCIYIWA FLAGTCGVLLLSLVITLYCRKGRKKLLYIFKQPFMRPVQTTQEEEDGCSCRFPEEEEGGCELRVKFS RSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDP PEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
274	QVQLVESGGGVVQPGRSRLRLSCAASGFTTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGT'TVTVSSGGGGSGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI PARFSGSGSGTDFTLTITSSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKESKYGPCCPPCIYIWA FLAGTCGVLLLSLVITLYCRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFS RSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDP PEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
275	QVQLVESGGGVVQPGRSRLRLSCAASGFTTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGT'TVTVSSGGGGSGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI

	PARFSGSGSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGGKVEIKESKYGPPCPPCPIYIWA PLAGTCGVLLLSLVIITLYCTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAP AYQQGQONQLYNELNLGRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGM KGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
276	QVQLVESGGGVVQPGRLSLRLSCAASGFTTFSSYGMHVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDMVWGQGTITVTVSSGGGGSGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASN RATGI PARFSGSGSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGGKVEIKESKYGPPCPPCFWVLV VVGGLVACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL VKFSRSADAPAYQQGQONQLYNELNLGRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
277	QVQLVESGGGVVQPGRLSLRLSCAASGFTTFSSYGMHVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDMVWGQGTITVTVSSGGGGSGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASN RATGI PARFSGSGSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGGKVEIKESKYGPPCPPCFWVLV VVGGLVACYSLLVTVAFIIFWVRSKRSLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRV KFSRSADAPAYQQGQONQLYNELNLGRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
278	QVQLVESGGGVVQPGRLSLRLSCAASGFTTFSSYGMHVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDMVWGQGTITVTVSSGGGGSGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASN RATGI PARFSGSGSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGGKVEIKESKYGPPCPPCFWVLV VVGGLVACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRS ADAPAYQQGQONQLYNELNLGRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQKDKMAEAYSE IGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
279	QVQLVESGGGVVQPGRLSLRLSCAASGFTTFSSYGMHVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDMVWGQGTITVTVSSGGGGSGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASN RATGI PARFSGSGSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGGKVEIKLEPKSCDKTHTCPPCP IYIWAPLAGTCGVLLLSLVIITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQONQLYNELNLGRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQKDK KMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
280	QVQLVESGGGVVQPGRLSLRLSCAASGFTTFSSYGMHVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDMVWGQGTITVTVSSGGGGSGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASN RATGI PARFSGSGSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGGKVEIKLEPKSCDKTHTCPPCP IYIWAPLAGTCGVLLLSLVIITLYCRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSR VKFSRSADAPAYQQGQONQLYNELNLGRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
281	QVQLVESGGGVVQPGRLSLRLSCAASGFTTFSSYGMHVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDMVWGQGTITVTVSSGGGGSGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASN RATGI PARFSGSGSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGGKVEIKLEPKSCDKTHTCPPCP IYIWAPLAGTCGVLLLSLVIITLYCTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRS ADAPAYQQGQONQLYNELNLGRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQKDKMAEAYS EIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
282	QVQLVESGGGVVQPGRLSLRLSCAASGFTTFSSYGMHVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDMVWGQGTITVTVSSGGGGSGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASN RATGI PARFSGSGSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGGKVEIKLEPKSCDKTHTCPPCP FWLVVVGGLVACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGG CEL RVKFSRSADAPAYQQGQONQLYNELNLGRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
283	QVQLVESGGGVVQPGRLSLRLSCAASGFTTFSSYGMHVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDMVWGQGTITVTVSSGGGGSGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASN RATGI PARFSGSGSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGGKVEIKLEPKSCDKTHTCPPCP FWLVVVGGLVACYSLLVTVAFIIFWVRSKRSLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAY RSRVKFSRSADAPAYQQGQONQLYNELNLGRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQ

	KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
284	QVQLVESGGGVVQPGRLRLSCAASGFTTFSSYGMHVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTITVTVSSGGGGSGGGSGGGSGGGSGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTIS SLEPEDFAVYYCQQRVDLWTFGGG TKVEIKLEPKSCDKTHTCPPCPFVWLVVVGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

In particular embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in SEQ ID NO: 40; a spacer domain comprising an amino acid sequence set forth in SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 148, or SEQ ID NO: 150; a transmembrane domain comprising an amino acid sequence set forth in SEQ ID NO: 151 or SEQ ID NO: 153; a costimulatory domain comprising an amino acid sequence set forth in SEQ ID NO: 159, SEQ ID NO: 160, or SEQ ID NO: 162; and a primary signaling domain comprising an amino acid sequence set forth in SEQ ID NO: 158. In particular embodiments, a CAR comprises an amino acid sequence set forth in any one of SEQ ID NOs: 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, and 308.

SEQ ID NO.	AMINO ACID SEQUENCE
285	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTIS SLEPEDFAVYYCQQRVDLWTFGGG TKVEIKGGGSGGGSGGGSGGGSGGGSGVQLVESGGGVVQPGRLRLSCAASGFTTFSSYGMHVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTITVTVSSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
286	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTIS SLEPEDFAVYYCQQRVDLWTFGGG TKVEIKGGGSGGGSGGGSGGGSGGGSGVQLVESGGGVVQPGRLRLSCAASGFTTFSSYGMHVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTITVTVSSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLSLVITLYCRSKRSRLHSDYMNMTPRRP GPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
287	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTIS SLEPEDFAVYYCQQRVDLWTFGGG TKVEIKGGGSGGGSGGGSGGGSGGGSGVQLVESGGGVVQPGRLRLSCAASGFTTFSSYGMHVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTITVTVSSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
288	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTIS SLEPEDFAVYYCQQRVDLWTFGGG TKVEIKGGGSGGGSGGGSGGGSGGGSGVQLVESGGGVVQPGRLRLSCAASGFTTFSSYGMHVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTITVTVSSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFVWLVVVGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYD

	VLDKRRGRDPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
289	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGVQLVESGGGVVQPGRSRLRLSCAASGFTTFSSYGMHWRQAPGKGLEWVAVISYEGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDMVWGQGT'TVTVSSSTTPAPRPPPTAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGVLACYSLLVTVAFIIFWVRSKRSRLLSHDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
290	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGVQLVESGGGVVQPGRSRLRLSCAASGFTTFSSYGMHWRQAPGKGLEWVAVISYEGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDMVWGQGT'TVTVSSSTTPAPRPPPTAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGVLACYSLLVTVAFIIFWVTKKYSSSVHDPNGEYMFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
291	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGVQLVESGGGVVQPGRSRLRLSCAASGFTTFSSYGMHWRQAPGKGLEWVAVISYEGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDMVWGQGT'TVTVSSIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLEPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTEEDGCSCRFP EEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
292	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGVQLVESGGGVVQPGRSRLRLSCAASGFTTFSSYGMHWRQAPGKGLEWVAVISYEGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDMVWGQGT'TVTVSSIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLEPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTEEDGCSCRFP EEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
293	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGVQLVESGGGVVQPGRSRLRLSCAASGFTTFSSYGMHWRQAPGKGLEWVAVISYEGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDMVWGQGT'TVTVSSIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLEPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
294	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGVQLVESGGGVVQPGRSRLRLSCAASGFTTFSSYGMHWRQAPGKGLEWVAVISYEGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDMVWGQGT'TVTVSSIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLEPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
295	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGVQLVESGGGVVQPGRSRLRLSCAASGFTTFSSYGMHWRQAPGKGLEWVAVISYEGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARELGDMVWGQGT'TVTVSSIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLEPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
296	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGVQL

	VESGGGVQPGRSRLRLSCAASGFTTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDN SKNTLYLQMN SLRAEDTAVYYCARELGDGMDVWGQGT'TVTVSSIEVMYPPPYLDNEKSNG TIIHVKGKHLCPSPLEFPGPSKPFVVLVVVGGVLACYLLVTVAFIIFWVTKKKYSSSVHDPNGEY MFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDP EMGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPP R
297	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGSGGGSGGGSGGGSGVQVQ VESGGGVQPGRSRLRLSCAASGFTTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDN SKNTLYLQMN SLRAEDTAVYYCARELGDGMDVWGQGT'TVTVSSSESKYGPPCPPCPYIYWA PLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEDGDCSCRFPEEEGGCELRVKE RSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQDKMAE AYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
298	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGSGGGSGGGSGGGSGVQVQ VESGGGVQPGRSRLRLSCAASGFTTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDN SKNTLYLQMN SLRAEDTAVYYCARELGDGMDVWGQGT'TVTVSSSESKYGPPCPPCPYIYWA PLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEDGDCSCRFPEEEGGCELRVKE RSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQDKMAEA YSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
299	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGSGGGSGGGSGGGSGVQVQ VESGGGVQPGRSRLRLSCAASGFTTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDN SKNTLYLQMN SLRAEDTAVYYCARELGDGMDVWGQGT'TVTVSSSESKYGPPCPPCPYIYWA PLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMAVNTAKKSRLTDVTLRVKFSRSADAP AYQQGQNLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQDKMAEAYSEIGM KGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
300	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGSGGGSGGGSGGGSGVQVQ VESGGGVQPGRSRLRLSCAASGFTTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDN SKNTLYLQMN SLRAEDTAVYYCARELGDGMDVWGQGT'TVTVSSSESKYGPPCPPCPFWVLV VVGVLACYLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEDGDCSCRFPEEEGGCELR VKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQDK MAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
301	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGSGGGSGGGSGGGSGVQVQ VESGGGVQPGRSRLRLSCAASGFTTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDN SKNTLYLQMN SLRAEDTAVYYCARELGDGMDVWGQGT'TVTVSSSESKYGPPCPPCPFWVLV VVGVLACYLLVTVAFIIFWVRSKRSLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRV KFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQDKM AEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
302	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGSGGGSGGGSGGGSGVQVQ VESGGGVQPGRSRLRLSCAASGFTTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDN SKNTLYLQMN SLRAEDTAVYYCARELGDGMDVWGQGT'TVTVSSSESKYGPPCPPCPFWVLV VVGVLACYLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMAVNTAKKSRLTDVTLRVKFSRSA DAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQDKMAEAYSE IGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
303	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGSGGGSGGGSGGGSGVQVQ VESGGGVQPGRSRLRLSCAASGFTTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDN SKNTLYLQMN SLRAEDTAVYYCARELGDGMDVWGQGT'TVTVSSLEPKSCDKTHTCPPCP IYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEDGDCSCRFPEEEGGCELR RVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQDK KMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
304	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSELEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGSGGGSGGGSGGGSGVQVQ VESGGGVQPGRSRLRLSCAASGFTTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDN SKNTLYLQMN SLRAEDTAVYYCARELGDGMDVWGQGT'TVTVSSLEPKSCDKTHTCPPCP I

	YIWAPLAGTCGVLLLSLVITILYCRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSR VKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
305	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSELEPDFAVYYCQQRVDLWTFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGVQL VESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDNKNTLYLQMNSLRAEDTAVYYCARELGDMVWGQGTITVTVSSLEPKSCDKTHTCPPCP YIWAPLAGTCGVLLLSLVITILYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRS ADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYS EIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
306	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSELEPDFAVYYCQQRVDLWTFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGVQL VESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDNKNTLYLQMNSLRAEDTAVYYCARELGDMVWGQGTITVTVSSLEPKSCDKTHTCPPCPF WVLVVVGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEDGCSCRFPEEEEEGG CELRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
307	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSELEPDFAVYYCQQRVDLWTFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGVQL VESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDNKNTLYLQMNSLRAEDTAVYYCARELGDMVWGQGTITVTVSSLEPKSCDKTHTCPPCPF WVLVVVGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAY RSRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
308	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSELEPDFAVYYCQQRVDLWTFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGVQL VESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDNKNTLYLQMNSLRAEDTAVYYCARELGDMVWGQGTITVTVSSLEPKSCDKTHTCPPCPF WVLVVVGVLACYSLLVTVAFIIFWVTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKF SRADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAE AYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR

In particular embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in SEQ ID NO: 49 or SEQ ID NO: 50; a spacer domain comprising an amino acid sequence set forth in SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 148, or SEQ ID NO: 150; a transmembrane domain
5 comprising an amino acid sequence set forth in SEQ ID NO: 151 or SEQ ID NO: 153; a costimulatory domain comprising an amino acid sequence set forth in SEQ ID NO: 159, SEQ ID NO: 160, or SEQ ID NO: 162; and a primary signaling domain comprising an amino acid sequence set forth in SEQ ID NO: 158. In particular embodiments, a CAR comprises an amino acid sequence set forth in any one of SEQ ID NOs: 309, 310, 311, 312, 313, 314, 315,
10 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, and 332. In particular embodiments, a CAR comprises an amino acid sequence set forth in any one of SEQ ID NOs: 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, and 356.

SEQ ID NO.	AMINO ACID SEQUENCE
309	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQNGYVDVWGQGTITVTVSSGGGGSGGGGSGG

	GGSGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTIISSLOPDDFATYYCQOVSSLPPTFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKLLYIF KQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQOGQONQLYNELNLGRREEYDV LDKRRGRDPGEMGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKD TYDALHMQALPPR
310	EVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSIISSSGSTIYYADSVK GRFTISRDNNAKNSLYLQMNLSRAEDTAVYYCARDQNGYGVVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTIISSLOPDDFATYYCQOVSSLPPTFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLHSD YMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQOGQONQLYNELNLGRREEYDVL DKRRGRDPGEMGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDT YDALHMQALPPR
311	EVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSIISSSGSTIYYADSVK GRFTISRDNNAKNSLYLQMNLSRAEDTAVYYCARDQNGYGVVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTIISSLOPDDFATYYCQOVSSLPPTFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKYSVHD PNGEYMFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQOGQONQLYNELNLGRREEYDVLDKRRGR DPGEMGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHM QALPPR
312	EVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSIISSSGSTIYYADSVK GRFTISRDNNAKNSLYLQMNLSRAEDTAVYYCARDQNGYGVVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTIISSLOPDDFATYYCQOVSSLPPTFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGVLACYSLLVTVAFIIFWVKRGRKLL YIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQOGQONQLYNELNLGRREE YDVLDKRRGRDPGEMGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTA TKDTYDALHMQALPPR
313	EVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSIISSSGSTIYYADSVK GRFTISRDNNAKNSLYLQMNLSRAEDTAVYYCARDQNGYGVVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTIISSLOPDDFATYYCQOVSSLPPTFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGVLACYSLLVTVAFIIFWVRSKRSRL HSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQOGQONQLYNELNLGRREEY DVLDKRRGRDPGEMGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTAT KDTYDALHMQALPPR
314	EVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSIISSSGSTIYYADSVK GRFTISRDNNAKNSLYLQMNLSRAEDTAVYYCARDQNGYGVVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTIISSLOPDDFATYYCQOVSSLPPTFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGVLACYSLLVTVAFIIFWVTKKKYSSS VHDPNGEYMFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQOGQONQLYNELNLGRREEYDVLDKR RGRDPGEMGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDA LHMQALPPR
315	EVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSIISSSGSTIYYADSVK GRFTISRDNNAKNSLYLQMNLSRAEDTAVYYCARDQNGYGVVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTIISSLOPDDFATYYCQOVSSLPPTFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKLLYIFKQPFMR PVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQOGQONQLYNELNLGRREEYDVLDKRRG RDPGEMGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALH MQALPPR
316	EVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSIISSSGSTIYYADSVK GRFTISRDNNAKNSLYLQMNLSRAEDTAVYYCARDQNGYGVVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTIISSLOPDDFATYYCQOVSSLPPTFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLHSDYMNMT P

	RRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
317	EVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYYSSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQNGYGVVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISLQPDFFATYYCQQVSSLPPTFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYM FMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
318	EVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYYSSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQNGYGVVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISLQPDFFATYYCQQVSSLPPTFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYM FMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
319	EVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYYSSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQNGYGVVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISLQPDFFATYYCQQVSSLPPTFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYM FMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
320	EVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYYSSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQNGYGVVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISLQPDFFATYYCQQVSSLPPTFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYM FMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
321	EVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYYSSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQNGYGVVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISLQPDFFATYYCQQVSSLPPTFGGGTKVEIKESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSAD APAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
322	EVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYYSSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQNGYGVVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISLQPDFFATYYCQQVSSLPPTFGGGTKVEIKESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSAD APAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
323	EVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYYSSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQNGYGVVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISLQPDFFATYYCQQVSSLPPTFGGGTKVEIKESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSAD APAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
324	EVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYYSSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQNGYGVVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISLQPDFFATYYCQQVSSLPPTFGGGTKVEIKESKYGPPCPPCFWV

	LVVVGGVLACYSLLVTVAFIIFWVKRGRKLLYIFKQPFMRPVQTTQEEDGCSCRFPPEEEEGGCE LRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
325	EVQLVESGGGLVKKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYYSSSGSTIYYADSVK GRFTISRDNKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISLQPDFFATYYCQQVSSLPPTFGGGTKVEIKESKYGPPCPPCFWV LVVVGGVLACYSLLVTVAFIIFWVRSKRSLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRS RVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQK KMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
326	EVQLVESGGGLVKKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYYSSSGSTIYYADSVK GRFTISRDNKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISLQPDFFATYYCQQVSSLPPTFGGGTKVEIKESKYGPPCPPCFWV LVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSR SADAPAYQQGQNLYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAY SEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
327	EVQLVESGGGLVKKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYYSSSGSTIYYADSVK GRFTISRDNKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISLQPDFFATYYCQQVSSLPPTFGGGTKVEIKLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCKRGRKLLYIFKQPFMRPVQTTQEEDGCSCRFPPEEEEGGC ELRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
328	EVQLVESGGGLVKKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYYSSSGSTIYYADSVK GRFTISRDNKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISLQPDFFATYYCQQVSSLPPTFGGGTKVEIKLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCKRGRKLLYIFKQPFMRPVQTTQEEDGCSCRFPPEEEEGGC SRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
329	EVQLVESGGGLVKKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYYSSSGSTIYYADSVK GRFTISRDNKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISLQPDFFATYYCQQVSSLPPTFGGGTKVEIKLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCKRGRKLLYIFKQPFMRPVQTTQEEDGCSCRFPPEEEEGGC RSADAPAYQQGQNLYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEA YSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
330	EVQLVESGGGLVKKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYYSSSGSTIYYADSVK GRFTISRDNKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISLQPDFFATYYCQQVSSLPPTFGGGTKVEIKLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKLLYIFKQPFMRPVQTTQEEDGCSCRFPPEEE GGCELRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
331	EVQLVESGGGLVKKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYYSSSGSTIYYADSVK GRFTISRDNKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISLQPDFFATYYCQQVSSLPPTFGGGTKVEIKLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSLHSDYMNMTPRRPGPTRKHYPYAPPRDFA AYRSRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
332	EVQLVESGGGLVKKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYYSSSGSTIYYADSVK GRFTISRDNKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISLQPDFFATYYCQQVSSLPPTFGGGTKVEIKLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRV KFSRSADAPAYQQGQNLYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

333	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESQVPSRFSGS GSGTEFTLTISSLQPDFFATYYCQOVSSLPPTFGGGTKVEIKGGGSGGGSGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIF KQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREYDVL LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKD TYDALHMQALPPR
334	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESQVPSRFSGS GSGTEFTLTISSLQPDFFATYYCQOVSSLPPTFGGGTKVEIKGGGSGGGSGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLHSD YMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDT YDALHMQALPPR
335	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESQVPSRFSGS GSGTEFTLTISSLQPDFFATYYCQOVSSLPPTFGGGTKVEIKGGGSGGGSGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHD PNGEYMFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDALHM QALPPR
336	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESQVPSRFSGS GSGTEFTLTISSLQPDFFATYYCQOVSSLPPTFGGGTKVEIKGGGSGGGSGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGVLACYSLLVTVAFIIFWVKRGRKKLL YIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTA TKDTYDALHMQALPPR
337	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESQVPSRFSGS GSGTEFTLTISSLQPDFFATYYCQOVSSLPPTFGGGTKVEIKGGGSGGGSGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGVLACYSLLVTVAFIIFWVRSKRSRL HSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTAT KDTYDALHMQALPPR
338	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESQVPSRFSGS GSGTEFTLTISSLQPDFFATYYCQOVSSLPPTFGGGTKVEIKGGGSGGGSGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGVLACYSLLVTVAFIIFWVTKKKYSSS VHDPNGEYMFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDA LHMQALPPR
339	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESQVPSRFSGS GSGTEFTLTISSLQPDFFATYYCQOVSSLPPTFGGGTKVEIKGGGSGGGSGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMR PVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREYDVLDKRRG RDPPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDALH MQALPPR
340	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESQVPSRFSGS GSGTEFTLTISSLQPDFFATYYCQOVSSLPPTFGGGTKVEIKGGGSGGGSGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF

	TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLHSDYMNMTF RRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRRGKHDGLYQGLSTATKDTYDALHMQALPPR
341	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESQVPSRFSGS GSGTEFTLTISSLQDDFATYYCQOVSSLPPTFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYM FMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRRGKHDGLYQGLSTATKDTYDALHMQALPPR
342	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESQVPSRFSGS GSGTEFTLTISSLQDDFATYYCQOVSSLPPTFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYM FMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRRGKHDGLYQGLSTATKDTYDALHMQALPPR
343	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESQVPSRFSGS GSGTEFTLTISSLQDDFATYYCQOVSSLPPTFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYM FMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRRGKHDGLYQGLSTATKDTYDALHMQALPPR
344	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESQVPSRFSGS GSGTEFTLTISSLQDDFATYYCQOVSSLPPTFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYM FMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRRGKHDGLYQGLSTATKDTYDALHMQALPPR
345	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESQVPSRFSGS GSGTEFTLTISSLQDDFATYYCQOVSSLPPTFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYM FMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRRGKHDGLYQGLSTATKDTYDALHMQALPPR
346	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESQVPSRFSGS GSGTEFTLTISSLQDDFATYYCQOVSSLPPTFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYM FMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRRGKHDGLYQGLSTATKDTYDALHMQALPPR
347	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESQVPSRFSGS GSGTEFTLTISSLQDDFATYYCQOVSSLPPTFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYM FMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRRGKHDGLYQGLSTATKDTYDALHMQALPPR
348	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESQVPSRFSGS GSGTEFTLTISSLQDDFATYYCQOVSSLPPTFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ

	LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSSESKYGPCCPPCFWV LVVVGGLVACYSLLVTVAFIIFWVKRGRKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCE LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
349	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESQVPSRFSGS GSGTEFTLTISSLQPDFFATYYCQOVSSLPPTFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSSESKYGPCCPPCFWV LVVVGGLVACYSLLVTVAFIIFWVRSKRSLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRS RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
350	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESQVPSRFSGS GSGTEFTLTISSLQPDFFATYYCQOVSSLPPTFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSSESKYGPCCPPCFWV LVVVGGLVACYSLLVTVAFIIFWVTKKYSVSDHPNGEYMFRAVNTAKKSRLTDVTLRVKFSR SADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAY SEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
351	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESQVPSRFSGS GSGTEFTLTISSLQPDFFATYYCQOVSSLPPTFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPCP PIYIWAPLAGTCGVLLSLVITLYCKRGRKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
352	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESQVPSRFSGS GSGTEFTLTISSLQPDFFATYYCQOVSSLPPTFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPCP PIYIWAPLAGTCGVLLSLVITLYCKRGRKLLYIFKQPFMRPVQTTQEEDGCSCRFPFAAYR SRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
353	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESQVPSRFSGS GSGTEFTLTISSLQPDFFATYYCQOVSSLPPTFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPCP PIYIWAPLAGTCGVLLSLVITLYCKKYSVSDHPNGEYMFRAVNTAKKSRLTDVTLRVKFS RSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEA YSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
354	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESQVPSRFSGS GSGTEFTLTISSLQPDFFATYYCQOVSSLPPTFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPCP PFWVLVVVGGLVACYSLLVTVAFIIFWVKRGRKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEE GGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
355	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESQVPSRFSGS GSGTEFTLTISSLQPDFFATYYCQOVSSLPPTFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPCP PFWVLVVVGGLVACYSLLVTVAFIIFWVRSKRSLHSDYMNMTPRRPGPTRKHYPYAPPRDFA AYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
356	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESQVPSRFSGS GSGTEFTLTISSLQPDFFATYYCQOVSSLPPTFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPCP PFWVLVVVGGLVACYSLLVTVAFIIFWVTKKYSVSDHPNGEYMFRAVNTAKKSRLTDVTLRV

	KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
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In preferred embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in SEQ ID NO: 59; a spacer domain comprising an amino acid sequence set forth in SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 148, or SEQ ID NO: 150; a transmembrane domain comprising an amino acid sequence set forth in SEQ ID NO: 151 or SEQ ID NO: 153; a costimulatory domain comprising an amino acid sequence set forth in SEQ ID NO: 159, SEQ ID NO: 160, or SEQ ID NO: 162; and a primary signaling domain comprising an amino acid sequence set forth in SEQ ID NO: 158. In preferred embodiments, a CAR comprises an amino acid sequence set forth in any one of SEQ ID NOS: 357, 358, 359, 360, 361, 362,363, 364, 365, 366, 367, 368, 369, 370 371, 372, 373, 374, 375, 376, 377, 378, 379, and 380.

SEQ ID NO.	AMINO ACID SEQUENCE
357	QVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGSGGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGSGSGTEFTLTITSSLPDDFATYYCQQSDSHPITFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
358	QVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGSGGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGSGSGTEFTLTITSSLPDDFATYYCQQSDSHPITFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLHSDYMNMTPRRPPTTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
359	QVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGSGGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGSGSGTEFTLTITSSLPDDFATYYCQQSDSHPITFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
360	QVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGSGGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGSGSGTEFTLTITSSLPDDFATYYCQQSDSHPITFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFVWLTVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
361	QVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGSGGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGSGSGTEFTLTITSSLPDDFATYYCQQSDSHPITFGGGTKVEIKTTTPAPRPPTPAPTI

	ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSLRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
362	QVQLVESGGGLVKKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGSGGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGSGSGTEFTLTISLQPDFFATYYCQQSDSHPITFGGGTKVEIKITTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
363	QVQLVESGGGLVKKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGSGGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGSGSGTEFTLTISLQPDFFATYYCQQSDSHPITFGGGTKVEIKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
364	QVQLVESGGGLVKKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGSGGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGSGSGTEFTLTISLQPDFFATYYCQQSDSHPITFGGGTKVEIKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRKRSLRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
365	QVQLVESGGGLVKKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGSGGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGSGSGTEFTLTISLQPDFFATYYCQQSDSHPITFGGGTKVEIKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
366	QVQLVESGGGLVKKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGSGGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGSGSGTEFTLTISLQPDFFATYYCQQSDSHPITFGGGTKVEIKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
367	QVQLVESGGGLVKKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGSGGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGSGSGTEFTLTISLQPDFFATYYCQQSDSHPITFGGGTKVEIKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
368	QVQLVESGGGLVKKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGSGGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGSGSGTEFTLTISLQPDFFATYYCQQSDSHPITFGGGTKVEIKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR

369	QVQLVESGGGLVQPKGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQOKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISLQPDFAFYCYCQSDSHPITFGGGTKVEIKESKYGPPCPPCPPIYI WAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEDGCSCRFPEEEEGGCELRV KFSRSADAPAYQQGQNLQYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
370	QVQLVESGGGLVQPKGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQOKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISLQPDFAFYCYCQSDSHPITFGGGTKVEIKESKYGPPCPPCPPIYI WAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEDGCSCRFPEEEEGGCELRV KFSRSADAPAYQQGQNLQYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
371	QVQLVESGGGLVQPKGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQOKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISLQPDFAFYCYCQSDSHPITFGGGTKVEIKESKYGPPCPPCPPIYI WAPLAGTCGVLLLSLVITLYCKKYSVSDHPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSAD APAYQQGQNLQYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI GMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
372	QVQLVESGGGLVQPKGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQOKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISLQPDFAFYCYCQSDSHPITFGGGTKVEIKESKYGPPCPPCPFWV LVVVGVLACYSLLVTVAFIIFWVGRGRKKLLYIFKQPFMRPVQTTQEDGCSCRFPEEEEGGCE LRVKFSRSADAPAYQQGQNLQYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
373	QVQLVESGGGLVQPKGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQOKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISLQPDFAFYCYCQSDSHPITFGGGTKVEIKESKYGPPCPPCPFWV LVVVGVLACYSLLVTVAFIIFWVRSKRSLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRS RVKFSRSADAPAYQQGQNLQYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
374	QVQLVESGGGLVQPKGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQOKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISLQPDFAFYCYCQSDSHPITFGGGTKVEIKESKYGPPCPPCPFWV LVVVGVLACYSLLVTVAFIIFWVTKKYSVSDHPNGEYMFMRVNTAKKSRLTDVTLRVKFSR SADAPAYQQGQNLQYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAY SEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
375	QVQLVESGGGLVQPKGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQOKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISLQPDFAFYCYCQSDSHPITFGGGTKVEIKLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQNLQYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
376	QVQLVESGGGLVQPKGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQOKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISLQPDFAFYCYCQSDSHPITFGGGTKVEIKLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQNLQYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
377	QVQLVESGGGLVQPKGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQOKPGKAPKLLIYEASSLESG

	VPSRFSGSGSGTEFTLTISLQPDFFATYYCQSDSHPITFGGGTKVEIKLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFS RSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEA YSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR
378	QVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNANKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISLQPDFFATYYCQSDSHPITFGGGTKVEIKLEPKSCDKTHTCPPC PFWVLVVGGLVACYSLLVTVAFIIFWVKRGRKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEE GGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR
379	QVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNANKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISLQPDFFATYYCQSDSHPITFGGGTKVEIKLEPKSCDKTHTCPPC PFWVLVVGGLVACYSLLVTVAFIIFWVRSKRSLHSDYMNMTPRRPGPTRKHYPYAPPRDFA AYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR
380	QVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNANKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISLQPDFFATYYCQSDSHPITFGGGTKVEIKLEPKSCDKTHTCPPC PFWVLVVGGLVACYSLLVTVAFIIFWVTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR

In particular embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in SEQ ID NO: 60; a spacer domain comprising an amino acid sequence set forth in SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 148, or SEQ ID NO: 150; a transmembrane domain comprising an amino acid sequence set forth in SEQ ID NO: 151 or SEQ ID NO: 153; a costimulatory domain comprising an amino acid sequence set forth in SEQ ID NO: 159, SEQ ID NO: 160, or SEQ ID NO: 162; and a primary signaling domain comprising an amino acid sequence set forth in SEQ ID NO: 158. In particular embodiments, a CAR comprises an amino acid sequence set forth in any one of SEQ ID NOs: 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, and 404.

SEQ ID NO.	AMINO ACID SEQUENCE
381	DIQMTQSPSTLSASVGRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISLQPDFFATYYCQSDSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNANKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKLLYIF KQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKD TYDALHMQALPPR
382	DIQMTQSPSTLSASVGRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISLQPDFFATYYCQSDSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNANKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKSRLLHSD

	YMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDT YDALHMQALPPR
383	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISLQPDFFATYYCQSDSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGQVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHD PNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDALHM QALPPR
384	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISLQPDFFATYYCQSDSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGQVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLVACYSLLVTVAFIIFWVRGRKRL YIFKQPFMRPVQTTQEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTA TKDTYDALHMQALPPR
385	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISLQPDFFATYYCQSDSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGQVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLVACYSLLVTVAFIIFWVRGRKRL HSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTAT KDTYDALHMQALPPR
386	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISLQPDFFATYYCQSDSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGQVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLVACYSLLVTVAFIIFWVTKKYSSSV VHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDA LHMQALPPR
387	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISLQPDFFATYYCQSDSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGQVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKLLYIFKQPFMR PVQTTQEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDALH MQALPPR
388	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISLQPDFFATYYCQSDSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGQVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKLLYIFKQPFMR RRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDALHM QALPPR
389	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISLQPDFFATYYCQSDSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGQVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYM FMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDALHMQALPPR
390	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS

	GSGTEFTLTISLQPDDEFATYYCQSDSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPFVWLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPF FMRPVQTTQEDGDCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYD ALHMQALPPR
391	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISLQPDDEFATYYCQSDSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPFVWLVVVGGVLACYSLLVTVAFIIFWVRSKRSLHSDYMN MTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDA LHMALPPR
392	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISLQPDDEFATYYCQSDSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPFVWLVVVGGVLACYSLLVTVAFIIFWVTKKYSVVHDPNG EYMFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDRGRDPE MGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDALHMQAL PPR
393	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISLQPDDEFATYYCQSDSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSSESKYPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEDGDCSCRFPEEEEGGCELRV KFSSADAPAYQQGQNLYNELNLGRREEYDVLDRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDALHMQALPPR
394	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISLQPDDEFATYYCQSDSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSSESKYPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCRSKRSRLHSDYMNMTTPRRPGPTRKHYQPYAPPRDFAAYRSRVK FRSADAPAYQQGQNLYNELNLGRREEYDVLDRGRDPEMGGKPRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDALHMQALPPR
395	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISLQPDDEFATYYCQSDSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSSESKYPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFRAVNTAKKSRLTDVTLRVKFSRSAD APAYQQGQNLYNELNLGRREEYDVLDRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI GMKGERRRRGKGDGLYQGLSTATKDTYDALHMQALPPR
396	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISLQPDDEFATYYCQSDSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSSESKYPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFRAVNTAKKSRLTDVTLRVKFSRSAD APAYQQGQNLYNELNLGRREEYDVLDRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI GMKGERRRRGKGDGLYQGLSTATKDTYDALHMQALPPR
397	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISLQPDDEFATYYCQSDSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSSESKYPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFRAVNTAKKSRLTDVTLRVKFSRSAD APAYQQGQNLYNELNLGRREEYDVLDRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI GMKGERRRRGKGDGLYQGLSTATKDTYDALHMQALPPR
398	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS

	GSGTEFTLTISLQPDFFATYYCQSDSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSSESKYGPPCPPCFWV LVVVGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSR SADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAY SEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
399	DIQMTQSPSTLSASVGRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISLQPDFFATYYCQSDSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEDGCSCRFPFEEEGGC ELRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
400	DIQMTQSPSTLSASVGRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISLQPDFFATYYCQSDSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYR SRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
401	DIQMTQSPSTLSASVGRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISLQPDFFATYYCQSDSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFS RSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEA YSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
402	DIQMTQSPSTLSASVGRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISLQPDFFATYYCQSDSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPPC PFWVLVVGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEDGCSCRFPFEEEE GGCELRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
403	DIQMTQSPSTLSASVGRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISLQPDFFATYYCQSDSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPPC PFWVLVVGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFA AYRSRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
404	DIQMTQSPSTLSASVGRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISLQPDFFATYYCQSDSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSGVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPPC PFWVLVVGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRV KFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

In particular embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in SEQ ID NO: 69; a spacer domain comprising an amino acid sequence set forth in SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 148, or SEQ ID NO: 150; a transmembrane domain comprising an amino acid sequence set forth in SEQ ID NO: 151 or SEQ ID NO: 153; a costimulatory domain comprising an amino acid sequence set forth in SEQ ID NO: 159, SEQ ID NO: 160, or SEQ

ID NO: 162; and a primary signaling domain comprising an amino acid sequence set forth in SEQ ID NO: 158. In particular embodiments, a CAR comprises an amino acid sequence set forth in any one of SEQ ID NOs: 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, and 428.

SEQ ID NO.	AMINO ACID SEQUENCE
405	EVQLVESGGGLVQPKGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVS YISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGGSGGGGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQOKPGKAPKLLIYEASSLESGVPSRFGSGSGSGTEFTLTISLQPDDEFATYYCQQANSHPITFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
406	EVQLVESGGGLVQPKGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVS YISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGGSGGGGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQOKPGKAPKLLIYEASSLESGVPSRFGSGSGSGTEFTLTISLQPDDEFATYYCQQANSHPITFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
407	EVQLVESGGGLVQPKGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVS YISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGGSGGGGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQOKPGKAPKLLIYEASSLESGVPSRFGSGSGSGTEFTLTISLQPDDEFATYYCQQANSHPITFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKYSVVDHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
408	EVQLVESGGGLVQPKGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVS YISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGGSGGGGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQOKPGKAPKLLIYEASSLESGVPSRFGSGSGSGTEFTLTISLQPDDEFATYYCQQANSHPITFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLVACYSLLVTVAFIIFWVRKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
409	EVQLVESGGGLVQPKGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVS YISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGGSGGGGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQOKPGKAPKLLIYEASSLESGVPSRFGSGSGSGTEFTLTISLQPDDEFATYYCQQANSHPITFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLVACYSLLVTVAFIIFWVRKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
410	EVQLVESGGGLVQPKGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVS YISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGGSGGGGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQOKPGKAPKLLIYEASSLESGVPSRFGSGSGSGTEFTLTISLQPDDEFATYYCQQANSHPITFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLVACYSLLVTVAFIIFWVTKKKYSSVDHPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
411	EVQLVESGGGLVQPKGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVS YISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGGSGGGGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQOKPGKAPKLLIYEASSLESGVPSRFGSGSGSGTEFTLTISLQPDDEFATYYCQQANSHPITFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLVACYSLLVTVAFIIFWVTKKKYSSVDHPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR

	GGSGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTIISSLOPDDFATYYCQOANSHPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKLLYIFKQPFMR PVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQOQONQLYNELNLGRREEYDVLDKRRG RDPFMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH MQALPPR
412	EVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSIISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTIISSLOPDDFATYYCQOANSHPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRSRRLHSDYMNMT RRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQOQONQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
413	EVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSIISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTIISSLOPDDFATYYCQOANSHPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYM FMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQOQONQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
414	EVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSIISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTIISSLOPDDFATYYCQOANSHPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPFVWLVVVGVLACYSLLVTVAFIIFWVKRGRKLLYIFKQ FMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQOQONQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
415	EVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSIISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTIISSLOPDDFATYYCQOANSHPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPFVWLVVVGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMN MTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQOQONQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
416	EVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSIISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTIISSLOPDDFATYYCQOANSHPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPFVWLVVVGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNG EYMFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQOQONQLYNELNLGRREEYDVLDKRRGRDPE MGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQAL PPR
417	EVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSIISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTIISSLOPDDFATYYCQOANSHPITFGGGTKVEIKESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCKRGRKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRV KFSRSADAPAYQOQONQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
418	EVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSIISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTIISSLOPDDFATYYCQOANSHPITFGGGTKVEIKESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCKRSRRLHSDYMNMTTPRRPGPTRKHYQPYAPPRDFAAYRSRVK FSRSADAPAYQOQONQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

419	EVQLVESGGGLVQPKGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVS YISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGT TTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTITSSLPDDFATYYCQQANSHPITFGGGTKVEIKESKYGPPCPPCPPIYI WAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSAD APAYQQGQNQLYNELNLRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEI GMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
420	EVQLVESGGGLVQPKGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVS YISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGT TTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTITSSLPDDFATYYCQQANSHPITFGGGTKVEIKESKYGPPCPPCPFWV LVVVGGLACYSLLVTVAFIIFWVKRGRKLLYIFKQPFMRPVQTTQEDGCSCRFP EEEEEGGCE LRVKFSRSADAPAYQQGQNQLYNELNLRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
421	EVQLVESGGGLVQPKGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVS YISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGT TTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTITSSLPDDFATYYCQQANSHPITFGGGTKVEIKESKYGPPCPPCPFWV LVVVGGLACYSLLVTVAFIIFWVRSKRSLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRS RVKFSRSADAPAYQQGQNQLYNELNLRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
422	EVQLVESGGGLVQPKGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVS YISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGT TTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTITSSLPDDFATYYCQQANSHPITFGGGTKVEIKESKYGPPCPPCPFWV LVVVGGLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSR SADAPAYQQGQNQLYNELNLRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAY SEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
423	EVQLVESGGGLVQPKGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVS YISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGT TTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTITSSLPDDFATYYCQQANSHPITFGGGTKVEIKLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCKRGRKLLYIFKQPFMRPVQTTQEDGCSCRFP EEEEEGGC ELRVKFSRSADAPAYQQGQNQLYNELNLRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQ DKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
424	EVQLVESGGGLVQPKGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVS YISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGT TTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTITSSLPDDFATYYCQQANSHPITFGGGTKVEIKLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCRSKRSLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYR SRVKFSRSADAPAYQQGQNQLYNELNLRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
425	EVQLVESGGGLVQPKGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVS YISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGT TTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTITSSLPDDFATYYCQQANSHPITFGGGTKVEIKLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFS RSADAPAYQQGQNQLYNELNLRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEA YSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
426	EVQLVESGGGLVQPKGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVS YISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGT TTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTITSSLPDDFATYYCQQANSHPITFGGGTKVEIKLEPKSCDKTHTCPPC PFWVLVVVGGLACYSLLVTVAFIIFWVKRGRKLLYIFKQPFMRPVQTTQEDGCSCRFP EEEEE GGCELRVKFSRSADAPAYQQGQNQLYNELNLRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYN ELQDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
427	EVQLVESGGGLVQPKGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVS YISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGT TTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG

	VPSRFSGSGSGTEFTLTISLQPDFFATYYCQOANSHPIITFGGGTKVEIKLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFA AYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
428	EVQLVESGGGLVVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSIISSSGSTIYYADSVK GRFTISRDNKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSGGGGSGGGSGG GGSGGGSDIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISLQPDFFATYYCQOANSHPIITFGGGTKVEIKLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

In more preferred embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in SEQ ID NO: 70; a spacer domain comprising an amino acid sequence set forth in SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 148, or SEQ ID NO: 150; a transmembrane domain comprising an amino acid sequence set forth in SEQ ID NO: 151 or SEQ ID NO: 153; a costimulatory domain comprising an amino acid sequence set forth in SEQ ID NO: 159, SEQ ID NO: 160, or SEQ ID NO: 162; and a primary signaling domain comprising an amino acid sequence set forth in SEQ ID NO: 158. In preferred embodiments, a CAR comprises an amino acid sequence set forth in any one of SEQ ID NOs: 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, and 452 and in even more preferred embodiments a CAR comprises an amino acid sequence set forth in SEQ ID NO: 429, 432, 435, or 438.

SEQ ID NO.	AMINO ACID SEQUENCE
429	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISLQPDFFATYYCQOANSHPIITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSIISSSGSTIYYADSVKGRF TISRDNKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSSTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIF KQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
430	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISLQPDFFATYYCQOANSHPIITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSIISSSGSTIYYADSVKGRF TISRDNKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSSTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLHSD YMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR
431	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISLQPDFFATYYCQOANSHPIITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSIISSSGSTIYYADSVKGRF TISRDNKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSSTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVH DPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR

432	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISSLQPDFFATYYCQQAANSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLVACYSLLVTVAFIIFWVKRGRKKLL YIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTA TKDITYDALHMQALPPR
433	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISSLQPDFFATYYCQQAANSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLVACYSLLVTVAFIIFWVRSKRSLRL HSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTAT KDTYDALHMQALPPR
434	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISSLQPDFFATYYCQQAANSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLVACYSLLVTVAFIIFWVTKKKYSSS VHDPNGEYMFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDA LHMQALPPR
435	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISSLQPDFFATYYCQQAANSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMR PVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRG RDPPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALH MQALPPR
436	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISSLQPDFFATYYCQQAANSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRSKRSLRLHSDYMNMT PRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRG RDPPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALH MQALPPR
437	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISSLQPDFFATYYCQQAANSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYM FRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
438	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISSLQPDFFATYYCQQAANSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITVAFIIFWVKRGRKKLLYIFKQ PFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYD ALHMQALPPR
439	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISSLQPDFFATYYCQQAANSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSIEVMYPPPYLDNEKS

	NGTIIHVKGKHLCPSPFLFPGPSKPFVVLVVGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMN MTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDR RGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
440	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISLQPDFFATYYCQQANSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPFLFPGPSKPFVVLVVGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNG EYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRRGRDPE MGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQAL PPR
441	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISLQPDFFATYYCQQANSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSSESKYGPPCPPCPIYI WAPLAGTCGVLVLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEDGCSCRFPEEEEGGCELRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQDKMA EAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
442	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISLQPDFFATYYCQQANSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSSESKYGPPCPPCPIYI WAPLAGTCGVLVLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEDGCSCRFPEEEEGGCELRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQDKMA EAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
443	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISLQPDFFATYYCQQANSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSSESKYGPPCPPCPIYI WAPLAGTCGVLVLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSAD APAYQQGQNQLYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEI GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
444	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISLQPDFFATYYCQQANSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSSESKYGPPCPPCFWV LVVVGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEDGCSCRFPEEEEGGCE LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
445	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISLQPDFFATYYCQQANSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSSESKYGPPCPPCFWV LVVVGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTTPRRPGPTRKHYPYAPPRDFAAYRS RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQK KMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
446	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISLQPDFFATYYCQQANSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSSESKYGPPCPPCFWV LVVVGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSR SADAPAYQQGQNQLYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAY SEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
447	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGS GSGTEFTLTISLQPDFFATYYCQQANSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTTFSDYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNLSRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLVLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEDGCSCRFPEEEEGGC

	ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
448	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGSGSGTEFTLTISSLQPDFFATYYCQQANSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNANKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSLEPKSCDKTHTCPPCPYYIWAPLAGTCGVLLLSLVITLYCRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
449	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGSGSGTEFTLTISSLQPDFFATYYCQQANSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNANKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSLEPKSCDKTHTCPPCPYYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
450	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGSGSGTEFTLTISSLQPDFFATYYCQQANSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNANKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSLEPKSCDKTHTCPPCPFWVLVVGGLVACYSLLVTVAFIIFWVKRGRKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
451	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGSGSGTEFTLTISSLQPDFFATYYCQQANSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNANKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSLEPKSCDKTHTCPPCPFWVLVVGGLVACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
452	DIQMTQSPSTLSASVGDRTTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESQVPSRFSGSGSGTEFTLTISSLQPDFFATYYCQQANSHPITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNANKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTITVTVSSLEPKSCDKTHTCPPCPFWVLVVGGLVACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

In particular embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in SEQ ID NO: 79 or SEQ ID NO: 80; a spacer domain comprising an amino acid sequence set forth in SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 148, or SEQ ID NO: 150; a transmembrane domain
5 comprising an amino acid sequence set forth in SEQ ID NO: 151 or SEQ ID NO: 153; a costimulatory domain comprising an amino acid sequence set forth in SEQ ID NO: 159, SEQ ID NO: 160, or SEQ ID NO: 162; and a primary signaling domain comprising an amino acid sequence set forth in SEQ ID NO: 158. In particular embodiments, a CAR comprises an amino acid sequence set forth in any one of SEQ ID NOs: 453, 454, 455, 456, 457, 458, 459,
10 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, and 476. In particular embodiments, a CAR comprises an amino acid sequence set forth in any one of

SEQ ID NOs: 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, and 500.

SEQ ID NO.	AMINO ACID SEQUENCE
453	EVQLLES GGGGLVQP GGSRLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARPGDGYEGVYFDYWGGQGLVTVSSGGGGSGGGSGSGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSPIITFGGGTKVEIKTTTPAPRPPTPAPTIIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
454	EVQLLES GGGGLVQP GGSRLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARPGDGYEGVYFDYWGGQGLVTVSSGGGGSGGGSGSGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSPIITFGGGTKVEIKTTTPAPRPPTPAPTIIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
455	EVQLLES GGGGLVQP GGSRLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARPGDGYEGVYFDYWGGQGLVTVSSGGGGSGGGSGSGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSPIITFGGGTKVEIKTTTPAPRPPTPAPTIIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKYSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
456	EVQLLES GGGGLVQP GGSRLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARPGDGYEGVYFDYWGGQGLVTVSSGGGGSGGGSGSGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSPIITFGGGTKVEIKTTTPAPRPPTPAPTIIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
457	EVQLLES GGGGLVQP GGSRLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARPGDGYEGVYFDYWGGQGLVTVSSGGGGSGGGSGSGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSPIITFGGGTKVEIKTTTPAPRPPTPAPTIIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWLVVVGGVLACYSLLVTVAFIIFWVRSKR SLLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
458	EVQLLES GGGGLVQP GGSRLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARPGDGYEGVYFDYWGGQGLVTVSSGGGGSGGGSGSGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSPIITFGGGTKVEIKTTTPAPRPPTPAPTIIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
459	EVQLLES GGGGLVQP GGSRLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARPGDGYEGVYFDYWGGQGLVTVSSGGGGSGGGSGSGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSPIITFGGGTKVEIKIEVMYPPPYLDNEKSNGTIIHVKGKHLCP SPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQ

	PFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLD KRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTY DALHMQALPPR
460	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARPGDGYEGVYFDYWGGQTLVTVSSGGGGSGGG GSGGGGSGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLPEDFATYYCQQAHSSTITFGGGTKVEIKIEVMYPPPYLD NEKSNGTIIHVKGKHLCP SPLFP GP SKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLHSDYM NMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDK RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYD ALHMQALPPR
461	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARPGDGYEGVYFDYWGGQTLVTVSSGGGGSGGG GSGGGGSGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLPEDFATYYCQQAHSSTITFGGGTKVEIKIEVMYPPPYLD NEKSNGTIIHVKGKHLCP SPLFP GP SKPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPN GEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRD PEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQA LPPR
462	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARPGDGYEGVYFDYWGGQTLVTVSSGGGGSGGG GSGGGGSGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLPEDFATYYCQQAHSSTITFGGGTKVEIKIEVMYPPPYLD NEKSNGTIIHVKGKHLCP SPLFP GP SKPFVWL VVVGVLACYSLLVTVAFIIFWVKRGRKKLLYI FKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATK DTYDALHMQALPPR
463	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARPGDGYEGVYFDYWGGQTLVTVSSGGGGSGGG GSGGGGSGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLPEDFATYYCQQAHSSTITFGGGTKVEIKIEVMYPPPYLD NEKSNGTIIHVKGKHLCP SPLFP GP SKPFVWL VVVGVLACYSLLVTVAFIIFWVSKRSRLHSDY MNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATK TYDALHMQALPPR
464	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARPGDGYEGVYFDYWGGQTLVTVSSGGGGSGGG GSGGGGSGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLPEDFATYYCQQAHSSTITFGGGTKVEIKIEVMYPPPYLD NEKSNGTIIHVKGKHLCP SPLFP GP SKPFVWL VVVGVLACYSLLVTVAFIIFWVTKKYSSSVH DPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRG RDPPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALH MQALPPR
465	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARPGDGYEGVYFDYWGGQTLVTVSSGGGGSGGG GSGGGGSGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLPEDFATYYCQQAHSSTITFGGGTKVEIKESKYGPCCPPC PIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
466	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARPGDGYEGVYFDYWGGQTLVTVSSGGGGSGGG GSGGGGSGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLPEDFATYYCQQAHSSTITFGGGTKVEIKESKYGPCCPPC PIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYR SRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
467	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARPGDGYEGVYFDYWGGQTLVTVSSGGGGSGGG

	GS GGGGSGGGSDIQMTQSPSSLSASVGRVTTITCRASQSISSYLNWYQOKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLOPEDFATYYCQQAHSPIITFGGGTKVEIKESKYGPCCPPC PIYIWAPLAGTCGVLLLSLVTITLYCTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFS RSADAPAYQOGQONQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEA YSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
468	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARPGDGYEGVYFDYWGQGLTIVTVSSGGGSGGG GSGGGGSGGGSDIQMTQSPSSLSASVGRVTTITCRASQSISSYLNWYQOKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLOPEDFATYYCQQAHSPIITFGGGTKVEIKESKYGPCCPPC PFWVLVVVGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEEDGCSCRFPEEEE GGCELRVKFSRSADAPAYQOGQONQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
469	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARPGDGYEGVYFDYWGQGLTIVTVSSGGGSGGG GSGGGGSGGGSDIQMTQSPSSLSASVGRVTTITCRASQSISSYLNWYQOKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLOPEDFATYYCQQAHSPIITFGGGTKVEIKESKYGPCCPPC PFWVLVVVGVLACYSLLVTVAFIIFWVRSKRSLHSDYMNMTPRRPGPTRKHYPYAPPRDFA AYRSRVKFSRSADAPAYQOGQONQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
470	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARPGDGYEGVYFDYWGQGLTIVTVSSGGGSGGG GSGGGGSGGGSDIQMTQSPSSLSASVGRVTTITCRASQSISSYLNWYQOKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLOPEDFATYYCQQAHSPIITFGGGTKVEIKESKYGPCCPPC PFWVLVVVGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRV KFSRSADAPAYQOGQONQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
471	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARPGDGYEGVYFDYWGQGLTIVTVSSGGGSGGG GSGGGGSGGGSDIQMTQSPSSLSASVGRVTTITCRASQSISSYLNWYQOKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLOPEDFATYYCQQAHSPIITFGGGTKVEIKLEPKSCDKTHT CPPCPIYIWAPLAGTCGVLLLSLVTITLYCKRGRKKLLYIFKQPFMRPVQTTQEEEDGCSCRFPEEE EGGCELRVKFSRSADAPAYQOGQONQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLY NELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
472	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARPGDGYEGVYFDYWGQGLTIVTVSSGGGSGGG GSGGGGSGGGSDIQMTQSPSSLSASVGRVTTITCRASQSISSYLNWYQOKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLOPEDFATYYCQQAHSPIITFGGGTKVEIKLEPKSCDKTHT CPPCPIYIWAPLAGTCGVLLLSLVTITLYCRSKRSLHSDYMNMTPRRPGPTRKHYPYAPPRDF AAYRSRVKFSRSADAPAYQOGQONQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
473	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARPGDGYEGVYFDYWGQGLTIVTVSSGGGSGGG GSGGGGSGGGSDIQMTQSPSSLSASVGRVTTITCRASQSISSYLNWYQOKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLOPEDFATYYCQQAHSPIITFGGGTKVEIKLEPKSCDKTHT CPPCPIYIWAPLAGTCGVLLLSLVTITLYCTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLR VKFSRSADAPAYQOGQONQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
474	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARPGDGYEGVYFDYWGQGLTIVTVSSGGGSGGG GSGGGGSGGGSDIQMTQSPSSLSASVGRVTTITCRASQSISSYLNWYQOKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLOPEDFATYYCQQAHSPIITFGGGTKVEIKLEPKSCDKTHT CPPCPFWVLVVVGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEEDGCSCRF EEEEGGCELRVKFSRSADAPAYQOGQONQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ GLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
475	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARPGDGYEGVYFDYWGQGLTIVTVSSGGGSGGG GSGGGGSGGGSDIQMTQSPSSLSASVGRVTTITCRASQSISSYLNWYQOKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLOPEDFATYYCQQAHSPIITFGGGTKVEIKLEPKSCDKTHT CPPCPFWVLVVVGVLACYSLLVTVAFIIFWVRSKRSLHSDYMNMTPRRPGPTRKHYPYAPP

	RDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
476	EVQLLSGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKLEWVSAISGGSGSTYYADSVK GRFTISRDNKNTLYLQMNSLRAEDTAVYYCARPGDGYEGVYFDYWGQGLTVTVSSGGGGSGGG GSGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQAHSPIITFGGGTKVEIKLEPKSCDKTHT CPPCFWVLVVVGVLACYSLLVTVAFIIFWVTKKYSVSDPNGEYMFMRVNTAKKSRLTDV TLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
477	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISLQPEDFATYYCQQAHSPIITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKLEWVSAISGGSGSTYYADSVKGRF TISRDNKNTLYLQMNSLRAEDTAVYYCARPGDGYEGVYFDYWGQGLTVTVSSSTTTPAPRPPTP APTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITILYCKRGRKKL LYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLST ATKDTYDALHMQALPPR
478	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISLQPEDFATYYCQQAHSPIITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKLEWVSAISGGSGSTYYADSVKGRF TISRDNKNTLYLQMNSLRAEDTAVYYCARPGDGYEGVYFDYWGQGLTVTVSSSTTTPAPRPPTP APTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITILYCKRGRKKL LHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA TKDTYDALHMQALPPR
479	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISLQPEDFATYYCQQAHSPIITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKLEWVSAISGGSGSTYYADSVKGRF TISRDNKNTLYLQMNSLRAEDTAVYYCARPGDGYEGVYFDYWGQGLTVTVSSSTTTPAPRPPTP APTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITILYCTKKKYS SVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
480	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISLQPEDFATYYCQQAHSPIITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKLEWVSAISGGSGSTYYADSVKGRF TISRDNKNTLYLQMNSLRAEDTAVYYCARPGDGYEGVYFDYWGQGLTVTVSSSTTTPAPRPPTP APTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGVLACYSLLVTVAFIIFWVKRGR KKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLG RREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGL LSTATKDTYDALHMQALPPR
481	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISLQPEDFATYYCQQAHSPIITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKLEWVSAISGGSGSTYYADSVKGRF TISRDNKNTLYLQMNSLRAEDTAVYYCARPGDGYEGVYFDYWGQGLTVTVSSSTTTPAPRPPTP APTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGVLACYSLLVTVAFIIFWVRSKR SRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGL STATKDTYDALHMQALPPR
482	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISLQPEDFATYYCQQAHSPIITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKLEWVSAISGGSGSTYYADSVKGRF TISRDNKNTLYLQMNSLRAEDTAVYYCARPGDGYEGVYFDYWGQGLTVTVSSSTTTPAPRPPTP APTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGVLACYSLLVTVAFIIFWVTKKK YSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
483	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISLQPEDFATYYCQQAHSPIITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ

	LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNKNTLYLQMNLSRAEDTAVYYCARPGDGYEGVYFDYWGQGTTLVTVSSIEVMYPPPYLD NEKSNGTIIHVKGKHLCP SPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQ PFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNLQYNEINLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTY DALHMQALPPR
484	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSPIITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNKNTLYLQMNLSRAEDTAVYYCARPGDGYEGVYFDYWGQGTTLVTVSSIEVMYPPPYLD NEKSNGTIIHVKGKHLCP SPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLHSDYM NMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNLQYNEINLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYD ALHMQALPPR
485	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSPIITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNKNTLYLQMNLSRAEDTAVYYCARPGDGYEGVYFDYWGQGTTLVTVSSIEVMYPPPYLD NEKSNGTIIHVKGKHLCP SPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPN GEYMFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLQYNEINLGRREEYDVLDKRRGRD PEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQA LPPR
486	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSPIITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNKNTLYLQMNLSRAEDTAVYYCARPGDGYEGVYFDYWGQGTTLVTVSSIEVMYPPPYLD NEKSNGTIIHVKGKHLCP SPLFPGPSKPFVVLVVGGLVACYSLLVTVAFIIFWVKRGRKKLLYI FKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNLQYNEINLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATK DTYDALHMQALPPR
487	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSPIITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNKNTLYLQMNLSRAEDTAVYYCARPGDGYEGVYFDYWGQGTTLVTVSSIEVMYPPPYLD NEKSNGTIIHVKGKHLCP SPLFPGPSKPFVVLVVGGLVACYSLLVTVAFIIFWVRSKRKRLLHS DYMNTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNLQYNEINLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATK DTYDALHMQALPPR
488	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSPIITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNKNTLYLQMNLSRAEDTAVYYCARPGDGYEGVYFDYWGQGTTLVTVSSIEVMYPPPYLD NEKSNGTIIHVKGKHLCP SPLFPGPSKPFVVLVVGGLVACYSLLVTVAFIIFWVTKKYSSSVH DPNGEYMFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLQYNEINLGRREEYDVLDKRRG RDPPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALH MQALPPR
489	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSPIITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNKNTLYLQMNLSRAEDTAVYYCARPGDGYEGVYFDYWGQGTTLVTVSSIEVMYPPPYLD PIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGG CELRVKFSRSADAPAYQQGQNLQYNEINLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR
490	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSPIITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNKNTLYLQMNLSRAEDTAVYYCARPGDGYEGVYFDYWGQGTTLVTVSSIEVMYPPPYLD PIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYR SRVKFSRSADAPAYQQGQNLQYNEINLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK

	DKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
491	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISLQPEDFATYYCQQAHSPTFTGGGKVEIKGGGSGGGSGGGSGGGSGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGGSGSTYYADSVKGRF TISRDNKNTLYLQMNLSRAEDTAVYYCARPGDGYEGVYFDYWGQGLTVTVSSSESKYGPCCPPC PIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFS RSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEA YSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
492	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISLQPEDFATYYCQQAHSPTFTGGGKVEIKGGGSGGGSGGGSGGGSGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGGSGSTYYADSVKGRF TISRDNKNTLYLQMNLSRAEDTAVYYCARPGDGYEGVYFDYWGQGLTVTVSSSESKYGPCCPPC PFWVLVVGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEDGDCSCRFPEEEE GGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
493	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISLQPEDFATYYCQQAHSPTFTGGGKVEIKGGGSGGGSGGGSGGGSGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGGSGSTYYADSVKGRF TISRDNKNTLYLQMNLSRAEDTAVYYCARPGDGYEGVYFDYWGQGLTVTVSSSESKYGPCCPPC PFWVLVVGVLACYSLLVTVAFIIFWVRSKRSLHSDYMNMTPRRPGPTRKHYPYAPPRDFA AYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
494	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISLQPEDFATYYCQQAHSPTFTGGGKVEIKGGGSGGGSGGGSGGGSGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGGSGSTYYADSVKGRF TISRDNKNTLYLQMNLSRAEDTAVYYCARPGDGYEGVYFDYWGQGLTVTVSSSESKYGPCCPPC PFWVLVVGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
495	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISLQPEDFATYYCQQAHSPTFTGGGKVEIKGGGSGGGSGGGSGGGSGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGGSGSTYYADSVKGRF TISRDNKNTLYLQMNLSRAEDTAVYYCARPGDGYEGVYFDYWGQGLTVTVSSLEPKSCDKTHT CPPCPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEDGDCSCRFPEEE EGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLY NELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
496	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISLQPEDFATYYCQQAHSPTFTGGGKVEIKGGGSGGGSGGGSGGGSGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGGSGSTYYADSVKGRF TISRDNKNTLYLQMNLSRAEDTAVYYCARPGDGYEGVYFDYWGQGLTVTVSSLEPKSCDKTHT CPPCPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDF AAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
497	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISLQPEDFATYYCQQAHSPTFTGGGKVEIKGGGSGGGSGGGSGGGSGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGGSGSTYYADSVKGRF TISRDNKNTLYLQMNLSRAEDTAVYYCARPGDGYEGVYFDYWGQGLTVTVSSLEPKSCDKTHT CPPCPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLR VKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
498	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISLQPEDFATYYCQQAHSPTFTGGGKVEIKGGGSGGGSGGGSGGGSGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGGSGSTYYADSVKGRF TISRDNKNTLYLQMNLSRAEDTAVYYCARPGDGYEGVYFDYWGQGLTVTVSSLEPKSCDKTHT CPPCPFWVLVVGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEDGDCSCRF EEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ GLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
499	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISLQPEDFATYYCQQAHSPTFTGGGKVEIKGGGSGGGSGGGSGGGSGGGSEVQ

	LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGGSGSTYYADSVKGRF TISRDNKNTLYLQMNLSRAEDTAVYYCARPGDGYEGVYFDYWGQGLTVTVSSLEPKSCDKTHT CPPCPFWVLVVVGVLACYSLLVTVAFIIFWVRSKRRLHSDYMNMTPRRPGPTRKHYPYAPP RDTFAAYRSRVKFSRSADAPAYQQGQNLNLYNELNLGRREEYDVLDKRRGRDPPEMGGKPRRKNPQEG LYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
500	DIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLPEDFATYYCQQAHSPIITFGGGTKVEIKGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGGSGSTYYADSVKGRF TISRDNKNTLYLQMNLSRAEDTAVYYCARPGDGYEGVYFDYWGQGLTVTVSSLEPKSCDKTHT CPPCPFWVLVVVGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFRAVNTAKKSRLTDV TLRVKFSRSADAPAYQQGQNLNLYNELNLGRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

In particular embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in SEQ ID NO: 89; a spacer domain comprising an amino acid sequence set forth in SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 148, or SEQ ID NO: 150; a transmembrane domain comprising an amino acid sequence set forth in SEQ ID NO: 151 or SEQ ID NO: 153; a costimulatory domain comprising an amino acid sequence set forth in SEQ ID NO: 159, SEQ ID NO: 160, or SEQ ID NO: 162; and a primary signaling domain comprising an amino acid sequence set forth in SEQ ID NO: 158. In particular embodiments, a CAR comprises an amino acid sequence set forth in any one of SEQ ID NOs: 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, and 524.

SEQ ID NO.	AMINO ACID SEQUENCE
501	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVLTMTNMDPVDTAIVYICAREGSHDYKSSNWFDPWGQGLTVTVSSGGGGSG GGGSGGGSGGGGSDIQMTQSPSSLSASVGRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVP SRFSGSGSGTDFTFITISSLPED IATYYCQHFNLPLTFGGGTKVEIKTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIAPLAGTCGVLLSLVITLYCKRGRK KLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNLNLYNELNLGR REEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGL STATKDTYDALHMQALPPR
502	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVLTMTNMDPVDTAIVYICAREGSHDYKSSNWFDPWGQGLTVTVSSGGGGSG GGGSGGGSGGGGSDIQMTQSPSSLSASVGRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVP SRFSGSGSGTDFTFITISSLPED IATYYCQHFNLPLTFGGGTKVEIKTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIAPLAGTCGVLLSLVITLYCKRGRK RLLHSDYMNMTPRRPGPTRKHYPYAPP RDTFAAYRSRVKFSRSADAPAYQQGQNLNLYNELNLGR REEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLS TATKDTYDALHMQALPPR
503	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVLTMTNMDPVDTAIVYICAREGSHDYKSSNWFDPWGQGLTVTVSSGGGGSG GGGSGGGSGGGGSDIQMTQSPSSLSASVGRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVP SRFSGSGSGTDFTFITISSLPED IATYYCQHFNLPLTFGGGTKVEIKTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIAPLAGTCGVLLSLVITLYCKKKY SSSVHDPNGEYMFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLNLYNELNLGRREEYDVL DKRRGRDPPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR
504	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVLTMTNMDPVDTAIVYICAREGSHDYKSSNWFDPWGQGLTVTVSSGGGGSG

	GGGSGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGSGSGTDFTFITISLQPED IATYYCQOHFNLP LTFGGGKVEIKTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGVLACYSLLVTVAFIIFWVKR GRKKLLYIFKQPFMRPVQTTQEEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR
505	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYWNDEKRYSPSLKSRLTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFD PWGQGLVTVSSGGGGSGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGSGSGTDFTFITISLQPED IATYYCQOHFNLP LTFGGGKVEIKTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGVLACYSLLVTVAFIIFWVRS KRSRLHSDYMNMTPRRP GPTRKHYPYAPPRDFAAYSRSRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR
506	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYWNDEKRYSPSLKSRLTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFD PWGQGLVTVSSGGGGSGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGSGSGTDFTFITISLQPED IATYYCQOHFNLP LTFGGGKVEIKTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGVLACYSLLVTVAFIIFWVTK KKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR
507	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYWNDEKRYSPSLKSRLTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFD PWGQGLVTVSSGGGGSGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGSGSGTDFTFITISLQPED IATYYCQOHFNLP LTFGGGKVEIKIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSP LFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR
508	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYWNDEKRYSPSLKSRLTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFD PWGQGLVTVSSGGGGSGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGSGSGTDFTFITISLQPED IATYYCQOHFNLP LTFGGGKVEIKIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSP LFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLHSDYMNMTPRRP GPTRKHYPYAPPRDFAAYSRSRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR
509	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYWNDEKRYSPSLKSRLTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFD PWGQGLVTVSSGGGGSGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGSGSGTDFTFITISLQPED IATYYCQOHFNLP LTFGGGKVEIKIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSP LFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR
510	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYWNDEKRYSPSLKSRLTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFD PWGQGLVTVSSGGGGSGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGSGSGTDFTFITISLQPED IATYYCQOHFNLP LTFGGGKVEIKIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSP LFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR
511	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYWNDEKRYSPSLKSRLTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFD PWGQGLVTVSSGGGGSGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGSGSGTDFTFITISLQPED IATYYCQOHFNLP LTFGGGKVEIKIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSP LFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR

	HSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNLQYNEINLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTAT KDTYDALHMQALPPR
512	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYWNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYICAREGSHDYKSSNWFDPWGQGLTVTVSSGGGGSG GGSGGGGGGGGGSDIQMTQSPSSLSASVGRDVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVP SRFSGSGSGTDFTFITISLQPED IATYYCQOHFNLP LTFGGG TKVEIKIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSP LFP GPSPKPFVWL VVVGVLACYSLLVTVAFIIFWVTKKKYSSS VHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLQYNEINLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDA LHMQALPPR
513	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYWNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYICAREGSHDYKSSNWFDPWGQGLTVTVSSGGGGSG GGSGGGGGGGGGSDIQMTQSPSSLSASVGRDVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVP SRFSGSGSGTDFTFITISLQPED IATYYCQOHFNLP LTFGGG TKVEIKESKYGPPCP PCPIYIWAPLAGTCGVLLLSLVITLYCKRGRKLLYIFKQPFMRPVQTTQEEDGCSCRFP EEEEE GCELRVKFSRSADAPAYQQGQNLQYNEINLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
514	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYWNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYICAREGSHDYKSSNWFDPWGQGLTVTVSSGGGGSG GGSGGGGGGGGGSDIQMTQSPSSLSASVGRDVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVP SRFSGSGSGTDFTFITISLQPED IATYYCQOHFNLP LTFGGG TKVEIKESKYGPPCP PCPIYIWAPLAGTCGVLLLSLVITLYCKRGRKLLYIFKQPFMRPVQTTQEEDGCSCRFP EEEEE GCELRVKFSRSADAPAYQQGQNLQYNEINLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
515	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYWNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYICAREGSHDYKSSNWFDPWGQGLTVTVSSGGGGSG GGSGGGGGGGGGSDIQMTQSPSSLSASVGRDVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVP SRFSGSGSGTDFTFITISLQPED IATYYCQOHFNLP LTFGGG TKVEIKESKYGPPCP PCPIYIWAPLAGTCGVLLLSLVITLYCKKYSVVHDPNGEYMFMRVNTAKKSRLTDVTLRVK FSRSADAPAYQQGQNLQYNEINLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
516	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYWNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYICAREGSHDYKSSNWFDPWGQGLTVTVSSGGGGSG GGSGGGGGGGGGSDIQMTQSPSSLSASVGRDVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVP SRFSGSGSGTDFTFITISLQPED IATYYCQOHFNLP LTFGGG TKVEIKESKYGPPCP PCPFWVLVVVGVLACYSLLVTVAFIIFWVKRGRKLLYIFKQPFMRPVQTTQEEDGCSCRFP EEE EGGCELRVKFSRSADAPAYQQGQNLQYNEINLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLY NELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
517	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYWNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYICAREGSHDYKSSNWFDPWGQGLTVTVSSGGGGSG GGSGGGGGGGGGSDIQMTQSPSSLSASVGRDVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVP SRFSGSGSGTDFTFITISLQPED IATYYCQOHFNLP LTFGGG TKVEIKESKYGPPCP PCPFWVLVVVGVLACYSLLVTVAFIIFWVRSKRSRLLSHSDYMNMTPRRPGPTRKHYPYAPPRD FAAYRSRVKFSRSADAPAYQQGQNLQYNEINLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLY NELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
518	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYWNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYICAREGSHDYKSSNWFDPWGQGLTVTVSSGGGGSG GGSGGGGGGGGGSDIQMTQSPSSLSASVGRDVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVP SRFSGSGSGTDFTFITISLQPED IATYYCQOHFNLP LTFGGG TKVEIKESKYGPPCP PCPFWVLVVVGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTL RVKFSRSADAPAYQQGQNLQYNEINLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK KMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
519	QITLKESGPTLVKPTQTLTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLALIIYWNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYICAREGSHDYKSSNWFDPWGQGLTVTVSSGGGGSG GGSGGGGGGGGGSDIQMTQSPSSLSASVGRDVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVP SRFSGSGSGTDFTFITISLQPED IATYYCQOHFNLP LTFGGG TKVEIKLEPKSCDKT HTCPPCPYIWAPLAGTCGVLLLSLVITLYCKRGRKLLYIFKQPFMRPVQTTQEEDGCSCRFP EEE GGCELRVKFSRSADAPAYQQGQNLQYNEINLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG

	LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
520	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYYCAREGSHDYKSSNWFDPWGQGTTLVTVSSGGGGSG GGGSGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVP SRFSGSGSGTDFFTTISLQPED IATYYCQHFNLPLTFGGGKVEIKLEPKSCDKT HTCPPCPYIWIAPLAGTCGVLLLSLVITLYCRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPR DFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
521	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYYCAREGSHDYKSSNWFDPWGQGTTLVTVSSGGGGSG GGGSGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVP SRFSGSGSGTDFFTTISLQPED IATYYCQHFNLPLTFGGGKVEIKLEPKSCDKT HTCPPCPYIWIAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFRAVNTAKKSRLTDVT LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
522	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYYCAREGSHDYKSSNWFDPWGQGTTLVTVSSGGGGSG GGGSGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVP SRFSGSGSGTDFFTTISLQPED IATYYCQHFNLPLTFGGGKVEIKLEPKSCDKT HTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEEDGCS CRFEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNP QEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
523	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYYCAREGSHDYKSSNWFDPWGQGTTLVTVSSGGGGSG GGGSGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVP SRFSGSGSGTDFFTTISLQPED IATYYCQHFNLPLTFGGGKVEIKLEPKSCDKT HTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTRKHYPYA PPRDFAAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNP QEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
524	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIIYNDEKRYSPSL KSRLTITKDTSKNQVVLMTNMDPVDTAIVYYCAREGSHDYKSSNWFDPWGQGTTLVTVSSGGGGSG GGGSGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVP SRFSGSGSGTDFFTTISLQPED IATYYCQHFNLPLTFGGGKVEIKLEPKSCDKT HTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKYSSSVHDPNGEYMFRAVNTAKKSRLT DVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

In preferred embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in SEQ ID NO: 90; a spacer domain comprising an amino acid sequence set forth in SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 148, or SEQ ID NO: 150; a transmembrane domain comprising an amino acid sequence set forth in SEQ ID NO: 151 or SEQ ID NO: 153; a costimulatory domain comprising an amino acid sequence set forth in SEQ ID NO: 159, SEQ ID NO: 160, or SEQ ID NO: 162; and a primary signaling domain comprising an amino acid sequence set forth in SEQ ID NO: 158. In preferred embodiments, a CAR comprises an amino acid sequence set forth in any one of SEQ ID NOs: 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, and 548.

SEQ ID NO.	AMINO ACID SEQUENCE
525	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGS SGTDFFTTISLQPED IATYYCQHFNLPLTFGGGKVEIKGGGGSGGGSGGGSGGGSGGQIT

	LKESGPTLVKPTQTTLTLCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWYNDKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFDWPWGQGLTVTVSSSTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIAPLAGTCGVLLLSLVITLYCKRGRK KLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNLYNELNLGR REEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGL STATKDTYDALHMQALPPR
526	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGS GSGTDFTF TISSLOPED IATYYCQHFNLPLTFGGGKVEIKGGGSGGGSGGGSGGGSGGGSQIT LKESGPTLVKPTQTTLTLCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWYNDKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFDWPWGQGLTVTVSSSTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIAPLAGTCGVLLLSLVITLYCRSKRS RLLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAAYRSRVKFSRSADAPAYQQGQNLYNELNLGR EEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLS TATKDTYDALHMQALPPR
527	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGS GSGTDFTF TISSLOPED IATYYCQHFNLPLTFGGGKVEIKGGGSGGGSGGGSGGGSGGGSQIT LKESGPTLVKPTQTTLTLCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWYNDKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFDWPWGQGLTVTVSSSTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIAPLAGTCGVLLLSLVITLYCTKKKY SSSVHDPNGEYMFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVL DKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDT YDALHMQALPPR
528	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGS GSGTDFTF TISSLOPED IATYYCQHFNLPLTFGGGKVEIKGGGSGGGSGGGSGGGSGGGSQIT LKESGPTLVKPTQTTLTLCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWYNDKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFDWPWGQGLTVTVSSSTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGVLACYSLLVTVAFIIFWVKR GRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNLYNELN LGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLY QGLSTATKDTYDALHMQALPPR
529	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGS GSGTDFTF TISSLOPED IATYYCQHFNLPLTFGGGKVEIKGGGSGGGSGGGSGGGSGGGSQIT LKESGPTLVKPTQTTLTLCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWYNDKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFDWPWGQGLTVTVSSSTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGVLACYSLLVTVAFIIFWVRS KRSRLLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAAYRSRVKFSRSADAPAYQQGQNLYNELN LGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQ GLSTATKDTYDALHMQALPPR
530	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGS GSGTDFTF TISSLOPED IATYYCQHFNLPLTFGGGKVEIKGGGSGGGSGGGSGGGSGGGSQIT LKESGPTLVKPTQTTLTLCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWYNDKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFDWPWGQGLTVTVSSSTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGVLACYSLLVTVAFIIFWVTK KKYSSSVHDPNGEYMFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEY DVLDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTAT KDTYDALHMQALPPR
531	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGS GSGTDFTF TISSLOPED IATYYCQHFNLPLTFGGGKVEIKGGGSGGGSGGGSGGGSGGGSQIT LKESGPTLVKPTQTTLTLCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWYNDKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFDWPWGQGLTVTVSSIEVMPPPY LDNEKSNGTIIHVKGKHLCPSP LFPGPSKPIYIAPLAGTCGVLLLSLVITLYCKRGRKKLLYIF KQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNLYNELNLGRREEYDV LDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKD TYDALHMQALPPR
532	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGS GSGTDFTF TISSLOPED IATYYCQHFNLPLTFGGGKVEIKGGGSGGGSGGGSGGGSGGGSQIT LKESGPTLVKPTQTTLTLCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIWYNDKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFDWPWGQGLTVTVSSIEVMPPPY LDNEKSNGTIIHVKGKHLCPSP LFPGPSKPIYIAPLAGTCGVLLLSLVITLYCRSKRSRLLHSD

	YMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR
533	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGS GSGTDFTFITISSLOPED IATYYCQQHFNLP LTFGGGKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLAL IYWNDEKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFD PWGQGLTVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSP LFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHD PNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVL DKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
534	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGS GSGTDFTFITISSLOPED IATYYCQQHFNLP LTFGGGKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLAL IYWNDEKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFD PWGQGLTVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSP LFPGPSKPFVWL VVVGVLACYSLLVTVAFIIFWVRGRKKLL YIFKQPFMRPVQTTQEEEDGCSCRFPEEEEGGCELVRVFSRSADAPAYQQGQNLYNELNLGRREE YDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA TKDTYDALHMQALPPR
535	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGS GSGTDFTFITISSLOPED IATYYCQQHFNLP LTFGGGKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLAL IYWNDEKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFD PWGQGLTVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSP LFPGPSKPFVWL VVVGVLACYSLLVTVAFIIFWVRGRKKLL YIFKQPFMRPVQTTQEEEDGCSCRFPEEEEGGCELVRVFSRSADAPAYQQGQNLYNELNLGRREE YDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA TKDTYDALHMQALPPR
536	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGS GSGTDFTFITISSLOPED IATYYCQQHFNLP LTFGGGKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLAL IYWNDEKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFD PWGQGLTVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSP LFPGPSKPFVWL VVVGVLACYSLLVTVAFIIFWVTKKYSSSV VHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVL DKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
537	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGS GSGTDFTFITISSLOPED IATYYCQQHFNLP LTFGGGKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLAL IYWNDEKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFD PWGQGLTVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSP LFPGPSKPFVWL VVVGVLACYSLLVTVAFIIFWVTKKYSSSV VHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVL DKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
538	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGS GSGTDFTFITISSLOPED IATYYCQQHFNLP LTFGGGKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLAL IYWNDEKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFD PWGQGLTVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSP LFPGPSKPFVWL VVVGVLACYSLLVTVAFIIFWVTKKYSSSV VHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVL DKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
539	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGS GSGTDFTFITISSLOPED IATYYCQQHFNLP LTFGGGKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLAL IYWNDEKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFD PWGQGLTVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSP LFPGPSKPFVWL VVVGVLACYSLLVTVAFIIFWVTKKYSSSV VHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVL DKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
540	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGS GSGTDFTFITISSLOPED IATYYCQQHFNLP LTFGGGKVEIKGGGSGGGGSGGGGSGGGGSGIT LKESGPTLVKPTQTTLTCTFSGFSLSSTSGVGVGWIRQPPGKALEWLAL IYWNDEKRYSPSLKSR

	LTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFD PWGQGLTVTVSSESKYGPPCP PCPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEE EEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDP EMGGKPRRKNPQEG LYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
541	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGS GSGTDFTFITISLQPED IATYYCQQHFNLP LTFGGG TKVEIKGGGSGGGSGGGSGGGSGGGSGQIT LKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLAL IYWNDEKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFD PWGQGLTVTVSSESKYGPPCP PCPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSLHSDYMNMTPRRPGPTRKHYPYAPPRD FAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDP EMGGKPRRKNPQEG LYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
542	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGS GSGTDFTFITISLQPED IATYYCQQHFNLP LTFGGG TKVEIKGGGSGGGSGGGSGGGSGGGSGQIT LKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLAL IYWNDEKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFD PWGQGLTVTVSSESKYGPPCP PCPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDP EMGGKPRRKNPQEGLYNELQDK MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
543	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGS GSGTDFTFITISLQPED IATYYCQQHFNLP LTFGGG TKVEIKGGGSGGGSGGGSGGGSGGGSGQIT LKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLAL IYWNDEKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFD PWGQGLTVTVSSLEPKSCDKT HTCPPCP IYIWAPLAGTCGVLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPE EEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDP EMGGKPRRKNPQEG LYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
544	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGS GSGTDFTFITISLQPED IATYYCQQHFNLP LTFGGG TKVEIKGGGSGGGSGGGSGGGSGGGSGQIT LKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLAL IYWNDEKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFD PWGQGLTVTVSSLEPKSCDKT HTCPPCP IYIWAPLAGTCGVLLSLVITLYCRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPR DFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDP EMGGKPRRKNPQEG LYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
545	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGS GSGTDFTFITISLQPED IATYYCQQHFNLP LTFGGG TKVEIKGGGSGGGSGGGSGGGSGGGSGQIT LKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLAL IYWNDEKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFD PWGQGLTVTVSSLEPKSCDKT HTCPPCP IYIWAPLAGTCGVLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVT LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDP EMGGKPRRKNPQEGLYNELQDK MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
546	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGS GSGTDFTFITISLQPED IATYYCQQHFNLP LTFGGG TKVEIKGGGSGGGSGGGSGGGSGGGSGQIT LKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLAL IYWNDEKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFD PWGQGLTVTVSSLEPKSCDKT HTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCR FPEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDP EMGGKPRRKNP QEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
547	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGS GSGTDFTFITISLQPED IATYYCQQHFNLP LTFGGG TKVEIKGGGSGGGSGGGSGGGSGGGSGQIT LKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLAL IYWNDEKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFD PWGQGLTVTVSSLEPKSCDKT HTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSLHSDYMNMTPRRPGPTRKHYPYA PPRDFAAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDP EMGGKPRRKNPQ EGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
548	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVP SRFSGS GSGTDFTFITISLQPED IATYYCQQHFNLP LTFGGG TKVEIKGGGSGGGSGGGSGGGSGGGSGQIT LKESGPTLVKPTQTTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLAL IYWNDEKRYSPSLKSR LTITKDTSKNQVVLMTNMDPVD TAVYYCAREGSHDYKSSNWFD PWGQGLTVTVSSLEPKSCDKT HTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKYSSSVHDPNGEYMFMRVNTAKKSRLT DVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDP EMGGKPRRKNPQEGLYNE

	LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
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In particular embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in SEQ ID NO: 99 or SEQ ID NO: 100; a spacer domain comprising an amino acid sequence set forth in SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 148, or SEQ ID NO: 150; a transmembrane domain
5 comprising an amino acid sequence set forth in SEQ ID NO: 151 or SEQ ID NO: 153; a costimulatory domain comprising an amino acid sequence set forth in SEQ ID NO: 159, SEQ ID NO: 160, or SEQ ID NO: 162; and a primary signaling domain comprising an amino acid sequence set forth in SEQ ID NO: 158. In particular embodiments, a CAR comprises an amino acid sequence set forth in any one of SEQ ID NOs: 549, 550, 551, 552, 553, 554, 555,
10 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, and 572. In particular embodiments, a CAR comprises an amino acid sequence set forth in any one of SEQ ID NOs: 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, and 596.

SEQ ID NO.	AMINO ACID SEQUENCE
549	EVQLVESGGGLVKPGGSLRLSCAASGFTTFSSYSMNWVRQAPGKGLEWVSSISSSSSSIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSGGGGSGGGSGGGSGGGSDIVMTQSPISLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVTILYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
550	EVQLVESGGGLVKPGGSLRLSCAASGFTTFSSYSMNWVRQAPGKGLEWVSSISSSSSSIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSGGGGSGGGSGGGSGGGSDIVMTQSPISLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVTILYCKRKRRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
551	EVQLVESGGGLVKPGGSLRLSCAASGFTTFSSYSMNWVRQAPGKGLEWVSSISSSSSSIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSGGGGSGGGSGGGSGGGSDIVMTQSPISLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVTILYCTKKYSSSVHDPNGEYMFMRVNTAKKSRITDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
552	EVQLVESGGGLVKPGGSLRLSCAASGFTTFSSYSMNWVRQAPGKGLEWVSSISSSSSSIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSGGGGSGGGSGGGSGGGSDIVMTQSPISLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

553	EVQLVESGGGLVQPKGGSLRLSCAASGFTTFSSYSMNWVRQAPGKLEWVSSISSSSSSIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSGGGGSGGGSGGGSGGGSDIVMTQSPSLPVTGPGEPAISCRSSQSLHNSNGYNLDWYLQKPGQSPQLLIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNLNLEINLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
554	EVQLVESGGGLVQPKGGSLRLSCAASGFTTFSSYSMNWVRQAPGKLEWVSSISSSSSSIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSGGGGSGGGSGGGSGGGSDIVMTQSPSLPVTGPGEPAISCRSSQSLHNSNGYNLDWYLQKPGQSPQLLIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGVLACYSLLVTVAFIIFWVTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLNLEINLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
555	EVQLVESGGGLVQPKGGSLRLSCAASGFTTFSSYSMNWVRQAPGKLEWVSSISSSSSSIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSGGGGSGGGSGGGSGGGSDIVMTQSPSLPVTGPGEPAISCRSSQSLHNSNGYNLDWYLQKPGQSPQLLIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITITLYCKRGRKKLLYIFKQPFMRPVQTTQEEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNLNLEINLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
556	EVQLVESGGGLVQPKGGSLRLSCAASGFTTFSSYSMNWVRQAPGKLEWVSSISSSSSSIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSGGGGSGGGSGGGSGGGSDIVMTQSPSLPVTGPGEPAISCRSSQSLHNSNGYNLDWYLQKPGQSPQLLIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITITLYCKRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNLNLEINLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
557	EVQLVESGGGLVQPKGGSLRLSCAASGFTTFSSYSMNWVRQAPGKLEWVSSISSSSSSIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSGGGGSGGGSGGGSGGGSDIVMTQSPSLPVTGPGEPAISCRSSQSLHNSNGYNLDWYLQKPGQSPQLLIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITITLYCTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLNLEINLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
558	EVQLVESGGGLVQPKGGSLRLSCAASGFTTFSSYSMNWVRQAPGKLEWVSSISSSSSSIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSGGGGSGGGSGGGSGGGSDIVMTQSPSLPVTGPGEPAISCRSSQSLHNSNGYNLDWYLQKPGQSPQLLIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPFWVLVVGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNLNLEINLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
559	EVQLVESGGGLVQPKGGSLRLSCAASGFTTFSSYSMNWVRQAPGKLEWVSSISSSSSSIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSGGGGSGGGSGGGSGGGSDIVMTQSPSLPVTGPGEPAISCRSSQSLHNSNGYNLDWYLQKPGQSPQLLIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPFWVLVVGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNLNLEINLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
560	EVQLVESGGGLVQPKGGSLRLSCAASGFTTFSSYSMNWVRQAPGKLEWVSSISSSSSSIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSGGGGSGGGSGGGSGGGSDIVMTQSPSLPVTGPGEPAISCRSSQSLHNSNGYNLDWYLQKPGQSPQL

	LIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGYYCMQALGLITFGGGTKVEIKIEVMY PPPYLDNEKSNGTIIHVKGKHLCPSPFLPGPSKPFWVLVVVGVLACYSLLVTVAFIIFWVTKKK YSSSVHDPNGEYMFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDV LDKRRGRDPGEMGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
561	EVQLVESGGGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKLEWVSSISSSSSSIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSGGGGSG GGGSGGGSGGGSDIVMTQSPISLPLVTPGEPASISCRSSQSLHNSNGYNLDWYLQKPGQSPQL LIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGYYCMQALGLITFGGGTKVEIKESKYG PPCPPCPYIYWAPLAGTCGVLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEDGCSCRFPE EEEGGCELRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDRRGRDPGEMGKPRRKNPQEG LYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
562	EVQLVESGGGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKLEWVSSISSSSSSIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSGGGGSG GGGSGGGSGGGSDIVMTQSPISLPLVTPGEPASISCRSSQSLHNSNGYNLDWYLQKPGQSPQL LIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGYYCMQALGLITFGGGTKVEIKESKYG PPCPPCPYIYWAPLAGTCGVLLSLVITLYCRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPR DFAAYRSRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDRRGRDPGEMGKPRRKNPQEG LYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
563	EVQLVESGGGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKLEWVSSISSSSSSIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSGGGGSG GGGSGGGSGGGSDIVMTQSPISLPLVTPGEPASISCRSSQSLHNSNGYNLDWYLQKPGQSPQL LIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGYYCMQALGLITFGGGTKVEIKESKYG PPCPPCPYIYWAPLAGTCGVLLSLVITLYCTKKYSSSVHDPNGEYMFRAVNTAKKSRLTDVT LRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDRRGRDPGEMGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
564	EVQLVESGGGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKLEWVSSISSSSSSIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSGGGGSG GGGSGGGSGGGSDIVMTQSPISLPLVTPGEPASISCRSSQSLHNSNGYNLDWYLQKPGQSPQL LIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGYYCMQALGLITFGGGTKVEIKESKYG PPCPPCPFWVLVVVGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEDGCSCR FPEEEGGCELRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDRRGRDPGEMGKPRRKNP QEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
565	EVQLVESGGGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKLEWVSSISSSSSSIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSGGGGSG GGGSGGGSGGGSDIVMTQSPISLPLVTPGEPASISCRSSQSLHNSNGYNLDWYLQKPGQSPQL LIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGYYCMQALGLITFGGGTKVEIKESKYG PPCPPCPFWVLVVVGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTRKHYPYA PPRDFAAAYRSRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDRRGRDPGEMGKPRRKNPQ EGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
566	EVQLVESGGGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKLEWVSSISSSSSSIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSGGGGSG GGGSGGGSGGGSDIVMTQSPISLPLVTPGEPASISCRSSQSLHNSNGYNLDWYLQKPGQSPQL LIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGYYCMQALGLITFGGGTKVEIKESKYG PPCPPCPFWVLVVVGVLACYSLLVTVAFIIFWVTKKYSSSVHDPNGEYMFRAVNTAKKSRLT DVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDRRGRDPGEMGKPRRKNPQEGLYNE LQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
567	EVQLVESGGGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKLEWVSSISSSSSSIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSGGGGSG GGGSGGGSGGGSDIVMTQSPISLPLVTPGEPASISCRSSQSLHNSNGYNLDWYLQKPGQSPQL LIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGYYCMQALGLITFGGGTKVEIKLEPKS CDKTHTCPPCPYIYWAPLAGTCGVLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEDGCSC RFPEEEGGCELRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDRRGRDPGEMGKPRRKN PQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
568	EVQLVESGGGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKLEWVSSISSSSSSIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSGGGGSG GGGSGGGSGGGSDIVMTQSPISLPLVTPGEPASISCRSSQSLHNSNGYNLDWYLQKPGQSPQL LIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGYYCMQALGLITFGGGTKVEIKLEPKS CDKTHTCPPCPYIYWAPLAGTCGVLLSLVITLYCRSKRSRLHSDYMNMTPRRPGPTRKHYPY

	APPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNP QEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
569	EVQLVESGGGLVKKPGGSLRLSCAASGFTFSYYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVK GRFTISRDNNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSGGGGSG GGGSGGGSGGGSDIVMTQSPSLPVTGPGEPAISCRSSQSLHNSNGYNYLDWYLQKPGQSPQL LIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKLEPKS CDKTHTCPPCPPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRVNTAKKSRL TDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
570	EVQLVESGGGLVKKPGGSLRLSCAASGFTFSYYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVK GRFTISRDNNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSGGGGSG GGGSGGGSGGGSDIVMTQSPSLPVTGPGEPAISCRSSQSLHNSNGYNYLDWYLQKPGQSPQL LIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKLEPKS CDKTHTCPPCPFWVLVVVGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEDG CSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPR RKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
571	EVQLVESGGGLVKKPGGSLRLSCAASGFTFSYYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVK GRFTISRDNNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSGGGGSG GGGSGGGSGGGSDIVMTQSPSLPVTGPGEPAISCRSSQSLHNSNGYNYLDWYLQKPGQSPQL LIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKLEPKS CDKTHTCPPCPFWVLVVVGVLACYSLLVTVAFIIFWVRSKRSLHSDYMNMTPRRPGPTRKH YQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRR KNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
572	EVQLVESGGGLVKKPGGSLRLSCAASGFTFSYYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVK GRFTISRDNNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSGGGGSG GGGSGGGSGGGSDIVMTQSPSLPVTGPGEPAISCRSSQSLHNSNGYNYLDWYLQKPGQSPQL LIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKLEPKS CDKTHTCPPCPFWVLVVVGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKK SRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
573	DIVMTQSPSLPVTGPGEPAISCRSSQSLHNSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVDP RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGGSGGGSGGGSGGGG SEVQLVESGGGLVKKPGGSLRLSCAASGFTFSYYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSTTT PA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCK RGRKKLLYIFKQPFMRPVQTTQEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNEL NLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGL YQGLSTATKDTYDALHMQALPPR
574	DIVMTQSPSLPVTGPGEPAISCRSSQSLHNSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVDP RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGGSGGGSGGGSGGGG SEVQLVESGGGLVKKPGGSLRLSCAASGFTFSYYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSTTT PA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCR SKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELN LGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGL YQGLSTATKDTYDALHMQALPPR
575	DIVMTQSPSLPVTGPGEPAISCRSSQSLHNSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVDP RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGGSGGGSGGGSGGGG SEVQLVESGGGLVKKPGGSLRLSCAASGFTFSYYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSTTT PA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCT KKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTA TKDTYDALHMQALPPR
576	DIVMTQSPSLPVTGPGEPAISCRSSQSLHNSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVDP RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGGSGGGSGGGSGGGG SEVQLVESGGGLVKKPGGSLRLSCAASGFTFSYYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSTTT PA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGVLACYSLLVTVAFIIF

	WVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
577	DIVMTQSPLSLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVDP RFSGSGSGTDFTLKISRVEAEDVGVIYCMQALGLITFGGGTKVEIKGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLEWVSSISSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTSSTTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGVLACYSLLVTVAFIIF WVRSKRSLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYN ELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHD GLYQGLSTATKDTYDALHMQALPPR
578	DIVMTQSPLSLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVDP RFSGSGSGTDFTLKISRVEAEDVGVIYCMQALGLITFGGGTKVEIKGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLEWVSSISSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTSSTTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGVLACYSLLVTVAFIIF WVTKKYSVVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGL STATKDTYDALHMQALPPR
579	DIVMTQSPLSLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVDP RFSGSGSGTDFTLKISRVEAEDVGVIYCMQALGLITFGGGTKVEIKGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLEWVSSISSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTSIEVMY PPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKL LYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGR EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLST ATKDTYDALHMQALPPR
580	DIVMTQSPLSLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVDP RFSGSGSGTDFTLKISRVEAEDVGVIYCMQALGLITFGGGTKVEIKGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLEWVSSISSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTSIEVMY PPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKL LHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGR EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA TKDTYDALHMQALPPR
581	DIVMTQSPLSLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVDP RFSGSGSGTDFTLKISRVEAEDVGVIYCMQALGLITFGGGTKVEIKGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLEWVSSISSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTSIEVMY PPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYS SVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
582	DIVMTQSPLSLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVDP RFSGSGSGTDFTLKISRVEAEDVGVIYCMQALGLITFGGGTKVEIKGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLEWVSSISSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTSIEVMY PPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYS SVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
583	DIVMTQSPLSLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVDP RFSGSGSGTDFTLKISRVEAEDVGVIYCMQALGLITFGGGTKVEIKGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLEWVSSISSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTSIEVMY PPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYS SVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR

584	DIVMTQSPISLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVDP RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSYSYMNWVRQAPKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSIEVMY PPPYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPFVVLVVVGVLACYSLLVTVAFIIFWVTKKK YSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKD TYDALHMQALPPR
585	DIVMTQSPISLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVDP RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSYSYMNWVRQAPKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSSESKYG PPCPPCPYIYWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEEDGCSRFE EEEGGCRLRVKFSRSADAPAYQQGQNQLYNELNLRREEYDVLDRRGRDPEMGGKPRRKNPQEG LYNELQDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKD TYDALHMQALPPR
586	DIVMTQSPISLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVDP RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSYSYMNWVRQAPKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSSESKYG PPCPPCPYIYWAPLAGTCGVLLLSLVITLYCRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPR DFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLRREEYDVLDRRGRDPEMGGKPRRKNPQEG LYNELQDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKD TYDALHMQALPPR
587	DIVMTQSPISLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVDP RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSYSYMNWVRQAPKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSSESKYG PPCPPCPYIYWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVT LRVKFSRSADAPAYQQGQNQLYNELNLRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKD TYDALHMQALPPR
588	DIVMTQSPISLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVDP RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSYSYMNWVRQAPKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSSESKYG PPCPPCPFWVLVVVGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEEDGCSR FPEEEEGGCRLRVKFSRSADAPAYQQGQNQLYNELNLRREEYDVLDRRGRDPEMGGKPRRKNP QEGLYNELQDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKD TYDALHMQALPPR
589	DIVMTQSPISLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVDP RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSYSYMNWVRQAPKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSSESKYG PPCPPCPFWVLVVVGVLACYSLLVTVAFIIFWVRSKRSLHSDYMNMTPRRPGPTRKHYPYA PPRDFAAAYRSRVKFSRSADAPAYQQGQNQLYNELNLRREEYDVLDRRGRDPEMGGKPRRKNPQ EGLYNELQDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKD TYDALHMQALPPR
590	DIVMTQSPISLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVDP RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSYSYMNWVRQAPKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSSESKYG PPCPPCPFWVLVVVGVLACYSLLVTVAFIIFWVTKKYSSSVHDPNGEYMFMRVNTAKKSRLT DVTLRVKFSRSADAPAYQQGQNQLYNELNLRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNE LQDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKD TYDALHMQALPPR
591	DIVMTQSPISLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVDP RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSYSYMNWVRQAPKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYMDVWGKGTITVTVSSLEPKS CDKTHTCPPCPYIYWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEEDGSC RFPEEEEGGCRLRVKFSRSADAPAYQQGQNQLYNELNLRREEYDVLDRRGRDPEMGGKPRRKN PQEGLYNELQDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKD TYDALHMQALPPR
592	DIVMTQSPISLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVDP RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGSGGGGSGGGGSGGGG

	SEVQLVESGGGLVQPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTITVTVSSLEPKS CDKTHTCPPCPYIWIAPLAGTCGVLLLSLVITLYCRSKRSRLHSDYMNMTPRRPGPTRKHYPY APPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNP QEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
593	DIVMTQSPISLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQLLIYLGNSRASGVDP RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVQPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTITVTVSSLEPKS CDKTHTCPPCPYIWIAPLAGTCGVLLLSLVITLYCTKKYSSVHDPNGEYMFMRVNTAKKSRL TDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
594	DIVMTQSPISLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQLLIYLGNSRASGVDP RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVQPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTITVTVSSLEPKS CDKTHTCPPCPFWVLVVGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTQEEDG CSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPR RKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
595	DIVMTQSPISLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQLLIYLGNSRASGVDP RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVQPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTITVTVSSLEPKS CDKTHTCPPCPFWVLVVGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTRKH QPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRR KNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
596	DIVMTQSPISLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQLLIYLGNSRASGVDP RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVQPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTITVTVSSLEPKS CDKTHTCPPCPFWVLVVGVLACYSLLVTVAFIIFWVTKKYSSSVHDPNGEYMFMRVNTAKK SRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR

In preferred embodiments, a CAR comprises an antibody or antigen binding
fragment thereof comprising an amino acid sequence set forth in SEQ ID NO: 101; a spacer
domain comprising an amino acid sequence set forth in SEQ ID NO: 145, SEQ ID NO: 146,
SEQ ID NO: 148, or SEQ ID NO: 150; a transmembrane domain comprising an amino acid
5 sequence set forth in SEQ ID NO: 151 or SEQ ID NO: 153; a costimulatory domain
comprising an amino acid sequence set forth in SEQ ID NO: 159, SEQ ID NO: 160, or SEQ
ID NO: 162; and a primary signaling domain comprising an amino acid sequence set forth in
SEQ ID NO: 158. In preferred embodiments, a CAR comprises an amino acid sequence set
forth in any one of SEQ ID NOs: 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608,
10 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, and 620.

SEQ ID NO.	AMINO ACID SEQUENCE
597	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVTYYADSVK GRFTISRDNKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSSTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWIAPLAGTCGVLLLSLVITLYCKRGRKKLLYI FKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYD VLDKRRGRDPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATK

	DTYDALHMQALPPR
598	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVITYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSTTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLSH DYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKD TYDALHMQALPPR
599	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVITYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSTTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVH DPNGEYMFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRG RDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDALH MQALPPR
600	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVITYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSTTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLVACYSLLVTVAFIIFWVKRGRKKL LYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRRE EYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLST ATKDTYDALHMQALPPR
601	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVITYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSTTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLVACYSLLVTVAFIIFWVRSKRSRL LHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTA TKDTYDALHMQALPPR
602	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVITYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSTTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLVACYSLLVTVAFIIFWVTKKKYSS SVHDPNGEYMFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK RRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYD ALHMQALPPR
603	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVITYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSIEVMYPPPYLDNEK SNGTIIHVKGKHLCP SPLFPGPSKP IYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFM RPVQTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRR GRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDAL HMQALPPR
604	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVITYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSIEVMYPPPYLDNEK SNGTIIHVKGKHLCP SPLFPGPSKP IYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLSHSDYMNMT PRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRG RDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDALH MQALPPR
605	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVITYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSIEVMYPPPYLDNEK SNGTIIHVKGKHLCP SPLFPGPSKP IYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEY MFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDP EMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDALHMQALPP R
606	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVITYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSIEVMYPPPYLDNEK SNGTIIHVKGKHLCP SPLFPGPSKPFWVLVVGGLVACYSLLVTVAFIIFWVKRGRKKLLYIFKQ PFMRPVQTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTY DALHMQALPPR
607	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVITYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSIEVMYPPPYLDNEK SNGTIIHVKGKHLCP SPLFPGPSKPFWVLVVGGLVACYSLLVTVAFIIFWVRSKRSRLLSHSDYM NMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK

	RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
608	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVITYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSIEVMYPPPYLDNEK SNGTIIHVKGKHLCPSPFLFPGPSKPFVWL VVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPN GEYMFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQA LPPR
609	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVITYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSSESKYGPPCPPCPIY IWAPLAGTCGVLLLSLVI TLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL VKSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
610	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVITYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSSESKYGPPCPPCPIY IWAPLAGTCGVLLLSLVI TLYCRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
611	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVITYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSSESKYGPPCPPCPIY IWAPLAGTCGVLLLSLVI TLYCTKKKYSSSVHDPNGEYMFRAVNTAKKSRLTDVTLRVKFSRSA DAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQKDKMAEAYSE IGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
612	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVITYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSSESKYGPPCPPCFW VLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
613	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVITYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSSESKYGPPCPPCFW VLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYR SRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
614	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVITYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSSESKYGPPCPPCFW VLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFRAVNTAKKSRLTDVTLRVKFS RSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQKDKMAEA YSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
615	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVITYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSSLEPKSCDKTHTCPP CPIYIWAPLAGTCGVLLLSLVI TLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGG CELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
616	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVITYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSSLEPKSCDKTHTCPP CPIYIWAPLAGTCGVLLLSLVI TLYCRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAY RSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
617	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVITYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSSLEPKSCDKTHTCPP CPIYIWAPLAGTCGVLLLSLVI TLYCTKKKYSSSVHDPNGEYMFRAVNTAKKSRLTDVTLRVKFS RSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLYNELQKDKMAE AYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
618	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVITYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSSLEPKSCDKTHTCPP CPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEE EGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPPEMGGKPRRKNPQEGLY NELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
619	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVITYYADSVK

	GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSLEPKSCDKTHTCPP CPFWVLVVGGLVACYSLLVTVAFIIFWVRSKRSRL LHS DYMNMTPRRP GPTRKHYPYAPPRDF AAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYN ELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
620	EVQLLES GGGVLVQPGGSLRLSCAASGFTFESEAMSWVRQAPGKERELVSAISGSGEVITYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSLEPKSCDKTHTCPP CPFWVLVVGGLVACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLR VKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQDK MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

In particular embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in SEQ ID NO: 105; a spacer domain comprising an amino acid sequence set forth in SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 148, or SEQ ID NO: 150; a transmembrane domain comprising an amino acid sequence set forth in SEQ ID NO: 151 or SEQ ID NO: 153; a costimulatory domain comprising an amino acid sequence set forth in SEQ ID NO: 159, SEQ ID NO: 160, or SEQ ID NO: 162; and a primary signaling domain comprising an amino acid sequence set forth in SEQ ID NO: 158. In particular embodiments, a CAR comprises an amino acid sequence set forth in any one of SEQ ID NOs: 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, and 644.

SEQ ID NO.	AMINO ACID SEQUENCE
621	EVQLLES GGGVLVQPGGSLRLSCAASGFTFESEAMSWVRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSSTTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYI FKQPFMRPVQTTQEEDGCSRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYD VLDKRRGRDP EMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR
622	EVQLLES GGGVLVQPGGSLRLSCAASGFTFESEAMSWVRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSSTTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRL LHS DYMNMTPRRP GPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDP EMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
623	EVQLLES GGGVLVQPGGSLRLSCAASGFTFESEAMSWVRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSSTTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVH DPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRG RDP EMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH MQALPPR
624	EVQLLES GGGVLVQPGGSLRLSCAASGFTFESEAMSWVRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSSTTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLVACYSLLVTVAFIIFWVKRGRKKL LYIFKQPFMRPVQTTQEEDGCSRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRRE EYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLST ATKDTYDALHMQALPPR
625	EVQLLES GGGVLVQPGGSLRLSCAASGFTFESEAMSWVRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSSTTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLVACYSLLVTVAFIIFWVRSKRSRL LHS DYMNMTPRRP GPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA

	TKD TYDALHMQALPPR
626	EVQLLES GGG LVQP GGS LRLSCAAS GFT FEFSEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSTTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLVACYSLLVTVAFIIFWVTKKKYSS SVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
627	EVQLLES GGG LVQP GGS LRLSCAAS GFT FEFSEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSIEVMYPPPYLDNEK SNGTIIHVKGKHLCPSP LFPGPSKP IYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFM RPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRR GRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDAL HMQALPPR
628	EVQLLES GGG LVQP GGS LRLSCAAS GFT FEFSEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSIEVMYPPPYLDNEK SNGTIIHVKGKHLCPSP LFPGPSKP IYIWAPLAGTCGVLLLSLVITLYCKRSRSLHSDYMNMT PRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRG RDPPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH MQALPPR
629	EVQLLES GGG LVQP GGS LRLSCAAS GFT FEFSEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSIEVMYPPPYLDNEK SNGTIIHVKGKHLCPSP LFPGPSKP IYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEY MFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPP R
630	EVQLLES GGG LVQP GGS LRLSCAAS GFT FEFSEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSIEVMYPPPYLDNEK SNGTIIHVKGKHLCPSP LFPGPSKPFWVLVVGGLVACYSLLVTVAFIIFWVKRGRKKLLYIFKQ PFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTY DALHMQALPPR
631	EVQLLES GGG LVQP GGS LRLSCAAS GFT FEFSEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSIEVMYPPPYLDNEK SNGTIIHVKGKHLCPSP LFPGPSKPFWVLVVGGLVACYSLLVTVAFIIFWVRSKRSLHSDYM NMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
632	EVQLLES GGG LVQP GGS LRLSCAAS GFT FEFSEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSIEVMYPPPYLDNEK SNGTIIHVKGKHLCPSP LFPGPSKPFWVLVVGGLVACYSLLVTVAFIIFWVTKKKYSSSVHDPN GEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRD PEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQA LPPR
633	EVQLLES GGG LVQP GGS LRLSCAAS GFT FEFSEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSSESKYGPPCPPCIY IWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELR VKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDK MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
634	EVQLLES GGG LVQP GGS LRLSCAAS GFT FEFSEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSSESKYGPPCPPCIY IWAPLAGTCGVLLLSLVITLYCKRSRSLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
635	EVQLLES GGG LVQP GGS LRLSCAAS GFT FEFSEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSSESKYGPPCPPCIY IWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSA DAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSE IGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
636	EVQLLES GGG LVQP GGS LRLSCAAS GFT FEFSEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG

	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAHIEWETRLNWGGQTQVTVSSSESKYGPPCPPCPFW VLVVVGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
637	EVQLLES GGGVLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAHIEWETRLNWGGQTQVTVSSSESKYGPPCPPCPFW VLVVVGVLACYSLLVTVAFIIFWVRSKRSLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYR SRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
638	EVQLLES GGGVLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAHIEWETRLNWGGQTQVTVSSSESKYGPPCPPCPFW VLVVVGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFS RSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEA YSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
639	EVQLLES GGGVLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAHIEWETRLNWGGQTQVTVSSLEPKSCDKTHTCPP CPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEEDGCSCRFPEEEEGG CELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
640	EVQLLES GGGVLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAHIEWETRLNWGGQTQVTVSSLEPKSCDKTHTCPP CPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAY RSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
641	EVQLLES GGGVLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAHIEWETRLNWGGQTQVTVSSLEPKSCDKTHTCPP CPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKF SRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAE AYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
642	EVQLLES GGGVLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAHIEWETRLNWGGQTQVTVSSLEPKSCDKTHTCPP CPFWVLVVVGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEEDGCSCRFPEEE EGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLY NELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
643	EVQLLES GGGVLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAHIEWETRLNWGGQTQVTVSSLEPKSCDKTHTCPP CPFWVLVVVGVLACYSLLVTVAFIIFWVRSKRSLHSDYMNMTPRRPGPTRKHYPYAPPRDF AAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
644	EVQLLES GGGVLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAHIEWETRLNWGGQTQVTVSSLEPKSCDKTHTCPP CPFWVLVVVGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLR VKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

In particular embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in SEQ ID NO: 109; a spacer domain comprising an amino acid sequence set forth in SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 148, or SEQ ID NO: 150; a transmembrane domain comprising an amino acid sequence set forth in SEQ ID NO: 151 or SEQ ID NO: 153; a costimulatory domain comprising an amino acid sequence set forth in SEQ ID NO: 159, SEQ ID NO: 160, or SEQ ID NO: 162; and a primary signaling domain comprising an amino acid sequence set forth in SEQ ID NO: 158. In particular embodiments, a CAR comprises an amino acid sequence set

forth in any one of SEQ ID NOs: 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, and 668.

SEQ ID NO.	AMINO ACID SEQUENCE
645	EVQLLESQGGGLVQPGGSLRLSCAASGFTTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSTTTTPAPRPPTPA PTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
646	EVQLLESQGGGLVQPGGSLRLSCAASGFTTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSTTTTPAPRPPTPA PTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
647	EVQLLESQGGGLVQPGGSLRLSCAASGFTTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSTTTTPAPRPPTPA PTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKKYYSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
648	EVQLLESQGGGLVQPGGSLRLSCAASGFTTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSTTTTPAPRPPTPA PTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
649	EVQLLESQGGGLVQPGGSLRLSCAASGFTTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSTTTTPAPRPPTPA PTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
650	EVQLLESQGGGLVQPGGSLRLSCAASGFTTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSTTTTPAPRPPTPA PTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
651	EVQLLESQGGGLVQPGGSLRLSCAASGFTTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSIEVMYPPPYLDN EKSNGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
652	EVQLLESQGGGLVQPGGSLRLSCAASGFTTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSIEVMYPPPYLDN EKSNGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
653	EVQLLESQGGGLVQPGGSLRLSCAASGFTTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSIEVMYPPPYLDN EKSNGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKKYYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR

	PPR
654	EVQLLESGGGLVQPGGSLRLSCAASGFTTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSIEVMYPPPYLDN EKSNGTIIHVKGKHLCP SPLFPGPSKPFVWL VVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIF KQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDP EMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRRGK GHDGLYQGLSTATKD TYDALHMQALPPR
655	EVQLLESGGGLVQPGGSLRLSCAASGFTTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSIEVMYPPPYLDN EKSNGTIIHVKGKHLCP SPLFPGPSKPFVWL VVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSD YMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDP EMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRRGK GHDGLYQGLSTATKD TYDALHMQALPPR
656	EVQLLESGGGLVQPGGSLRLSCAASGFTTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSIEVMYPPPYLDN EKSNGTIIHVKGKHLCP SPLFPGPSKPFVWL VVVGGVLACYSLLVTVAFIIFWVTKKYS SSVHD PNGEYMFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGR DP EMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRRGK GHDGLYQGLSTATKD TYDALHM QALPPR
657	EVQLLESGGGLVQPGGSLRLSCAASGFTTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSSESKYGP PCPPCP IYIWAPLAGTCGVLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCE LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDP EMGGKPRRKNPQEGLYNELQK DMAEAYSEIGMKGERRRRGK GHDGLYQGLSTATKD TYDALHMQALPPR
658	EVQLLESGGGLVQPGGSLRLSCAASGFTTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSSESKYGP PCPPCP IYIWAPLAGTCGVLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRS RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDP EMGGKPRRKNPQEGLYNELQK DMAEAYSEIGMKGERRRRGK GHDGLYQGLSTATKD TYDALHMQALPPR
659	EVQLLESGGGLVQPGGSLRLSCAASGFTTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSSESKYGP PCPPCP IYIWAPLAGTCGVLLSLVITLYCTKKYSSSVHDPNGEYMFRAVNTAKKSRLTDVTLRVKFSR SADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDP EMGGKPRRKNPQEGLYNELQDKMAEAY SEIGMKGERRRRGK GHDGLYQGLSTATKD TYDALHMQALPPR
660	EVQLLESGGGLVQPGGSLRLSCAASGFTTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSSESKYGP PCPPCP FWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEG GCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDP EMGGKPRRKNPQEGLYNE LQDKDMAEAYSEIGMKGERRRRGK GHDGLYQGLSTATKD TYDALHMQALPPR
661	EVQLLESGGGLVQPGGSLRLSCAASGFTTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSSESKYGP PCPPCP FWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYPYAPPRDFAA YRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDP EMGGKPRRKNPQEGLYNEL QDKDMAEAYSEIGMKGERRRRGK GHDGLYQGLSTATKD TYDALHMQALPPR
662	EVQLLESGGGLVQPGGSLRLSCAASGFTTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSSESKYGP PCPPCP FWVLVVVGGVLACYSLLVTVAFIIFWVTKKYSSSVHDPNGEYMFRAVNTAKKSRLTDVTLRVK FSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDP EMGGKPRRKNPQEGLYNELQDKMA EAYSEIGMKGERRRRGK GHDGLYQGLSTATKD TYDALHMQALPPR
663	EVQLLESGGGLVQPGGSLRLSCAASGFTTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSLEPKSCDKTHTC PPCPIYIWAPLAGTCGVLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEG GCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDP EMGGKPRRKNPQEGLYN ELQDKDMAEAYSEIGMKGERRRRGK GHDGLYQGLSTATKD TYDALHMQALPPR
664	EVQLLESGGGLVQPGGSLRLSCAASGFTTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSLEPKSCDKTHTC PPCPIYIWAPLAGTCGVLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYPYAPPRDFA AYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDP EMGGKPRRKNPQEGLYNE LQDKDMAEAYSEIGMKGERRRRGK GHDGLYQGLSTATKD TYDALHMQALPPR

665	EVQLLESGGGLVQPGGSLRLSCAASGFTTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSLEPKSCDKTHTCPCPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
666	EVQLLESGGGLVQPGGSLRLSCAASGFTTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSLEPKSCDKTHTCPCPFVWL VVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEDGCSCRFPFEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
667	EVQLLESGGGLVQPGGSLRLSCAASGFTTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSLEPKSCDKTHTCPCPFVWL VVVGGVLACYSLLVTVAFIIFWVRSKRSLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
668	EVQLLESGGGLVQPGGSLRLSCAASGFTTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSLEPKSCDKTHTCPCPFVWL VVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

In particular embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in SEQ ID NO: 113; a spacer domain comprising an amino acid sequence set forth in SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 148, or SEQ ID NO: 150; a transmembrane domain comprising an amino acid sequence set forth in SEQ ID NO: 151 or SEQ ID NO: 153; a costimulatory domain comprising an amino acid sequence set forth in SEQ ID NO: 159, SEQ ID NO: 160, or SEQ ID NO: 162; and a primary signaling domain comprising an amino acid sequence set forth in SEQ ID NO: 158. In particular embodiments, a CAR comprises an amino acid sequence set forth in any one of SEQ ID NOs: 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, and 692.

SEQ ID NO.	AMINO ACID SEQUENCE
669	EVQLLESGGGLVQPGGSLRLSCAASGFTTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEDGCSCRFPFEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
670	EVQLLESGGGLVQPGGSLRLSCAASGFTTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
671	EVQLLESGGGLVQPGGSLRLSCAASGFTTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKYS SVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

672	EVQ LLES GGG LVQ PGGSLRLSCAASGFTTFEDYAMSWFRQAPGKERE GVS AISGKGGSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAVLDEEAGAEGGYWGOGTQVTVSSTTTPAPRPPT PAPTIIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGVLACYSLLVTVAFIIFWVKRG RKKLLYIFKQPFMRPVQTTQEE DGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNL GRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKKMAEAYSEIGMKGERRRRGK GHDGLYQ GLSTATKDTYDALHMQALPPR
673	EVQ LLES GGG LVQ PGGSLRLSCAASGFTTFEDYAMSWFRQAPGKERE GVS AISGKGGSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAVLDEEAGAEGGYWGOGTQVTVSSTTTPAPRPPT PAPTIIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGVLACYSLLVTVAFIIFWVRSK RSRL LHS DY MNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLG RREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKKMAEAYSEIGMKGERRRRGK GHDGLYQ LSTATKDTYDALHMQALPPR
674	EVQ LLES GGG LVQ PGGSLRLSCAASGFTTFEDYAMSWFRQAPGKERE GVS AISGKGGSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAVLDEEAGAEGGYWGOGTQVTVSSTTTPAPRPPT PAPTIIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGVLACYSLLVTVAFIIFWVTKK KYSSSVHDPNGEYMFMRVANTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKKMAEAYSEIGMKGERRRRGK GHDGLYQGLSTATK DTYDALHMQALPPR
675	EVQ LLES GGG LVQ PGGSLRLSCAASGFTTFEDYAMSWFRQAPGKERE GVS AISGKGGSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAVLDEEAGAEGGYWGOGTQVTVSSIEVMYPPPYL DNEKSNGTIIHVKGKHLCPSP LFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFK QPFMRPVQTTQEE DGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQDKKMAEAYSEIGMKGERRRRGK GHDGLYQGLSTATKDT YDALHMQALPPR
676	EVQ LLES GGG LVQ PGGSLRLSCAASGFTTFEDYAMSWFRQAPGKERE GVS AISGKGGSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAVLDEEAGAEGGYWGOGTQVTVSSIEVMYPPPYL DNEKSNGTIIHVKGKHLCPSP LFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRL LHS DY MNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQDKKMAEAYSEIGMKGERRRRGK GHDGLYQGLSTATKDTY DALHMQALPPR
677	EVQ LLES GGG LVQ PGGSLRLSCAASGFTTFEDYAMSWFRQAPGKERE GVS AISGKGGSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAVLDEEAGAEGGYWGOGTQVTVSSIEVMYPPPYL DNEKSNGTIIHVKGKHLCPSP LFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDP NGEYMFMRVANTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRD PEMGGKPRRKNPQEGLYNELQDKKMAEAYSEIGMKGERRRRGK GHDGLYQGLSTATKDTYDALHMQ ALPPR
678	EVQ LLES GGG LVQ PGGSLRLSCAASGFTTFEDYAMSWFRQAPGKERE GVS AISGKGGSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAVLDEEAGAEGGYWGOGTQVTVSSIEVMYPPPYL DNEKSNGTIIHVKGKHLCPSP LFPGPSKPFWVLVVVGVLACYSLLVTVAFIIFWVKRGRKKLLY IFKQPFMRPVQTTQEE DGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKKMAEAYSEIGMKGERRRRGK GHDGLYQGLSTAT KDTYDALHMQALPPR
679	EVQ LLES GGG LVQ PGGSLRLSCAASGFTTFEDYAMSWFRQAPGKERE GVS AISGKGGSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAVLDEEAGAEGGYWGOGTQVTVSSIEVMYPPPYL DNEKSNGTIIHVKGKHLCPSP LFPGPSKPFWVLVVVGVLACYSLLVTVAFIIFWVRSKRSRL LHS SDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQDKKMAEAYSEIGMKGERRRRGK GHDGLYQGLSTATK DTYDALHMQALPPR
680	EVQ LLES GGG LVQ PGGSLRLSCAASGFTTFEDYAMSWFRQAPGKERE GVS AISGKGGSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAVLDEEAGAEGGYWGOGTQVTVSSIEVMYPPPYL DNEKSNGTIIHVKGKHLCPSP LFPGPSKPFWVLVVVGVLACYSLLVTVAFIIFWVTKK KYSSSV HDPNGEYMFMRVANTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRR GRDPEMGGKPRRKNPQEGLYNELQDKKMAEAYSEIGMKGERRRRGK GHDGLYQGLSTATKDTYDAL HMQALPPR
681	EVQ LLES GGG LVQ PGGSLRLSCAASGFTTFEDYAMSWFRQAPGKERE GVS AISGKGGSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAVLDEEAGAEGGYWGOGTQVTVSSSESKYGPPCPP CPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEE DGCSCRFPEEEEGG CEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QDKKMAEAYSEIGMKGERRRRGK GHDGLYQGLSTATKDTYDALHMQALPPR

682	EVQLLES GGGVLVQPGGSLRLSCAASGFTTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSSESKYGPPCPP CPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAY RSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR
683	EVQLLES GGGVLVQPGGSLRLSCAASGFTTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSSESKYGPPCPP CPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSVVHDPNGEYMFMRVNTAKKSRLTDVTLRVKF SRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAE AYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR
684	EVQLLES GGGVLVQPGGSLRLSCAASGFTTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSSESKYGPPCPP CPFWVLVVVGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDF AAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLY NELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR
685	EVQLLES GGGVLVQPGGSLRLSCAASGFTTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSSESKYGPPCPP CPFWVLVVVGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDF AAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR
686	EVQLLES GGGVLVQPGGSLRLSCAASGFTTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSSESKYGPPCPP CPFWVLVVVGVLACYSLLVTVAFIIFWVTKKKYSVVHDPNGEYMFMRVNTAKKSRLTDVTLR VKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR
687	EVQLLES GGGVLVQPGGSLRLSCAASGFTTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSLEPKSCDKTH TCPPCPIYIWAPLAGTCGVLLLSLVITLYCYCRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEE EEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR
688	EVQLLES GGGVLVQPGGSLRLSCAASGFTTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSLEPKSCDKTH TCPPCPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRD FAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR
689	EVQLLES GGGVLVQPGGSLRLSCAASGFTTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSLEPKSCDKTH TCPPCPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSVVHDPNGEYMFMRVNTAKKSRLTDVTL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR
690	EVQLLES GGGVLVQPGGSLRLSCAASGFTTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSLEPKSCDKTH TCPPCPFWVLVVVGVLACYSLLVTVAFIIFWVRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRF PEEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNP QEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR
691	EVQLLES GGGVLVQPGGSLRLSCAASGFTTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSLEPKSCDKTH TCPPCPFWVLVVVGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTRKHYPYAP PRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNP QEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR
692	EVQLLES GGGVLVQPGGSLRLSCAASGFTTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSLEPKSCDKTH TCPPCPFWVLVVVGVLACYSLLVTVAFIIFWVTKKKYSVVHDPNGEYMFMRVNTAKKSRLTD VTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR

In preferred embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in SEQ ID NO: 117; a spacer

domain comprising an amino acid sequence set forth in SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 148, or SEQ ID NO: 150; a transmembrane domain comprising an amino acid sequence set forth in SEQ ID NO: 151 or SEQ ID NO: 153; a costimulatory domain comprising an amino acid sequence set forth in SEQ ID NO: 159, SEQ ID NO: 160, or SEQ ID NO: 162; and a primary signaling domain comprising an amino acid sequence set forth in SEQ ID NO: 158. In preferred embodiments, a CAR comprises an amino acid sequence set forth in any one of SEQ ID NOs: 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, and 716.

SEQ ID NO.	AMINO ACID SEQUENCE
693	EVQLLES GGGGLVQP GGSRLRLSCAASGFTFD RYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAE GGYWGQGTQVTVSSTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
694	EVQLLES GGGGLVQP GGSRLRLSCAASGFTFD RYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAE GGYWGQGTQVTVSSTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
695	EVQLLES GGGGLVQP GGSRLRLSCAASGFTFD RYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAE GGYWGQGTQVTVSSTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKYS SSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
696	EVQLLES GGGGLVQP GGSRLRLSCAASGFTFD RYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAE GGYWGQGTQVTVSSTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGVLACYSLLVTVAFIIFWVKRG RKLLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
697	EVQLLES GGGGLVQP GGSRLRLSCAASGFTFD RYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAE GGYWGQGTQVTVSSTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
698	EVQLLES GGGGLVQP GGSRLRLSCAASGFTFD RYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAE GGYWGQGTQVTVSSTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGVLACYSLLVTVAFIIFWVTKK KYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
699	EVQLLES GGGGLVQP GGSRLRLSCAASGFTFD RYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAE GGYWGQGTQVTVSSIEVMYPPPYLDNEKSGTIIHVKGKHLCPSP LFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDALHMQALPPR

700	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSIEVMYPPPYL DNEKSNGTIIHVKGKHLCPSP LFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRL LHSDY MNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL D KRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTY DALHMQALPPR
701	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSIEVMYPPPYL DNEKSNGTIIHVKGKHLCPSP LFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDP NGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRD PEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQ ALPPR
702	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSIEVMYPPPYL DNEKSNGTIIHVKGKHLCPSP LFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDP IFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT KDTYDALHMQALPPR
703	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSIEVMYPPPYL DNEKSNGTIIHVKGKHLCPSP LFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDP SDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYD VL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR
704	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSIEVMYPPPYL DNEKSNGTIIHVKGKHLCPSP LFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDP HDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRR GRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDAL HMQALPPR
705	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSIEVMYPPPYL CPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGG CELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
706	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSIEVMYPPPYL CPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRL LHSDYMNMTPRRPGPTRKHYPYAPPRDFAAY RSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
707	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSIEVMYPPPYL CPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFS RSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAE AYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
708	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSIEVMYPPPYL CPFWVLVVGGLVACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEE EGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLY NELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
709	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSIEVMYPPPYL CPFWVLVVGGLVACYSLLVTVAFIIFWVRSKRSRL LHSDYMNMTPRRPGPTRKHYPYAPPRDFA AYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
710	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSIEVMYPPPYL CPFWVLVVGGLVACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLR VKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDK

	MAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
711	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSLEPKSCDKTH TCPPCP IYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEE EEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLY YNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
712	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSLEPKSCDKTH TCPPCP IYIWAPLAGTCGVLLLSLVITLYCRSKRSRLHSDYMNMTPRRPGRPTRKHYPYAPPRD FAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLY NELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
713	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSLEPKSCDKTH TCPPCP IYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDK KMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
714	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSLEPKSCDKTH TCPPCPFWVLVVVGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRF PEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ EGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
715	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSLEPKSCDKTH TCPPCPFWVLVVVGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGRPTRKHYPYAP PRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ GLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
716	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSLEPKSCDKTH TCPPCPFWVLVVVGVLACYSLLVTVAFIIFWVTKKYSSSVHDPNGEYMFMRVNTAKKSRLTD VTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR

In particular embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in SEQ ID NO: 121; a spacer domain comprising an amino acid sequence set forth in SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 148, or SEQ ID NO: 150; a transmembrane domain comprising an amino acid sequence set forth in SEQ ID NO: 151 or SEQ ID NO: 153; a costimulatory domain comprising an amino acid sequence set forth in SEQ ID NO: 159, SEQ ID NO: 160, or SEQ ID NO: 162; and a primary signaling domain comprising an amino acid sequence set forth in SEQ ID NO: 158. In particular embodiments, a CAR comprises an amino acid sequence set forth in any one of SEQ ID NOs: 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, and 740.

SEQ ID NO.	AMINO ACID SEQUENCE
717	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRK KLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGL STATKDTYDALHMQALPPR
718	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK

	GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSSTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRS RLLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNLYNELNLGRR EYDVL DKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLS TATKDTYDALHMQALPPR
719	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMS WYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSSTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKY SSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVL DKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDT YDALHMQALPPR
720	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMS WYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSSTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGVLACYSLLVTVAFIIFWVKR GRKKLLYIFKQPFMRPVQTTQEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNLYNELN LGRREEYDVL DKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLY QGLSTATKDTYDALHMQALPPR
721	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMS WYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSSTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGVLACYSLLVTVAFIIFWVRS KRSRLLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNLYNELN LGRREEYDVL DKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQ GLSTATKDTYDALHMQALPPR
722	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMS WYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSSTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGVLACYSLLVTVAFIIFWVTK KKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEY DVL DKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTA KDTYDALHMQALPPR
723	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMS WYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSP LFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIF KQPFMRPVQTTQEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNLYNELNLGRREEYDV LDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKD TYDALHMQALPPR
724	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMS WYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSP LFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSD YMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVL DKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDT YDALHMQALPPR
725	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMS WYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSP LFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHD PNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVL DKRRGR DP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDALHM QALPPR
726	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMS WYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSP LFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHD YIFKQPFMRPVQTTQEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNLYNELNLGRREE YDVL DKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTA TKDTYDALHMQALPPR
727	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMS WYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSP LFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHD HSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNLYNELNLGRREEY DVL DKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTA KDTYDALHMQALPPR

728	EVQLLES GGGVLVQPGGSLRLSCAASGFTTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSPLEFPGPSKPFVWLVVVGVLACYSLLVTVAFIIFWVTKKKYSSS VHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDR RGRDP EMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDAL LHMQALPPR
729	EVQLLES GGGVLVQPGGSLRLSCAASGFTTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSSESKYGPPCP PCPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEG GCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRGRDP EMGGKPRRKNPQEGLYNE LQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
730	EVQLLES GGGVLVQPGGSLRLSCAASGFTTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSSESKYGPPCP PCPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAA YRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRGRDP EMGGKPRRKNPQEGLYNEL QDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
731	EVQLLES GGGVLVQPGGSLRLSCAASGFTTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSSESKYGPPCP PCPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVK FSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRGRDP EMGGKPRRKNPQEGLYNELQDKMA EAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
732	EVQLLES GGGVLVQPGGSLRLSCAASGFTTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSSESKYGPPCP PCPFWVLVVGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEE EEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRGRDP EMGGKPRRKNPQEG LYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
733	EVQLLES GGGVLVQPGGSLRLSCAASGFTTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSSESKYGPPCP PCPFWVLVVGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRD FAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRGRDP EMGGKPRRKNPQEG LYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
734	EVQLLES GGGVLVQPGGSLRLSCAASGFTTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSSESKYGPPCP PCPFWVLVVGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRGRDP EMGGKPRRKNPQEGLYNELQDK MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
735	EVQLLES GGGVLVQPGGSLRLSCAASGFTTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSLEPKSCDKT HTCPPCPYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPE EEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRGRDP EMGGKPRRKNPQEG LYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
736	EVQLLES GGGVLVQPGGSLRLSCAASGFTTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSLEPKSCDKT HTCPPCPYIWAPLAGTCGVLLLSLVITLYCRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPR DFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRGRDP EMGGKPRRKNPQEG LYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
737	EVQLLES GGGVLVQPGGSLRLSCAASGFTTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSLEPKSCDKT HTCPPCPYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVT LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRGRDP EMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
738	EVQLLES GGGVLVQPGGSLRLSCAASGFTTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSLEPKSCDKT HTCPPCPFWVLVVGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCR FPEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRGRDP EMGGKPRRKNP QEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
739	EVQLLES GGGVLVQPGGSLRLSCAASGFTTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSLEPKSCDKT HTCPPCPFWVLVVGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTRKHYPYA

	PPRDFAAYSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQ EGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
740	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMSWYRQAPGKERELVSAISGGSGSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSSLEPKSCDKT HTCPPCPFWVLVVGGLVACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLT DVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR

In particular embodiments, a CAR comprises an antibody or antigen binding
fragment thereof comprising an amino acid sequence set forth in SEQ ID NO: 125; a spacer
domain comprising an amino acid sequence set forth in SEQ ID NO: 145, SEQ ID NO: 146,
SEQ ID NO: 148, or SEQ ID NO: 150; a transmembrane domain comprising an amino acid
5 sequence set forth in SEQ ID NO: 151 or SEQ ID NO: 153; a costimulatory domain
comprising an amino acid sequence set forth in SEQ ID NO: 159, SEQ ID NO: 160, or SEQ
ID NO: 162; and a primary signaling domain comprising an amino acid sequence set forth in
SEQ ID NO: 158. In particular embodiments, a CAR comprises an amino acid sequence set
forth in any one of SEQ ID NOs: 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752,
10 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, and 764.

SEQ ID NO.	AMINO ACID SEQUENCE
741	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKERELVSAISGHGDSITYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSSTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRK KLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGR REEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGL STATKDTYDALHMQALPPR
742	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKERELVSAISGHGDSITYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSSTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRS RLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGR EEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLS TATKDTYDALHMQALPPR
743	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKERELVSAISGHGDSITYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSSTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKY SSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDT YDALHMQALPPR
744	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKERELVSAISGHGDSITYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSSTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLVACYSLLVTVAFIIFWVKR GRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELN LGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLY QGLSTATKDTYDALHMQALPPR
745	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKERELVSAISGHGDSITYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSSTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLVACYSLLVTVAFIIFWVRS KRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNL GRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQ GLSTATKDTYDALHMQALPPR
746	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKERELVSAISGHGDSITYYADSVK

	GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSSTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGVLACYSLLVTVAFIIFWVTK KKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEY DVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTAT KDTYDALHMQALPPR
747	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTM SWYRQAPGKERELVSAISGHGDSITYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSP LFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIF KQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNLYNELNLGRREEYDV LDKRRGRDPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKD TYDALHMQALPPR
748	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTM SWYRQAPGKERELVSAISGHGDSITYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSP LFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLHSD YMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVL DKRRGRDPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDT YDALHMQALPPR
749	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTM SWYRQAPGKERELVSAISGHGDSITYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSP LFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHD PNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGR DPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDALHM QALPPR
750	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTM SWYRQAPGKERELVSAISGHGDSITYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSP LFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLL YIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNLYNELNLGRREE YDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTA TKDTYDALHMQALPPR
751	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTM SWYRQAPGKERELVSAISGHGDSITYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSP LFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIF HSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNLYNELNLGRREEY DVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTAT KDTYDALHMQALPPR
752	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTM SWYRQAPGKERELVSAISGHGDSITYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSP LFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIF VHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKR RGRDPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDA LHMQALPPR
753	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTM SWYRQAPGKERELVSAISGHGDSITYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSIEVMYPPPY PCPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEG GCEL RVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDALHMQALPPR
754	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTM SWYRQAPGKERELVSAISGHGDSITYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSIEVMYPPPY PCPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAA YRSRVKFSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDALHMQALPPR
755	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTM SWYRQAPGKERELVSAISGHGDSITYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSIEVMYPPPY PCPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVK FSRSADAPAYQQGQNLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDALHMQALPPR
756	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTM SWYRQAPGKERELVSAISGHGDSITYYADSVK GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSIEVMYPPPY PCPFWVLVVGGVLACYSLLVTVAFIIFWVTKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEE

	EEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
757	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMWYRQAPGKERELVSAISGHGDSITYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSSESKYGPPCPFCPFWVLVVGGLVACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
758	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMWYRQAPGKERELVSAISGHGDSITYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSSESKYGPPCPFCPFWVLVVGGLVACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
759	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMWYRQAPGKERELVSAISGHGDSITYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSLEPKSCDKTHTCPPCPYIYWAPLAGTCGVLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEDGCSCRFPFEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
760	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMWYRQAPGKERELVSAISGHGDSITYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSLEPKSCDKTHTCPPCPYIYWAPLAGTCGVLLSLVITLYCRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
761	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMWYRQAPGKERELVSAISGHGDSITYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSLEPKSCDKTHTCPPCPYIYWAPLAGTCGVLLSLVITLYCTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
762	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMWYRQAPGKERELVSAISGHGDSITYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSLEPKSCDKTHTCPPCPFWVLVVGGLVACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEDGCSCRFPFEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
763	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMWYRQAPGKERELVSAISGHGDSITYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSLEPKSCDKTHTCPPCPFWVLVVGGLVACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
764	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMWYRQAPGKERELVSAISGHGDSITYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSLEPKSCDKTHTCPPCPFWVLVVGGLVACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

In particular embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in SEQ ID NO: 129; a spacer domain comprising an amino acid sequence set forth in SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 148, or SEQ ID NO: 150; a transmembrane domain comprising an amino acid sequence set forth in SEQ ID NO: 151 or SEQ ID NO: 153; a costimulatory domain comprising an amino acid sequence set forth in SEQ ID NO: 159, SEQ ID NO: 160, or SEQ ID NO: 162; and a primary signaling domain comprising an amino acid sequence set forth in SEQ ID NO: 158. In particular embodiments, a CAR comprises an amino acid sequence set

forth in any one of SEQ ID NOs: 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, and 788.

SEQ ID NO.	AMINO ACID SEQUENCE
765	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSTTTTPAPRPPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRG RKKLLYIFKQPFMRPVQTTQEEDGCSCRFP EEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
766	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSTTTTPAPRPPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
767	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSTTTTPAPRPPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
768	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSTTTTPAPRPPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFP EEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
769	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSTTTTPAPRPPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
770	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSTTTTPAPRPPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
771	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFP EEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
772	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
773	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFLPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR

	HMQALPPR
774	EVQLLES GGGGLVQP GGSRLRLSCAASGFT FSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSIEVMYPP PYLDNEK SNGTIIHVKGKHLCPSP LFPGPSKPFWVLV VVGVLACYSLLVTVAFIIFWVKRGRKK LLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRR EYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRRGK GHDGLYQGLS TATKDTYDALHMQALPPR
775	EVQLLES GGGGLVQP GGSRLRLSCAASGFT FSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSIEVMYPP PYLDNEK SNGTIIHVKGKHLCPSP LFPGPSKPFWVLV VVGVLACYSLLVTVAFIIFWVRSKRSR LLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRRE EYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRRGK GHDGLYQGLS ATKDTYDALHMQALPPR
776	EVQLLES GGGGLVQP GGSRLRLSCAASGFT FSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSIEVMYPP PYLDNEK SNGTIIHVKGKHLCPSP LFPGPSKPFWVLV VVGVLACYSLLVTVAFIIFWVTKKKYS SSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQDKMAEAYSEIGMKGERRRRGK GHDGLYQGLSTATKDTY DALHMQALPPR
777	EVQLLES GGGGLVQP GGSRLRLSCAASGFT FSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSIESKYGPP CPPCP IYIWAPLAGTCGVLLLSLVI TLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEE EGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREYDVL DKRRGRDPEMGGKPRRKNPQEGLY NELQDKMAEAYSEIGMKGERRRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
778	EVQLLES GGGGLVQP GGSRLRLSCAASGFT FSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSIESKYGPP CPPCP IYIWAPLAGTCGVLLLSLVI TLYCKSRKSRLLHSDYMNMTPRRPGPTRKHYPYAPPRDF AAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREYDVL DKRRGRDPEMGGKPRRKNPQEGLYN ELQDKMAEAYSEIGMKGERRRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
779	EVQLLES GGGGLVQP GGSRLRLSCAASGFT FSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSIESKYGPP CPPCP IYIWAPLAGTCGVLLLSLVI TLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLR VKFSRSADAPAYQQGQNQLYNELNLGRREYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQDK MAEAYSEIGMKGERRRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
780	EVQLLES GGGGLVQP GGSRLRLSCAASGFT FSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSIESKYGPP CPPCPFWVLV VVGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRF EEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREYDVL DKRRGRDPEMGGKPRRKNPQ GLYNELQDKMAEAYSEIGMKGERRRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
781	EVQLLES GGGGLVQP GGSRLRLSCAASGFT FSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSIESKYGPP CPPCPFWVLV VVGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYPYAP RDFAAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREYDVL DKRRGRDPEMGGKPRRKNPQ GLYNELQDKMAEAYSEIGMKGERRRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
782	EVQLLES GGGGLVQP GGSRLRLSCAASGFT FSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSIESKYGPP CPPCPFWVLV VVGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDV TLRVKFSRSADAPAYQQGQNQLYNELNLGRREYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQ DKMAEAYSEIGMKGERRRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
783	EVQLLES GGGGLVQP GGSRLRLSCAASGFT FSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSLEPKSCD KTHTCPPCP IYIWAPLAGTCGVLLLSLVI TLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRF PEEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREYDVL DKRRGRDPEMGGKPRRKNPQ EGLYNELQDKMAEAYSEIGMKGERRRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
784	EVQLLES GGGGLVQP GGSRLRLSCAASGFT FSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSLEPKSCD KTHTCPPCP IYIWAPLAGTCGVLLLSLVI TLYCKSRKSRLLHSDYMNMTPRRPGPTRKHYPYAP PRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREYDVL DKRRGRDPEMGGKPRRKNPQ GLYNELQDKMAEAYSEIGMKGERRRRGK GHDGLYQGLSTATKDTYDALHMQALPPR

785	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSLEPKSCDKTHTCPPCPFIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
786	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSLEPKSCDKTHTCPPCPFWVLVVVGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCS CRFP EEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRK NPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
787	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSLEPKSCDKTHTCPPCPFWVLVVVGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTRKHYP YAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKN PQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
788	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSLEPKSCDKTHTCPPCPFWVLVVVGVLACYSLLVTVAFIIFWVTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLY NELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

In particular embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in SEQ ID NO: 133; a spacer domain comprising an amino acid sequence set forth in SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 148, or SEQ ID NO: 150; a transmembrane domain comprising an amino acid sequence set forth in SEQ ID NO: 151 or SEQ ID NO: 153; a costimulatory domain comprising an amino acid sequence set forth in SEQ ID NO: 159, SEQ ID NO: 160, or SEQ ID NO: 162; and a primary signaling domain comprising an amino acid sequence set forth in SEQ ID NO: 158. In particular embodiments, a CAR comprises an amino acid sequence set forth in any one of SEQ ID NOs: 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, and 812.

SEQ ID NO.	AMINO ACID SEQUENCE
789	EVQLLESGGGLVQPGGSLRLSCAASGFTTFDYDMSWYRQAPGKERELVSVIHSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAPGYSDLSFDYINFQYWGQGTQVTVSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCS CRFP EEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
790	EVQLLESGGGLVQPGGSLRLSCAASGFTTFDYDMSWYRQAPGKERELVSVIHSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAPGYSDLSFDYINFQYWGQGTQVTVSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
791	EVQLLESGGGLVQPGGSLRLSCAASGFTTFDYDMSWYRQAPGKERELVSVIHSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAPGYSDLSFDYINFQYWGQGTQVTVSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

792	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAPGYSDLSFDYYNFDYWGQGTQVTVSSTTTTPAPR PPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAF I IFVW KRGRKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNOLYNE LNLGRREYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDG LYQGLSTATKDTYDALHMQALPPR
793	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAPGYSDLSFDYYNFDYWGQGTQVTVSSTTTTPAPR PPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAF I IFVW RSKRSRL LHS DYMNMTPRRPGPTRKH YQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNOLYNEI NLGRREYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGI YQGLSTATKDTYDALHMQALPPR
794	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAPGYSDLSFDYYNFDYWGQGTQVTVSSTTTTPAPR PPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAF I IFVW TKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNOLYNE LNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLST ATKDTYDALHMQALPPR
795	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAPGYSDLSFDYYNFDYWGQGTQVTVSSIEVMYPP PYLDNEKSNGTIIHVKGKHLCPSPLEFPGPSKPIYIWAPLAGTCGVLLLSLIVITLYCKRGRKKLLY IFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNOLYNE LNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT KDTYDALHMQALPPR
796	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAPGYSDLSFDYYNFDYWGQGTQVTVSSIEVMYPP PYLDNEKSNGTIIHVKGKHLCPSPLEFPGPSKPIYIWAPLAGTCGVLLLSLIVITLYCKRSKRSRLH SDYMNMTPRRPGPTRKH YQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNOLYNE LNLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR
797	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAPGYSDLSFDYYNFDYWGQGTQVTVSSIEVMYPP PYLDNEKSNGTIIHVKGKHLCPSPLEFPGPSKPIYIWAPLAGTCGVLLLSLIVITLYC'TKKYSSSV HDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNOLYNE LNLGRREEYDVLDKRR GRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDAL HMQALPPR
798	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAPGYSDLSFDYYNFDYWGQGTQVTVSSIEVMYPP PYLDNEKSNGTIIHVKGKHLCPSPLEFPGPSKPFVWLVVVGGVLACYSLLVTVAF I IFVWKRGRK LLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNOLYNE LNLGRR EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLS TATKDTYDALHMQALPPR
799	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAPGYSDLSFDYYNFDYWGQGTQVTVSSIEVMYPP PYLDNEKSNGTIIHVKGKHLCPSPLEFPGPSKPFVWLVVVGGVLACYSLLVTVAF I IFVWRSKRSR LLHSDYMNMTPRRPGPTRKH YQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNOLYNE LNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLST ATKDTYDALHMQALPPR
800	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAPGYSDLSFDYYNFDYWGQGTQVTVSSIEVMYPP PYLDNEKSNGTIIHVKGKHLCPSPLEFPGPSKPFVWLVVVGGVLACYSLLVTVAF I IFVWTKKKYS SSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNOLYNE LNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTY DALHMQALPPR
801	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAPGYSDLSFDYYNFDYWGQGTQVTVSSSESKYGP CPPCPIYIWAPLAGTCGVLLLSLIVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEE EGGCEL RVKFSRSADAPAYQQGQNOLYNE LNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLY NELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

802	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYMDSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAPGYSDLSFDYNNFDYWGQGTQVTVSSESKEYGPP CPPCP IYIWAPLAGTCGVLLLSLVITLYCRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDF AAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
803	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYMDSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAPGYSDLSFDYNNFDYWGQGTQVTVSSESKEYGPP CPPCP IYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLR VKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
804	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYMDSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAPGYSDLSFDYNNFDYWGQGTQVTVSSESKEYGPP CPPCPFWVLVVVGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRF EEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ GLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
805	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYMDSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAPGYSDLSFDYNNFDYWGQGTQVTVSSESKEYGPP CPPCPFWVLVVVGVLACYSLLVTVAFIIFWVRSKRSLHSDYMNMTPRRPGPTRKHYPYAP RDFAAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
806	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYMDSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAPGYSDLSFDYNNFDYWGQGTQVTVSSESKEYGPP CPPCPFWVLVVVGVLACYSLLVTVAFIIFWVTKKYSSSVHDPNGEYMFMRVNTAKKSRLTDV TLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
807	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYMDSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAPGYSDLSFDYNNFDYWGQGTQVTVSSELPKSCD KTHTCPPCP IYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRF PEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ EGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
808	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYMDSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAPGYSDLSFDYNNFDYWGQGTQVTVSSELPKSCD KTHTCPPCP IYIWAPLAGTCGVLLLSLVITLYCRSKRSRLHSDYMNMTPRRPGPTRKHYPYAP PRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ GLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
809	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYMDSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAPGYSDLSFDYNNFDYWGQGTQVTVSSELPKSCD KTHTCPPCP IYIWAPLAGTCGVLLLSLVITLYCTKKYSSSVHDPNGEYMFMRVNTAKKSRLTD VTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
810	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYMDSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAPGYSDLSFDYNNFDYWGQGTQVTVSSELPKSCD KTHTCPPCPFWVLVVVGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRR KNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
811	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYMDSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAPGYSDLSFDYNNFDYWGQGTQVTVSSELPKSCD KTHTCPPCPFWVLVVVGVLACYSLLVTVAFIIFWVRSKRSLHSDYMNMTPRRPGPTRKHYP YAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKN PQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
812	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYMDSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAPGYSDLSFDYNNFDYWGQGTQVTVSSELPKSCD KTHTCPPCPFWVLVVVGVLACYSLLVTVAFIIFWVTKKYSSSVHDPNGEYMFMRVNTAKKSRL LTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLY NELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

In particular embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in SEQ ID NO: 137; a spacer

domain comprising an amino acid sequence set forth in SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 148, or SEQ ID NO: 150; a transmembrane domain comprising an amino acid sequence set forth in SEQ ID NO: 151 or SEQ ID NO: 153; a costimulatory domain comprising an amino acid sequence set forth in SEQ ID NO: 159, SEQ ID NO: 160, or SEQ ID NO: 162; and a primary signaling domain comprising an amino acid sequence set forth in SEQ ID NO: 158. In particular embodiments, a CAR comprises an amino acid sequence set forth in any one of SEQ ID NOs: 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, and 836.

SEQ ID NO.	AMINO ACID SEQUENCE
813	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSTTTTPAPR PPTPAPTIIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRG RKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNL GRREYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQ GLSTATKDTYDALHMQALPPR
814	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSTTTTPAPR PPTPAPTIIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSK RSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLG RREYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQ LSTATKDTYDALHMQALPPR
815	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSTTTTPAPR PPTPAPTIIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKK KYSSSVHDPNGEYMFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATK DTYDALHMQALPPR
816	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSTTTTPAPR PPTPAPTIIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLVACYSLLVTVAFIIFWV KRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNE LNLGRREYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDG LYQGLSTATKDTYDALHMQALPPR
817	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSTTTTPAPR PPTPAPTIIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLVACYSLLVTVAFIIFWV RSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNEL NLGRREYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGL YQGLSTATKDTYDALHMQALPPR
818	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSTTTTPAPR PPTPAPTIIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVGGLVACYSLLVTVAFIIFWV TKKKYSSSVHDPNGEYMFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLST ATKDTYDALHMQALPPR
819	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDN SKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSIEVMYPP PYLDNEKSNGTIIHVKGKHLCPSPFLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLY IFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTAT KDTYDALHMQALPPR

820	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYC NAGFKGDHPHPKDAFDIWGGQTQVTVSSIEV MYPP PYLDNEKSNGTIIHVKGKHLCPSPLEFPGPSKPIYIWAPLAGTCGVLLLSLVTLYCYCRSKRSRLH SDYMMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK TDYDALHMQALPPR
821	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYC NAGFKGDHPHPKDAFDIWGGQTQVTVSSIEV MYPP PYLDNEKSNGTIIHVKGKHLCPSPLEFPGPSKPIYIWAPLAGTCGVLLLSLVTLYCTKKKYSSSV HDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRR GRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKTDYDAL HMQALPPR
822	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYC NAGFKGDHPHPKDAFDIWGGQTQVTVSSIEV MYPP PYLDNEKSNGTIIHVKGKHLCPSPLEFPGPSKPFVWL VVVGVLACYSLLVTVAFIIFVWKRGRK LLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGR EYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLS TATKTDYDALHMQALPPR
823	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYC NAGFKGDHPHPKDAFDIWGGQTQVTVSSIEV MYPP PYLDNEKSNGTIIHVKGKHLCPSPLEFPGPSKPFVWL VVVGVLACYSLLVTVAFIIFVWRSKR LLHSDYMMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGR EYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLS TATKTDYDALHMQALPPR
824	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYC NAGFKGDHPHPKDAFDIWGGQTQVTVSSIEV MYPP PYLDNEKSNGTIIHVKGKHLCPSPLEFPGPSKPFVWL VVVGVLACYSLLVTVAFIIFVWTKKKYS SSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKTDY DALHMQALPPR
825	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYC NAGFKGDHPHPKDAFDIWGGQTQVTVSSIESKYGP CPPCPYIYWAPLAGTCGVLLLSLVTLYCYCRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEE EGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLY NELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKTDYDALHMQALPPR
826	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYC NAGFKGDHPHPKDAFDIWGGQTQVTVSSIESKYGP CPPCPYIYWAPLAGTCGVLLLSLVTLYCYCRSKRSRLHSDYMMNMTPRRPGPTRKHYPYAPPRD FAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLY NELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKTDYDALHMQALPPR
827	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYC NAGFKGDHPHPKDAFDIWGGQTQVTVSSIESKYGP CPPCPYIYWAPLAGTCGVLLLSLVTLYCTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLR VKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKTDYDALHMQALPPR
828	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYC NAGFKGDHPHPKDAFDIWGGQTQVTVSSIESKYGP CPPCPFVWL VVVGVLACYSLLVTVAFIIFVWKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRF EEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKTDYDALHMQALPPR
829	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYC NAGFKGDHPHPKDAFDIWGGQTQVTVSSIESKYGP CPPCPFVWL VVVGVLACYSLLVTVAFIIFVWKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRF RDFAAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKTDYDALHMQALPPR
830	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYC NAGFKGDHPHPKDAFDIWGGQTQVTVSSIESKYGP CPPCPFVWL VVVGVLACYSLLVTVAFIIFVWTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDV TLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRRGRDPEMGGKPRRKNPQEGLYNELQ

	KDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
831	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSLEPKSCD KTHTCPPCP IYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRF PEEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDP EMGGKPRRKNPQ EGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
832	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSLEPKSCD KTHTCPPCP IYIWAPLAGTCGVLLLSLVITLYCRSKRSRLHSDYMNMPRRPGPTRKHYPYAP PRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDP EMGGKPRRKNPQ EGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
833	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSLEPKSCD KTHTCPPCP IYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTD VTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDP EMGGKPRRKNPQ EGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
834	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSLEPKSCD KTHTCPPCPFWVLVVGGLVACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSC CRFP EEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDP EMGGKPRRK NPQ EGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
835	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSLEPKSCD KTHTCPPCPFWVLVVGGLVACYSLLVTVAFIIFWVRSKRSRLHSDYMNMPRRPGPTRKHYP YAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDP EMGGKPRRKN PQ EGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR
836	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDN SKNTLYLQMN SLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSLEPKSCD KTHTCPPCPFWVLVVGGLVACYSLLVTVAFIIFWVTKKYSSSVHDPNGEYMFMRVNTAKKSR LTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDP EMGGKPRRKNPQ EGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALPPR

In particular embodiments, a CAR comprises an antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in SEQ ID NO: 141; a spacer domain comprising an amino acid sequence set forth in SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 148, or SEQ ID NO: 150; a transmembrane domain comprising an amino acid sequence set forth in SEQ ID NO: 151 or SEQ ID NO: 153; a costimulatory domain comprising an amino acid sequence set forth in SEQ ID NO: 159, SEQ ID NO: 160, or SEQ ID NO: 162; and a primary signaling domain comprising an amino acid sequence set forth in SEQ ID NO: 158. In particular embodiments, a CAR comprises an amino acid sequence set forth in any one of SEQ ID NOs: 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, and 860.

SEQ ID NO.	AMINO ACID SEQUENCE
837	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCNALEGGPTTAIQGGPDYWGQGTQVTVSSSTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCK RGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNQLYNEL NLGRREEYDVL DKRRGRDP EMGGKPRRKNPQ EGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGL YQGLSTATKDTYDALHMQALPPR
838	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR

	GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSTTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLIVITLYCR SKRSRL LHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELN LGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLY QGLSTATKDTYDALHMQALPPR
839	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGM SWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSTTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLIVITLYCT KKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTA TKDTYDALHMQALPPR
840	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGM SWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSTTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWLVVVVGGVLACYSLLVTVAFIIF WVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFP EEEEGGCEL RVKFSRSADAPAYQQGQNQLY NELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR
841	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGM SWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSTTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWLVVVVGGVLACYSLLVTVAFIIF WVRSKRSL LHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYN ELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR
842	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGM SWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSTTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWLVVVVGGVLACYSLLVTVAFIIF WVTKKYSVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGR REEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGL STATKDTYDALHMQALPPR
843	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGM SWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSIEVMY PPPYLDNEKSGNTIIHVKGKHLCP SPLFPGPSKPIYIWAPLAGTCGVLLLSLIVITLYCKRGRKKL LYIFKQPFMRPVQTTQEEDGCSCRFP EEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRRE EYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLST ATKDTYDALHMQALPPR
844	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGM SWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSIEVMY PPPYLDNEKSGNTIIHVKGKHLCP SPLFPGPSKPIYIWAPLAGTCGVLLLSLIVITLYCKRSRL LHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTA TKDTYDALHMQALPPR
845	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGM SWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSIEVMY PPPYLDNEKSGNTIIHVKGKHLCP SPLFPGPSKPIYIWAPLAGTCGVLLLSLIVITLYCTKKKYSS SVHDPNGEYMFMRVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DK RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYD ALHMQALPPR
846	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGM SWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSIEVMY PPPYLDNEKSGNTIIHVKGKHLCP SPLFPGPSKPIYIWAPLAGTCGVLLLSLIVITLYCTKKKYSS KKLLYIFKQPFMRPVQTTQEEDGCSCRFP EEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLG RREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQG LSTATKDTYDALHMQALPPR
847	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGM SWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDN SKNTLYLQMN SLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSIEVMY PPPYLDNEKSGNTIIHVKGKHLCP SPLFPGPSKPIYIWAPLAGTCGVLLLSLIVITLYCTKKKYSS SRL LHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGR REEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGDGLYQGL STATKDTYDALHMQALPPR

848	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTTISRDN SKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSIEVMY PPPYLDNEKSNGTIIHVKGKHLCPSPFLPGPSKPFVWL VVVGVLACYSLLVTVAFIIFWVTKKK YSSSVHDPNGEYMFRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQDKDMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKD TYDALHMQALPPR
849	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTTISRDN SKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSSESKYG PPCPPCPYIYWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFE EEEGGCCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG LYNELQDKDMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDALHMQALPPR
850	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTTISRDN SKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSSESKYG PPCPPCPYIYWAPLAGTCGVLLLSLVITLYCKSRKSRLLHSDYMNMTPRRPGPTRKHYPYAPPR DFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG LYNELQDKDMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDALHMQALPPR
851	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTTISRDN SKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSSESKYG PPCPPCPYIYWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFRAVNTAKKSRLTDVT LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDALHMQALPPR
852	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTTISRDN SKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSSESKYG PPCPPCPFWVLVVVGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCR FPEEEEGGCCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNP QEGLYNELQDKDMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDALHMQALPPR
853	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTTISRDN SKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSSESKYG PPCPPCPFWVLVVVGVLACYSLLVTVAFIIFWVSRKSRLLHSDYMNMTPRRPGPTRKHYPYA PPRDFAAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNP QEGLYNELQDKDMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDALHMQALPPR
854	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTTISRDN SKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSSESKYG PPCPPCPFWVLVVVGVLACYSLLVTVAFIIFWVTKKYSVHDPNGEYMFRAVNTAKKSRLT DVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQDKDMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDALHMQALPPR
855	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTTISRDN SKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSLEPKS CDKTHTCPPCPYIYWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSC RFPEEEEGGCCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKN PQEGLYNELQDKDMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDALHMQALPPR
856	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTTISRDN SKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSLEPKS CDKTHTCPPCPYIYWAPLAGTCGVLLLSLVITLYCKSRKSRLLHSDYMNMTPRRPGPTRKHYPY APPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNP QEGLYNELQDKDMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDALHMQALPPR
857	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTTISRDN SKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSLEPKS CDKTHTCPPCPYIYWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFRAVNTAKKSRL TDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQDKDMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDALHMQALPPR
858	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTTISRDN SKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSLEPKS CDKTHTCPPCPFWVLVVVGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDG CSCRFPPEEEEGGCCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPR RKNPQEGLYNELQDKDMAEAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDALHMQALPPR
859	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTTISRDN SKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSLEPKS CDKTHTCPPCPFWVLVVVGVLACYSLLVTVAFIIFWVSRKSRLLHSDYMNMTPRRPGPTRKHYPY

	QPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNEINLGRREEYDVLDKRRGRDPGEMGGKPRR KNPQOGLYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
860	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDN SKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSLEPKS CDKTHTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRVNTAKK SRLTDVTLRVKFSRSADAPAYQQGQNQLYNEINLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEG LYNELQDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

F. POLYPEPTIDES

Polypeptides, fusion polypeptides, and polypeptide variants are contemplated in particular embodiments. Exemplary polypeptides contemplated herein include but not limited to, antibodies and antigen binding fragments thereof, fusion polypeptides, bispecific antibodies, bispecific T cell engagers (BiTEs), antibody conjugates, chimeric antigen receptors (CARs) and components thereof, and variants and/or fragments thereof, *e.g.*, SEQ ID NOs: 1-873 and 954-979. Polypeptides contemplated herein also include those encoded by polynucleotide sequences set forth in any one of SEQ ID NOs: 874-953.

Polypeptide,” “polypeptide,” “peptide,” and “protein” are used interchangeably, unless specified to the contrary, and according to conventional meaning, *i.e.*, as a sequence of amino acids. In particular embodiments, a “polypeptide” is a fusion polypeptide or polypeptide variant. Polypeptides can be prepared using any of a variety of well-known recombinant and/or synthetic techniques. Polypeptides are not limited to a specific length, *e.g.*, they may comprise a full-length protein sequence, a fragment of a full-length protein, or a fusion protein, and may include post-translational modifications, *e.g.*, glycosylations, acetylations, phosphorylations and the like, as well as other modifications known in the art, both naturally occurring and non-naturally occurring.

An “isolated peptide,” “isolated protein” or an “isolated polypeptide” as used herein, refers to isolation, separation, and/or purification of a polypeptide molecule from a cellular environment, and from association with other components of the cell, *i.e.*, it is not significantly associated with *in vivo* substances.

Polypeptides include “polypeptide variants.” In particular embodiments, a polypeptide variant is referred to as a “modified polypeptide.” Polypeptide variants may differ from a naturally occurring polypeptide in one or more amino acid substitutions, deletions, additions and/or insertions. For example, in particular embodiments, it may be desirable to modulate one or more biological activities of a chimeric antigen receptor by introducing one or more amino acid substitutions, deletions, additions and/or insertions into the polypeptide. Such variants may be naturally occurring or may be synthetically

generated. In particular embodiments, polypeptides include polypeptide variants having at least about 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 86%, 97%, 98%, or 99% amino acid identity to any reference sequence contemplated herein, typically where the variant maintains at least one biological activity of the reference sequence.

Polypeptides variants include “polypeptide fragments.” Illustrative examples of polypeptide fragments include but are not limited to binding domains, hinges, transmembrane domains, intracellular domains, and the like. In particular embodiment, the polypeptide fragment is a biologically active polypeptide fragment. As used herein, the term “biologically active polypeptide fragment” refers to a polypeptide fragment that retains at least 100%, at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 65%, at least 60%, at least 55%, or at least 50% of the naturally occurring polypeptide activity. In certain embodiments, a polypeptide fragment comprises an amino acid sequence at least 5 to about 500 amino acids long. It will be appreciated that in certain embodiments, fragments are at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 150, 200, 250, 300, 350, 400, 450, or 500 or more amino acids long. In particular embodiments, a polypeptide fragment comprises an antibody or antigen binding fragment thereof that binds BCMA.

In particular embodiments, a polypeptide comprises one or more amino acid substitutions, deletions, truncations, or insertions using methods that are well known in the art. See, for example, Kunkel (Proc. Natl. Acad. Sci. USA. 82: 488-492. (1985)), Kunkel *et al.*, (Methods in Enzymol, 154: 367-382. (1987)), U.S. Pat. No. 4,873,192, Watson, J. D. *et al.*, (Molecular Biology of the Gene, Fourth Edition, Benjamin/Cummings, Menlo Park, Calif. (1987)) and the references cited therein. Guidance as to appropriate amino acid substitutions that do not affect biological activity of the protein of interest may be found in the model of Dayhoff *et al.*, Atlas of Protein Sequence and Structure (Natl. Biomed. Res. Found., Washington, D.C. (1978)).

In certain embodiments, a polypeptide variant comprises one or more conservative substitutions. A “conservative substitution” is one in which an amino acid is substituted for another amino acid that has similar properties. Guidance in determining which amino acid residues can be substituted, inserted, or deleted can be found using computer programs well

known in the art, such as DNASTAR, DNA Strider, Geneious, Mac Vector, or Vector NTI software. In particular embodiments, amino acid changes in the polypeptide variants contemplated herein comprise one or more conservative amino acid substitutions. A conservative amino acid substitution involves substituting an amino acid with an amino acid
5 having a related side chain. Naturally occurring amino acids are generally divided into four families: acidic (aspartate, glutamate), basic (lysine, arginine, histidine), non-polar (alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), and uncharged polar (glycine, asparagine, glutamine, cysteine, serine, threonine, tyrosine) amino acids. Phenylalanine, tryptophan, and tyrosine are sometimes classified jointly as aromatic amino
10 acids. In particular embodiments, a conservative amino acid substitution refers to substituting amino acids within the same group or family. Those of skill in this art recognize that, in general, single amino acid substitutions in non-essential regions of a polypeptide do not substantially alter biological activity (see, *e.g.*, Watson *et al.*, Molecular Biology of the Gene, 4th Edition, 1987, The Benjamin/Cummings Pub. Co., p.224).

15 In particular embodiments, a conservative amino acid substitution refers to substituting amino acids having a similar hydropathic index or score. The importance of the hydropathic amino acid index in conferring interactive biologic function on a protein is generally understood in the art (Kyte and Doolittle, 1982, incorporated herein by reference). Each amino acid has been assigned a hydropathic index on the basis of its hydrophobicity
20 and charge characteristics (Kyte and Doolittle, 1982). These values are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cysteine (+2.5); methionine (+1.9); alanine (+1.8); glycine (-0.4); threonine (-0.7); serine (-0.8); tryptophan (-0.9); tyrosine (-1.3); proline (-1.6); histidine (-3.2); glutamate (-3.5); glutamine (-3.5); aspartate (-3.5); asparagine (-3.5); lysine (-3.9); and arginine (-4.5). In particular embodiments, a
25 conservative amino acid substitution refers to substituting amino acids having a similar hydropathic index or score. In particular embodiments, substitution of amino acids whose hydropathic indices are within ± 2 is preferred, those within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred. It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity.

30 In particular embodiments, a conservative amino acid substitution refers to substituting amino acids having a similar hydrophilic index or score. As detailed in U.S. Patent No. 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0 $\pm$ 1); glutamate (+3.0 $\pm$ 1); serine

(+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (-0.4); proline (-0.5 $\pm$ 1); alanine (-0.5); histidine (-0.5); cysteine (-1.0); methionine (-1.3); valine (-1.5); leucine (-1.8); isoleucine (-1.8); tyrosine (-2.3); phenylalanine (-2.5); tryptophan (-3.4). In particular embodiments, a conservative amino acid substitution refers to substituting amino acids
 5 having a similar hydrophilic index or score. In particular embodiments, substitution of amino acids whose hydrophilic indices are substitution of amino acids whose hydrophilicity values are within ± 2 is preferred, those within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred.

In particular embodiments, a conservative amino acid substitution may be based on
 10 the relative similarity of the amino acid side-chain substituents, for example, their hydrophobicity, hydrophilicity, charge, size, and the like.

In particular embodiments, a polypeptide comprises an anti-BCMA antibody or antigen binding fragment thereof comprises a heavy chain variable region (VH) comprising a CDRH1, a CDRH2, and a CDRH3 of an antibody or antigen binding fragment thereof set
 15 forth in Table 1; a polypeptide linker; and a light chain variable region (VL) comprising a CDRL1, a CDRL2, and a CDRL3 of an antibody or antigen binding fragment thereof set forth in Table 1; and optionally a polypeptide linker and an anti-CD3 antibody.

In particular embodiments, a polypeptide comprises an anti-BCMA antibody or antigen binding fragment thereof comprises in either orientation (*e.g.*, VL-linker-VH or VH-linker-VL): a VH that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 12, 13, and 14, a polypeptide linker, and a VL that comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 16, 17, and 18; a VH that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 22, 23, and 24, a polypeptide
 25 linker, and a VL that comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 26, 27, and 28; a VH that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 32, 33, and 34, a polypeptide linker, and a VL that comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 36, 37, and 38; a VH that
 30 comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 42, 43, and 44, a polypeptide linker, and a VL that comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 46, 47, and 48; a VH that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino

acid sequences set forth in SEQ ID NOs: 52, 53, and 54, a polypeptide linker, and a VL that comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 56, 57, and 58; a VH that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 62, 63, and 64, a polypeptide linker, and a VL that comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 66, 67, and 68; a VH that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 72, 73, and 74, a polypeptide linker, and a VL that comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 76, 77, and 78; a VH that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 82, 83, and 84, a polypeptide linker, and a VL that comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 86, 87, and 88; and a VH that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 92, 93, and 94, a polypeptide linker, and a VL that comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 96, 97, and 98; and optionally a polypeptide linker and an anti-CD3 antibody. In particular embodiments, the polypeptide linker is selected from the group consisting of: (GGGS)_n wherein n = 1, 2, 3, 4 or 5; GEGTSTGSGGSGGSGGAD, GSTSGSGKPGSGEGSTKG and variants thereof comprising an amino acid sequence at least 90% identical thereto.

In particular embodiments, a polypeptide comprises an anti-BCMA antibody or antigen binding fragment thereof comprises in either orientation (*e.g.*, VL-linker-VH or VH-linker-VL): a VH that comprises the amino acid sequence set forth in any one of SEQ ID NOs: 11, 21, 31, 41, 51, 61, 71, 81, and 91 a polypeptide linker, and a corresponding VL that comprises the amino acid sequence set forth in SEQ ID NO: 15, 25, 35, 45, 55, 65, 75, 85, and 95; and optionally a polypeptide linker and an anti-CD3 antibody; wherein the polypeptide linker is selected from the group consisting of: (GGGS)_n wherein n = 1, 2, 3, 4 or 5, GEGTSTGSGGSGGSGGAD, GSTSGSGKPGSGEGSTKG and variants thereof comprising an amino acid sequence 95% identical thereto.

In particular embodiments, a polypeptide comprises an anti-BCMA antibody or antigen binding fragment thereof comprises the amino acid sequence set forth in any one of SEQ ID NOs: 19, 20, 29, 30, 39, 40, 49, 50, 59, 60, 69, 70, 79, 80, 89, 90, 99, and 100 or an amino acid sequence with at least 85%, at least 90%, at least 91%, at least 92%, at least 93%,

at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identity thereto; and optionally a polypeptide linker and an anti-CD3 antibody.

In particular embodiments, a polypeptide comprises an anti-BCMA antibody or antigen binding fragment thereof comprises a VHH domain comprising a CDRH1, a CDRH2, and a CDRH3 of an antibody or antigen binding fragment thereof set forth in Table 1; and optionally a polypeptide linker and an anti-CD3 antibody.

In particular embodiments, a polypeptide comprises an anti-BCMA antibody or antigen binding fragment thereof comprises: a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 102, 103, and 104; a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 106, 107, and 108; a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 110, 111, and 112; a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 114, 115, and 116; a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 118, 119, and 120; a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 122, 123, and 124; a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 126, 127, and 128; a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 130, 131, and 132; a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 134, 135, and 136; a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 138, 139, and 140; or a VHH domain that comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 142, 143, and 144; and optionally a polypeptide linker and an anti-CD3 antibody.

In particular embodiments, a polypeptide comprises an anti-BCMA antibody or antigen binding fragment thereof comprises a VHH that comprises the amino acid sequence set forth in any one of SEQ ID NOs: 101, 105, 109, 113, 117, 121, 125, 129, 133, 137, and 141 or an amino acid sequence with at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identity thereto; and optionally a polypeptide linker and an anti-CD3 antibody.

Polypeptides contemplated in particular embodiments include fusion polypeptides. In particular embodiments, fusion polypeptides and polynucleotides encoding fusion polypeptides are provided. Fusion polypeptides can include one or more polypeptide domains or segments including but not limited to signal peptides, antibodies or antigen binding fragments thereof, polypeptide linkers, spacer domains, transmembrane domains, intracellular signaling domains, and polypeptide cleavage signals. Fusion proteins and polypeptides are typically linked C-terminus to N-terminus, although they can also be linked C-terminus to C-terminus, N-terminus to N-terminus, or N-terminus to C-terminus. Fusion polypeptides and fusion proteins refer to a polypeptide having at least two, three, four, five, six, seven, eight, nine, or ten polypeptide segments.

In particular embodiments, a fusion polypeptide, *e.g.*, CAR, comprises signal peptide set forth in any one of SEQ ID NOs: 861-873 that is subsequently cleaved from the fusion polypeptide. Signal peptides are short 16 to 30 amino acid N-terminal sequences of nascently synthesized polypeptide chains that mediate protein targeting to the membrane of the endoplasmic reticulum (ER). Typically, signal peptides are cleaved cotranslationally by signal peptidase, a heterooligomeric polypeptide complex. In particular embodiments, a polypeptide comprises a signal peptide. In preferred embodiments, a polynucleotide encoding a polypeptide comprises a polynucleotide encoding a signal polypeptide; and the translated polypeptide does not comprise a signal peptide. Exemplary signal peptides are set forth in Table 5.

Table 5: Exemplary Signal Peptides

SEQ ID NO	AMINO ACID SEQUENCE
861	MALPVTALLLPLALLHAARP
862	METDTLLLWVLLWVPGSTG
863	MDMRVPAQLLGLLLWLRGARC
864	MPLLLLLPILLWAGALA
865	MDAMKRGLCCVLLLCGAVFVSPS
866	MLLLLLLLGLRLQLSLG
867	MWLQSLLLLGTVACSIS
868	MGVKVLFALICIAVAEA
869	MLLLVTSLLLCELPHPAFLIP
870	MSRSVALAVLALLSLSGLEA
871	MGHTRRQGTSPSKCPYLNFFQLLVLAGLSHFCSG
872	MWWRLWWLLLLLLLLLWPMVWA
873	MLLLLLLLLLLALALA

In particular embodiments, a polypeptide comprises a signal peptide set forth in any one of SEQ ID NOs: 861-973 and a chimeric antigen receptor comprising an amino acid sequence set forth in any one of SEQ ID NOs: 165-860.

In particular embodiments, a polypeptide comprises a signal peptide set forth in any one of SEQ ID NOs: 861-973 and a chimeric antigen receptor encoded by a polynucleotide sequence set forth in any one of SEQ ID NOs: 904-944.

5 Fusion polypeptides may optionally comprise a polypeptide linker contemplated elsewhere herein that can be used to link one or more polypeptides or domains within a polypeptide. Exemplary linkers are set forth in SEQ ID NOs: 2-10.

In particular embodiments, two or more polypeptides can be expressed as a fusion polypeptide that comprises one or more polypeptide cleavage signals disposed between the two or more polypeptides.

10 Exemplary polypeptide cleavage signals include, but are not limited to, protease cleavage sites, nuclease cleavage sites and ribosomal skipping polypeptide or self-cleaving viral polypeptides (see, *e.g.*, in Ryan *et al.*, 1997. J. Gener. Virol. 78, 699-722; deFelipe and Ryan, 2004. Traffic, 5(8); 616-26; and Scymczak *et al.*, (2004) Nature Biotech. 5, 589-594).

15 Exemplary protease cleavage sites include, but are not limited to the cleavage sites of potyvirus NIa proteases (*e.g.*, tobacco etch virus protease), poty virus HC proteases, potyvirus PI (P35) proteases, byovirus NIa proteases, byovirus RNA-2-encoded proteases, aphthovirus L proteases, enterovirus 2A proteases, rhinovirus 2 A proteases, picorna 3C proteases, comovirus 24K proteases, nepovirus 24K proteases, RTSV (rice tungro spherical virus) 3C-like protease, PYVF (parsnip yellow fleck virus) 3C-like protease, heparin, 20 thrombin, factor Xa and enterokinase.

Illustrative examples of ribosomal skipping polypeptides include but are not limited to: a viral 2A peptide or sequence (Donnelly *et al.*, 2001. J. Gen. Virol. 82: 1027- 1041). In a particular embodiment, the viral 2A peptide is an aphthovirus 2A peptide, a potyvirus 2A peptide, or a cardiovirus 2A peptide.

25 In one embodiment, the viral 2A peptide is selected from the group consisting of: a foot-and-mouth disease virus (FMDV) 2A peptide, an equine rhinitis A virus (ERAV) 2A peptide, a Thosa asigna virus (TaV) 2A peptide, a porcine teschovirus-1 (PTV-1) 2A peptide, a Theilovirus 2A peptide, and an encephalomyocarditis virus 2A peptide.

30 Illustrative examples of viral 2A sequences include, but are not limited to: GSGATNFSLLKQAGDVEENPGP (SEQ ID NO: 956); ATNFSLLKQAGDVEENPGP (SEQ ID NO: 957); LLKQAGDVEENPGP (SEQ ID NO: 958); GSGEGRGSLLTCGDVEENPGP (SEQ ID NO: 959); EGRGSLLTCGDVEENPGP (SEQ ID NO: 960); LLTCGDVEENPGP (SEQ ID NO: 961);

GSGQCTNYALLKLAGDVESNPGP (SEQ ID NO: 962);
 QCTNYALLKLAGDVESNPGP (SEQ ID NO: 963); LLKLAGDVESNPGP (SEQ ID NO:
 964); GSGVKQTLNFDLLKLAGDVESNPGP (SEQ ID NO: 965);
 VKQTLNFDLLKLAGDVESNPGP (SEQ ID NO: 966); LLNFDLLKLAGDVESNPGP
 5 (SEQ ID NO: 967); TLNFDLLKLAGDVESNPGP (SEQ ID NO: 968);
 NFDLLKLAGDVESNPGP (SEQ ID NO: 969); QLLNFDLLKLAGDVESNPGP (SEQ ID
 NO: 970); APVKQTLNFDLLKLAGDVESNPGP (SEQ ID NO: 971);
 VTELLYRMKRAETYCPRLLAIHPTEARHKQKIVAPVKQT (SEQ ID NO: 972);
 LNFDLLKLAGDVESNPGP (SEQ ID NO: 973);
 10 LLAIHPTEARHKQKIVAPVKQTLNFDLLKLAGDVESNPGP (SEQ ID NO: 974); and
 EARHKQKIVAPVKQTLNFDLLKLAGDVESNPGP (SEQ ID NO: 975).

G. POLYNUCLEOTIDES

Polynucleotides comprising or encoding antibodies and antigen binding fragments
 thereof, bispecific antibodies, BiTEs, antibody conjugates, chimeric antigen receptors,
 15 vectors, promoters, enhancers, Kozak sequences, polyadenylation signals, untranslated
 regions, and posttranscriptional response elements as well as other polynucleotides are
 contemplated in various embodiments.

As used herein, the terms “polynucleotide” or “nucleic acid” refer to
 deoxyribonucleic acid (DNA), ribonucleic acid (RNA) and DNA/RNA hybrids.
 20 Polynucleotides may be single-stranded or double-stranded and either recombinant,
 synthetic, or isolated. Polynucleotides include but are not limited to: pre-messenger RNA
 (pre-mRNA), messenger RNA (mRNA), RNA, circular RNA (circRNA), synthetic RNA,
 short interfering RNA (siRNA), short hairpin RNA (shRNA), microRNA (miRNA),
 ribozymes, genomic RNA (gRNA), viral genomic RNA, plus strand RNA (RNA(+)), minus
 25 strand RNA (RNA(-)), tracrRNA, crRNA, single guide RNA (sgRNA), Doggybone DNA
 (dbDNA), linear DNA, circular DNA, PCR amplified DNA, complementary DNA (cDNA),
 synthetic DNA, or recombinant DNA. Polynucleotides refer to a polymeric form of
 nucleotides of at least 5, at least 10, at least 15, at least 20, at least 25, at least 30, at least 40,
 at least 50, at least 100, at least 200, at least 300, at least 400, at least 500, at least 1000, at
 30 least 5000, at least 10000, or at least 15000 or more nucleotides in length, either
 ribonucleotides or deoxyribonucleotides or a modified form of either type of nucleotide, as
 well as all intermediate lengths. It will be readily understood that “intermediate lengths,” in

this context, means any length between the quoted values, such as 6, 7, 8, 9, *etc.*, 101, 102, 103, *etc.*, 151, 152, 153, *etc.*, 201, 202, 203, *etc.*

As used herein, “isolated polynucleotide” refers to a polynucleotide that has been isolated from or purified from the sequences which flank it in a naturally-occurring state. In particular embodiments, an isolated polynucleotide is a synthetic polynucleotide, a semi-synthetic polynucleotide, or a polynucleotide obtained or derived from a recombinant source, or other polynucleotide that does not exist in nature and that has been made by the hand of man.

In particular embodiments, polynucleotides contemplated herein are polynucleotide variants. As used herein, the terms “polynucleotide variant” and “variant” and the like refer to polynucleotides displaying substantial sequence identity with a reference polynucleotide sequence or polynucleotides that hybridize with a reference sequence under stringent conditions that are defined hereinafter. These terms also encompass polynucleotides that are distinguished from a reference polynucleotide by the addition, deletion, substitution, or modification of one or more nucleotides. Accordingly, the terms “polynucleotide variant” and “variant” include polynucleotides in which one or more nucleotides have been added or deleted, or modified, or replaced with different nucleotides. In this regard, it is well understood in the art that certain alterations inclusive of mutations, additions, deletions and substitutions can be made to a reference polynucleotide whereby the altered polynucleotide retains the biological function or activity of the reference polynucleotide or wherein the function or activity of the altered polynucleotide is modulated. In particular embodiments, polynucleotides or polynucleotide variants have at least or about 50%, 55%, 60%, 65%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to a reference sequence.

In particular embodiments, a polynucleotide variant includes a polynucleotide fragment that encodes biologically active polypeptide fragments or variants. As used herein, the term “polynucleotide fragment” refers to a polynucleotide fragment at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700 or more nucleotides in length that encodes a polypeptide variant that retains at least 100%, at least 90%, at least 80%, at least

70%, at least 60%, at least 50%, at least 40%, at least 30%, at least 20%, at least 10%, or at least 5% of the naturally occurring polypeptide activity. Polynucleotide fragments refer to a polynucleotide that encodes a polypeptide that has an amino-terminal deletion, a carboxyl-terminal deletion, and/or an internal deletion or substitution of one or more amino acids of a naturally occurring or recombinantly-produced polypeptide.

As used herein, the phrases “sequence identity” or, for example, comprising a “sequence 50% identical to,” refer to the extent that sequences are identical on a nucleotide-by-nucleotide basis or an amino acid-by-amino acid basis over a window of comparison. A “percentage of sequence identity” may be calculated by comparing two optimally aligned sequences over the window of comparison, determining the number of positions at which the identical nucleic acid base (*e.g.*, A, T, C, G, I) or the identical amino acid residue (*e.g.*, Ala, Pro, Ser, Thr, Gly, Val, Leu, Ile, Phe, Tyr, Trp, Lys, Arg, His, Asp, Glu, Asn, Gln, Cys and Met) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of sequence identity. In particular embodiments, polynucleotides and polypeptides comprise at least about 50%, 55%, 60%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 86%, 97%, 98%, or 99% sequence identity to any of the reference sequences described herein, *e.g.*, SEQ ID NOs: 1-979.

Illustrative examples of polynucleotides include, but are not limited to, polynucleotide sequences set forth in any one of SEQ ID NOs: 874-953 and polynucleotides encoding polypeptides set forth in SEQ ID NOs: 1-873 and 954-979.

In various embodiments, a polynucleotide encodes a polypeptide comprising an amino acid sequence set forth in any one of SEQ ID NOs: 1-873 and 954-979.

In various embodiments, a polynucleotide encodes an antigen or antigen binding fragment thereof comprising an amino acid sequence set forth in any one of SEQ ID NOs: 11-144. In particular embodiments, a polynucleotide encoding an antigen or antigen binding fragment thereof comprises a polynucleotide sequence set forth in any one of SEQ ID NOs: 874-893.

Table 6 sets forth the SEQ ID NOs. and associated nucleic acid sequences encoding anti-BCMA antibodies or antigen binding fragments thereof and the corresponding amino acid SEQ ID NO (AA SEQ ID NO.) encoded by the nucleic acid sequence.

Table 6

SEQ ID NO.	AA SEQ ID NO.	NUCLEIC ACID SEQUENCE
874	20	GAGATCGTGCTGACACAGTCTCCCGCCACACTGTCACTGTCTCCAGGC GAAAGAGCCACACTGAGCTGTAGAGCCAGCCAGAGCGTGTCTCTTAC CTGGCCTGGTATCAGCAGAAGCCTGGACAGGCTCCCCGGCTGCTGATC TACGATGCCAGCAATAGAGCCACAGGCATCCCCGCCAGATTTTCTGGC AGCGGCTCTGGCACCATTTCACCTGACCATAGCAGCCTGGAACCT GAGGACTTCGCCGTGTACTACTGCCAGCAGAGAGTGGTGTACCCCATC ACCTTTGGCGGAGGCACCAAGGTGGAATCAAAGCGGCGGAGGAAGC GGAGGCGGAGGATCTGGTGGTGGTGGATCTGGCGGAGGTGGCAGCCAG ATCACACTGAAAGAGTCTGGCCCCACACTGGTCAAGCCCACACAGACC CTGACACTGACCTGCACCTTCAGCGGCTTTAGCCTGAGCACATCTGGC GTCGGCGTTGGCTGGATTAGACAGCCTCCTGGAAGGCCCTGGAATGG CTGGCCCTGATCTACTGGAACGACGAGAAGAGATACAGCCCCAGCCTG AAGTCCCGGCTGACCATCACCAAGGACACCAGCAAGAACCAGGTGGTG CTGACCATGACAAACATGGACCCCGTGGACACCGCCGTGTATTATTGC GCCAGAGATGAGTACGGCGGCTTCGACATTTGGGGCCAGGGCACAATG GTCACCGTGTCTAGT
875	30	GAGATCGTGCTGACCCAGTCCCCTGCTACCCCTGAGCCTGTCTCCAGGC GAGCGGGCCACACTGAGCTGTAGAGCTTCTCAGAGCGTGTCCAGCTAC CTGGCCTGGTATCAGCAGAAACCTGGCCAGGCCCTAGACTGCTGATC TACGACGCCAGCAACCGGGCCACCGGCATCCCCGCCAGATTACGCGGA TCTGGCAGCGGCACAGATTTTACCCTCACCATCAGCAGCCTGGAACCT GAGGACTTCGCCGTGTACTACTGCCAGCAAAGATTGCACTACCCCATC ACCTTCGGCGGCGGAACAAAGGTGGAATTAAGGGTGGTGGGGGAGC GGTGGAGGTGGGAGCGGAGGCGGGGGTAGCGGAGGCGGGGGTAGCCAA ATCACACTGAAAGAGAGCGGCCCTACACTCGTGAACCTACCCAGACC CTGACACTGACATGTACCTTCAGCGGCTTCTCCCTGAGCACCTCTGGC GTCGGCGTTGGATGGATCAGACAGCCTCCAGGCAAGGCCCTGGAATGG CTGGCTCTGATCTATTGGAACGACGACAAGCGGTACAGCCCCAGCCTG AAGTCTAGACTGACCATCACAAAGGACACCAGCAAGAACCAGGTGGTG CTGACCATGACAAATATGGACCCCGTGGACACCGCCGTGTACTACTGC GCCAGAGATGAGTACGGCGGATTTGATATCTGGGGCCAGGGCACCATG GTGACCGTGTCCAGC
876	39	CAAGTGCAGCTCGTGGAAAGCGGGCGGCGGAGTGGTGCAGCCCCGGCCG AGCCTGAGACTGTCTGCGCCGCTTCTGGATTTACCTTCAGCAGCTAC GGCATGCACTGGGTGAGACAGGCCCTGGCAAAGGCCTGGAGTGGGTG GCCGTTATCAGCTACGAGGGCAGCAACAAGTATTACGCCGACAGCGTG AAGGGCCGCTTCACAATCTCTAGAGATAATAGCAAGAACACCTGTAC CTGCAGATGAACAGCCTGCGGGCCGAAGATACCGCCGTGTACTACTGT GCTAGAGAGCTGGGCGACGGCATGGACGTGTGGGGACAGGGCACAACC GTGACCGTGTCTCTGGTGGTGGGGGAGCGGTGGAGGTGGGAGCGGA GGCGGGGGTAGCGGAGGCGGGGGTAGCGAGATCGTGCTGACCCAGTCC CCTGCTACACTGAGCCTGTCTCCAGGCGAGCGGGCCACACTGAGCTGT AGAGCTTCTCAGAGCGTGTCCAGCTATCTGGCCTGGTTCAGCAGAAA CCTGGCCAGGCCCTAGACTGCTGATCTACGACGCCAGCAACCGGGCC ACCGGCATCCCCGCCAGATTACGCGGCTCTGGCAGCGGCACCGACTTC ACCCTCACCATCAGCAGCCTGGAACCCGAGGATTTTGCCGTCTACTAC TGCCAGCAAAGAGTGGACCTGTGGACCTTCGGCGGAGGAACAAAGGTG GAAATCAAG
877	45	GACATCCAGATGACCCAGAGCCCTTCGACCCATCCGCTTCCGTGGGT GACCGTGTGACCATCACCTGTCGCGCGTGCAGAGCATCTCTCCTGG CTCGCGTGGTACCAACAGAAGCCTGGCAAGGCCCAAGCTGCTGATT TACGACGCCAGTTCCCTGGAGTCTGGCGTGCCATCCCGCTTCTCCGGC AGCGGCAGCGGTACCGAGTTCACCTGACGATCAGCTCCCTGCAGCCG GATGACTTTGCTACTACTACTGTCAGCAGGTCTCCTCCCTCCCCCCC ACCTTCGGTGGCGGTACCAAGGTGGAGATCAAGGGCGGCGGCGGCTCT

		GGTGGCGAGGTTCTGGCGGGGAGGTTCTGGGGGGGGAGGCTCCGAG GTGCAACTGGTAGAGAGCGGCGGGGACTGGTAAAACCCGGCGGCTCC CTGCGGCTGTCTATGCGCTGCTAGCGGCTTCACGTTTCAGCGATTACTAC ATGAGTTGGATCCGCCAGGCCCGGGGAAGGGTTTGGAGTGGGTCTCG TATATCTCTTCCAGCGGATCTACCATTACTATGCGGACAGCGTGAAG GGGCGCTTCACCATACTCTCGGGACAACGCCAAGAACTCCCTGTACCTG CAGATGAATTCCCTGCGTGCCGAGGACACGGCCGTGTATTACTGTGCC CGCGACCAGGGCAACTACGGCGTCGACGTGTGGGGCCAGGGTACAACC GTCACCGTGTCCAGT
878	59	CAAGTGCAGCTGGTCGAGAGCGGAGGAGGCCTGGTTAAGCCCGGCGGA TCTCTCAGACTGAGCTGCGCCGCTAGCGGCTTTACATTACAGCGACTAC TACATGAGCTGGATCCGGCAGGCCCTGGCAAGGGCCTGGAATGGGTG TCCTACATCAGCTCCTCCGGCAGCACCATCTACTACGCCGACAGCGTG AAAGGCAGATTACAAATCTCTAGAGATAATGCCAAGAACAGCCTGTAC CTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTATTGT GCTAGAGATCAGGGCAACTACGGCGTGGACGTGTGGGGCCAGGGCACC ACCGTGACCGTGTCTAGCGGTGGTGGGGGCAGCGGTGGAGGTGGGAGC GGAGGCGGGGGTAGCGGAGGCGGGGGTAGCGATATCCAGATGACCCAG TCCCCATCTACACTGAGCGCCTCTGTGGGCGACCGGGTGACCATTACA TG TAGAGCCAGCCAGAGCATCAGCAGCTGGCTGGCTTGGTATCAGCAG AAACCTGGCAAGGCCCTAAGCTGCTGATCTACGAGGCCAGCAGCCTG GAAAGCGCGTCCCCAGCAGATTACGCGGCAGCGGCTCTGGAACAGAG TTCACCTGACCATCTCTCCCTGCAGCCTGACGACTTCGCCACCTAC TACTGCCAGCAATCTGATAGCCACCCCATCACCTTTGGCGGAGGCACC AAGGTGGAAATCAAG
879	70	GATATCCAGATGACCCAGTCCCCATCTACACTGAGCGCCTCTGTGGGC GACCGGGTGACAATTACCTGTAGAGCTAGCCAGAGCATCTCTCCTGG CTGGCTTGGTACCAGCAAAAACCTGGCAAGGCCCTAAGCTGCTGATC TACGAGGCCAGCAGCCTGGAAGCGGCGTCCCCCTAGATTACGCGGC AGCGGCTCTGGAACCGAGTTACCCCTGACAATCAGCAGCCTGCAGCCT GACGACTTCGCCACCTATTACTGCCAGCAGGCCAACAGCCACCCCATC ACCTTTGGCGGAGGCACCAAGGTGGAAATCAAGGGTGGTGGGGGCAGC GGTGGAGGTGGGAGCGGAGGCGGGGGTAGCGGAGGCGGGGGTAGCGAG GTGCAGCTGGTGGAAAGCGGCGGAGGACTCGTTAAGCCCGCGGCGAGC CTGAGACTGAGCTGCGCCGCTAGCGGATTTACCTTCAGCGACTACTAC ATGAGCTGGATCCGGCAGGCCCTGGCAAGGGCCTGGAATGGGTGAGC TACATCAGCTCCTCTGGCTCTACAATCTACTACGCCGACAGCGTGAAA GGCAGATTCACCATCTCTAGAGATAATGCCAAGAACAGCCTGTACCTG CAAATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTATTGTGCT AGAGATCAGGGCAACTACGGCGTGGACGTGTGGGGCCAGGGCACCACC GTGACAGTGTCTCC
880	80	GACATCCAGATGACCCAGAGCCCTAGCTCCCTGAGCGCCAGCGTGGGC GATAGAGTGACCATTACCTGTAGAGCCTCTCAGAGCATCTCTCCTAC CTGAACTGGTATCAGCAGAAACCCGGCAAGGCCCTAAGCTGCTGATC TACGCCGCTAGCAGCCTGCAGTCTGGCGTCCCCAGCCGGTTACGCGGC AGCGGATCTGGCACCGACTTCACCTGACAATCAGCAGCCTGCAACCT GAGGACTTTGCTACATACTACTGCCAGCAGGCCACAGCTTCCAATC ACCTTCGGCGGCGGAACAAAGGTGGAAATCAAGGGTGGTGGGGGCAGC GGTGGAGGTGGGAGCGGAGGCGGGGGTAGCGGAGGCGGGGGTAGCGAG GTGCAGCTGCTGGAAAGCGGAGGCGGACTCGTTCAACCTGGCGGCAGC CTGAGACTGAGCTGCGCCGCTTCTGGATTTACCTTCAGCAACTACGCC ATGAGCTGGGTGCGGCAGGCCCTGGCAAAGGCCTGGAATGGGTCTCC GCCATCAGCGGCTCTGGCGGCTCCACCTACTACGCCGACAGCGTGAAG GGCAGATTCACCATCTCTAGAGATAATAGCAAGAACACCCTGTACCTG CAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTATTGTGCT AGACCCGAGATGGCTACTACGAGGGCGTGTACTTCGACTACTGGGGC CAGGGCACACTGGTGACAGTGTCCAGC
881	90	GATATTCAGATGACCCAGAGCCCATCTAGCCTGAGCGCCAGCGTGGGC GATAGAGTGACCATCACCTGTAGGCTCTCAGGACATCGCTAATTAC

		CTGAACTGGTATCAGCAGAAACCCGGCAAGGCCCTAAGCTGCTGATC TACGACGCCTCCAACCTGGAACCCGGCGTGCCAGCCGGTTACGCGGC AGCGGATCTGGCACAGACTTACCTTTACCATCAGCTCCCTCCAGCCT GAGGACATCGCCACATACTACTGCCAGCAACACTTCAACCTGCCTCTG ACCTTCGGCGGGCGGAACAAAGGTCGAGATCAAGGGTGGTGGGGGCGAGC GGTGGAGGTGGGAGCGGAGGCGGGGGTAGCGGAGGCGGGGGTAGCCAA ATCACCTGAAAGAGAGCGGACCTACACTGGTCAAGCCTACCCAGACA CTGACCCTCACATGTACATTACGCGGCTTTAGCCTGAGCACCTCCGGC GTGGGAGTGGGCTGGATCAGACAGCCCCCGGCAAGGCCCTGGAATGG CTGGCTCTGATCTATTGGAATGACGAGAAGCGGTACAGCCCTAGCCTG AAATCTAGACTGACAATCACCAGGACACCAGCAAGAACCAGGTGGTG CTGACCATGACCAACATGGATCCTGTGGATACCGCGTGTACTACTGC GCCAGAGAAGGCTCTCACGACTACAAGAGCTCCAAGTGGTTCGACCCA TGGGGCCAGGGCACCTGGTTACAGTGTCTAGC
882	100	GATATCGTGATGACCAATCTCCACTGAGCCTGCCTGTGACACCTGGC GAGCCTGCTTCTATCAGCTGTAGAAGCAGCCAGTCCCTGCTGCACAGC AACGGCTACAACCTACCTGGACTGGTATCTGCAGAAACCCGGCCAGAGC CCCCAGCTGCTGATCTACCTCGGCTCTAATCGGGCCAGCGGAGTGCCT GATAGATTACGCGGAAGCGGCTCCGGCACCGACTTACCCCTGAAGATC AGCAGAGTGAAGCCGAGGACGTGGGCGTCTACTACTGCATGCAGGCC CTGGGCTGATTACATTTGGCGGCGGAACCAAGGTGGAAATCAAGGGT GGTGGGGGCGAGCGGTGGAGGTGGGAGCGGAGGCGGGGGTAGCGGAGGC GGGGGTAGCGAAGTGCAGCTGGTTGAGAGCGGCGGGGACTGGTGAAG CCCGGAGGCAGCCTCAGACTGAGCTGTGCTGCTTCTGGCTTTACCTTC AGCTCTTATAGCATGAACTGGGTGCGGCAGGCCCTGGCAAGGGCCTG GAATGGGTCAGCTCCATCAGCTCTTCTAGCAGCTACATCTACTACGCC GACAGCGTGAAGGGCAGATTACCATCAGCAGAGATAACGCCAAGAAC AGCCTGTACCTGCAGATGAATAGCCTGCGGGCCGAGGACACCGCCGTG TACTACTGCGCCAGAGCCGGCGACACCTACAGCGCCGCGGATTACTAC TACATGGACGTGTGGGGCAAGGAACAACCGTGACAGTGTCTCTCC
883	101	GAAGTGCAACTGCTGGAAAGCGGCGGAGGCCTGGTCCAGCCCGCGGC TCTCTGCGGCTCAGCTGCGCCGCTTCTGGATTTACCTTCGGCAGCGAG GCTATGAGCTGGGTGCGGCAGGCCCTGGAAAAGAGAGAGAGCTGGTG TCCGCCATCAGCGGCAGCGGCGAGGTGACCTACTACGCCGACAGCGTG AAGGGCAGATTACCATCTCTAGAGATAATAGCAAGAACACCTGTAC CTGCAGATGAACAGCCTGAGAGCCGAGGACACCGCCGTGTACTATTGT CAGAGACTGGTGAAGCCAAGCGGCACTGGGGCCAGGGCACACAGGTT ACAGTGTCCAGC
884	105	GAAGTGCAACTGCTGGAATCTGGCGGAGGACTGGTGCAGCCCGCGGC AGCCTGCGGCTGAGCTGTGCTGCTTCTGGCTTTACCTTCGAGTCTGAG GCCATGAGCTGGTATAGACAGGCCCTGGCAAGGAAAGAGAGCTGGTC AGCGTGATCACCAGCGAGGGCTCCACCTACTACGCCGACAGCGTGAAA GGCAGATTACAATCAGCCGGGACAATAGCAAGAACACCTGTACTCTG CAGATGAACAGCCTGCGCGCCGAAGATACAGCCGTGTACTACTGCGCC CACATCGAGTGGGAGACAAGACTCAACTGGGGCCAGGGCACCCAGGTG ACCGTGTCCAGC
885	109	GAGGTGCAGCTGCTGGAAAGCGGAGGGGGCCTGGTCCAACCCGGCGGG TCTCTTCGCCTAAGCTGTGCCGCTTCTGGCTTCACCTTCGACGAGTAC ACCATGCACTGGTTACAGACAGGCCCCCGCAAGGAGCGCGAGTTCGTC AGTGCAATCAGCGGAGGCGGTAGCGAGACTTATTACGCGGACTCCGTG AAGGGCCGCTTCACCATTAGCCGCGACAACCTCAAGAACACGCTGTAC CTGCAGATGAATTCGCTGCGCGCCGAAGATACAGCCGTGTACTACTGT GCCGCTGGTGGGAGGAGGCTGGCGTGGGCTATTGGGGCCAGGGCACCC CAGGTACCGTGTCTGCC
886	113	GAGGTGCAGCTGCTGGAGAGCGGAGGCGGCCTCGTGCAGCCAGGAGGT TCCCTACGACTCTCCTGTGCCGCCAGCGGCTTCACCTTCGAGGACTAC GCCATGAGTTGGTTCCGCCAGGCCCGGGGAAGGAGCGCGAGGGCGTG AGCGCGATTTCTGGAAGGGCGGCTCCACCTATTACGCGGACTCCGTG AAGGTCGCTTTACCATCTCTCGCGACAACCTCAAGAACACGCTGTAC

		CTGCAGATGAATAGCCTGCGCGCTGAGGACACTGCCGTGTACTACTGT GCTGTCTTGGACGAGGAGGCCGCGCAGAGGGCGGCTATTGGGGCCAG GGTACCCAGGTACCGTGTCTCGTCC
887	117	GAGGTGCAACTGCTGGAAAGCGGCGGTGGACTGGTGCAGCCCGGCGGC AGCCTGAGACTGTCTTGTGCTGCTTCTGGATTTACATTTCAGACAGATAC GCCATGAGCTGGTTCCGCCAGGCCCTGGCAAAGAGCGGGAAGGCGTG TCCGCCATCTCCACAAGCGGAGATAGCACATACTATGCCGACAGCGTG AAGGGCAGATTACCATCAGCAGAGATAATAGCAAGAACACCCGTGTAC CTGCAGATGAACAGCCTCCGGGCGGAGGACACCGCCGTCTACTACTGC GCCGTGCTGGACGAGGAAGCCGGCGCCGAGGGCGGCTACTGGGGCCAG GGCACCCAGGTGACCGTGTCTAGC
888	121	GAGGTGCAACTGCTGGAAAGCGGCGGAGGACTCGTCCAGCCCGGCGGC AGCCTGCGGCTGAGCTGTGCTGCTTCTGGATTTACCTTCGCCAGCGAC GCCATGAGCTGGTATAGACAGGCCCTGGCAAAGAGCGGGAAGTGGTG TCCGCCATCAGCGGCTCTGGCGGCTCCACCTACTACGCCGATAGCGTG AAGGGCAGATTACAAATCTCTAGAGATAATAGCAAGAACACCCGTGTAC CTGCAGATGAACAGCCTGAGAGCCGAGGACACCGCCGTGTACTACTGC GCCGCTCACGACAGCGCGGAGGCCCTACCTGGCCTTCGACTACTGGGGC CAGGGCACACAGGTGACCGTGTCTAGC
889	125	GAGGTGCAACTGCTGGAAAGCGGCGGAGGACTCGTCCAGCCCGGCGGC AGCCTGAGGCTGAGCTGTGCTGCTTCTGGCTTTACCTTCGACTCCTAC ACAATGAGCTGGTATAGACAGGCCCTGGCAAAGAGCGGGAACTGGTG TCCGCCATCAGCGGCCACGGCGACTCTACATACTACGCCGACAGCGTG AAAGGCAGATTACAAATCTCTAGAGATAATAGCAAGAACACCCGTGTAC CTGCAGATGAACAGCCTGCGGGCGGAGGACACCGCCGTGTACTACTGC ACCAGAATCAGCATCACACCGAGTGGCTGGCCGGAGATTACTGGGGC CAGGGCACCCAGGTGACAGTGTCCAGC
890	129	GAGGTGCACTGCTGGAAGCGGAGGAGGCCTGGTCCAACCTGGCGGC AGCCTGCGGCTGAGCTGCGCCGCTTCTGGCTTCACCTTCAGCAGTAC GCCATGAGCTGGTTCCGCCAGGCCCTGGCAAAGGAAAGAGAGTTCTGTG TCTTTTATCAGCGGATCTGGCGACTCCACCTACTACGCTGATAGCGTG AAAGGCAGATTTACCATCTCTAGAGATAATAGCAAGAACACCCGTGTAC CTCCAGATGAACAGCCTGCGCGCCGAGGACACAGCCGTGTACTATTGT ACCAGATGGCCTTACGACTTCGAGGAACCAAGCGAGCCCGGCGGTGTAC TGGGGCCAGGGCACACAGGTGACAGTGTCTCTCC
891	133	GAGGTGCACTGCTGGAAGCGGCGGAGGCCTGGTGCAACCTGGCGGA TCTCTCAGACTGAGCTGTGCTGCTTCTGGCTTCACATTACCGACTAC GACATGAGCTGGTATAGACAGGCCCTGGAAAAGAGCGGGAAGTGGTC TCCGTGATCCACAGCGCGGCTCCACCTACTACGCCGATAGCGTGAAG GGCAGATTCACCATCAGCAGAGATAATAGCAAGAACACCCGTGTACCTG CAGATGAACAGCCTGCGGGCGGAGGACACCGCCGTGTACTACTGCGCC CCCGGCTACTACAGCGACCTGTCTTTTGATTATTACAACCTTCGACTAC TGGGGCCAGGGCACACAGGTGACAGTGTCTCAGC
892	137	GAGGTGCACTGCTGGAGAGCGGTGGAGGGTTGGTGCAGCCCGGGGGT AGCCTGCGTCTGTCTGTCGCGCTTCCGGCTTCACGTTCTCTGATTAC GCCATGCACTGGTTCCGGCAGGCCCCCGGTAAGGAGCGCGTGTGGTG TCGTCTATTGACTCCGGCGGCTCCACTTACTACGCAGACAGTGTCAAG GGCCGTTTACCATCAGCCGCGACAACAGCAAGAACAGCTGTACCTG CAGATGAACTCCCTTCGAGCAGAGGACACCGCGGTGTACTACTGTAAT GCGGGCTTCAAGGGCGATCACCCCAACCCCAAGGATGCCTTCGACATT TGGGGCCAGGGCACCCAGGTACCGTGTCTCGTCC
893	141	GAGGTGCAACTGCTGGAATCCGGCGGAGGCCTGGTGCAGCCCGGCGGC AGCCTCAGACTGAGCTGTGCCGCTTCTGGCTTTACCTTCAGCAGCGAG GGCATGAGCTGGGTGCGGCGAGGCCCTGGCAAAGGAAAGAGAGTGGTC TCCGCCATCAGCGGATCTGGCGACCAACCTACTATGCCGATAGCGTG CGCGGAAGATTACAAATCTCTAGAGATAATAGCAAGAACACCCGTGTAC CTGCAGATGAACAGCCTGCGGGCGGAGGACACCGCCGTGTACTACTGC AACGCCCTGGAAGGCGGCCCTACAACAGCTATCCAGCCAGGAGGCCCT GACTACTGGGGCCAGGGCACCCAGGTGACCGTGTCTCAGC

In various embodiments, a polynucleotide encodes a chimeric antigen receptor comprising an anti-BCMA antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in any one of SEQ ID NOs: 11-144. In particular embodiments, a polynucleotide encodes a chimeric antigen receptor comprising an anti-BCMA antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in any one of SEQ ID NOs: 20, 30, 39, 50, 59, 70, 80, 90, 100, 101, 105, 109, 113, 117, 121, 125, 129, 133, 137, and 141; and optionally a polypeptide linker and an anti-CD3 antibody.

In particular embodiments, a polynucleotide encodes a chimeric antigen receptor comprising an amino acid sequence set forth in any one of SEQ ID NOs: 165-860. In particular embodiments, a polynucleotide encodes a chimeric antigen receptor comprising an amino acid sequence set forth in any one of SEQ ID NOs: 189, 237, 261, 333, 357, 429, 477, 525, 573, 597, 621, 645, 669, 693, 717, 741, 765, 789, 813, and 837. In particular embodiments, a polynucleotide encoding a chimeric antigen receptor comprises a polynucleotide sequence set forth in any one of SEQ ID NOs: 905-944.

In particular embodiments, polynucleotides encoding a chimeric antigen receptor may be codon-optimized. As used herein, the term “codon-optimized” refers to substituting codons in a polynucleotide encoding a polypeptide in order to modulate polypeptide expression, stability and/or activity. Factors that influence codon optimization include, but are not limited to one or more of: (i) variation of codon biases between two or more organisms or genes or synthetically constructed bias tables, (ii) variation in the degree of codon bias within an organism, gene, or set of genes, (iii) systematic variation of codons including context, (iv) variation of codons according to their decoding tRNAs, (v) variation of codons according to GC %, either overall or in one position of the triplet, (vi) variation in degree of similarity to a reference sequence for example a naturally occurring sequence, (vii) variation in the codon frequency cutoff, (viii) structural properties of mRNAs transcribed from the DNA sequence, (ix) prior knowledge about the function of the DNA sequences upon which design of the codon substitution set is to be based, (x) systematic variation of codon sets for each amino acid, and/or (xi) isolated removal of spurious translation initiation sites.

A “nucleic acid cassette,” “expression cassette” or “nucleic acid expression cassette” refers to polynucleotide sequences sufficient to transcribe an RNA, which is ultimately translated to a polypeptide. In particular embodiments, a nucleic acid cassette comprises a polynucleotide-of-interest, a polynucleotide that encodes a polypeptide, *e.g.*, a CAR. Nucleic

acid expression cassettes contemplated in particular embodiments comprise one or more expression control sequences, *e.g.*, a promoter, enhancer, poly(A) sequence, and one or more polynucleotide(s)-of-interest. In particular embodiments, a vector contemplated herein comprises one or more nucleic acid cassettes. In particular embodiments, a nucleic acid cassette is oriented in a vector to enable transcription of a polynucleotide-of-interest.

In particular embodiments, a polynucleotide encoding a polypeptide may be combined with other polynucleotide sequences, such as expression control sequences, promoters and/or enhancers, untranslated regions (UTRs), polynucleotides encoding signal peptides, Kozak sequences, polyadenylation signals, restriction enzyme sites, multiple cloning sites, internal ribosomal entry sites (IRES), recombinase recognition sites, termination codons, transcriptional termination signals, and polynucleotides encoding self-cleaving polypeptides or epitope tags, as disclosed elsewhere herein or as known in the art.

Polynucleotides can be prepared, manipulated, expressed and/or delivered using any of a variety of well-established techniques known and available in the art. In order to express a desired polypeptide, a nucleotide sequence encoding the polypeptide, can be inserted into an appropriate vector.

In particular embodiments, a polynucleotide is inserted into a non-viral vector. Illustrative examples of non-viral vectors include but are not limited to autonomously replicating sequences; plasmids; phagemids; cosmids; artificial chromosomes such as yeast artificial chromosomes (YAC), bacterial artificial chromosomes (BAC), or P1-derived artificial chromosomes (PAC); bacteriophages such as lambda phage or M13 phage; and transposable elements including but not limited to piggyBac, Sleeping Beauty, Mos1, Tc1/mariner, Tol2, mini-Tol2, Tc3, MuA, Himar I, Frog Prince, and derivatives thereof.

In particular embodiments, a polynucleotide is inserted into a viral vector. Illustrative examples of viral vectors include but are not limited to Adenoviral (Ad) vectors, adeno-associated virus (AAV) vectors, rhabdovirus (*e.g.*, lyssavirus, vesiculovirus) vectors, paramyxovirus (*e.g.*, henipavirus, morbillivirus, respirovirus, rubelavirus) vectors, herpes simplex virus (*e.g.*, HSV-1, HSV-2) vectors, vaccinia virus vectors, and retroviral vectors, preferably lentiviral vectors (LVV).

In particular embodiments, a vector comprises a polynucleotide comprising or encoding one or more exogenous, endogenous, or heterologous expression control sequences operably linked to a polynucleotide encoding one or more polynucleotides and/or polypeptides contemplated herein.

“Expression control sequences,” “control elements,” or “regulatory sequences” contemplated in particular embodiments include but not limited to promoters, enhancers, translation initiation signals (Shine Dalgarno sequence or Kozak sequence), introns, polyadenylation signals, 5′ and 3′ untranslated regions, all of which may interact with host
5 cell proteins to carry out transcription and translation.

The term “promoter” as used herein refers to a recognition site of a polynucleotide (DNA or RNA) to which an RNA polymerase binds. An RNA polymerase initiates and transcribes polynucleotides operably linked to the promoter. In particular embodiments, promoters operative in mammalian cells comprise an AT-rich region located approximately
10 25 to 30 bases upstream from the site where transcription is initiated and/or another sequence found 70 to 80 bases upstream from the start of transcription, a CNCAAT region where N may be any nucleotide. The term “enhancer” refers to a segment of DNA which contains sequences capable of providing enhanced transcription and in some instances can function independent of their orientation relative to another control sequence. An enhancer can
15 function cooperatively or additively with promoters and/or other enhancer elements. The term “promoter/enhancer” refers to a segment of DNA which contains sequences capable of providing both promoter and enhancer functions.

The term “operably linked”, refers to a juxtaposition wherein the components described are in a relationship permitting them to function in their intended manner. In one
20 embodiment, the term refers to a functional linkage between an expression control sequence (such as a promoter, and/or enhancer) and a second polynucleotide sequence encoding a polypeptide, wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

Illustrative ubiquitous expression control sequences suitable for use in particular
25 embodiments include, but are not limited to, a β -actin promoter, a cytomegalovirus (CMV) immediate early promoter, a simian virus 40 (SV40) (*e.g.*, early or late) promoter, a Moloney murine leukemia virus (MoMLV) promoter, a Rous sarcoma virus (RSV) promoter, a herpes simplex virus (HSV) (thymidine kinase) promoter, an SV40/CD43 promoter, a spleen focus forming virus (SFFV) promoter, an elongation factor 1-alpha (EF1 α) short promoter
30 (intronless), an EF1 α long promoter containing an intron, a Ubiquitin C (UBC) promoter, a phosphoglycerate kinase-1 (PGK) promoter, a cytomegalovirus enhancer/chicken β -actin (CAG) promoter, and a myeloproliferative sarcoma virus enhancer, negative control region

deleted, dl587rev primer-binding site substituted (MND) U3 promoter (Haas *et al.*, Journal of Virology. 2003;77(17): 9439-9450).

Illustrative examples of ubiquitous expression control sequences suitable for use in particular embodiments contemplated herein include those comprising polynucleotide sequences set forth in Table 7.

Table 7

SEQ ID NO:	NUCLEIC ACID SEQUENCE
948	GCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCTACTTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTCGAGGTGAGCCCCACGTTCTGCTTCACTCTCCCCATCTCCCCCCCCCTCCCCACCCCAATTTGTATTTATTTATTTTAAATTATTTTGTGCAGCATGGGGGCGGGGGGGGGGGGGGGCGCGCCAGCGGGGGCGGGGCGCGGGCGAGGGCGGGGCGGGGCGAGAGGTGCGGGCGGCAGCCAATCAGAGCGGGCGGCTCCGAAAGTTTCCTTTTATGGCGAGGCGGGCGGGCGGGCGGGCCCTATAAAAAGCGAAGCGCGCGCGGGGCG
949	CGTGAGGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACCGGTGCCCTAGAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCCTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCCGTAACGTTCTTTTTTCGCAACGGGTTTGCCGCCGAGAACACAGGTAAGTGCCGTGTGTGGTTCCGCGGGCCTGGCCTCTTTACGGGTTATGGCCCTTGCGTGCCTTGAATTACTTCCACCTGGCTGCAGTACGTGATTCTTGATCCCGAGCTTCGGGTTGGAAGTGGGTGGGAGAGTTCGAGGCCTTGCGCTTAAGGAGCCCCCTCGCCTCGTGCTTGAGTTGAGGCTGGCCTGGGCGCTGGGGCCGCCCGCTGCGAATCTGGTGGCACCTTCGCGCCTGTCTCGCTGCTTTGATAAGTCTCTAGCCATTTAAAAATTTTTGATGACCTGCTGCGACGCTTTTTTCTGGCAAGATAGTCTTGTAATGCGGGCCAGATCTGACACTGGTATTTTCGGTTTTTGGGGCGCGGGGCGGCGACGGGGCCCGTGCCTCCAGCGCACATGTTTCGGCGAGGCGGGGCTGCGAGCGCGGCCACCGAGAATCGGACGGGGGTAGTCTCAAGCTGGCCGGCTGCTCTGGTGCCTGGCCTCGCGCCGCCGTGATCGCCCCGCCCTGGGCGGCAAGGCTGGCCCCGCTCGGCACCAAGTTGCGTGAGCGGAAAGATGGCCGCTTCCCGGCCCTGCTGCAGGGAGCTCAAAATGGAGGACGCGGCGCTCGGGAGAGCGGGCGGGTGAGTCACCCACACAAGGAAAAGGGCTTTTCCGTCTCAGCCGTGCTTTCATGTGACTCCACGGAGTACCGGGCGCCGTCCAGGCACCTCGATTAGTCTCGAGCTTTTGGAGTACGTGCTTTTAGGTTGGGGGAGGGGTTTTATGCGATGGAGTTTCCCACTGAGTGGGTGGAGACTGAAGTTAGGCCAGCTTGGCACTTGATGTAATTCCTTTGGAATTTGCCCTTTTGGATTTGGATCTTGGTTCATTCTCAAGCCTCAGACAGTGGTTCAAAGTTTTTTTCTTCCATTTCAAGGTGTCGTGA
950	AATGAAAGACCCACCTGTAGGTTTGGCAAGCTAGGATCAAGGTTAGGAACAGAGAGACAGCAGAAATATGGGCAACAGGATATCTGTGGTAAGCAGTTCTGCCCCGGCTCAGGGCCAAGACAGTTGGAACAGCAGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCTGCCCCGGCTCAGGGCCAAGAAGCAGATGGTCCCCAGATGCGGTCCCGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTTCGCTTCTCGCTTCTGTTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCACAAACCCCTCACTCGGC
951	GGGTAGGGGAGGCGCTTTTCCCAAGGCAGTCTGGAGCATGCGCTTTAGCAGCCCCGCTGGGCAC TTGGCGCTACACAAGTGGCCTCTGGCCTCGCACACATTCCACATCCACCGGTAGCGCCAACCGGCTCCGTTCTTTGGTGGCCCCCTTCGCGCCACCTTCTACTCCTCCCTAGTCAGGAAGTTCCCCC CCGCCCCGCAGCTCGCGTGTGTCAGGACGTGACAAATGGAAGTAGCACGTCTCACTAGTCTCGTGCAGATGGACAGCACCGCTGAGCAATGGAAGCGGGTAGGCCTTTGGGGCAGCGGCCAATAGCAGCTTTGCTCCTTCGCTTTCTGGGCTCAGAGGCTGGGAAGGGGTGGGTCCGGGGCGGGCTCAGGGGCGGGGCGGGGCGCCGAAGGTCTCCGGAGGCCCGGCAATTCGACGCTTCAAAAGCGCACGTCTGCGCGCTGTTCTCCTCTTCTCATCTCCGGGCTTTTCG
952	TGAAAGACCCACCTGTAGGTTTGGCAAGATAGCTGCAGTAACGCCATTTTGCAAGGCATGGAA

	AAATACCAACCAAGAATAGAGAAGTTCAGATCAAGGGCGGGTACATGAAAATAGCTAACGTTG GGCCAAACAGGATATCTGCGGTGAGCAGTTTCGGCCCCGGCCCGGGGCAAGAACAGATGGTCA CCGCAGTTTCGGCCCCGGCCCGAGGCCAAGAACAGATGGTCCCCAGATATGGCCCAACCTCAG CAGTTTCTTAAGACCCATCAGATGTTTCCAGGCTCCCCAAGGACCTGAAATGACCCTGCGCCT TATTTGAATTAACCAATCAGCCTGCTTCTCGCTTCTGTTGCGCGCTTCTGCTTCCCGAGCTCT ATAAAAGAGCTCACAAACCCCTCACTCGGCGCGCCAGTCCCTCCGATTGACTGAGTCGCCC
953	GGCCTCCGCGCGGGTTTTGGCGCCTCCCGCGGGCGCCCCCTCCTCACGGCGAGCGCTGCCAC GTCAGACGAAGGGCGCAGCGAGCGTCTGATCCTTCCGCCCCGACGCTCAGGACAGCGGCCCGC TGCTCATAAGACTCGGCCTTAGAACCCAGTATCAGCAGAAGGACATTTTAGGACGGGACTTGG GTGACTCTAGGGCACTGGTTTTCTTTCCAGAGAGCGGAACAGGCGAGGAAAAGTAGTCCCTTCT CGGCGATTCTGCGGAGGGATCTCCGTGGGGCGGTGAACGCCGATGATTATATAAGGACGCGCCG GGTGTGGCACAGCTAGTTCCGTGCGAGCCGGGATTTGGGTGCGCGTTCTTGTTTGGGATCGCT GTGATCGTCACTTGTTGAGTAGCGGGCTGCTGGGCTGGCCGGGGCTTTGCTGGCGCGCGGGCCG CTCGGTGGGACGGAAGCGTGTGGAGAGACCGCCAAGGGCTGTAGTCTGGGTCCGCGAGCAAGGT TGCCCTGAACTGGGGGTTGGGGGAGCGCAGCAAAATGGCGGCTGTCCCGAGTCTTGAATGGA AGACGCTTGTGAGGCGGGCTGTGAGGTCGTTGAAACAAGGTGGGGGCGATGGTGGGCGGCAAGA ACCCAAGTCTTGAGGCCTTCGCTAATGCGGGAAAGCTCTTATTCGGGTGAGATGGGCTGGGGC ACCATCTGGGGACCCTGACGTGAAGTTTGTCACTGACTGGAGAACTCGGTTTGTGCTCTGTTGC GGGGGCGGCAGTTATGGCGGTGCCGTTGGGCAGTGCACCCGTACCTTTGGGAGCGCGGCCCTC GTCGTGTCGTGACGTACCCGTTCTGTTGGCTTATAATGCAGGGTGGGGCCACCTGCCGGTAGG TGTGCGGTAGGCTTTTTCTCGTTCGAGGACGCGAGGTTTCGGGCCTAGGGTAGGCTCTCCTGAAT CGACAGGCGCCGGACCTCTGGTGAGGGGAGGGATAAGTGAGGCGTCAGTTTCTTTGGTTCGGTTT TATGTACCTATCTTCTTAAGTAGCTGAAGCTCCGGTTTGAACATATGCGCTCGGGTTGGCGAG TGTGTTTTGTGAAGTTTTTTAGGCACCTTTTGAATGTAATCATTGGGTCAATATGTAATTTT CAGTGTTAGACTAGTAAATTGTCCGCTAAATTCTGGCGTTTTTGGCTTTTTTGTAGAC

In particular embodiments, a polynucleotide comprises one or more cell type- or tissue-specific expression control sequences. In particular embodiments a cell type-specific expression control sequence is specific for immune effector cells. In particular embodiments a cell type-specific expression control sequence is a T cell specific promoter, an NK cell specific promoter, an NKT cell specific promoter, or a mucosal-associated invariant T (MAIT) cell promoter.

In particular embodiments, a cell type-specific expression control sequence is selected from the group consisting of a distal lymphocyte protein tyrosine kinase (LCK) promoter (Brenner *et al.*, Proc. Natl. Acad. Sci. USA 99:2936-2941 (2002)), a CD3δ promoter (Ji *et al.*, J Biol Chem. 277(49):47898-906 (2002)), a CD4 gene promoter (Salmon *et al.*, Proc. Natl. Acad. Sci. USA 90:7739 (1993)), a CD2 promoter (Greaves *et al.*, Cell 56:979-86 (1989)), and a TCF7 promoter (van de Wetering *et al.* J. of Bio. Chem. 267: 8530-8536 (1992)).

In particular embodiments, expression of polynucleotide sequences may be modulated by incorporating posttranscriptional regulatory elements into vectors. A variety of posttranscriptional regulatory elements may increase expression of a heterologous nucleic acid, *e.g.* woodchuck hepatitis virus posttranscriptional regulatory element (WPRE; Zufferey *et al.*, 1999, J. Virol., 73: 2886); the posttranscriptional regulatory element present in hepatitis

B vims (HPRE) (Huang *et al.*, Mol. Cell. Biol., 5:3864); and the like (Liu *et al.*, 1995, Genes Dev., 9:1766).

Illustrative examples of posttranscriptional control sequences suitable for use in particular embodiments contemplated herein include those comprising polynucleotide sequences set forth in Table 8.

Table 8

SEQ ID NO:	NUCLEIC ACID SEQUENCE
945	AATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTTCATTTCTCCTCCTTGTATAAATCCTGGTTGCTGTCTCTTTATGAGGAGTTGTGGCCCGTTGTCAAGGCAACGTGGCGTGGTGTGCACTGTGTTTGCTGACGCAACCCCCACTGGTTGGGGCATTGCCACCACCTGTCAGCTCCTTTCCGGGACTTTTCGCTTTCCCCCTCCCTATTGCCACGGCGGAACCTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCCTGACAATTCCCGTGGTGTGTGCGGGGAAGCTGACGTCCTTTCCATGGCTGCTCGCCTGTGTTGCCACCTGGATTCTGCGCGGGACGTCCTTCTGCTACGTCCTTCGGCCCTCAATCCAGCGGACCTTCCTTCCC CGCGCCTGCTGCCGGCTCTGCGGCCTCTTCCGCGTCTTCGCCTTCGCCTCAGACGAGTCGGATCTCCCTTTGGGCCGCTCCCCGCCTG
946	AATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTTCATTTCTCCTCCTTGTATAAATCCTGGTTGCTGTCTCTTTATGAGGAGTTGTGGCCCGTTGTCAAGGCAACGTGGCGTGGTGTGCACTGTGTTTGCTGACGCAACCCCCACTGGTTGGGGCATTGCCACCACCTGTCAGCTCCTTTCCGGGACTTTTCGCTTTCCCCCTCCCTATTGCCACGGCGGAACCTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCCTGACAATTCCCGTGGTGTGTGCGGGGAAGGTCTGCTGAGACTCGGGGCTGCTCGCCTGTGTTGCCACCTGGATTCTGCGCGGGACGTCCTTCTGCTACGTCCTTCGGCCCTCAATCCAGCGGACCTTCCTTCCC CGCGCCTGCTGCCGGCTCTGCGGCCTCTTCCGCGTCTTCGCCTTCGCCTCAGACGAGTCGGATCTCCCTTTGGGCCGCTCCCCGCCTG
947	AATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGATATTCTTAACTATGTTGCTCCTTTTACGCTGTGTGGATATGCTGCTTTAATGCCTCTGTATCATGCTATTGCTTCCCGTACGGCTTTTCGTTTTCTCCTCCTTGTATAAATCCTGGTTGCTGTCTCTTTATGAGGAGTTGTGGCCCGTTGTCCGTC AACGTGGCGTGGTGTGCTCTGTGTTTGCTGACGCAACCCCCACTGGCTGGGGCATTGCCACCACCTGTCAACTCCTTTCTGGGACTTTTCGCTTTCCCCCTCCCGATCGCCACGGCAGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTAGGTTGCTGGGCCTGATAATTCCGTGGTGTGTC

In particular embodiments, a vector comprises or encodes (in the case of an RNA vector, *e.g.*, a retroviral vector) an MNDU3 promoter (*e.g.*, SEQ ID NO: 950) operably linked to a polynucleotide encoding a chimeric antigen receptor comprising an anti-BCMA antibody or antigen binding fragment thereof comprising an amino acid set forth in any one of SEQ ID NOs: 11-144, and optionally a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947. In particular embodiments, a vector comprises or encodes an MNDU3 promoter operably linked to a polynucleotide encoding a chimeric antigen receptor comprising an anti-BCMA antibody or antigen binding fragment thereof comprising an amino acid set forth in any one of SEQ ID NOs: 20, 30, 39, 50, 59, 70, 80, 90, 100, 101, 105, 109, 113, 117, 121, 125, 129, 133, 137, and 141, and

optionally a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947. In particular embodiments, a vector comprises or encodes an MNDU3 promoter operably linked to a polynucleotide encoding a chimeric antigen receptor comprising an amino acid sequence set forth in any one of SEQ ID NOs: 165-860, and optionally a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947. In particular embodiments, a vector comprises or encodes an MNDU3 promoter operably linked to a polynucleotide encoding a signal peptide comprising an amino acid sequence set forth in any one of SEQ ID NOs: 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, and 873 and a polynucleotide encoding a chimeric antigen receptor comprising an amino acid sequence set forth in any one of SEQ ID NOs: 165-860, and optionally a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947. In particular embodiments, a vector comprises or encodes an MNDU3 promoter operably linked to a polynucleotide encoding a chimeric antigen receptor comprising an amino acid sequence set forth in any one of SEQ ID NOs: 189, 237, 261, 333, 357, 429, 477, 525, 573, 597, 621, 645, 669, 693, 717, 741, 765, 789, 813, and 837, and optionally a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947. In particular embodiments, a vector comprises or encodes an MNDU3 promoter operably linked to a polynucleotide encoding a signal peptides comprising an amino acid sequence set forth in SEQ ID NO: 861 and a polynucleotide encoding a chimeric antigen receptor comprising an amino acid sequence set forth in any one of SEQ ID NOs: 189, 237, 261, 333, 357, 429, 477, 525, 573, 597, 621, 645, 669, 693, 717, 741, 765, 789, 813, and 837, and optionally a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947. In particular embodiments, a vector comprises or encodes an MNDU3 promoter operably linked to a polynucleotide encoding a chimeric antigen receptor comprising a polynucleotide sequence set forth in any one of SEQ ID NOs: 905-944, and optionally a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947. In particular embodiments, a vector comprises or encodes an MNDU3 promoter operably linked to a polynucleotide encoding a signal peptide comprising a polynucleotide sequence set forth in SEQ ID NO: 904 and a chimeric antigen receptor comprising a polynucleotide sequence set forth in any one of SEQ ID NOs: 905-924, and optionally a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947. In particular embodiments, a vector comprises or encodes an

MNDU3 promoter operably linked to a polynucleotide encoding a signal peptide and a chimeric antigen receptor comprising a polynucleotide sequence set forth in any one of SEQ ID NOs: 925-944, and optionally a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

- 5 In particular embodiments, a vector comprises or encodes (in the case of an RNA vector, *e.g.*, a retroviral vector) an EF1 α promoter (*e.g.*, SEQ ID NO: 949) operably linked to a polynucleotide encoding a chimeric antigen receptor comprising an anti-BCMA antibody or antigen binding fragment thereof comprising an amino acid set forth in any one of SEQ ID NOs: 11-144, and optionally a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947. In particular embodiments,
- 10 a vector comprises or encodes an EF1 α promoter operably linked to a polynucleotide encoding a chimeric antigen receptor comprising an anti-BCMA antibody or antigen binding fragment thereof comprising an amino acid set forth in any one of SEQ ID NOs: 20, 30, 39, 50, 59, 70, 80, 90, 100, 101, 105, 109, 113, 117, 121, 125, 129, 133, 137, and 141, and
- 15 optionally a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947. In particular embodiments, a vector comprises or encodes an EF1 α promoter operably linked to a polynucleotide encoding a chimeric antigen receptor comprising an amino acid sequence set forth in any one of SEQ ID NOs: 165-860, and optionally a polynucleotide comprising a posttranscriptional regulatory element set forth in
- 20 any one of SEQ ID NOs: 945-947. In particular embodiments, a vector comprises or encodes an EF1 α promoter operably linked to a polynucleotide encoding a signal peptide comprising an amino acid sequence set forth in any one of SEQ ID NOs: 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, and 873 and a polynucleotide encoding a chimeric antigen receptor comprising an amino acid sequence set forth in any one of SEQ ID NOs: 165-860,
- 25 and optionally a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947. In particular embodiments, a vector comprises or encodes an EF1 α promoter operably linked to a polynucleotide encoding a chimeric antigen receptor comprising an amino acid sequence set forth in any one of SEQ ID NOs: 189, 237, 261, 333, 357, 429, 477, 525, 573, 597, 621, 645, 669, 693, 717, 741, 765, 789, 813, and 837,
- 30 and optionally a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947. In particular embodiments, a vector comprises or encodes an EF1 α promoter operably linked to a polynucleotide encoding a signal peptide comprising an amino acid sequence set forth in any one of SEQ ID NOs: 861, 862, 863, 864,

865, 866, 867, 868, 869, 870, 871, 872, and 873 and a chimeric antigen receptor comprising an amino acid sequence set forth in any one of SEQ ID NOs: 189, 237, 261, 333, 357, 429, 477, 525, 573, 597, 621, 645, 669, 693, 717, 741, 765, 789, 813, and 837, and optionally a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947. In particular embodiments, a vector comprises or encodes an EF1 α promoter operably linked to a polynucleotide encoding a chimeric antigen receptor comprising a polynucleotide sequence set forth in any one of SEQ ID NOs: 905-924, and optionally a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947. In particular embodiments, a vector comprises or encodes an EF1 α promoter operably linked to a polynucleotide encoding a signal peptide comprising a polynucleotide sequence set forth in SEQ ID NO: 904 and a chimeric antigen receptor comprising a polynucleotide sequence set forth in any one of SEQ ID NOs: 905-924, and optionally a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947. In particular embodiments, a vector comprises or encodes an EF1 α promoter operably linked to a polynucleotide encoding a signal peptide and a chimeric antigen receptor comprising a polynucleotide sequence set forth in any one of SEQ ID NOs: 925-944, and optionally a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

Efficient expression of polynucleotides can also be increased in some embodiments, by using sequences that increase translational efficiency, *e.g.*, through an increase in mRNA ribosomal binding or an increase in mRNA stability. In certain embodiments, polynucleotides encoding a chimeric antigen receptor comprise a short recognition sequence, *i.e.*, a Kozak sequence, that greatly facilitates the initial binding of mRNA to the small subunit of the ribosome and increases translation. The consensus Kozak sequence is (GCC)RCCATGG, where R is a purine (A or G) (Kozak, Cell. 44:283-92 (1986), and Kozak, Nucleic Acids Res. 15:8125-48 (1987)).

Elements directing the efficient termination and polyadenylation of heterologous nucleic acid transcripts may also increase heterologous gene expression. Transcription termination signals are generally found downstream of the polyadenylation signal. In particular embodiments, vectors comprise a polyadenylation sequence 3' to a sequence to be transcribed and/or expressed. The term "polyadenylation (or poly(A)) signal" refers to a DNA sequence which directs both the termination and polyadenylation of the nascent RNA transcript by RNA polymerase II. Polyadenylation signals can promote mRNA stability by

addition of a poly(A) tail to the 3' end of the coding sequence and thus, contribute to increased translational efficiency. Cleavage and polyadenylation are directed by a poly(A) signal in the RNA. The core poly(A) signal for mammalian pre-mRNAs has two recognition elements flanking a cleavage-polyadenylation site. Typically, an almost invariant AAUAAA hexamer
 5 lies 20-50 nucleotides upstream of a more variable element rich in U or GU residues. Cleavage of the nascent transcript occurs between these two elements and is coupled to the addition of up to 250 adenosines to the 5' cleavage product. In particular embodiments, the core poly(A) signal is an ideal poly(A) signal (*e.g.*, AATAAA, ATTAAA, AGTAAA). In particular embodiments, the poly(A) signal is an SV40 poly(A) signal, a bovine growth
 10 hormone poly(A) signal (BGHpA), a rabbit β -globin poly(A) signal (r β gpA), variants thereof, or another suitable heterologous or endogenous poly(A) signal known in the art. In particular embodiments, the poly(A) signal is synthetic.

In particular embodiments, a polynucleotide comprises or encodes a promoter operably a polynucleotide sequence encoding a chimeric antigen receptor comprising a signal
 15 peptide isolated from a polypeptide selected from the group consisting of CD8 α , murine IgG κ , human IgG κ , CD33, tPA, SEAP, hGM-CSF, gaussian luciferase, CSF2R, B2M, and CD80, wherein the signal peptide is subsequently cleaved from the translated chimeric antigen receptor. In particular embodiments, a polynucleotide comprises or encodes a promoter operably linked to a polynucleotide sequence encoding a chimeric antigen receptor
 20 comprising a signal peptide comprising an amino acid sequence set forth in any one of SEQ ID NOs: 861-873. An illustrative example of a polynucleotide encoding a signal peptide is set forth in SEQ ID NO: 904 (ATGGCTCTTCCCGTAACAGCCCTTTTGTGCCCCCTTGCACTCCTTCTGCATGCA GCACGACCG).

25 In particular embodiments, a polynucleotide comprises one or more miR target sequences inserted into a 5' UTR, intron, and/or 3' UTR to restrict expression in undesired or off-target cell types.

In some embodiments, a polynucleotide comprises an inducible suicide gene to reduce the risk of direct toxicity and/or uncontrolled proliferation. In some embodiment, the
 30 suicide gene is caspase-8 or caspase-9. Caspase-9 can be activated using a specific chemical inducer of dimerization (CID).

In some embodiments, a polynucleotide comprises a gene or gene segment that when introduced into a cell, renders the cell susceptible to negative selection. Negative selection

suitable for use in particular embodiments include but are not limited to the HSV-TK gene which confers ganciclovir sensitivity; the cellular hypoxanthine phosphoribosyltransferase (HPRT) gene, the cellular adenine phosphoribosyltransferase (APRT) gene, and bacterial cytosine deaminase.

5 In some embodiments, a polynucleotide comprises a gene or gene segment that when introduced into a cell, renders the cell susceptible to positive selection. Positive selection genes suitable for use in particular embodiments contemplated herein include but are not limited to hygromycin-B phosphotransferase gene (hph) which confers resistance to hygromycin B, the amino glycoside phosphotransferase gene (neo or aph) from Tn5 which
10 codes for resistance to the antibiotic G418, the dihydrofolate reductase (DHFR) gene, the adenosine deaminase gene (ADA), and the multi-drug resistance (MDR) gene.

Table 9 sets forth the SEQ ID NOs. and associated nucleic acid sequences encoding chimeric antigen receptor components and chimeric antigen receptors and the corresponding amino acid SEQ ID NO (AA SEQ ID NO.) encoded by the nucleic acid sequence.

15 Table 9

SEQ ID NO.	AA SEQ ID NO.	NUCLEIC ACID SEQUENCE
894	145	ACCACAACACCTGCTCCAAGGCCCCCACACCCGCTCCAACTATAGCCA GCCAACCATTGAGCCTCAGACCTGAAGCTTGCAGGCCCGCAGCAGGAGG CGCCGTCCATACGCGAGGCCCTGGACTTCGCGTGTGAT
895	146	ATTGAAGTTATGTATCCTCCTCCTTACCTAGACAATGAGAAGAGCAATG GAACCATTATCCATGTGAAAGGGAAACACCTTTGTCCAAGTCCCCTATT TCCCGGACCTTCTAAGCCC
896	148	GAGTCCAAATATGGTCCCCCGTGCCCAACCATGCCCCA
897	150	CTTGAGCCCCAAATCTTGTGACAAAACCTCACACATGCCCAACCGTGCCCCA
898	151	ATTTATATTTGGGCACCTTTGGCCGGAACATGTGGGGTGTGCTTCTCT CCCTTGTGATCACTCTGTATTGT
899	153	TTTTGGGTGCTGGTGGTGGTGGTGGAGTCTGGCTTGCTATAGCTTGC TAGTAACAGTGGCCTTTATTATTTTCTGGGTG
900	159	AAGCGCGGGAGAAAGAAGCTCCTGTACATCTTCAAGCAGCCTTTTATGC GACCTGTGCAAAACCACTCAGGAAGAAGATGGGTGTTTCATGCCGCTTCCC CGAGGAGGAAGAAGGAGGGTGTGAAGT
901	160	AGGAGTAAGAGGAGCAGGCTCCTGCACAGTGACTACATGAACATGACTC CCCGCCGCCCGGGCCACCCGCAAGCATTACCAGCCCTATGCCCCACC ACGCGACTTCGACGCTATCGCTCC
902	162	ACAAAAAAGAAGTATTTCATCCAGTGTGCACGACCCTAACGGTGAATACA TGTTTCATGAGAGCAGTGAACACAGCCAAAAAATCTAGACTCACAGATGT GACCCTA
903	158	AGGGTGAAATTTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAGGGTC AGAATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAGAAGAGTACGA TGTTCTGGACAAAAGACGGGGCAGGGATCCCGAGATGGGGGAAAGCCC CGGAGAAAAAATCCTCAGGAGGGGTGTGACAATGAGCTGCAGAAGGACA AGATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGAAAGACGCAG AGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTACAGCCACCAAG GACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCCCGC
904	861	ATGGCTCTTCCCGTAACAGCCCTTTTGTGCCCCCTTGCACTCCTTCTGC ATGCAGCACGACCG

905	189	GAGATCGTGCTGACACAGTCTCCCGCCACACTGTCTACTGTCTCCAGGCG AAAGAGCCACACTGAGCTGTAGAGCCAGCCAGAGCGTGTCTCTTACCT GGCTTGGTATCAGCAGAAGCCTGGACAGGCTCCCCGGCTGCTGATCTAC GATGCCAGCAATAGAGCCACAGGCATCCCCGCCAGATTTTCTGGCAGCG GCTCTGGCACCATTTCACCTGACCATAAGCAGCCTGGAACCTGAGGA CTTCGCCGTGTACTACTGCCAGCAGAGAGTGGTGTACCCCATCACCTTT GGCGGAGGCACCAAGGTGGAATCAAAGCGCGGAGGAAGCGGAGGCG GAGGATCTGGTGGTGGTGGATCTGGCGGAGGTGGCAGCCAGATCACACT GAAAGAGTCTGGCCCCACACTGGTCAAGCCACACAGACCCTGACACTG ACCTGCACCTTCAGCGGCTTTAGCCTGAGCACATCTGGCGTCCGCGTTG GCTGGATTAGACAGCCTCCTGGAAAGGCCCTGGAATGGCTGGCCCTGAT CTACTGGAACGACGAGAAGAGATACAGCCCCAGCCTGAAGTCCCGGTG ACCATCACCAAGGACACCAGCAAGAACCAGGTGGTGTGACCATGACAA ACATGGACCCCGTGGACACCGCCGTGTATTATTGCGCCAGAGATGAGTA CGCGCGCTTCGACATTTGGGGCCAGGGCACAATGGTCACCGTGTCTAGT ACCACAACACCTGTCTCAAGGCCCCCCACACCCGCTCCAACATATAGCCA GCCAACCATTGAGCCTCAGACCTGAAGCTTGCAGGCCCGCAGCAGGAGG CGCCGTCCATACGCGAGGCCCTGGACTTCGCGTGTGATATTTATATTTGG GCACCTTTGGCCGGAACATGTGGGGTGTGCTTCTCTCCCTTGTGATCA CTCTGTATTGTAAGCGCGGGAGAAAGAAGCTCCTGTACATCTTCAAGCA GCCTTTTATGCGACCTGTGCAAACCACTCAGGAAGAAGATGGGTGTTCA TGCCGCTTCCCCGAGGAGGAAGAAGGAGGGTGTGAACCTGAGGGTGAAT TTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAGGGTCAGAATCAGCT CTACAATGAATTGAATCTCGGCAGGCGAGAAGAGTACGATGTTCTGGAC AAAAGACGGGGCAGGGATCCCGAGATGGGGGGAAAGCCCCGAGAAAAA ATCCTCAGGAGGGGTGTACAATGAGCTGCAGAAGGACAAGATGGCTGA AGCCTATAGCGAGATCGGAATGAAAGGCGAAAAGACGCAGAGGCAAGGGG CATGACGGTCTGTACCAGGGTCTCTCTACAGCCACCAAGGACACTTATG ATGCGTTGCATATGCAAGCCTTGCCACCCCGC
906	237	GAGATCGTGCTGACCCAGTCCCCTGCTACCCTGAGCCTGTCTCCAGGCG AGCGGGCCACACTGAGCTGTAGAGCTTCTCAGAGCGTGTCCAGCTACCT GGCTTGGTATCAGCAGAAACCTGGCCAGGCCCTTAGACTGCTGATCTAC GACGCCAGCAACCGGGCCACCGGCATCCCCGCCAGATTAGCGGATCTG GCAGCGGCACAGATTTTACCCTCACCATCAGCAGCCTGGAACCTGAGGA CTTCGCCGTGTACTACTGCCAGCAAGATTGACTACCCCATCACCTTC GGCGGCGGAACAAAGGTGGAATTAAGGGTGGTGGGGCAGCGGTGGAG GTGGGAGCGGAGGCGGGGTAGCGGAGGCGGGGTAGCCAAATCACACT GAAAGAGAGCGGCCCTACACTCGTGAAACCTACCCAGACCCTGACACTG ACATGTACCTTCAGCGGCTTCTCCCTGAGCACCTCTGGCGTCCGCGTTG GATGGATCAGACAGCCTCCAGGCAAGGCCCTGGAATGGCTGGCTCTGAT CTATTGGAACGACGACAAGCGGTACAGCCCCAGCCTGAAGTCTAGACTG ACCATCACAAAGGACACCAGCAAGAACCAGGTGGTGTGACCATGACAA ATATGGACCCCGTGGACACCGCCGTGTACTACTGCGCCAGAGATGAGTA CGCGGGATTTGATATCTGGGGCCAGGGCACCATGGTGACCGTGTCCAGC ACCACAACACCTGTCTCAAGGCCCCCCACACCCGCTCCAACATATAGCCA GCCAACCATTGAGCCTCAGACCTGAAGCTTGCAGGCCCGCAGCAGGAGG CGCCGTCCATACGCGAGGCCCTGGACTTCGCGTGTGATATTTATATTTGG GCACCTTTGGCCGGAACATGTGGGGTGTGCTTCTCTCCCTTGTGATCA CTCTGTATTGTAAGCGCGGGAGAAAGAAGCTCCTGTACATCTTCAAGCA GCCTTTTATGCGACCTGTGCAAACCACTCAGGAAGAAGATGGGTGTTCA TGCCGCTTCCCCGAGGAGGAAGAAGGAGGGTGTGAACCTGAGGGTGAAT TTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAGGGTCAGAATCAGCT CTACAATGAATTGAATCTCGGCAGGCGAGAAGAGTACGATGTTCTGGAC AAAAGACGGGGCAGGGATCCCGAGATGGGGGGAAAGCCCCGAGAAAAA ATCCTCAGGAGGGGTGTACAATGAGCTGCAGAAGGACAAGATGGCTGA AGCCTATAGCGAGATCGGAATGAAAGGCGAAAAGACGCAGAGGCAAGGGG CATGACGGTCTGTACCAGGGTCTCTCTACAGCCACCAAGGACACTTATG ATGCGTTGCATATGCAAGCCTTGCCACCCCGC
907	261	CAAGTGCAGCTCGTGGAAAGCGGCGGAGTGGTGCAGCCCGGCCGGA

		GCCTGAGACTGTCTGCGCCGCTTCTGGATTACCTTCAGCAGCTACGG CATGCACTGGGTGAGACAGGCCCTGGCAAAGGCTGGAGTGGGTGGCC GTTATCAGCTACGAGGGCAGCAACAAGTATTACGCCGACAGCGTGAAGG GCCGCTTCACAACTCTCTAGAGATAATAGCAAGAACACCTGTACCTGCA GATGAACAGCCTGCGGGCCGAAGATACCGCCGTGTACTACTGTGCTAGA GAGCTGGGCGACGGCATGGACGTGTGGGGACAGGGCACAACCGTGACCG TGTCTCTGGTGGTGGGGGACGCGGTGGAGGTGGGAGCGGAGGCGGGGG TAGCGGAGGCGGGGGTAGCGAGATCGTGCTGACCCAGTCCCCTGCTACA CTGAGCCTGTCTCCAGGCGAGCGGGCCACACTGAGCTGTAGAGCTTCTC AGAGCGTGTCCAGCTATCTGGCTGGTTCAGCAGAAACCTGGCCAGGC CCCTAGACTGCTGATCTACGACGCCAGCAACCGGGCCACCGGCATCCCC GCCAGATTACGCGGCTCTGGCAGCGGCACCGACTTCACCTCACCATCA GCAGCCTGGAACCCGAGGATTTGCGCTCTACTACTGCCAGCAAAGAGT GGACCTGTGGACCTTCGGCGGAGGAACAAGGTGGAAATCAAGACCACA ACACCTGCTCCAAGGCCCCCACACCCGCTCCAATATAGCCAGCCAAC CATTGAGCCTCAGACCTGAAGCTTGACGGCCGACGAGGAGGCGCGGT CCATACGCGAGGCTGGACTTCGCGTGTGATATTTATATTTGGGCACCT TTGGCCGGAACATGTGGGTGTGTCTTCTCTCCCTTGTGATCACTCTGT ATTGTAAGCGCGGGAGAAAGAAGCTCCTGTACATCTTCAAGCAGCCTTT TATGCGACCTGTGCAAACCACTCAGGAAGAAGATGGGTGTTTCATGCCGC TTCCCCGAGGAGGAAGAAGGAGGGTGTGAAGTGAAGGTGAAATTTCTA GAAGCGCCGATGCTCCCGCATATCAGCAGGGTCAGAATCAGCTCTACAA TGAATTGAATCTCGGCAGGCGAGAAGAGTACGATGTTCTGGACAAAAGA CGGGGCAGGGATCCCGAGATGGGGGAAAGCCCCGGAGAAAAAATCCTC AGGAGGGGTTGTACAATGAGCTGCAGAAGGACAAGATGGCTGAAGCCTA TAGCGAGATCGGAATGAAAGGCGAAAGACGAGAGGCAAGGGGCATGAC GGTCTGTACCAGGTCTCTCTACAGCCACCAAGGACACTTATGATGCGT TGCATATGCAAGCCTTGCCACCCCGC
908	333	GACATCCAGATGACCCAGAGCCCTTCGACCCTATCCGCTTCCGTGGGTG ACCGTGTGACCATCACCTGTGCGCGCTCGCAGAGCATCTCCTCCTGGGT CGCGTGGTACCAACAGAAGCCTGGCAAGGCCCCCAAGCTGCTGATTTAC GACGCCAGTTCCCTGGAGTCTGGCGTGCCATCCCGCTTCTCCGGCAGCG GCAGCGGTACCGAGTTACCCGTGACGATCAGCTCCCTGACGCCGGATGA CTTTGCTACCTACTACTGTGAGCAGGTCTCCTCCCTCCCCCCCACCTTC GGTGGCGGTACCAAGGTGGAGATCAAGGGCGGCGGCGCTCTGTTGGCG GAGGTTCTGGCGGGGAGGTTCGGGGGGGGGAGGCTCCGAGGTGCAACT GGTAGAGAGCGGCGGGGACTGGTAAAACCCGGCGGCTCCCTGCGGCTG TCATGCGCTGCTAGCGGCTTCAGGTTACGCGATTACTACATGAGTTGGA TCCGCCAGGCCCCCGGGAAGGGTTTGGAGTGGGTCTCGTATATCTCTTC CAGCGGATCTACCATTACTATGCGGACAGCGTGAAGGGGCGCTTCACC ATATCTCGGGACAACGCCAAGAACTCCCTGTACCTGAGATGAATTCCT TGCGTGCCGAGGACACGGCCGTGTATTACTGTGCCCCGACACAGGGCAA CTACGGCGTGCAGCTGTGGGGCCAGGTTACAACCGTCACCGTGTCCAGT ACCACAACACCTGCTCCAAGGCCCCACACCCGCTCCAATATAGCCA GCCAACCATTGAGCCTCAGACCTGAAGCTTGACAGGCCCGCAGCAGGAGG CGCCGTCCATACGCGAGGCTGGACTTCGCGTGTGATATTTATATTTGG GCACCTTTGGCCGGAACATGTGGGTGTTGCTTCTCTCCCTTGTGATCA CTCTGTATTGTAAAGCGGGAGAAAGAAGCTCCTGTACATCTTCAAGCA GCCTTTTATGCGACCTGTGCAAACCACTCAGGAAGAAGATGGGTGTTCA TGCCGCTTCCCCGAGGAGGAAGAAGGAGGTGTGAAGTGAAGGTGAAAT TTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAGGGTCAGAATCAGCT CTACAATGAATTGAATCTCGGCAGGCGAGAAGAGTACGATGTTCTGGAC AAAAGACGGGGCAGGGATCCCGAGATGGGGGAAAGCCCCGGAGAAAAA ATCCTCAGGAGGGGTTGTACAATGAGCTGCAGAAGGACAAGATGGCTGA AGCCTATAGCGAGATCGGAATGAAAGGCGAAAGACGAGAGGCAAGGGG CATGACGGTCTGTACCAGGTCTCTCTACAGCCACCAAGGACACTTATG ATGCGTTGCATATGCAAGCCTTGCCACCCCGC
909	357	CAAGTGACAGCTGGTTCGAGAGCGGAGGAGGCTGGTTAAGCCCGGCGGAT CTCTCAGACTGAGCTGCGCGCTAGCGGCTTACATTACGCGACTACTA

		CATGAGCTGGATCCGGCAGGCCCTGGCAAGGGCCTGGAATGGGTGTCC TACATCAGCTCCTCCGGCAGCACCATCTACTACGCCGACAGCGTGAAAG GCAGATTACAACTCTCTAGAGATAATGCCAAGAACAGCCTGTACCTGCA GATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTATTGTGCTAGA GATCAGGGCAACTACGGCGTGGACGTGTGGGGCCAGGGCACCACCGTGA CCGTGTCTAGCGGTGGTGGGGGCAGCGGTGGAGGTGGGAGCGGAGGCGG GGGTAGCGGAGGCGGGGGTAGCGATATCCAGATGACCCAGTCCCCATCT AACTGAGCGCCTCTGTGGGCGACCGGGTGACCATTACATGTAGAGCCA GCCAGAGCATCAGCAGCTGGCTGGCTTGGTATCAGCAGAAACCTGGCAA GGCCCCAAGCTGTGTATCTACGAGGCCAGCAGCCTGGAAAGCGGCGTC CCCAGCAGATTACGCGGCAGCGGCTCTGGAACAGAGTTACCCCTGACCA TCTCCTCCCTGCAGCCTGACGACTTCGCCACCTACTACTGCCAGCAATC TGATAGCCACCCCATCACCTTTGGCGGAGGCACCAAGGTGGAAATCAAG ACCACAACACCTGCTCCAAGGCCCCCACACCCGCTCCAACATAGCCA GCCAACCATTGAGCCTCAGACCTGAAGCTTGCAGGCCCGCAGCAGGAGG CGCCGTCCATACGCGAGGCCCTGGACTTCGCGTGTGATATTTATATTTGG GCACCTTTGGCCGGAACATGTGGGGTGTGCTTCTCTCCCTTGTGATCA CTCTGTATTGTAAGCGCGGGAGAAAGAAGCTCCTGTACATCTTCAAGCA GCCTTTTATGCGACCTGTGCAAACCACTCAGGAAGAAGATGGGTGTTCA TGCCGCTTCCCCGAGGAGGAAGAAGGAGGTGTGAACAGGGGTGAAAT TTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAGGGTCAGAATCAGCT CTACAATGAATTGAATCTCGGCAGGCGAGAAGAGTACGATGTTCTGGAC AAAAGACGGGGCAGGGATCCCGAGATGGGGGGAAGCCCCGGAGAAAAA ATCCTCAGGAGGGGTGTACAATGAGCTGCAGAAGGACAAGATGGCTGA AGCCTATAGCGAGATCGGAATGAAAGGCGAAAGACGCAGAGGCAAGGGG CATGACGGTCTGTACCAGGGTCTCTCTACAGCCACCAAGGACACTTATG ATGCGTTGCATATGCAAGCCTTGCCACCCCGC
910	429	GATATCCAGATGACCCAGTCCCCATCTACTGAGCGCCTCTGTGGGCG ACCGGGTGACAAATACCTGTAGAGCTAGCCAGAGCATCTCCTCTGGCT GGCTTGGTACCAGCAAAAACCTGGCAAGGCCCTAAGCTGTCTGATCTAC GAGGCCAGCAGCCTGGAAAGCGGCGTCCCCCTCTAGATTACGCGGCAGCG GCTCTGGAACCGAGTTCACCCTGACAATCAGCAGCCTGCAGCCTGACGA CTTCCGCCACCTATTACTGCCAGCAGGCCAACAGCCACCCCATCACCTTT GCGCGAGGCACCAAGGTGGAAATCAAGGGTGGTGGGGGCAGCGGTGGAG GTGGGAGCGGAGCGGGGGTAGCGGAGGCGGGGGTAGCAGAGTGCAGCT GGTGAAAGCGCGGAGGACTCGTTAAGCCCGGCGGCGCCTGAGACTG AGCTGCGCCGCTAGCGGATTTACCTTCAGCGACTACTACATGAGCTGGA TCCGGCAGGCCCTGGCAAGGGCCTGGAATGGGTGAGTACATCAGCTC CTCTGGCTCTACAATCTACTACGCCGACAGCGTGAAAGGCAGATTACCC ATCTCTAGAGATAATGCCAAGAACAGCCTGTACCTGCAAATGAACAGCC TGCGGGCCGAGGACACCGCGTGTACTATTGTGCTAGAGATCAGGGCAA CTACGGCGTGGACGTGTGGGGCCAGGGCACACCGTGACAGTGTCTCTCC ACCACAACACCTGCTCCAAGGCCCCCACACCCGCTCCAACATAGCCA GCCAACCATTGAGCCTCAGACCTGAAGCTTGCAGGCCCGCAGCAGGAGG CGCCGTCCATACGCGAGGCCCTGGACTTCGCGTGTGATATTTATATTTGG GCACCTTTGGCCGGAACATGTGGGGTGTGCTTCTCTCCCTTGTGATCA CTCTGTATTGTAAGCGCGGGAGAAAGAAGCTCCTGTACATCTTCAAGCA GCCTTTTATGCGACCTGTGCAAACCACTCAGGAAGAAGATGGGTGTTCA TGCCGCTTCCCCGAGGAGGAAGAAGGAGGTGTGAACAGGGGTGAAAT TTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAGGGTCAGAATCAGCT CTACAATGAATTGAATCTCGGCAGGCGAGAAGAGTACGATGTTCTGGAC AAAAGACGGGGCAGGGATCCCGAGATGGGGGGAAGCCCCGGAGAAAAA ATCCTCAGGAGGGGTGTACAATGAGCTGCAGAAGGACAAGATGGCTGA AGCCTATAGCGAGATCGGAATGAAAGGCGAAAGACGCAGAGGCAAGGGG CATGACGGTCTGTACCAGGGTCTCTCTACAGCCACCAAGGACACTTATG ATGCGTTGCATATGCAAGCCTTGCCACCCCGC
911	477	GACATCCAGATGACCCAGAGCCCTAGCTCCCTGAGCGCCAGCGTGGGCG ATAGAGTGACCATTACCTGTAGAGCCTCTCAGAGCATCTCCTCCTACCT GAACTGGTATCAGCAGAAACCCGGCAAGGCCCTAAGCTGCTGATCTAC

		GCCGCTAGCAGCCTGCAGTCTGGCGTCCCCAGCCGGTTCAGCGGCAGCG GATCTGGCACCGACTTCACCTTGACAATCAGCAGCCTGCAACCTGAGGA CTTTGCTACATACTACTGCCAGCAGGCCACAGCTCTCCAATCACCTTC GGCGGCGGAACAAAGGTGGAATCAAGGGTGGTGGGGGAGCGGTGGAG GTGGGAGCGGAGGCGGGGTAGCGGAGGCGGGGTAGCGAGGTGCAGCT GCTGGAAAGCGGAGGCGGACTCGTTCAACCTGGCGGCAGCCTGAGACTG AGCTGCGCCGCTTCTGGATTACCTTCAGCAACTACGCCATGAGCTGGG TGCGGCAGGCCCCCTGGCAAAGGCCTGGAATGGGTCTCCGCCATCAGCGG CTCTGGCGGCTCCACCTACTACGCCGACAGCGTGAAGGGCAGATTACCC ATCTCTAGAGATAATAGCAAGAACACCCGTGTACCTGCAGATGAACAGCC TGCGGGCCGAGGACACCGCCGTGTACTATTGTGCTAGACCCGGAGATGG CTACTACGAGGGCGTGTACTTCGACTACTGGGGCCAGGGCAGACTGGTG ACAGTGCTCCAGCACCACAACACCTGCTCCAAGGCCCCCACACCCGCTC CAACTATAGCCAGCCAACCATTGAGCCTCAGACCTGAAGCTTGAGGCC CGCAGCAGGAGGCGCCGTCCATACGCGAGGCGCTGGACTTCGCGTGTGAT ATTTATATTTGGGCACCTTTGGCCGGAACATGTGGGGTGTGCTTCTCT CCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGAAAGAAGCTCCTGTA CATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAACCACTCAGGAAGAA GATGGGTGTTTATGCCGCTTCCCCGAGGAGGAAGAAGGAGGGTGTGAAC TGAGGGTGAAATTTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAGGG TCAGAATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAGAAGAGTAC GATGTTCTGGACAAAAGACGGGGCAGGGATCCCGAGATGGGGGGAAAGC CCCGAGAAAAAATCCTCAGGAGGGGTGTACAATGAGCTGCAGAAGGA CAAGATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGAAAGACCC AGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTACAGCCACCA AGGACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCCCGC
912	525	GATATTGATGACCCAGAGCCCATCTAGCCTGAGCGCCAGCGTGGGCG ATAGAGTGACCATCACCTGTGAGGCCTCTCAGGACATCGCTAATTACCT GAACTGGTATCAGCAGAAACCGGCAAGGCCCTAAGCTGTGATCTAC GACGCTTCAACCTGGAACCGGCGTGCCAGCCGTTTTCAGCGGAGCG GATCTGGCACAGACTTCACCTTTACCATCAGCTCCCTCCAGCCTGAGGA CATCGCCACATACTACTGCCAGCAACACTTCAACCTGCCTCTGACCTTC GGCGGCGGAACAAAGGTGAGATCAAGGGTGGTGGGGGAGCGGTGGAG GTGGGAGCGGAGGCGGGGTAGCGGAGGCGGGGTAGCCAAATCACCTC GAAAGAGAGCGGACCTACACTGGTCAAGCCTACCCAGACACTGACCTC ACATGTACATTAGCGGCTTTAGCCTGAGCACCTCCGGCGTGGGAGTGG GCTGGATCAGACAGCCCCCGGCAAGGCCCTGGAATGGCTGGCTCTGAT CTATTGGAATGACGAGAAGCGGTACAGCCCTAGCCTGAAATCTAGACTG ACAATCACCAAGGACACCAGCAAGAACCAGGTGGTGTGACCATGACCA ACATGGATCCTGTGGATACCGCCGTGTACTACTGCGCCAGAGAAGGCTC TCACGACTACAAGAGCTCCAAGTGGTTCGACCCATGGGGCCAGGGCACC CTGGTTACAGTGTCTAGCACCAACACCTGCTCCAAGGCCCCCACAC CCGCTCCAATATAGCCAGCCAACCATTGAGCCTCAGACCTGAAGCTTG CAGGCCCCGAGCAGGAGGCGCCGTCCATACGCGAGGCGCTGGACTTCGCG TGTGATATTTTATTTGGGCACCTTTGGCCGGAACATGTGGGGTGTGTC TTCTCTCCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGAAAGAAGCT CCTGTACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAACCACTCAG GAAGAAGATGGGTGTTTATGCCGCTTCCCCGAGGAGGAAGAAGGAGGT GTGAACTGAGGGTGAAATTTTCTAGAAGCGCCGATGCTCCCGCATATCA GCAGGGTCAGAAATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAGAA GAGTACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCGAGATGGGGG GAAAGCCCCGAGAAAAAATCCTCAGGAGGGGTGTACAATGAGCTGCA GAAGGACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGAA AGACGCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTACAG CCACCAAGGACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCCCG C
913	573	GATATCGTGATGACCCAATCTCCACTGAGCCTGCCTGTGACACCTGGCG AGCCTGCTTCTATCAGCTGTAGAAGCAGCCAGTCCCTGCTGCACAGCAA CGGCTACAACCTACCTGGACTGGTATCTGCAGAAACCGGCCAGAGCCCC

		CAGCTGCTGATCTACCTCGGCTCTAATCGGGCCAGCGGAGTGCCTGATA GATTTCAGCGGAAGCGGCTCCGGCACCGACTTCACCCTGAAGATCAGCAG AGTGGAAGCCGAGGACGTGGGCGTCTACTACTGCATGCAGGCCCTGGGC CTGATTACATTTGGCGGCGGAACCAAGGTGGAATCAAGGGTGGTGGGG GCAGCGGTGGAGGTGGGAGCGGAGGCGGGGGTAGCGGAGGCGGGGGTAG CGAAGTGCAGCTGGTTGAGAGCGGCGGCGGACTGGTGAAGCCCGAGGC AGCCTCAGACTGAGCTGTGCTGCTTCTGGCTTTACCTTCAGCTCTTATA GCATGAACTGGGTGCGGCAGGCCCCCTGGCAAGGGCCTGGAATGGGTGAG CTCCATCAGCTCTTCTAGCAGCTACATCTACTACGCCGACAGCGTGAAG GGCAGATTACCATCAGCAGAGATAACGCCAAGAACAGCCTGTACCTGC AGATGAATAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCGCCAG AGCCGGCGACACCTACAGCGCGCCGATTACTACTACATGGACGTGTGG GGCAAAGGAACAACCGTGACAGTGTCTCCACCACAACCTGCTCCAA GGCCCCCACACCCGCTCCAATATAGCCAGCCAACCATGAGCCTCAG ACCTGAAGCTTGCGAGGCCCGCAGCAGGAGGCGCCGTCCATACGCGAGGC CTGGACTTCGCGTGTGATATTATATTGGGACCTTTGGCCGGAACAT GTGGGGTGTGTCTCTCTCCCTTGTGATCACTCTGTATTGTAAGCGCGG GAGAAAGAAGCTCCTGTACATCTTCAAGCAGCCTTTTATGCGACCTGTG CAAACCACTCAGGAAGAAGATGGGTGTTTCATGCCGCTTCCCGAGGAGG AAGAAGGAGGGTGTGAATGAGGGTGAAATTTCTAGAAGCGCCGATGC TCCCGCATATCAGCAGGGTCAGAATCAGCTCTACAATGAATTGAATCTC GGCAGGCGAGAAGAGTACGATGTTCTGGACAAAAGACGGGGCAGGGATC CCGAGATGGGGGAAAGCCCCGGAGAAAAATCCTCAGGAGGGGTGTGA CAATGAGCTGCAGAAGGACAAGATGGCTGAAGCCTATAGCGGAGATCGGA ATGAAAGGCGAAAGACGCGAGGCAAGGGGCATGACGGTCTGTACCAGG GTCTCTCTACAGCCACCAAGGACACTTATGATGCGTTGCATATGCAAGC CTTGCCACCCCGC
914	597	GAAGTGCAACTGCTGGAAGCGGCGGAGGCCTGGTCCAGCCCCGGCGGCT CTCTGCGGCTCAGCTGCGCCGCTTCTGGATTACCTTCGGCAGCGAGGC TATGAGCTGGGTGCGGCAGGCCCCCTGGAAGAGAGAGAGCTGGTGTCC GCCATCAGCGGCAGCGCGAGGTGACCTACTACGCCGACAGCGTGAAGG GCAGATTACCATCTCTAGAGATAATAGCAAGAACACCTGTACCTGCA GATGAACAGCCTGAGAGCCGAGGACACCGCCGTGTACTATTGTGAGAGA CTGGTGGAAGCCAAGCGGCACTGGGGCCAGGGCACACAGGTTACAGTGT CCAGCACCAACACCTGCTCCAAGGCCCCCACACCGCTCCAACATAT AGCCAGCCAACCATTTAGCCTCAGACCTGAAGCTTGAGGCCCGCAGCA GGAGGCGCCGTCCATACGCGAGGCCTGGACTTCGCGTGTGATATTTATA TTTGGGCACCTTTGGCCGGAACATGTGGGGTGTGCTTCTCTCCCTTGT GATCACTCTGTATTGTAAGCGCGGGAGAAAGAAGCTCCTGTACATCTTC AAGCAGCCTTTTATGCGACCTGTGCAAAACCACTCAGGAAGAAGATGGGT GTTTCATGCCGCTTCCCCGAGGAGGAAGAAGGAGGTGTGAAGTGAAGGT GAAATTTTCTAGAAGCGCGATGCTCCCGCATATCAGCAGGGTCAGAAT CAGCTCTACAATGAATTGAATCTCGGCAGGCGAGAAGAGTACGATGTTT TGGACAAAAGACGGGGCAGGGATCCCGAGATGGGGGGAAAGCCCCGGAG AAAAATCCTCAGGAGGGGTGTACAATGAGCTGCAGAAGGACAAGATG GCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGAAAGACGCGAGGCA AGGGGCATGACGGTCTGTACCAGGGTCTCTCTACAGCCACCAAGGACAC TTATGATGCGTTGCATATGCAAGCCTTGCCACCCCGC
915	621	GAAGTGCAACTGCTGGAATCTGGCGGAGGACTGGTGCAGCCCCGGCGGCA GCCTGCGGCTGAGCTGTGCTGCTTCTGGCTTTACCTTCGAGTCTGAGGC CATGAGCTGGTATAGACAGGCCCCCTGGCAAGGAAAGAGAGCTGGTCAGC GTGATCACCAGCGAGGGCTCCACCTACTACGCCGACAGCGTGAAAGGCA GATTACAAATCAGCCGGGACAATAGCAAGAACACCTGTACCTGCAGAT GAACAGCCTGCGCGCCGAAGATACAGCCGTGTACTACTGCGCCACATC GAGTGGGAGACAAGACTCAACTGGGGCCAGGGCACCCAGGTGACCGTGT CCAGCACCAACACCTGCTCCAAGGCCCCCACACCCGCTCCAACATAT AGCCAGCCAACCATTTAGCCTCAGACCTGAAGCTTGACGCCCCGACGCA GGAGGCGCCGTCCATACGCGAGGCCTGGACTTCGCGTGTGATATTTATA TTTGGGCACCTTTGGCCGGAACATGTGGGGTGTGCTTCTCTCCCTTGT

		GATCACTCTGTATTGTAAGCGCGGGAGAAAGAAGCTCCTGTACATCTTC AAGCAGCCTTTTATGCGACCTGTGCAAACCACTCAGGAAGAAGATGGGT GTTTCATGCCGCTTCCCCGAGGAGGAAGAAGGAGGGTGTGAAGTGGGGT GAAATTTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAGGGTCAGAAT CAGCTCTACAATGAATTGAATCTCGGCAGGCGAGAAGAGTACGATGTT TGGACAAAAGACGGGGCAGGGATCCCGAGATGGGGGGAAAGCCCCGGAG AAAAAATCCTCAGGAGGGGTGTACAATGAGCTGCAGAAGGACAAGATG GCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGAAAGACGCAGAGGCA AGGGGCATGACGGTCTGTACCAGGGTCTCTCTACAGCCACCAAGGACAC TTATGATGCGTTGCATATGCAAGCCTTGCCACCCCGC
916	645	GAGGTGCAGCTGCTGGAAAGCGGAGGGGGCCTGGTCCAACCCGGCGGGT CTCTTCGCCTAAGCTGTGCCGCTTCTGGCTTCACCTTCGACGAGTACAC CATGCACTGGTTCAGACAGGCCCCCGGCAAGGAGCGCGAGTTTCGTCACT GCAATCAGCGGAGGCGGTAGCGAGACTTATTACGCGGACTCCGTGAAGG GCCGCTTCACCATTAGCCGCGACAACCTCCAAGAACACGCTGTACCTGCA GATGAATTTCGCTGCGCGCCGAAGATACGGCCGTGTACTACTGTGCCGT GGTGGGGAGGAGGCTGGCGTGGGCTATTGGGGCCAGGGCAGCCAGGTCA CCGTGTGTCCTCCACCACAACACCTGCTCCAAGGCCCCCACACCCGCTCC AACTATAGCCAGCCAACCATGAGCCTCAGACCTGAAGCTTGCAAGGCC GCAGCAGGAGGCGCCGTCCATACGCGAGGCTGGACTTCGCGTGTGATA TTTATATTTGGGCACCTTTTGCCCGGAACATGTGGGGTGTGTCTTCTCTC CCTTGTGATCACTCTGTATTGTAAGCGCGGGAGAAAGAAGCTCCTGTAC ATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAACCACTCAGGAAGAAG ATGGGTGTTTCATGCCGCTTCCCCGAGGAGGAAGAAGGAGGGTGTGAAC GAGGGTGAATTTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAGGGT CAGAATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAGAAGAGTACG ATGTTCTGGACAAAAGACGGGGCAGGGATCCCGAGATGGGGGGAAAGCC CCGGAGAAAAATCCTCAGGAGGGGTGTACAATGAGCTGCAGAAGGAC AAGATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGAAAGACGCA GAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTACAGCCACCAA GGACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCCCGC
917	669	GAGGTGCAGCTGCTGGAGAGCGGAGGCGGCCTCGTGCAGCCAGGAGGTT CCCTACGACTCTCCTGTGCCGCCAGCGGCTTCACCTTCGAGGACTACGC CATGAGTTGGTTCGCCAGGCCCCGGGGAAGGAGCGCGAGGGCGTGAGC GCGATTTCTGGAAAGGCGGCTCCACCTATTACGCGGACTCCGTGAAGG GTCGCTTTACCATCTCTCGCGACAACCTCCAAGAACACGCTGTACTCTGA GATGAATAGCCTGCGCGCTGAGGACACTGCCGTGTACTACTGTGCTGTC TTGGACGAGGAGGCGCGCGCAGAGGCGGCTATTGGGGCCAGGGTACCC AGGTCACCGTGTGTCCTCCACCACAACACCTGCTCCAAGGCCCCCACACC CGCTCCAACCTATAGCCAGCCAACCATGAGCCTCAGACCTGAAGCTTGC AGGCCCCGACGAGGAGGCGCGTCCATACGCGAGGCTGGACTTCGCGT GTGATATTTATATTTGGGCACCTTTGGCCGGAACATGTGGGGTGTGTGCT TCTCTCCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGAAAGAAGCTC CTGTACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAACCACTCAGG AAGAAGATGGGTGTTTCATGCCGCTTCCCCGAGGAGGAAGAAGGAGGGTG TGAAGTGAAGGTGAATTTTCTAGAAGCGCCGATGCTCCCGCATATCAG CAGGGTCAGAATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAGAAG AGTACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCGAGATGGGGGG AAAGCCCCGAGAAAAAATCCTCAGGAGGGGTGTACAATGAGCTGCAG AAGGACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGAAA GACGCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTACAGC CACCAAGGACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCCCGC
918	693	GAGGTGCAACTGCTGGAAAGCGCGGTGGACTGGTGCAGCCCCGGCGGCA GCCTGAGACTGTCTGTGCTGCTTCTGGATTACATTTCGACAGATACGC CATGAGCTGGTTCGCCAGGCCCCCTGGCAAAGAGCGGGAAGGCGTGTCC GCCATCTCCACAAGCGGAGATAGCACATACTATGCCGACAGCGTGAAGG GCAGATTACCATCAGCAGAGATAATAGCAAGAACACCTGTACCTGCA GATGAACAGCCTCCGGGCCGAGGACACCGCCGTCTACTACTGCGCCGTG CTGGACGAGGAAGCCGCGCGGAGGGCGGCTACTGGGGCCAGGGCACCC

		AGGTGACCGTGTCTAGCACCACAACACCTGCTCCAAGGCCCCCACACC CGCTCCAACCTATAGCCAGCCAACCATTGAGCCTCAGACCTGAAGCTTGC AGGCCCCGAGCAGGAGGCGCGCTCCATACGCGAGGCCTGGACTTCGCGT GTGATATTTATATTTGGGCACCTTTGGCCGGAACATGTGGGGTGTGTCT TCTCTCCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGAAAGAAGCTC CTGTACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAACCACTCAGG AAGAAGATGGGTGTTTCATGCCGCTTCCCCGAGGAGGAAGAAGGAGGGTG TGAAGTGAAGGTGAAATTTTCTAGAAGCGCCGATGCTCCCGCATATCAG CAGGGTCAGAATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAGAAG AGTACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCAGATGGGGGG AAAGCCCCGGAGAAAAATCCTCAGGAGGGGTGTACAATGAGCTGCAG AAGGACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGAAA GACGCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTACAGC CACCAAGGACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCCCGC
919	717	GAGGTGCAACTGCTGGAAAGCGGCGGAGGACTCGTCCAGCCCGGCGGCA GCCTGCGGCTGAGCTGTGCTGCTTCTGGATTTACCTTCGCCAGCGACGC CATGAGCTGGTATAGACAGGCCCTGGCAAAGAGCGGGAAGTGGTGTCC GCCATCAGCGGCTCTGGCGGCTCCACCTACTACGCCGATAGCGTGAAGG GCAGATTCACAATCTCTAGAGATAATAGCAAGAACACCTGTACCTGCA GATGAACAGCCTGAGAGCCGAGGACACCGCCGTGTACTACTGCGCCGCT CACGACAGCGGCGAGGCTTACCTGGCCTTCGACTACTGGGGCCAGGGCA CACAGGTGACCGTGTCTAGCACCACAACACCTGCTCCAAGGCCCCCAC ACCCGCTCCAACCTATAGCCAGCCAACCATTGAGCCTCAGACCTGAAGCT TGCAGGCCCGCAGCAGGAGGCGCCGTCCATACGCGAGGCCTGGACTTCG CGTGTGATATTTATATTTGGGCACCTTTGGCCGGAACATGTGGGGTGT GCTTCTCTCCCTTGTGATCACTCTGTATTGTAAGCGCGGAGAAAGAAG CTCCTGTACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAACCACTC AGGAAGAAGATGGGTGTTTCATGCCGCTTCCCCGAGGAGGAAGAAGGAGG GTGTGAAGTGAAGGTGAAATTTTCTAGAAGCGCCGATGCTCCCGCATAT CAGCAGGGTCAGAATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAG AAGAGTACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCAGATGGG GGGAAAGCCCCGGAGAAAAATCCTCAGGAGGGGTGTACAATGAGCTG CAGAAGGACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCG AAAGACGCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTAC AGCCACCAAGGACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCC CGC
920	741	GAGGTGCAACTGCTGGAAAGCGGCGGAGGACTCGTCCAGCCCGGCGGCA GCCTGAGGCTGAGCTGTGCTGCTTCTGGCTTTACCTTCGACTCCTACAC AATGAGCTGGTATAGACAGGCCCTGGCAAGGAGCGGGAAGTGGTGTCC GCCATCAGCGGCCACGGCGACTCTACATACTACGCCGACAGCGTGAAG GCAGATTCACAATCTCTAGAGATAATAGCAAGAACACCTGTACCTGCA GATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCACCAGA ATCAGCATCACCACCGAGTGGCTGGCCGGAGATTACTGGGGCCAGGGCA CCCAGGTGACAGTGTCCAGCACCACAACACCTGCTCCAAGGCCCCCAC ACCCGCTCCAACCTATAGCCAGCCAACCATTGAGCCTCAGACCTGAAGCT TGCAGGCCCGCAGCAGGAGGCGCCGTCCATACGCGAGGCCTGGACTTCG CGTGTGATATTTATATTTGGGCACCTTTGGCCGGAACATGTGGGGTGT GCTTCTCTCCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGAAAGAAG CTCCTGTACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAACCACTC AGGAAGAAGATGGGTGTTTCATGCCGCTTCCCCGAGGAGGAAGAAGGAGG GTGTGAAGTGAAGGTGAAATTTTCTAGAAGCGCCGATGCTCCCGCATAT CAGCAGGGTCAGAATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAG AAGAGTACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCAGATGGG GGGAAAGCCCCGGAGAAAAATCCTCAGGAGGGGTGTACAATGAGCTG CAGAAGGACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCG AAAGACGCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTAC AGCCACCAAGGACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCC CGC
921	765	GAGGTGCAGCTGCTGGAAAGCGGAGGAGGCCTGGTCCAACCTGGCGGCA

		GCCTGCGGCTGAGCTGCGCCGCTTCTGGCTTCACCTTCAGCAGCTACGC CATGAGCTGGTTCCGGCAGGCCCTTGGCAAGGAAAGAGAGTTCTGTGTCT TTTATCAGCGGATCTGGCGACTCCACCTACTACGCTGATAGCGTGAAG GCAGATTTACCATCTCTAGAGATAATAGCAAGAACACCCGTGTACCTCCA GATGAACAGCCTGCGCGCCGAGGACACAGCCGTGTACTATTGTACCAGA TGGCCTTACGACTTCGAGGAACCAAGCGAGCCCGCGTGTACTGGGGCC AGGGCACACAGGTGACAGTGTCTCCACCACAACACCTGCTCCAAGGCC CCCCACACCCGCTCCAACCTATAGCCAGCCAACCATTTAGCCTCAGACCT GAAGCTTGCAGGCCCGCAGCAGGAGGCGCCGTCCATACGCGAGGCCTGG ACTTCGCGTGTGATATTTATATTTGGGCACCTTTGGCCGGAACATGTGG GGTGTGTCTTCTCTCCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGA AAGAAGCTCCTGTACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAA CCACTCAGGAAGAAGATGGGTGTTTCATGCCGCTTCCCCGAGGAGGAAGA AGGAGGGTGTGAACTGAGGGTGAAATTTTCTAGAAGCGCCGATGCTCCC GCATATCAGCAGGGTCAGAATCAGCTCTACAATGAATTGAATCTCGGCA GGCGAGAAGAGTACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCCGA GATGGGGGGAAGCCCCGGAGAAAAAATCCTCAGGAGGGGTGTACAAAT GAGCTGCAGAAGGACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGA AAGGCGAAAGACGCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCT CTCTACAGCCACCAAGGACACTTATGATGCGTTGCATATGCAAGCCTTG CCACCCCGC
922	789	GAGGTGCAGCTGCTGGAAAGCGGCGGAGGCCTGGTGCAACCTGGCGGAT CTCTCAGACTGAGCTGTGCTGCTTCTGGCTTCACATTACCGACTACGA CATGAGCTGGTATAGACAGGCCCTGGAAAAGAGCGGGAACCTGGTCTCC GTGATCCACAGCGCGGCTCCACCTACTACGCCGATAGCGTGAAGGGCA GATTCACCATCAGCAGAGATAATAGCAAGAACACCCGTGTACCTGCAGAT GAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCGCCCCCGGC TACTACAGCGACCTGTCTTTTGATTATTACAACCTCGACTACTGGGGCC AGGGCACACAGGTGACAGTGTCCAGCACCACAACACCTGCTCCAAGGCC CCCCACACCCGCTCCAACCTATAGCCAGCCAACCATTTAGCCTCAGACCT GAAGCTTGCAGGCCCGCAGCAGGAGGCGCCGTCCATACGCGAGGCCTGG ACTTCGCGTGTGATATTTATATTTGGGCACCTTTGGCCGGAACATGTGG GGTGTGTCTTCTCTCCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGA AAGAAGCTCCTGTACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAA CCACTCAGGAAGAAGATGGGTGTTTCATGCCGCTTCCCCGAGGAGGAAGA AGGAGGGTGTGAACTGAGGGTGAAATTTTCTAGAAGCGCGATGCTCCC GCATATCAGCAGGGTCAGAATCAGCTCTACAATGAATTGAATCTCGGCA GGCGAGAAGAGTACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCCGA GATGGGGGGAAGCCCCGGAGAAAAAATCCTCAGGAGGGGTGTACAAAT GAGCTGCAGAAGGACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGA AAGGCGAAAGACGCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCT CTCTACAGCCACCAAGGACACTTATGATGCGTTGCATATGCAAGCCTTG CCACCCCGC
923	813	GAGGTGCAGCTGCTGGAGAGCGGTGGAGGGTGGTGAGCCCGGGGTA GCCTGCGTCTGTGCTGCGCCGCTTCCGGCTTCACGTTCTCTGATTACGC CATGCACTGGTTCCGGCAGGCCCCCGGTAAGGAGCGCGTGTGGTGTCTG TCTATTGACTCCGGCGGCTCCACTTACTACGCAGACAGTGTCAAGGGCC GTTTCACCATCAGCCCGCACAACAGCAAGAACACGCTGTACCTGCAGAT GAACTCCCTTCGAGCAGAGGACACCGCGGTGTACTACTGTAATGCGGGC TTCAAGGGCGATCACCCCAACCAAGGATGCCTTCGACATTTGGGGCC AGGGCACCCAGGTACCCGTGTGCTCCACCACAACACCTGCTCCAAGGCC CCCCACACCCGCTCCAACCTATAGCCAGCCAACCATTTAGCCTCAGACCT GAAGCTTGCAGGCCCGCAGCAGGAGGCGCCGTCCATACGCGAGGCCTGG ACTTCGCGTGTGATATTTATATTTGGGCACCTTTGGCCGGAACATGTGG GGTGTGTCTTCTCTCCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGA AAGAAGCTCCTGTACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAA CCACTCAGGAAGAAGATGGGTGTTTCATGCCGCTTCCCCGAGGAGGAAGA AGGAGGGTGTGAACTGAGGGTGAAATTTTCTAGAAGCGCCGATGCTCCC GCATATCAGCAGGGTCAGAATCAGCTCTACAATGAATTGAATCTCGGCA

		GGCGAGAAGAGTACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCCGAGATGGGGGAAAGCCCCGGAGAAAAAATCCTCAGGAGGGGTGTACAATGAGCTGCAGAAGGACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGAAGGCGAAAGACGCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTACAGCCACCAAGGACACTTATGATGCGTTGCATATGCAAGCCTGCCACCCCGC
924	837	GAGGTGCAACTGCTGGAATCCGGCGGAGGCCTGGTGCAGCCCGGCGGCA GCCCTCAGACTGAGCTGTGCCGCTTCTGGCTTTACCTTCAGCAGCGAGGG CATGAGCTGGGTGCGGCAGGCCCTGGCAAGGAAAGAGAGCTGGTCTCCGCCATCAGCGGATCTGGCGACCACACCTACTATGCCGATAGCGTGC GCGGAAGATTACAATCTCTAGAGATAATAGCAAGAACACCTGTACCTGCA GATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCAACGCC CTGGAAGGCGGCCCTACAACAGCTATCCAGCCAGGAGGCCCTGACTACT GGGGCCAGGGCACCCAGGTGACCGTGTCCAGCACCACAACCTGTCTCC AAGCCCCCCCACCCCGCTCCAACCTATAGCCAGCCAACCATGAGCCTC AGACCTGAAGCTTGCAAGCCCCGAGCAGGAGGCGCGCTCCATACGCGAG GCCTGGACTTCGCGTGTGATATTTATATTTGGGCACCTTTGGCCGGAAC ATGTGGGGTGTGCTTCTCTCCCTTGTGATCACTCTGTATTGTAAGCGC GGGAGAAAGAAGCTCCTGTACATCTTCAAGCAGCCTTTTATGCGACCTG TGCAAACCACTCAGGAAGAAGATGGGTGTTATGCCGCTTCCCCGAGGA GGAAGAAGGAGGGTGTGAACGAGGGTGAAATTTCTAGAAGCGCCGAT GCTCCCGCATATCAGCAGGGTCAGAATCAGCTCTACAATGAATTGAATC TCGGCAGGCGAGAAGAGTACGATGTTCTGGACAAAAGACGGGGCAGGGA TCCCGAGATGGGGGAAAGCCCCGGAGAAAAAATCCTCAGGAGGGGTG TACAATGAGCTGCAGAAGGACAAGATGGCTGAAGCCTATAGCGAGATCG GAATGAAAGGCGAAAGACGCAGAGGCAAGGGGCATGACGGTCTGTACCA GGGTCTCTCTACAGCCACCAAGGACACTTATGATGCGTTGCATATGCAA GCCTTGCCACCCCGC
925	861 + 189	ATGGCTCTTCCCGTAACAGCCCTTTTGTGGCCCTTGCACTCCTTCTGC ATGCAGCACGACCGGAGATCGTGCTGACACAGTCTCCCCCACACTGTCT ACTGTCTCCAGGCGAAAGAGCCACACTGAGCTGTAGAGCCAGCCAGAGC GTGTCTCTTACCTGGCTTGGTATCAGCAGAAGCCTGGACAGGCTCCCC GGCTGCTGATCTACGATGCCAGCAATAGAGCCACAGGCAATCCCCGCCAG ATTTTCTGGCAGCGGCTCTGGCACCGATTTACCCCTGACCATAAGCAGC CTGGAACCTGAGGACTTCGCCGTGTACTACTGCCAGCAGAGAGTGTGT ACCCCATCACCTTTGGCGGAGGCACCAAGGTGGAAATCAAAGCGGCGG AGGAAGCGGAGGCGGAGGATCTGGTGGTGGTGGATCTGGCGGAGGTGGC AGCCAGATCACACTGAAAGAGTCTGGCCCCACACTGGTCAAGCCCACAC AGACCCCTGACACTGACCTGCACCTTCAGCGGCTTTAGCCTGAGCACATC TGGCGTCGGCGTTGGCTGGATTAGACAGCCTCCTGGAAGGCCCTGGAA TGGCTGGCCCTGATCTACTGGAACGACGAGAAGAGATACAGCCCCAGCC TGAAGTCCCGGCTGACCATCACCAGGACACCAGCAAGAACCAGGTGGT GCTGACCATGACAAACATGGACCCCGTGGACACCGCCGTGTATTATTGC GCCAGAGATGAGTACGGCGGCTTCGACATTTGGGGCCAGGGCACAATGG TCACCGTGTCTAGTACCACAACACCTGCTCCAAGGCCCCCACACCCGC TCCAACCTATAGCCAGCCAACCATGAGCCTCAGACCTGAAGCTTGCAAG CCGGCAGCAGGAGGCGCGTCCATACGCGAGGCCTGGACTTCGCGTGTG ATATTTATATTTGGGCACCTTTGGCCGGAACATGTGGGGTGTGCTTCT CTCCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGAAAGAAGCTCCTG TACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAACCACTCAGGAAG AAGATGGGTGTTATGCGCTTCCCCGAGGAGGAAGAAGGAGGGTGTGA ACTGAGGGTGAAATTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAG GGTGAGAATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAGAAGAGT ACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCGAGATGGGGGGA AAA GCCCCGAGAAAAAATCCTCAGGAGGGGTGTACAATGAGCTGCAGAAG GACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGAAAGAC GCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTACAGCCAC CAAGGACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCCCGC
926	861 + 237	ATGGCTCTTCCCGTAACAGCCCTTTTGTGGCCCTTGCACTCCTTCTGC

		ATGCAGCACGACCGGAGATCGTGCTGACCCAGTCCCCCTGCTACCCGTGAG CCTGTCTCCAGGCGAGCGGGCCACACTGAGCTGTAGAGCTTCTCAGAGC GTGTCCAGCTACCTGGCCTGGTATCAGCAGAAACCTGGCCAGGCCCCCTA GACTGCTGATCTACGACGCCAGCAACCGGGCCACCGGCATCCCCGCCAG ATTCAGCGGATCTGGCAGCGGCACAGATTTACCCCTCACCATCAGCAGC CTGGAACCTGAGGACTTCGCCGTCTACTACTGCCAGCAAAGATTTCGACT ACCCATCACCTTCGGCGGCGGAACAAAGGTGGAAATTAAGGGTGGTGG GGGCAGCGGTGGAGGTGGGAGCGGAGGCGGGGGTAGCGGAGGCGGGGGT AGCCAAATCACACTGAAAGAGAGCGGCCCTACACTCGTGAAACCTACCC AGACCCTGACACTGACATGTACCTTCAGCGGCTTCTCCCTGAGCACCTC TGGCGTCGGCGTTGGATGGATCAGACAGCCTCCAGGCAAGGCCCTGGAA TGGCTGGCTCTGATCTATTGGAACGACGACAAGCGGTACAGCCCCAGCC TGAAGTCTAGACTGACCATCACAAAGGACACCAGCAAGAACCAGGTGGT GCTGACCATGACAAATATGGACCCCGTGGACACCGCCGTGTACTACTGC GCCAGAGATGAGTACGGCGGATTTGATATCTGGGGCCAGGGCACCATGG TGACCGTGTCCAGCACCAACACCTGCTCCAAGGCCCCCACACCCGC TCCAACCTATAGCCAGCCAACCATTGAGCCTCAGACCTGAAGCTTGCAGG CCGCAGCAGGAGGCGCCGTCATACGCGAGGCCTGGACTTCGCGTGTG ATATTTATATTTGGGCACCTTTGGCCGGAACATGTGGGGTGTGTCTCT CTCCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGAAAGAAGCTCCTG TACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAACCACTCAGGAAG AAGATGGGTGTTTCATGCCGCTTCCCCGAGGAGGAAGAAGGAGGGTGTGA ACTGAGGGTGAATTTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAG GGTGAGAATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAGAAGAGT ACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCGAGATGGGGGGAAA GCCCGGAGAAAAATCCTCAGGAGGGGTGTACAATGAGCTGCAGAAG GACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGAAAGAC GCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTACAGCCAC CAAGGACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCCCGC
927	861 + 261	ATGGCTCTTCCCGTAACAGCCCTTTTGTGGCCCTTGCACTCCTTCTGC ATGCAGCACGACCGCAAGTGCAGCTCGTGGAAAGCGGCGGCGAGTGGT GCAGCCCCGGCCGAGCCTGAGACTGTCTGCGCCGCTTCTGGATTTACC TTCAGCAGCTACGGCATGCACTGGGTGAGCAGGCCCCCTGGCAAAGGCC TGGAGTGGGTGGCCGTTATCAGCTACGAGGGCAGCAACAAGTATTACGC CGACAGCGTGAAGGGCCGCTTACAATCTCTAGAGATAATAGCAAGAAC ACCCTGTACCTGCAGATGAACAGCCTGCGGGCCGAAGATACCGCGTGT ACTACTGTGCTAGAGAGCTGGGCGACGGCATGGACGTGTGGGGACAGGG CACAACCGTGACCGTGTCTCTGGTGGTGGGGCAGCGGTGGAGGTGGG AGCGGAGGCGGGGGTAGCGGAGGCGGGGGTAGCGAGATCGTGCTGACCC AGTCCCCGTGTACACTGAGCCTGTCTCCAGGCGAGCGGGCCACACTGAG CTGTAGAGCTTCTCAGAGCGTGTCCAGCTATCTGGCCTGGTTCCAGCAG AAACCTGGCCAGGCCCCCTAGACTGTCTGATCTACGACGCCAGCAACCGGG CCACCGGCATCCCCGCCAGATTGAGCGGCTCTGGCAGCGGCACCGACTT CACCCTCACCATCAGCAGCCTGGAACCCGAGGATTTTGGCGTCTACTAC TGCCAGCAAAGAGTGGACCTGTGGACCTTCGGCGGAGGAACAAAGGTGG AAATCAAGACCACAACACCTGCTCCAAGGCCCCCACACCCGCTCCAAC TATAGCCAGCCAACCATTGAGCCTCAGACCTGAAGCTTGACGGCCCGCA GCAGGAGGCGCCGTCATACGCGAGGCCTGGACTTCGCGTGTGATATTT ATATTTGGGCACCTTTGGCCGGAACATGTGGGGTGTGTCTCTCTCCCT TGTGATCACTCTGTATTGTAAGCGCGGGAGAAAGAAGCTCCTGTACATC TTCAAGCAGCCTTTTATGCGACCTGTGCAAACCACTCAGGAAGAAGATG GGTGTTTCATGCCGCTTCCCCGAGGAGGAAGAAGGAGGGTGTGAACCTGAG GGTGAAATTTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAGGGTCAG AATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAGAAGAGTACGATG TTCTGGACAAAAGACGGGGCAGGGATCCCGAGATGGGGGGAAAGCCCCG GAGAAAAAATCCTCAGGAGGGGTGTACAATGAGCTGCAAGAAGGACAG ATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGAAAGACGCAGAG GCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTACAGCCACCAAGGA CACTTATGATGCGTTGCATATGCAAGCCTTGCCACCCCGC

928	861 + 333	ATGGCTCTTCCCGTAACAGCCCTTTTGTGGCCCTTGCACTCCTTCTGC ATGCAGCACGACCGGACATCCAGATGACCCAGAGCCCTTCGACCCTATC CGCTTCCGTGGGTGACCGTGTGACCATCACCTGTGCGCGGTGCGAGAGC ATCTCCTCCTGGCTCGCGTGGTACCAACAGAAGCCTGGCAAGGCCCCCA AGCTGCTGATTTACGACGCCAGTTCCCTGGAGTCTGGCGTGCCATCCCG CTTCTCCGGCAGCGGCAGCGGTACCGAGTTCACCCTGACGATCAGCTCC CTGCAGCCGGATGACTTTGCTACCTACTACTGTGACGAGGTCTCCTCCC TCCCCCCCACCTTCGGTGGCGGTACCAAGGTGGAGATCAAGGGCGGCGG CGGCTCTGGTGGCGGAGGTTCTGGCGGGGAGGTTTCGGGGGGGGAGGC TCCGAGGTGCAACTGGTAGAGAGCGGCGGGGGGACTGGTAAAAACCGGCG GCTCCCTGCGGCTGTGATGCGCTGTAGCGGCTTCACGTTACGCGATTA CTACATGAGTTGGATCCGCCAGGCCCGCGGAAGGTTTGGAGTGGGTCT TCGTATATCTCTTCCAGCGGATCTACCATTACTATGCGGACAGCGTGA AGGGGCGCTTCACCATATCTCGGGACAACGCCAAGAATCCCTGTACCT GCAGATGAATCCCTGCGTGCAGGAGACACGGCCGTGTATTACTGTGCC CGCGACCAGGGCAACTACGGCGTGCAGGTGTGGGGCCAGGGTACAACCG TCACCGTGTCCAGTACCACAACACCTGCTCCAAGGCCCGCCACACCCGC TCCAACCTATAGCCAGCCAACCATTTAGCCTCAGACCTGAAGCTTGCAAG CCCGAGCAGGAGGCGCGTCCATACGCGAGGCCTGGACTTCGCGTGTG ATATTTATATTTGGGCACCTTTGGCCGGAACATGTGGGTGTGCTTCT CTCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGAAAGAAGCTCCTG TACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAACCACTCAGGAAG AAGATGGGTGTTTATGCCGCTTCCCCGAGGAGGAAGAAGGAGGTGTGA ACTGAGGGTGAAATTTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAG GGTGAGAATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAGAAGAGT ACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCGAGATGGGGGGAAA GCCCGGAGAAAAAATCCTCAGGAGGGGTGTACAATGAGCTGCAGAAG GACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGAAAGAC CAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTACAGCCAC CAAGGACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCCCGC
929	861 + 357	ATGGCTCTTCCCGTAACAGCCCTTTTGTGGCCCTTGCACTCCTTCTGC ATGCAGCACGACCGCAAGTGCAGCTGGTGCAGAGCGGAGGAGGCTGGT TAAGCCCGGGCGATCTCTCAGACTGAGCTGCGCCGCTAGCGGCTTTACA TTCAGCGACTACTACATGAGCTGGATCCGGCAGGCCCCCTGGCAAGGGCC TGAATGGGTGTCCTACATCAGCTCCTCCGGCAGCACCATCTACTACGC CGACAGCGTGAAAGGCAGATTACAATCTCTAGAGATAATGCAAGAAC AGCCTGTACCTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGT ACTATTGTGCTAGAGATCAGGGCAACTACGGCGTGGACGTGTGGGGCCA GGGCACCACCGTGACCGTGTCTAGCGGTGGTGGGGGACGGGTGGAGGT GGGAGCGGAGGCGGGGTAGCGGAGGCGGGGTAGCGATATCCAGATGA CCCAGTCCCCATCTACACTGAGCGCCTCTGTGGGCGACCGGGTGACCAT TACATGTAGAGCCAGCCAGAGCATCAGCAGCTGGCTGGCTTGGTATCAG CAGAAACCTGGCAAGGCCCTTAAGCTGCTGATCTACGAGGCCAGCAGCC TGGAAAGCGGCGTCCCCAGCAGATTAGCGGCAGCGGCTCTGGAACAGA GTTCAACCCTGACCATCTCCTCCCTGCAGCCTGACGACTTCGCCACCTAC TACTGCCAGCAATCTGATAGCCACCCATCACCTTTGGCGGAGGCACCA AGGTGGAATCAAGACCACAACACCTGCTCCAAGGCCCGCCACACCCGC TCCAACCTATAGCCAGCCAACCATTTAGCCTCAGACCTGAAGCTTGCAAG CCCGAGCAGGAGGCGCGTCCATACGCGAGGCCTGGACTTCGCGTGTG ATATTTATATTTGGGCACCTTTGGCCGGAACATGTGGGTGTGCTTCT CTCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGAAAGAAGCTCCTG TACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAACCACTCAGGAAG AAGATGGGTGTTTATGCCGCTTCCCCGAGGAGGAAGAAGGAGGTGTGA ACTGAGGGTGAAATTTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAG GGTGAGAATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAGAAGAGT ACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCGAGATGGGGGGAAA GCCCGGAGAAAAAATCCTCAGGAGGGGTGTACAATGAGCTGCAGAAG GACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGAAAGAC GCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTACAGCCAC

		CAAGGACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCCCGC
930	861 + 429	ATGGCTCTTCCCGTAACAGCCCTTTTGTGGCCCTTGCACTCCTTCTGC ATGCAGCAGACCGGATATCCAGATGACCCAGTCCCCATCTACACTGAG CGCCTCTGTGGGCGACCGGGTGACAATTACCTGTAGAGCTAGCCAGAGC ATCTCCTCCTGGCTGGCTTGGTACCAGCAAAAACCTGGCAAGGCCCTTA AGCTGCTGATCTACGAGGCCAGCAGCCTGGAAAGCGGCGTCCCCTCTAG ATTCAGCGGCAGCGGCTCTGGAACCGAGTTCACCCTGACAATCAGCAGC CTGCAGCCTGACGACTTCGCCACCTATTACTGCCAGCAGGCCAACAGCC ACCCATCACCTTTGGCGGAGGCACCAAGGTGGAAATCAAGGGTGGTGG GGGCAGCGGTGGAGGTGGGAGCGGAGGCGGGGGTAGCGAGGCGGGGGT AGCGAGGTGCAGCTGGTGGAAAGCGGCGGAGGACTCGTTAAGCCCGGCG GCAGCCTGAGACTGAGCTGCGCCGCTAGCGGATTTACCTTCAGCGACTA CTACATGAGCTGGATCCGGCAGGCCCTTGCAAGGGCTGGAATGGGTC AGCTACATCAGTCTCTTGGCTCTACAATCTACTACGCCGACAGCGTGA AAGGCAGATTACCATCTCTAGAGATAATGCCAAGAACAGCCTGTACCT GCAAAATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTATTGTGCT AGAGATCAGGGCAACTACGGCGTGGACGTGTGGGGCCAGGGCACCACCG TGACAGTGTCTCCACCACAACACCTGCTCCAAGGCCCCCAACCCCGC TCCAATATAGCCAGCCAACCATTGAGCCTCAGACCTGAAGCTTGACAGG CCCGACGAGGAGGCGCGTCCATACGCGAGGCTGGACTTCGCGTGTG ATATTTATATTTGGGCACCTTTGGCCGGAACATGTGGGGTGTGTGCTTCT CTCCTTGTGATCACTCTGTATTGTGAAGCGCGGGAGAAAGAAGCTCCTG TACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAAACCACTCAGGAAG AAGATGGGTGTTTATGCCGCTTCCCCGAGGAGGAAGAAGGAGGGTGTGA ACTGAGGGTGAAATTTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAG GGTGAGAATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAGAAGAGT ACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCGAGATGGGGGGGAAA GCCCCGGAGAAAAAATCCTCAGGAGGGGTGTACAATGAGCTGCAGAAG GACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGAAAGAC GCAGAGGCAAGGGGCATGACGCTCTGTACCAGGGTCTCTTACAGCCAC CAAGGACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCCCGC
931	861 + 477	ATGGCTCTTCCCGTAACAGCCCTTTTGTGGCCCTTGCACTCCTTCTGC ATGCAGCAGACCGGACATCCAGATGACCCAGAGCCCTAGCTCCCTGAG CGCCAGCGTGGGCGATAGAGTGACCATTACCTGTAGAGCCTCTCAGAGC ATCTCCTCCTACCTGAACCTGGTATCAGCAGAAACCGGCAAGGCCCTTA AGCTGCTGATCTACGCCGCTAGCAGCCTGCAGTCTGGCGTCCCCAGCCG GTTCAGCGGCAGCGGATCTGGCACCGACTTCACCCTGACAATCAGCAGC CTGCAACCTGAGGACTTTGCTACATACTACTGCCAGCAGGCCACAGCT CTCCAATCACCTTCGGCGGCGGAACAAAGGTGGAAATCAAGGGTGGTGG GGGCAGCGGTGGAGGTGGGAGCGGAGGCGGGGGTAGCGAGGCGGGGGT AGCGAGGTGCAGCTGCTGGAAAGCGGAGGCGGACTCGTTCAACCTGGCG GCAGCCTGAGACTGAGCTGCGCCGCTTCTGGATTTACCTTCAGCAACTA CGCCATGAGCTGGGTGCGGCAGGCCCTTGCAAGGGCTGGAATGGGTC TCCGCCATCAGCGGCTCTGGCGGCTCCACCTACTACGCCGACAGCGTGA AGGGCAGATTACCATCTCTAGAGATAATAGCAAGAACACCCTGTACCT GCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTATTGTGCT AGACCCGGAGATGGCTACTACGAGGGCGTGTACTTCGACTACTGGGGCC AGGGCACACTGGTGACAGTGTCCAGCACCACAACACCTGCTCCAAGGCC CCCCACACCCGCTCCAATATAGCCAGCCAACCATTGAGCCTCAGACCT GAAGCTTGACAGCCCGCAGCAGGAGGCGCGTCCATACGCGAGGCCTGG ACTTCGCGTGTGATATTTATATTTGGGCACCTTTGGCCGGAACATGTGG GGTGTTGCTTCTCTCCCTTGTGATCACTCTGTATTGTGAAGCGCGGGAGA AAGAAGCTCCTGTACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAA CCACTCAGGAAGAAGATGGGTGTTTATGCCGCTTCCCCGAGGAGGAAGA AGGAGGGTGTGAACAGGGTGAAATTTTCTAGAAGCGCCGATGCTCCC GCATATCAGCAGGGTCAGAATCAGCTCTACAATGAATTGAATCTCGGCA GGCAGAGAAGGTACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCGA GATGGGGGGAAAGCCCCGAGAAAAAATCCTCAGGAGGGGTGTACAAT GAGCTGCAGAAGGACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGA

		AAGGCGAAAGACGCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTACAGCCACCAAGGACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCCCGC
932	861 + 525	ATGGCTCTTCCCGTAACAGCCCTTTTGTGCCCCCTTGCACTCCTTCTGCATGCAGCACGACCGGATATTCAGATGACCCAGAGCCCATCTAGCCTGAGCGCCAGCGTGGGCGATAGAGTGACCATCACCTGTGAGGCTCTCAGGACATCGCTAATTACCTGAACTGGTATCAGCAGAAACCCGGCAAGGCCCTAAGCTGCTGATCTACGACGCCTCCAACCTGGAAACCGCGTGCCAGCCGGTTCAGCGGCAGCGGATCTGGCACAGACTTCACCTTTACCATCAGCTCCCTCCAGCCTGAGGACATCGCCACATACTACTGCCAGCAACACTTCAACC TGCCCTCTGACCTTCGGCGGGGGAACAAAGGTCGAGATCAAGGGTGGTGGGGCAGCGGTGGAGGTGGGAGCGGAGGCGGGGTAGCGGAGGCGGGGTAGCCAAATCACCCTGAAAGAGAGCGGACCTACACTGGTCAAGCCTACCCAGACTGACCCCTCACATGTACATTGAGCGGCTTTAGCCTGAGCACCTCCGGCGTGGGAGTGGGCTGGATCAGACAGCCCCCGGCAAGGCCCTGGAA TGCTGGCTCTGATCTATTGGAATGACGAGAAGCGGTACAGCCCTAGCC TGAATCTAGACTGACAATCACCAAGGACACCAGCAAGAACCAGGTGGTGCTGACCATGACCAACATGGATCCTGTGGATACCGCCGTGTACTACTGC GCCAGAGAAGGCTCTCAGACTACAAGAGCTCCAACCTGGTTCGACCCAT GGGGCCAGGGCACCCCTGGTTACAGTGTCTAGCACCAACACCTGCTCC AAGGCCCCCACCACCGCTCCAACCTATAGCCAGCCAACATTGAGCCTC AGACCTGAAGCTTGAGGCCCCGAGCAGGAGGCGCGCTCCATACGCGAG GCCTGGACTTCGCGTGTGATATTTATATTTGGGCACCTTTGGCCGGAAC ATGTGGGGTGTGCTTCTCTCCCTTGTGATCACTCTGTATTGTAAGCCG GGGAGAAAGAAGCTCCTGTACATCTTCAAGCAGCCTTTTATGCGACCTG TGCAAACCACTCAGGAAGAAGATGGGTGTTGATGCCGCTTCCCCGAGGA GGAAGAAGGAGGGTGTGAAC TGAGGGTGAATTTTCTAGAAGCGCCGAT GCTCCCGCATATCAGCAGGGTCAGAATCAGCTCTACAATGAATTGAATC TCGGCAGGCGAGAAGAGTACGATGTTCTGGACAAAAGACGGGGCAGGGA TCCCGAGATGGGGGGAAGCCCCGGAGAAAAAATCCTCAGGAGGGGTG TACAATGAGCTGCAGAAGGACAAGATGGCTGAAGCCTATAGCGAGATCG GAATGAAAGGCGAAAGACGCAGAGGCAAGGGGCATGACGGTCTGTACCA GGGTCTCTCTACAGCCACCAAGGACACTTATGATGCGTTGCATATGCAA GCCTTGCCACCCCGC
933	861 + 573	ATGGCTCTTCCCGTAACAGCCCTTTTGTGCCCCCTTGCACTCCTTCTGCATGCAGCACGACCGGATATCGTGATGACCAATCTCCACTGAGCCTGCC TGTGACACCTGGCGAGCCTGCTTCTATCAGCTGTAGAAGCAGCCAGTCC CTGCTGCACAGCAACGGCTACAACCTACCTGGACTGGTATCTGCAGAAAC CCGCCAGAGCCCCAGCTGCTGATCTACCTCGGCTCTAATCGGGCCAG CGGAGTGCCCTGATAGATTGAGCGGAAGCGGCTCCGGCACCGACTTCACC CTGAAGATCAGCAGAGTGGAAGCCGAGGACGTGGGCGTCTACTACTGCA TGCAGGCCCTGGGCCTGATTACATTTGGCGCGGAACCAAGGTGGAAAT CAAGGGTGGTGGGGGCAGCGGTGGAGGTGGGAGCGGAGGCGGGGTAGC GGAGGCGGGGTAGCGAAGTGCAGCTGGTTGAGAGCGGCGGCGGACTGG TGAAGCCCGAGGCAGCCTCAGACTGAGCTGTGCTGCTTCTGGCTTTAC CTTCAGCTCTTATAGCATGAAC TGGGTGCGGCAGGCCCTTGCAAGGGC CTGGAATGGGTGAGCTCCATCAGCTCTTCTAGCAGCTACATCTACTACG CCGACAGCGTGAAGGGCAGATTACCATCAGCAGAGATAACGCCAAGAA CAGCCTGTACCTGCAGATGAATAGCCTGCGGGCCGAGGACACCGCCGTG TACTACTGCGCCAGAGCCGGCGACACCTACAGCGCCGCCGATTACTACT ACATGGACGTGTGGGGCAAAGGAACAACCGTGACAGTGTCTCCACCAC AACACCTGCTCCAAGGCCCCCCACACCCGCTCCAACCTATAGCCAGCCAA CCATTGAGCCTCAGACCTGAAGCTTGAGGCCCGCAGCAGGAGGCGCCG TCCATACGCGAGGCTGGACTTCGCGTGTGATATTTATATTTGGGCACC TTTGGCCGGAACATGTGGGGTGTGCTTCTCTCCCTTGTGATCACTCTG TATTGTAAGCGCGGGAGAAAGAAGCTCCTGTACATCTTCAAGCAGCCTT TTATGCGACCTGTGCAAACCACTCAGGAAGAAGATGGGTGTTGATGCCG CTCCCCGAGGAGGAAGAAGGAGGGTGTGAAC TGAGGGTGAATTTTCT AGAAGCGCCGATGCTCCCGCATATCAGCAGGGTCAGAATCAGCTCTACA

		ATGAATTGAATCTCGGCAGGCGAGAAGGTACGATGTTCTGGACAAAAG ACGGGGCAGGGATCCCGAGATGGGGGAAAGCCCCGGAGAAAAATCCT CAGGAGGGGTTGTACAATGAGCTGCAGAAGGACAAGATGGCTGAAGCCT ATAGCGAGATCGGAATGAAAGGCGAAAGACGCAGAGGCAAGGGGCATGA CGGTCTGTACCAGGGTCTCTCTACAGCCACCAAGGACACTTATGATGCG TTGCATATGCAAGCCTTGCCACCCCGC
934	861 + 597	ATGGCTCTTCCCGTAACAGCCCTTTTGTGGCCCTTGCACTCCTTCTGC ATGCAGCACGACCGGAAGTGCAACTGCTGGAAAGCGGCGGAGGCTGGT CCAGCCCGGCGGCTCTCTGCGGCTCAGCTGCGCCGCTTCTGGATTTACC TTCGGCAGCGAGGCTATGAGCTGGGTGCGGCAGGCCCTTGGAAAAGAGA GAGAGCTGGTGTCCGCCATCAGCGGCAGCGGCGAGGTGACCTACTACGC CGACAGCGTGAAAGGGCAGATTACCATCTCTAGAGATAATAGCAAGAAC ACCCTGTACCTGCAGATGAACAGCCTGAGAGCCGAGGACACCGCCGTGT ACTATTGTCAGAGACTGGTGGAAAGCCAAGCGGCACTGGGGCCAGGGCAC ACAGGTTACAGTGTCCAGCACCACAACACCTGCTCCAAGGCCCCCACA CCCCTCCAACATATAGCCAGCCAACCATGAGCCTCAGACCTGAAGCTT GCAGGCCCCGAGCAGGAGGCGCCGTCCATACGCGAGGCGCTGGACTTCGC GTGTGATATTTATATTTGGGCACCTTTGGCCGGAACATGTGGGGTGTG CTTCTCTCCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGAAAGAAGC TCCTGTACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAACCACTCA GGAAGAAGATGGGTGTTTCATGCCGCTTCCCGAGGAGGAAGAAGGAGGG TGTGAACTGAGGGTGAAATTTTCTAGAAGCGCCGATGCTCCCGCATATC AGCAGGGTCAGAATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAGA AGAGTACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCGAGATGGGG GGAAAGCCCCGGAGAAAAAATCCTCAGGAGGGGTGTACAATGAGCTGC AGAAGGACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGA AAGACGCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTACA GCCACCAAGGACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCCC GC
935	861 + 621	ATGGCTCTTCCCGTAACAGCCCTTTTGTGGCCCTTGCACTCCTTCTGC ATGCAGCACGACCGGAAGTGCAACTGCTGGAATCTGGCGGAGGACTGGT GCAGCCCGGCGGCGAGCCTGCGGCTGAGCTGTGCTGCTTCTGGCTTTACC TTCGAGTCTGAGGCCATGAGCTGGTATAGACAGGCCCTTGGCAAGGAAA GAGAGCTGGTCAGCGTGATCACCAGCGAGGGCTCCACCTACTACGCCGA CAGCGTGAAAGGCAGATTACAATCAGCCGGGACAATAGCAAGAACACC CTGTACCTGCAGATGAACAGCCTGCGCGCCGAAGATACAGCCGTGTACT ACTGCGCCACATCGAGTGGGAGACAAGACTCAACTGGGGCCAGGGCAC CCAGGTGACCGTGTCCAGCACCACAACACCTGCTCCAAGGCCCCCACA CCCCTCCAACATATAGCCAGCCAACCATGAGCCTCAGACCTGAAGCTT GCAGGCCCCGAGCAGGAGGCGCCGTCCATACGCGAGGCGCTGGACTTCGC GTGTGATATTTATATTTGGGCACCTTTGGCCGGAACATGTGGGGTGTG CTTCTCTCCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGAAAGAAGC TCCTGTACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAACCACTCA GGAAGAAGATGGGTGTTTCATGCCGCTTCCCGAGGAGGAAGAAGGAGGG TGTGAACTGAGGGTGAAATTTTCTAGAAGCGCCGATGCTCCCGCATATC AGCAGGGTCAGAATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAGA AGAGTACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCGAGATGGGG GGAAAGCCCCGGAGAAAAAATCCTCAGGAGGGGTGTACAATGAGCTGC AGAAGGACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGA AAGACGCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTACA GCCACCAAGGACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCCC GC
936	861 + 645	ATGGCTCTTCCCGTAACAGCCCTTTTGTGGCCCTTGCACTCCTTCTGC ATGCAGCACGACCGGAGGTGCAGCTGCTGGAAAGCGGAGGGGGCTGGT CCAACCCGGCGGGTCTCTTCGCCTAAGCTGTGCCGCTTCTGGCTTCACC TTCGACGAGTACACCATGCACTGGTTTCAGACAGGCCCCCGGCAAGGAGC GCGAGTTCGTCAGTGCAATCAGCGGAGGCGGTAGCGAGACTTATTACGC GGACTCCGTGAAGGGCCGCTTACCATTAGCCGCGACAACCTCCAAGAAC ACGCTGTACCTGCAGATGAATTCGCTGCGGCCGAAGATACGGCCGTGT

		ACTACTGTGCCGCTGGTGGGGAGGAGGCTGGCGTGGGCTATTGGGGCCA GGGCACCCAGGTCAACGTGTCTGCCACCACAACACCTGCTCCAAGGCCC CCACACCCCGCTCCAACCTATAGCCAGCCAACCATTTAGCCTCAGACCTG AAGCTTGCAGGCCCCGAGCAGGAGGCGCCGTCCATACGCGAGGCGCTGGA CTTCGCGTGTGATATTTATATTTGGGCACCTTTGGCCGGAACATGTGGG GTGTGTCTTCTCTCCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGAA AGAAGCTCCTGTACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAAC CACTCAGGAAGAAGATGGGTGTTTCATGCCGCTTCCCCGAGGAGGAAGAA GGAGGGTGTGAACTGAGGGTGAAATTTTCTAGAAGCGCCGATGCTCCCG CATATCAGCAGGGTCAGAATCAGCTCTACAATGAATTGAATCTCGGCAG GCGAGAAGAGTACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCGAG ATGGGGGAAAAGCCCCGGAGAAAAAATCCTCAGGAGGGGTGTGACAAATG AGCTGCAGAAGGACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGAA AGGCGAAAGACGCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTC TCTACAGCCACCAAGGACACTTATGATGCGTTGCATATGCAAGCCTTGC CACCCCGC
937	861 + 669	ATGGCTCTTCCCGTAACAGCCCTTTTGTGGCCCTTGCACTCCTTCTGC ATGCAGCACGACCGGAGGTGCAGCTGCTGGAGAGCGGAGCGGCTCGT GCAGCCAGGAGGTTCCCTACGACTCTCCTGTGCCGCCAGCGGCTTACC TTCGAGGACTACGCCATGAGTTGGTTCCGCCAGGCCCCGGGAAGGAGC GCGAGGGCGTGAGCGCGATTCTGGAAAGGGCGGCTCCACCTATTACGC GGACTCCGTGAAGGGTCGCTTTACCATCTCTCGCGACAACCTCAAGAAC ACGCTGTACCTGCAGATGAATAGCCTGCGCGCTGAGGACACTGCCGTGT ACTACTGTGCTGTCTTGGACGAGGAGGCCGCGCAGAGGGCGGCTATTG GGGCCAGGGTACCCAGGTCACCGTGTCTGCCACCACAACACCTGTCCA AGGCCCCCCACACCCGCTCCAACCTATAGCCAGCCAACCATTTAGCCTCA GACCTGAAGCTTGCAGGCCCCGAGCAGGAGGCGCGCTCCATACGCGAGG CCTGGACTTCGCGTGTGATATTTATATTTGGGCACCTTTGGCCGGAACA TGTGGGGTGTGCTTCTCTCCCTTGTGATCACTCTGTATTGTAAGCGCG GGAGAAAGAAGCTCCTGTACATCTTCAAGCAGCCTTTTATGCGACCTGT GCAAACCACTCAGGAAGAAGATGGGTGTTTCATGCCGCTTCCCCGAGGAG GAAGAAGGAGGGTGTGAACGAGGGTGAAATTTTCTAGAAGCGCCGATG CTCCCGCATATCAGCAGGGTCAGAATCAGCTCTACAATGAATTGAATCT CGGCAGGCGAGAAGAGTACGATGTTCTGGACAAAAGACGGGGCAGGGAT CCCGAGATGGGGGAAAAGCCCCGGAGAAAAAATCCTCAGGAGGGTGTG ACAATGAGCTGCAGAAGGACAAGATGGCTGAAGCCTATAGCGAGATCGG AATGAAAGGCGAAAAGACGCAGAGGCAAGGGGCATGACGGTCTGTACCAG GGTCTCTCTACAGCCACCAAGGACACTTATGATGCGTTGCATATGCAAG CCTTGCCACCCCGC
938	861 + 693	ATGGCTCTTCCCGTAACAGCCCTTTTGTGGCCCTTGCACTCCTTCTGC ATGCAGCACGACCGGAGGTGCAACTGCTGGAAAGCGGCGGTGGACTGGT GCAGCCCCGGCGGCAGCCTGAGACTGTCTTGTGCTGCTTCTGGATTACA TTCGACAGATACGCCATGAGCTGGTTCCGCCAGGCCCCCTGGCAAAGAGC GGGAAGGCGTGTCCGCCATCTCCACAAGCGGAGATAGCACATACTATGC CGACAGCGTGAAGGGCAGATTCAACATCAGCAGAGATAATAGCAAGAAC ACCCTGTACCTGCAGATGAACAGCCTCCGGGCGGAGGACACCGCGCTCT ACTACTGCGCCGTGCTGGACGAGGAAGCCGGCGCGGAGGCGGCTACTG GGGCCAGGGCACCCAGGTGACCGTGTCTAGCACCAACAACACCTGTCCA AGGCCCCCCACACCCGCTCCAACCTATAGCCAGCCAACCATTTAGCCTCA GACCTGAAGCTTGCAGGCCCCGAGCAGGAGGCGCGCTCCATACGCGAGG CCTGGACTTCGCGTGTGATATTTATATTTGGGCACCTTTGGCCGGAACA TGTGGGGTGTGCTTCTCTCCCTTGTGATCACTCTGTATTGTAAGCGCG GGAGAAAGAAGCTCCTGTACATCTTCAAGCAGCCTTTTATGCGACCTGT GCAAACCACTCAGGAAGAAGATGGGTGTTTCATGCCGCTTCCCCGAGGAG GAAGAAGGAGGGTGTGAACGAGGGTGAAATTTTCTAGAAGCGCCGATG CTCCCGCATATCAGCAGGGTCAGAATCAGCTCTACAATGAATTGAATCT CGGCAGGCGAGAAGAGTACGATGTTCTGGACAAAAGACGGGGCAGGGAT CCCGAGATGGGGGAAAAGCCCCGGAGAAAAAATCCTCAGGAGGGGTGTG ACAATGAGCTGCAGAAGGACAAGATGGCTGAAGCCTATAGCGAGATCGG

		AATGAAAGGCGAAAAGACGCAGAGGCAAGGGGCATGACGGTCTGTACCAG GGTCTCTCTACAGCCACCAAGGACACTTATGATGCGTTGCATATGCAAG CCTTGCCACCCCGC
939	861 + 717	ATGGCTCTTCCCGTAACAGCCCTTTTGTGGCCCTTGCACTCCTTCTGC ATGCAGCAGCAGCCGGAGGTGCAACTGCTGGAAAGCGGCGGAGGACTCGT CCAGCCCGGCGGCAGCCTGCGGCTGAGCTGTGCTGCTTCTGGATTTACC TTCGCCAGCGACGCCATGAGCTGGTATAGACAGGCCCTTGCCAAAGAGC GGGAACTGGTGTCCGCCATCAGCGGCTCTGGCGGCTCCACCTACTACGC CGATAGCGTGAAAGGGCAGATTACAATCTCTAGAGATAATAGCAAGAAC ACCCTGTACCTGCAGATGAACAGCCTGAGAGCCGAGGACACCGCCGTGT ACTACTGCGCCGCTCACGACAGCGGCGAGGCCCTACCTGGCCTTCGACTA CTGGGGCCAGGGCACACAGGTGACCGTGTCTAGCACCAACAACCTGCT CCAAGGCCCCCACACCCGCTCCAACCTATAGCCAGCCAACCATTTAGGCC TCAGACCTGAAGCTTGAGGCCCGCAGCAGGAGGCGCGCTCCATACGCG AGGCCTGGACTTCGCGTGTGATATTTATATTTGGGCACCTTTGGCCGGA ACATGTGGGGTGTGCTTCTCTCCCTTGTGATCACTCTGTATTGTAAGC GCGGGAGAAAGAAGCTCCTGTACATCTTCAAGCAGCCTTTTATGCGACC TGTGCAAACCACTCAGGAAGAAGATGGGTGTTTCATGCCGCTTCCCGGAG GAGGAAGAAGGAGGGTGTGAAGTGAAGGTGAAATTTTCTAGAAGCGCCG ATGCTCCCGCATATCAGCAGGGTCAGAATCAGCTCTACAATGAATTGAA TCTCGGCAGGCGAGAAGAGTACGATGTTCTGGACAAAAGACGGGGCAGG GATCCCGAGATGGGGGAAAGCCCCGGAGAAAAAATCCTCAGGAGGGGT TGTACAATGAGCTGCAGAAGGACAAGATGGCTGAAGCCTATAGCGAGAT CGGAATGAAAGGCGAAAGACGCAGAGGCAAGGGGCATGACGGTCTGTAC CAGGGTCTCTCTACAGCCACCAAGGACACTTATGATGCGTTGCATATGC AAGCCTTGCCACCCCGC
940	861 + 741	ATGGCTCTTCCCGTAACAGCCCTTTTGTGGCCCTTGCACTCCTTCTGC ATGCAGCAGCAGCCGGAGGTGCAACTGCTGGAAAGCGGCGGAGGACTCGT CCAGCCCGGCGGCAGCCTGAGGCTGAGCTGTGCTGCTTCTGGCTTTACC TTCGACTCCTACACAATGAGCTGGTATAGACAGGCCCTTGCCAAAGAGC GGGAACTGGTGTCCGCCATCAGCGGCCACGGCGACTCTACATACTACGC CGACAGCGTGAAAGGCAGATTACAATCTCTAGAGATAATAGCAAGAAC ACCCTGTACCTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGT ACTACTGCACCAAGATCAGCATCACCACCGAGTGGCTGGCCGGAGATTA CTGGGGCCAGGGCACCCAGGTGACAGTGTCCAGCACCACAACACCTGCT CCAAGGCCCCCACACCCGCTCCAACCTATAGCCAGCCAACCATTTAGGCC TCAGACCTGAAGCTTGAGGCCCGCAGCAGGAGGCGCGCTCCATACGCG AGGCCTGGACTTCGCGTGTGATATTTATATTTGGGCACCTTTGGCCGGA ACATGTGGGGTGTGCTTCTCTCCCTTGTGATCACTCTGTATTGTAAGC GCGGGAGAAAGAAGCTCCTGTACATCTTCAAGCAGCCTTTTATGCGACC TGTGCAAACCACTCAGGAAGAAGATGGGTGTTTCATGCCGCTTCCCCGAG GAGGAAGAAGGAGGGTGTGAAGTGAAGGTGAAATTTTCTAGAAGCGCCG ATGCTCCCGCATATCAGCAGGGTCAGAATCAGCTCTACAATGAATTGAA TCTCGGCAGGCGAGAAGAGTACGATGTTCTGGACAAAAGACGGGGCAGG GATCCCGAGATGGGGGAAAGCCCCGGAGAAAAAATCCTCAGGAGGGGT TGTACAATGAGCTGCAGAAGGACAAGATGGCTGAAGCCTATAGCGAGAT CGGAATGAAAGGCGAAAGACGCAGAGGCAAGGGGCATGACGGTCTGTAC CAGGGTCTCTCTACAGCCACCAAGGACACTTATGATGCGTTGCATATGC AAGCCTTGCCACCCCGC
941	861 + 765	ATGGCTCTTCCCGTAACAGCCCTTTTGTGGCCCTTGCACTCCTTCTGC ATGCAGCAGCAGCCGGAGGTGCAACTGCTGGAAAGCGGAGGAGGCTGGT CCAACCTGGCGGCAGCCTGCGGCTGAGCTGCGCCGCTTCTGGCTTACC TTCAGCAGCTACGCCATGAGCTGGTTCCGGCAGGCCCTTGCAAGGAAA GAGAGTTCTGTGCTTTTATCAGCGGATCTGGCGACTCCACCTACTACGC TGATAGCGTGAAAGGCAGATTTACCATCTCTAGAGATAATAGCAAGAAC ACCCTGTACCTCCAGATGAACAGCCTGCGCGCCGAGGACACAGCCGTGT ACTATTGTACCAGATGGCCTTACGACTTCGAGGAACCAAGCGAGCCCGG CGTGTACTGGGGCCAGGGCACACAGGTGACAGTGTCTCCACCACAACA CCTGCTCCAAGGCCCCCACACCCGCTCCAACCTATAGCCAGCCAACCAT

		TGAGCCTCAGACCTGAAGCTTGCAGGCCCGCAGCAGGAGGCGCCGTCCA TACGCGAGGCCCTGGACTTCGCGTGTGATATTTATATTTGGGCACCTTTG GCCGGAACATGTGGGGTGTGCTTCTCTCCCTTGTGATCACTCTGTATT GTAAGCGCGGGAGAAAGAAGCTCCTGTACATCTTCAAGCAGCCTTTTAT GCGACCTGTGCAAACCACTCAGGAAGAAGATGGGTGTTTCATGCCGCTTC CCCGAGGAGGAAGAAGGAGGGTGTGAAC TGAGGGTGAAATTTTCTAGAA GCGCCGATGCTCCCGCATATCAGCAGGGTCAGAATCAGTCTTACAATGA ATTGAATCTCGGCAGGCGAGAAGAGTACGATGTTCTGGACAAAAGACGG GGCAGGGATCCCGAGATGGGGGGAAAGCCCCGGAGAAAAAATCCTCAGG AGGGGTGTACAAATGAGCTGCAGAAGGACAAGATGGCTGAAGCCTATAG CGAGATCGGAATGAAAGGCGAAAGACGCAGAGGCAAGGGGCATGACGGT CTGTACCAGGGTCTCTCTACAGCCACCAAGGACACTTATGATGCGTTGC ATATGCAAGCCTTGCCACCCCGC
942	861 + 789	ATGGCTCTTCCCGTAACAGCCCTTTTGTGCCCCCTTGCACTCCTTCTGC ATGCAGCACGACCGGAGGTGCAGCTGCTGGAAAGCGGCGAGGCGCTGGT GCAACCTGGCGGATCTCTCAGACTGAGCTGTGCTGCTTCTGGCTTCACA TTCACCGACTACGACATGAGCTGGTATAGACAGGCCCTTGAAAAGAGC GGGAAGTGGTCTCCGTGATCCACAGCGGCGGCTCCACCTACTACGCCGA TAGCGTGAAGGGCAGATTACCATCAGCAGAGATAATAGCAAGAACACC CTGTACCTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACT ACTGCGCCCCCGCTACTACAGCGACCTGTCTTTTGATTATTACAACCTT CGACTACTGGGGCCAGGGCACACAGGTGACAGTGTCCAGCACCAACA CCTGCTCCAAGGCCCCCCACACCCGCTCCAATATAGCCAGCCAACCAT TGAGCCTCAGACCTGAAGCTTGAGGCCCGCAGCAGGAGGCGCCGCTCCA TACGCGAGGCGCTGGACTTCGCGTGTGATATTTATATTTGGGCACCTTTG GCCGGAACATGTGGGGTGTGCTTCTCTCCCTTGTGATCACTCTGTATT GTAAGCGCGGGAGAAAGAAGCTCCTGTACATCTTCAAGCAGCCTTTTAT GCGACCTGTGCAAACCACTCAGGAAGAAGATGGGTGTTTCATGCCGCTTC CCCGAGGAGGAAGAAGGAGGGTGTGAAC TGAGGGTGAAATTTTCTAGAA GCGCCGATGCTCCCGCATATCAGCAGGGTCAGAATCAGTCTTACAATGA ATTGAATCTCGGCAGGCGAGAAGAGTACGATGTTCTGGACAAAAGACGG GGCAGGGATCCCGAGATGGGGGGAAAGCCCCGGAGAAAAAATCCTCAGG AGGGGTGTACAAATGAGCTGCAGAAGGACAAGATGGCTGAAGCCTATAG CGAGATCGGAATGAAAGGCGAAAGACGCAGAGGCAAGGGGCATGACGGT CTGTACCAGGGTCTCTCTACAGCCACCAAGGACACTTATGATGCGTTGC ATATGCAAGCCTTGCCACCCCGC
943	861 + 813	ATGGCTCTTCCCGTAACAGCCCTTTTGTGCCCCCTTGCACTCCTTCTGC ATGCAGCACGACCGGAGGTGCAGCTGCTGGAGAGCGGTGGAGGGTTGGT GCAGCCCGGGGGTAGCCTGCGTCTGTGCTGCGCCGCTTCCGGCTTCACG TTCTCTGATTACGCCATGCACTGGTTCCGGCAGGCCCCCGGTAAGGAGC GCGTGCTGGTGTGCTCTATTGACTCCGGCGGCTCCACTTACTACGCAGA CAGTGTCAAGGGCCGTTTACCATCAGCCCGGACAAACAGCAAGAACACG CTGTACCTGCAGATGAACCTCCCTTCGAGCAGAGGACACCGCGGTGTACT ACTGTAATGCGGGCTTCAAGGGCGATCACCCCCACCCCAAGGATGCCTT CGACATTTGGGGCCAGGGCACCCAGGTACCGTGTGCTCCACCACAACA CCTGCTCCAAGGCCCCCCACACCCGCTCCAATATAGCCAGCCAACCAT TGAGCCTCAGACCTGAAGCTTGAGGCCCGCAGCAGGAGGCGCCGTCCA TACGCGAGGCCCTGGACTTCGCGTGTGATATTTATATTTGGGCACCTTTG GCCGGAACATGTGGGGTGTGCTTCTCTCCCTTGTGATCACTCTGTATT GTAAGCGCGGGAGAAAGAAGCTCCTGTACATCTTCAAGCAGCCTTTTAT GCGACCTGTGCAAACCACTCAGGAAGAAGATGGGTGTTTCATGCCGCTTC CCCGAGGAGGAAGAAGGAGGGTGTGAAC TGAGGGTGAAATTTTCTAGAA GCGCCGATGCTCCCGCATATCAGCAGGGTCAGAATCAGTCTTACAATGA ATTGAATCTCGGCAGGCGAGAAGAGTACGATGTTCTGGACAAAAGACGG GGCAGGGATCCCGAGATGGGGGGAAAGCCCCGGAGAAAAAATCCTCAGG AGGGGTGTACAAATGAGCTGCAGAAGGACAAGATGGCTGAAGCCTATAG CGAGATCGGAATGAAAGGCGAAAGACGCAGAGGCAAGGGGCATGACGGT CTGTACCAGGGTCTCTCTACAGCCACCAAGGACACTTATGATGCGTTGC ATATGCAAGCCTTGCCACCCCGC

944	861 + 837	ATGGCTCTTCCCGTAACAGCCCTTTTGTGTGCCCTTGCACTCCTTCTGCG ATGCAGCACGACCGGAGGTGCAACTGCTGGAATCCGGCGGAGGCCTGGT GCAGCCCGGCGGCAGCCTCAGACTGAGCTGTGCCGCTTCTGGCTTTACC TTCAGCAGCGAGGGCATGAGCTGGGTGCGGCAGGCCCTTGGCAAGGAAA GAGAGCTGGTCTCCGCCATCAGCGGATCTGGCGACCACCTACTATGCG CGATAGCCTGCGCGGAAGATTCACAATCTCTAGAGATAATAGCAAGAAC ACCCTGTACCTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGT ACTACTGCAACGCCCTGGAAGGCGGCCCTACAACAGCTATCCAGCCAGG AGGCCCTGACTACTGGGGCCAGGGCACCCAGGTGACCGTGTCCAGCACC ACAACACCTGCTCCAAGGCCCCCCACACCCGCTCCAACCTATAGCCAGCC AACCATTGAGCCTCAGACCTGAAGCTTGCAAGGCCCGCAGCAGGAGGCGC CGTCCATACGCGAGGCCTGGACTTCGCGTGTGATATTTATATTTGGGCA CCTTTGGCCGGAACATGTGGGGTGTGCTTCTCTCCCTTGTGATCACTC TGTATTGTAAGCGCGGGAGAAAGAGCTCCTGTACATCTTCAAGCAGCC TTTTATGCGACCTGTGCAAACTCAGGAAGAAGATGGGTGTTCATGCG CGCTTCCCGGAGGAGGAAGAAGGAGGTTGTGAAGTGAAGTGAATTTT CTAGAAGCGCCGATGCTCCCGCATATCAGCAGGCTCAGAATCAGCTCTA CAATGAATTGAATCTCGGCAGGCAGAGAAGGTACGATGTTCTGGACAAA AGACGGGGCAGGGATCCCGAGATGGGGGGAAAGCCCCGGAGAAAAAATC CTCAGGAGGGGTTGTACAATGAGCTGCAGAAGGACAAGATGGCTGAAGC CTATAGCGAGATCGGAATGAAAGGCGAAAGACGCGAGAGGCAAGGGGCAT GACGGTCTGTACCGAGGTCTCTCTACAGCCACCAAGGACACTTATGATG CGTTGCATATGCAAGCCTTGCCACCCCGC
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In particular embodiments, a vector comprises a polynucleotide encoding a polypeptide contemplated herein. In particular embodiments, the polypeptide is selected from the group consisting of an antibody, an antigen binding fragment of an antibody, a bispecific antibody, a BiTE, and a chimeric antigen receptor.

5 In particular embodiments, a vector comprises a polynucleotide that encodes a polypeptide comprising an anti-BCMA antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in any one of SEQ ID NOs: 11-144.

In particular embodiments, a vector comprises a polynucleotide that encodes a bispecific antibody comprising an anti-BCMA antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in any one of SEQ ID NOs: 11-144; and optionally a polypeptide linker and an anti-CD3 antibody.

In particular embodiments, a cell, *e.g.*, an immune effector cell, is modified to express a polypeptide, *e.g.*, a chimeric antigen receptor, that comprises an anti-BCMA antibody or antigen binding fragment thereof comprising an amino acid sequence set forth in any one of

15 SEQ ID NOs: 11-144.

In particular embodiments, a polynucleotide contemplated herein or vector comprising or encoding the same is introduced into a cell, *e.g.*, an immune effector cell. In particular embodiments, a non-viral vector comprising a polynucleotide is introduced into a cell. Illustrative examples non-viral vectors include but are not limited to: autonomously
20 replicating sequences; plasmids; phagemids; cosmids; artificial chromosomes such as yeast

artificial chromosomes (YAC), bacterial artificial chromosomes (BAC), or P1-derived artificial chromosomes (PAC); bacteriophages such as lambda phage or M13 phage; and transposable elements including but not limited to piggyBac, Sleeping Beauty, Mos1, Tc1/mariner, Tol2, mini-Tol2, Tc3, MuA, Himar I, Frog Prince, and derivatives thereof.

5 In particular embodiments, a viral vector comprising a polynucleotide is introduced into a cell. Illustrative examples of viral vectors include but are not limited to Adenoviral (Ad) vectors, adeno-associated virus (AAV) vectors, rhabdovirus (*e.g.*, lyssavirus, vesiculovirus) vectors, paramyxovirus (*e.g.*, henipavirus, morbillivirus, respirovirus, rubelavirus) vectors, herpes simplex virus (*e.g.*, HSV-1, HSV-2) vectors, vaccinia virus
10 vectors, and retroviral vectors, preferably lentiviral vectors (LVV).

A “viral vector” is a nucleic acid molecule derived from a viral genome that is used to transfer or deliver another nucleic acid to a cell. A viral vector is based on, and derived from, a virus genome that has been engineered to remove viral accessory proteins but leave elements intact for packaging, reverse transcription and integration. In preferred
15 embodiments, viral vectors contemplated herein comprise a polynucleotide comprising or encoding a promoter operably linked to a polynucleotide encoding a polypeptide comprising an anti-BCMA binding protein, *e.g.*, an anti-BCMA antibody or antigen binding fragment thereof, an anti-BCMA-antiCD3 bispecific antibody, or a chimeric antigen receptor (CAR).

In particular embodiments, an adenoviral vector comprises a polynucleotide
20 comprising or encoding a promoter operably linked to a polynucleotide encoding a polypeptide comprising an anti-BCMA binding protein, *e.g.*, an anti-BCMA antibody or antigen binding fragment thereof, an anti-BCMA-antiCD3 bispecific antibody, or a CAR. High-capacity adenoviral vectors (HC-Ads) (third generation) only retain short non-coding regions from the Ad genome (ITRs and ψ signal), which enables the vector to carry large
25 polynucleotide payloads (~37kb).

In particular embodiments, an AAV vector comprises a polynucleotide comprising or encoding a promoter operably linked to a polynucleotide encoding a polypeptide comprising an anti-BCMA binding protein, *e.g.*, an anti-BCMA antibody or antigen binding fragment thereof, an anti-BCMA-antiCD3 bispecific antibody, or a CAR. Recombinant
30 AAV (rAAV) vectors are primarily episomally maintained and have a polynucleotide payload capacity of about 4.7kb. rAAV vectors are typically composed of, at a minimum, a transgene and its regulatory sequences, and 5' and 3' AAV inverted terminal repeats (ITRs). rAAV vectors may comprise ITRs from any one of AAV1, AAV2, AAV3, AAV4, AAV5,

AAV6, AAV7, AAV8, AAV9, or AAV10. Construction of rAAV vectors, and production, and purification of AAV have been disclosed, *e.g.*, in U.S. Patent Nos. 9,169,494; 9,169,492; 9,012,224; 8,889,641; 8,809,058; and 8,784,799, each of which is incorporated by reference herein, in its entirety.

5 In particular embodiments, an HSV vector comprises a polynucleotide comprising or encoding a promoter operably linked to a polynucleotide encoding a polypeptide comprising an anti-BCMA binding protein, *e.g.*, an anti-BCMA antibody or antigen binding fragment thereof, an anti-BCMA-antiCD3 bispecific antibody, or a CAR. HSV vectors are relatively large, *e.g.*, up to 152 kb. Typically, HSV vectors are rendered replication deficient;
10 moreover, one or more essential or non-essential HSV genes are removed from the vector backbone to make room for polynucleotide payloads. Most replication deficient HSV vectors contain a deletion to remove one or more intermediate-early, early, or late HSV genes to prevent replication. Advantages of the HSV vector are its ability to enter a latent stage that can result in long-term DNA expression and its large viral DNA genome that can
15 accommodate exogenous DNA inserts of up to 25 kb. HSV-based vectors are described in, for example, U.S. Pat. Nos. 5,837,532, 5,846,782, and 5,804,413, and International Patent Applications WO 91/02788, WO 96/04394, WO 98/15637, and WO 99/06583, each of which are incorporated by reference herein in its entirety.

 In particular embodiments, a retroviral vector or a lentiviral vector comprises a
20 polynucleotide comprising or encoding a promoter operably linked to a polynucleotide encoding a polypeptide comprising an anti-BCMA binding protein, *e.g.*, an anti-BCMA antibody or antigen binding fragment thereof, an anti-BCMA-antiCD3 bispecific antibody, or a CAR. In particular embodiments, a recombinant particle comprises two copies of a vector, a genomic RNA comprising backbone sequences derived from a retrovirus genome,
25 *e.g.*, a lentivirus genome.

 In various embodiments, a retroviral vector is engineered or derived from a retrovirus genome selected from the group consisting of: an alpharetrovirus genome, a betaretrovirus genome, a gammaretrovirus genome, a deltaretrovirus genome, or a spumavirus genome (*e.g.*, an epsilon retrovirus genome, a simiispumavirus genome, a bovispumavirus genome,
30 an equispumavirus genome, a felispumavirus genome, and a prosimiispumavirus genome).

 In particular embodiments, a retroviral vector comprises a 5' LTR and a 3' LTR each isolated, obtained, or derived from a retrovirus genome selected from the group consisting

of: an alpharetrovirus genome, a betaretrovirus genome, a gammaretrovirus genome, a deltaretrovirus genome, an epsilonretrovirus genome, and a spumavirus genome.

Illustrative examples of alpharetroviruses from which a retroviral vector may be isolated, obtained, or derived from include but are not limited to avian leukosis virus, avian carcinoma Mill Hill virus 2, avian myeloblastosis virus, avian myelocytomatosis virus 29, 5 avian sarcoma virus CT10, fujinami sarcoma virus, rous sarcoma virus, UR2 sarcoma virus and Y73 sarcoma virus.

Illustrative examples of betaretroviruses from which a retroviral vector may be isolated, obtained, or derived from include but are not limited to mouse mammary tumor 10 virus, Jaagsiekte sheep retrovirus, langur virus, Mason-Pfizer monkey virus, and squirrel monkey retrovirus (SMRV).

Illustrative examples of deltaretroviruses from which a retroviral vector may be isolated, obtained, or derived from include but are not limited to bovine leukemia virus, primate T-lymphotropic virus 1, primate T-lymphotropic virus 2, primate T-lymphotropic 15 virus 3, and primate T-lymphotropic virus 4.

Illustrative examples of epsilonretroviruses from which a retroviral vector may be isolated, obtained, or derived from include but are not limited to walleye dermal sarcoma virus, walleye epidermal hyperplasia virus 1, and walleye epidermal hyperplasia virus 2.

Illustrative examples of gammaretrovirus from which a retroviral vector may be 20 isolated, obtained, or derived from include but are not limited to baboon endogenous virus (BaEV), chick syncytial virus, feline endogenous virus (*e.g.*, RD114), feline leukemia virus (FeLV), Finkel-Biskis-Jenkins murine sarcoma virus, Gardner-Arnstein feline sarcoma virus, gibbon ape leukemia virus (GALV), guinea pig type-C oncovirus, Hardy-Zuckerman feline sarcoma virus, Harvey murine sarcoma virus, Kirsten murine sarcoma virus, koala retrovirus, 25 murine leukemia virus (MLV), Moloney murine leukemia virus (MoMLV), Moloney murine sarcoma virus, porcine endogenous virus (PERV), Porcine type-C oncovirus, reticuloendotheliosis virus (REV), Snyder-Theilen feline sarcoma virus, Trager duck spleen necrosis virus, viper retrovirus, xenotropic murine leukemia virus- related virus (XMRV), and woolly monkey sarcoma virus.

30 Illustrative examples of spumaviruses from which a retroviral vector may be isolated, obtained, or derived from include but are not limited to simian foamy virus, bovine foamy virus, equine foamy virus, feline foamy virus, human foamy virus (HFV), and brown greater galago prosimian foamy virus.

In various embodiments, a lentiviral vector (lentivector) is engineered or derived from a lentivirus genome. Illustrative lentiviruses include, but are not limited to, HIV (human immunodeficiency virus; including HIV type 1, and HIV type 2); visna-maedi virus (VMV); caprine arthritis-encephalitis virus (CAEV); equine infectious anemia virus (EIAV); feline immunodeficiency virus (FIV); bovine immune deficiency virus (BIV); and simian immunodeficiency virus (SIV). In particular embodiments, lentiviral vectors are derived from HIV viral genomes, preferably HIV-1 or HIV-2 viral genomes and more preferably, HIV-1 viral genomes (*i.e.*, HIV-1 cis-acting sequence elements are preferred).

In various embodiments, a lentivirus comprises two copies of a lentiviral vector-based RNA genome comprising a 5' long terminal repeat (LTR) comprising R and U5 regions; a Psi (Ψ) packaging signal; a cPPT/FLAP, an export element; a polynucleotide comprising or encoding a promoter operably linked to a polynucleotide encoding a polypeptide comprising an anti-BCMA binding protein, *e.g.*, an anti-BCMA antibody or antigen binding fragment thereof, an anti-BCMA-antiCD3 bispecific antibody, or a CAR; a 3' LTR comprising U3 and R regions; optionally a WPRE or HPRE; a polyadenylation signal and a poly(A) tail.

The term "long terminal repeat (LTR)," as used herein, refers to elements located at the ends of retroviral polynucleotides which, in their natural sequence context, are direct repeats and contain U3, R and U5 regions. LTRs generally provide functions fundamental to the expression of retroviral genes (*e.g.*, promotion, initiation and polyadenylation of gene transcripts) and to viral replication. The LTR contains numerous regulatory signals including transcriptional control elements, polyadenylation signals and sequences needed for replication and integration of the viral genome. The viral LTR is divided into three regions called U3, R and U5. The U3 region contains the enhancer and promoter elements. The U5 region is the sequence between the primer binding site and the R region and contains the polyadenylation signal. The R (repeat) region is flanked by the U3 and U5 regions. A transfer plasmid, which is used to package a vector genome comprises a 5' LTR comprising U3, R and/or U5 regions and a 3' LTR comprising U3, R and/or U5 regions. Adjacent to the 5' LTR are sequences necessary for reverse transcription of the genome (the tRNA primer binding site) and for efficient packaging of viral RNA into particles (the Psi " Ψ " site). A retroviral vector-based genome packaged in a particle comprises a 5' LTR comprising R and U5 regions and a 3' LTR comprising U3 and R regions. The retroviral vector-based genome is reverse transcribed and integrated into the host cell genome as a provector. Through

reverse transcription and second strand synthesis of the retroviral vector genome, provectors comprise two copies of the 3' LTR, one copy that replaces the 5' LTR and the 3' LTR.

A "TAR" element as used herein, refers to the "trans-activation response" genetic element located in the R region of lentiviral vector LTRs. This element interacts with the
5 lentiviral trans-activator (tat) genetic element to enhance lentiviral vector genome replication. In third generation lentiviral vectors, this element is not usually present because lentiviral vector transfer vectors comprise a 5' LTR U3 region replaced by a heterologous promoter.

An "R region," as used herein, refers to the region within LTRs beginning at the start of the capping group (*i.e.*, the start of transcription) and ending immediately prior to the start
10 of the polyA tract. The R region is also defined as being flanked by the U3 and U5 regions. The R region plays a role during reverse transcription in permitting the transfer of nascent DNA from one end of the genome to the other.

As used herein, a "packaging signal" or "packaging sequence" refers to sequences located within the retroviral genome which are required for insertion of the viral RNA into
15 the viral capsid or particle, see *e.g.*, Clever et al., 1995. J. of Virology, Vol. 69, No. 4; pp. 2101-2109. Several retroviral vectors use the minimal packaging signal (also referred to as the psi [Ψ] or [Ψ +] sequence) needed for encapsidation of the viral genome. Thus, as used herein, the terms "packaging sequence," "packaging signal," "psi" and the symbol " Ψ ," are used in reference to the non-coding sequence required for encapsidation of retroviral RNA
20 strands during viral particle formation.

A "FLAP element" or "cPPT/FLAP," as used herein refers to a nucleic acid whose sequence includes the central polypurine tract and central termination sequences (cPPT and CTS) of a lentivirus, *e.g.*, HIV-1 or HIV-2. "FLAP element" and "cPPT/FLAP" may used interchangeably to refer to the foregoing FLAP element. Suitable FLAP elements are
25 described in U.S. Pat. No. 6,682,907 and in Zennou, et al., 2000, Cell, 101:173. During HIV-1 reverse transcription, central initiation of the plus-strand DNA at the central polypurine tract (cPPT) and central termination at the central termination sequence (CTS) lead to the formation of a three-stranded DNA structure: the HIV-1 central DNA flap. While not wishing to be bound by any particular theory, the DNA flap may act as a cis-active
30 determinant of lentiviral genome nuclear import and/or may increase virus titer.

As used herein, an "export element" refers to a cis-acting post-transcriptional regulatory element which regulates the transport of an RNA transcript from the nucleus to the cytoplasm of a cell. Examples of RNA export elements include, but are not limited to,

the human immunodeficiency virus (HIV) rev response element (RRE) (see *e.g.*, Cullen et al., 1991. J. Virol. 65: 1053; and Cullen et al., 1991. Cell 58: 423), the woodchuck hepatitis virus posttranscriptional regulatory element (WPRE), and the hepatitis B virus post-transcriptional regulatory element (HPRE).

5 Expression of heterologous sequences in viral vectors may be increased by incorporating posttranscriptional regulatory elements, efficient polyadenylation signals, and optionally, transcription termination signals into the vectors. A variety of posttranscriptional regulatory elements can increase expression of a heterologous nucleic acid at the protein, *e.g.*, WPRE, HPRE.

10 Lentiviral vectors may contain one or more safety enhancements to reduce the risk of replication, insertional mutagenesis, and off-target transduction and/or expression. In particular embodiments, a lentiviral vector comprises one or more of the following safety enhancements: one or more modifications of the 5' and 3' LTRs, cell or tissue specific expression control sequences, *e.g.*, promoters, enhancers, miRNA target sequences. A
15 “modified LTR,” as used herein, refers to one or more nucleotide additions, deletions or substitutions in the native HIV-1 5' LTR and/or 3' LTR. The skilled artisan would be able to determine whether an LTR is modified by comparison to a reference LTR.

 “Self-inactivating” (SIN) vectors, as used herein, refer to replication-defective vectors, *e.g.*, retroviral or lentiviral vectors, in which the right (3') LTR enhancer-promoter
20 region, known as the U3 region, has been modified (*e.g.*, by deletion or substitution) to prevent viral transcription beyond the first round of viral replication. Self-inactivation is achieved through a deletion in the U3 region of the 3' LTR of the lentiviral vector transfer plasmid that removes the LTR TATA box (*e.g.*, deletions from -418 to -18), without significant reductions in titers.

25 An additional safety enhancement is provided by replacing the U3 region of the 5' LTR with a heterologous promoter to drive transcription of the viral genome during production of recombinant viral particles. Examples of heterologous promoters which can be used include, for example, viral simian virus 40 (SV40) (*e.g.*, early or late), cytomegalovirus (CMV) (*e.g.*, immediate early), Moloney murine leukemia virus
30 (MoMLV), Rous sarcoma virus (RSV), and herpes simplex virus (HSV) (thymidine kinase) promoters.

 In particular embodiments, a lentiviral vector is engineered to integrate into the host cell genome.

In certain embodiments, a lentiviral vector is engineered to be integration defective, episomal, and not integrate in the cell genome. As used herein, the term “integration defective lentivirus” or “IDLV” refers to a lentivirus having an integrase that lacks the capacity to integrate the viral vector into the host cell genome. Integration-incompetent viral
 5 vectors have been described in patent application WO 2006/010834, which is herein incorporated by reference in its entirety. Illustrative mutations in HIV-1 integrase suitable to reduce integrase activity include, but are not limited to: H12N, H12C, H16C, H16V, S81R, D41A, K42A, H51A, Q53C, D55V, D64E, D64V, E69A, K71A, E85A, E87A, D116N, D116I, D116A, N120G, N120I, N120E, E152G, E152A, K156E, K156A, E157A, K159E,
 10 K159A, K160A, R166A, D167A, E170A, H171A, K173A, K186Q, K186T, K188T, E198A, R199C, R199T, R199A, D202A, K211A, Q214L, Q216L, Q221L, W235F, W235E, K236S, K236A, K246A, G247W, D253A, R262A, R263A and K264H. In particular embodiments, an HIV-1 integration deficient integrase comprises a D64V, D161I, D116A, E152G, or E152A mutation; D64V, D116A, and E152G mutations; D64V, D116A, and E152A
 15 mutations; or a D64V mutation.

H. CELLS

In particular embodiments, a polynucleotide encoding a polypeptide contemplated herein is introduced into a cell, *e.g.*, an immune effector cell. In particular embodiments, a cell, *e.g.*, an immune effector cell, is modified to express a polypeptide that comprises an
 20 anti-BCMA binding protein an anti-BCMA binding protein, *e.g.*, an anti-BCMA antibody or antigen binding fragment thereof, an anti-BCMA-antiCD3 bispecific antibody, or a CAR.

In particular embodiments, a cell, *e.g.*, an immune effector cell, is modified to express a polypeptide contemplated that comprises an anti-BCMA binding protein, *e.g.*, an anti-BCMA antibody or antigen binding fragment thereof, an anti-BCMA-antiCD3 bispecific
 25 antibody, or a CAR comprising an amino acid sequence set forth in any one of SEQ ID NOs: 11-144 or a CAR comprising the amino acid sequence set forth in any one of SEQ ID NOs: 165-860.

An “immune effector cell” is any cell of the immune system that has one or more effector functions (*e.g.*, cytotoxic cell killing activity, secretion of cytokines, induction of
 30 ADCC and/or CDC). Illustrative types of immune effector cells contemplated in particular embodiments include, without limitation, T lymphocytes, dendritic cells (DC), Treg cells, natural killer (NK) cells, natural killer T (NKT) cells, and macrophages. The terms “T cell”

or “T lymphocyte” are art-recognized and are intended, in particular embodiments, to include thymocytes, immature T lymphocytes, mature T lymphocytes, resting T lymphocytes, and/or activated T lymphocytes. Illustrative examples of T lymphocytes suitable for use in particular embodiments, include but not limited to cytotoxic T cells (CTLs; CD8⁺ T cells),
5 TILs, helper T cells (HTLs; CD4⁺ T cells), CD4⁺CD8⁺ T cells, CD4⁺ CD8⁻ T cells, or any other subset of T cells that has an effector function. In a particular embodiment, the cells comprise αβ T cells. In a particular embodiment, the cells comprise γδ T cells.

In particular embodiments, immune effector cells include natural killer (NK) cells. NK cells do not express T cell antigen receptors (TCR), CD3 or surface immunoglobulins
10 (Ig) B cell receptor, but usually express the surface markers CD16 (FcγRIII) and CD56 in humans.

In particular embodiments, immune effector cells include natural killer T (NKT) cells.

In particular embodiments, a polynucleotide encoding a polypeptide contemplated
15 herein is introduced into a progenitor of an immune effector cell that is subsequently induced to differentiate, or differentiates, into one or more immune effector cells. In particular embodiments, progenitors of immune effectors cells include hematopoietic stem cells (HSCs) contained within the CD34⁺ population of cells derived from cord blood, bone marrow or mobilized peripheral blood which naturally differentiate into mature immune
20 effector cells, or which can be induced to differentiate into mature immune effector cells.

I. COMPOSITIONS AND FORMULATIONS

Compositions contemplated herein comprise one or more antibodies or antigen binding fragments thereof, bispecific antibodies, antibody conjugates, polypeptides, fusion polypeptides, chimeric antigen receptors, polynucleotides, vectors, and/or immune
25 effector cells modified *ex vivo*.

In particular embodiments, a composition comprises one or more polynucleotides and/or polypeptides.

In particular embodiments, a composition comprises a polynucleotide comprising or encoding a promoter operably linked to one or more polynucleotide
30 encoding one or more anti-BCMA binding proteins, *e.g.*, an anti-BCMA antibody or antigen binding fragment thereof, an anti-BCMA-antiCD3 bispecific antibody, or a CAR.

In particular embodiments, a composition comprises a vector comprising a polynucleotide comprising or encoding a promoter operably linked to a polynucleotide encoding the amino acid sequence set forth in any one of SEQ ID NOs: 165-860 or a polynucleotide sequence set forth in any one of SEQ ID NOs: 905-944.

5 In particular embodiments, a composition is a pharmaceutical composition. A “pharmaceutical composition” refers to a composition formulated in a pharmaceutically-acceptable or physiologically-acceptable solution for administration to a cell or a subject, either alone, or in combination with one or more other modalities of therapy.

 “Pharmaceutically acceptable” refers to molecular entities and compositions that
10 do not produce excessive toxicity, irritation, allergic response, or other problems or complications, commensurate with a reasonable benefit/risk ratio when administered to a human.

 In particular embodiments, a composition comprises a pharmaceutically acceptable carrier and a recombinant particle contemplated herein. The term “pharmaceutically
15 acceptable carrier” refers to a diluent, adjuvant, excipient, vehicle and the like with which a polypeptide, a polynucleotide or a vector is physiologically compatible with administration to a human, including but not limited to pharmaceutically acceptable cell culture media, Dulbecco's phosphate buffered saline (PBS), Ringer's solution, 5% dextrose in water (D5W), and normal/physiologic saline (0.9% NaCl).

20 In particular embodiments, a composition comprises a polypeptide, a polynucleotide or a vector and a pharmaceutically acceptable carrier suitable for enteral or parenteral, *e.g.*, intravascular (intravenous or intraarterial), intraosseous, intraperitoneal, intraventricular, intracerebral, intracranial, intraspinal, intrathecal, intramuscular, and intramedullary, administration and formulation.

25 In particular embodiments, a composition is substantially free of mycoplasma, endotoxin, and microbial contamination. By “substantially free” with respect to endotoxin is meant that there is less endotoxin per dose of cells than is allowed by the FDA for a biologic, which is a total endotoxin of 5 EU/kg body weight per day, which for an average 70 kg person is 350 EU per total dose of cells. In particular embodiments, compositions
30 contemplated herein contain about 0.5 EU/mL to about 5.0 EU/mL, or about 0.5 EU/mL, 1.0 EU/mL, 1.5 EU/mL, 2.0 EU/mL, 2.5 EU/mL, 3.0 EU/mL, 3.5 EU/mL, 4.0 EU/mL, 4.5 EU/mL, or 5.0 EU/mL.

In particular embodiments, compositions contemplated herein are used in the treatment of a cancer, GVHD, an infectious disease, an autoimmune disease, an inflammatory disease, or an immunodeficiency. In particular embodiments, a composition comprises a recombinant particle contemplated herein and one or more cytokines, growth
5 factors, steroids, NSAIDs, DMARDs, anti-inflammatories, chemotherapeutics, radiotherapeutics, therapeutic antibodies, or other active and ancillary agents, either alone or in combination.

It would be understood by the skilled artisan that particular embodiments contemplated herein may comprise other formulations, such as those that are well known
10 in the pharmaceutical art, and are described, for example, in *Remington: The Science and Practice of Pharmacy*, Volume I and Volume II. 23rd Edition. Edited by Adeboye Adejare. Academic Press, 2020, which is incorporated by reference herein, in its entirety.

J. ENUMERATED EMBODIMENTS

15 Embodiment 1: An antibody or antigen binding fragment thereof comprising:

(a) a heavy chain variable region (VH) comprising a CDRH1, a CDRH2, and a CDRH3 of an antibody or antigen binding fragment thereof set forth in Table 1; a polypeptide linker; and a light chain variable region (VL) comprising a CDRL1, a CDRL2, and a CDRL3 of an antibody or antigen binding fragment thereof set forth in Table 1; or

20 (b) a VHH domain comprising a CDRH1, a CDRH2, and a CDRH3 of an antibody or antigen binding fragment thereof set forth in Table 1.

Embodiment 2: The antibody or antigen binding fragment thereof of embodiment 1, wherein:

(a) the VH comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino
25 acid sequences set forth in SEQ ID NOs: 12, 13, and 14 and the VL comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 16, 17, and 18;

(b) the VH comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 22, 23, and 24 and the VL comprises a CDRL1, a
30 CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 26, 27, and 28;

(c) the VH comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 32, 33, and 34 and the VL comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 36, 37, and 38;

5 (d) the VH comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 42, 43, and 44 and the VL comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 46, 47, and 48;

(e) the VH comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino
10 acid sequences set forth in SEQ ID NOs: 52, 53, and 54 and the VL comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 56, 57, and 58;

(f) the VH comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 62, 63, and 64 and the VL comprises a CDRL1, a
15 CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 66, 67, and 68;

(g) the VH comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 72, 73, and 74 and the VL comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 76,
20 77, and 78;

(h) the VH comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 82, 83, and 84 and the VL comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 86, 87, and 88;

25 (i) the VH comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 92, 93, and 94 and the VL comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 96, 97, and 98;

(j) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the
30 amino acid sequences set forth in SEQ ID NOs: 102, 103, and 104;

(k) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 106, 107, and 108;

- (l) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 110, 111, and 112;
- (m) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 114, 115, and 116;
- 5 (n) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 118, 119, and 120;
- (o) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 122, 123, and 124;
- (p) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 126, 127, and 128;
- 10 (q) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 130, 131, and 132;
- (r) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 134, 135, and 136;
- 15 (s) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 138, 139, and 140; or
- (t) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 142, 143, and 144.
- Embodiment 3: The antibody or antigen binding fragment thereof of embodiment 1 or embodiment 2, wherein:
- 20 (a) the VH comprises the amino acid sequence set forth in SEQ ID NO: 11 and the VL comprises the amino acid sequence set forth in SEQ ID NO: 15;
- (b) the VH comprises the amino acid sequence set forth in SEQ ID NO: 21 and the VL comprises the amino acid sequence set forth in SEQ ID NO: 25;
- 25 (c) the VH comprises the amino acid sequence set forth in SEQ ID NO: 31 and the VL comprises the amino acid sequence set forth in SEQ ID NO: 35;
- (d) the VH comprises the amino acid sequence set forth in SEQ ID NO: 41 and the VL comprises the amino acid sequence set forth in SEQ ID NO: 45;
- (e) the VH comprises the amino acid sequence set forth in SEQ ID NO: 51 and the VL comprises the amino acid sequence set forth in SEQ ID NO: 55;
- 30 (f) the VH comprises the amino acid sequence set forth in SEQ ID NO: 61 and the VL comprises the amino acid sequence set forth in SEQ ID NO: 65;

(g) the VH comprises the amino acid sequence set forth in SEQ ID NO: 71 and the VL comprises the amino acid sequence set forth in SEQ ID NO: 75;

(h) the VH comprises the amino acid sequence set forth in SEQ ID NO: 81 and the VL comprises the amino acid sequence set forth in SEQ ID NO: 85;

5 (i) the VH comprises the amino acid sequence set forth in SEQ ID NO: 91 and the VL comprises the amino acid sequence set forth in SEQ ID NO: 95; or

(a) the VHH domain comprises the amino acid sequence set forth in any one of SEQ ID NOs: 101, 105, 109, 113, 117, 121, 125, 129, 133, 137, and 141.

Embodiment 4: The antibody or antigen binding fragment thereof of any one of
10 embodiments 1 to 3, wherein the polypeptide linker is selected from the group consisting of: TGEKP (SEQ ID NO: 2); (GGGS)_n wherein n = 1, 2, 3, 4 or 5 (SEQ ID NOs: 3 and 976-979); EGKSSGSGSESKVD (SEQ ID NO: 4); KESGSVSSEQLAQFRSLD (SEQ ID NO: 5); LRQRDGERP (SEQ ID NO: 6); LRQKDGGGSRP (SEQ ID NO: 7); LRQKD(GGGS)₂ERP (SEQ ID NO: 8), GEGTSTGSGSGSGGGAD (SEQ ID NO: 9),
15 and GSTSGSGKPGSGEGSTKG (SEQ ID NO: 10) and variants thereof comprising an amino acid sequence 95% identical thereto.

Embodiment 5: The antibody or antigen binding fragment thereof of any one of
embodiments 1 to 4, wherein the antibody or antigen binding fragment thereof comprises the amino acid sequence set forth in any one of SEQ ID NOs: 19, 20, 29, 30, 39, 40, 49, 50, 59,
20 60, 69, 70, 79, 80, 89, 90, 99, 100, 101, 105, 109, 113, 117, 121, 125, 129, 133, 137, and 141.

Embodiment 6: A bispecific antibody comprising the antibody or antigen binding fragment thereof of any one of embodiments 1 to 5.

Embodiment 7: The bispecific antibody of embodiment 6, further comprising an anti-CD3 antibody that binds CD3δ, CD3ε, CD3γ, or CD3ζ.

25 Embodiment 8: An antibody conjugate comprising the antibody or antigen binding fragment thereof of any one of embodiments 1 to 5.

Embodiment 9: The antibody conjugate of embodiment 8, wherein the antigen or antigen binding fragment thereof is conjugated to a cytotoxic agent.

Embodiment 10: The antibody conjugate of embodiment 8 or embodiment 9,
30 wherein:

(a) the cytotoxic agent is a toxin selected from the group consisting of: saporin, diphtheria toxin, pseudomonas exotoxin A, Ricin A chain derivatives, a small molecule toxin, and combinations thereof;

(b) the cytotoxic agent is a radioisotope selected from the group consisting of: ^{131}I , ^{90}Y , ^{177}Lu , ^{188}Re , ^{67}Cu , ^{213}Bi , ^{211}At , and ^{227}Ac ;

(c) the cytotoxic agent is an RNA polymerase II inhibitor and/or RNA polymerase III inhibitor selected from the group consisting of: an amatoxin, α -amanitin, β -amanitin, γ -amanitin, ϵ -amanitin, amanin, amaninamide, amanullin, amanullinic acid and any functional fragments, derivatives or analogs thereof; or

(d) the cytotoxic agent is a DNA-damaging agent selected from the group consisting of: an antitubulin agent, a DNA crosslinking agent, a DNA alkylating agent and a mitotic disrupting agent.

10 Embodiment 11: A chimeric antigen receptor (CAR) comprising the antibody or antigen binding fragment thereof of any one of embodiments 1 to 5; a spacer domain; a transmembrane domain, and one or more intracellular signaling domains.

Embodiment 12: The CAR of embodiment 11, wherein the spacer domain comprises a hinge domain or fragment thereof selected from the group consisting of: a CD4 hinge, a CD8 β hinge, a CD8 α hinge, a CD28 hinge, a CD134 hinge, a CD137 hinge, a CD152 hinge, 15 a CD278 hinge, an IgG1 hinge, an IgG2 hinge, an IgG3 hinge, and an IgG4 hinge.

Embodiment 13: The CAR of embodiment 11 or embodiment 12, wherein the spacer domain comprises an amino acid sequence set forth in any one of SEQ ID NOs: 145, 146, 147, 148, 149, and 150 or an amino acid sequence at least 95% identical thereto.

20 Embodiment 14: The CAR of any one of embodiments 11 to 13, wherein the transmembrane domain is isolated or derived from a polypeptide selected from the group consisting of an alpha, beta, gamma, or delta chain of the T-cell receptor, CD3 δ , CD3 ϵ , CD3 γ , CD3 ζ , CD4, CD5, CD8 α , CD9, CD16, CD22, CD27, CD28, CD33, CD37, CD45, CD64, CD80, CD86, CD134, CD137, CD152, CD154, CD278, amnionless (AMN), and 25 programmed cell death 1 (PDCD1).

Embodiment 15: The CAR of any one of embodiments 11 to 14, wherein the transmembrane domain comprises an amino acid sequence set forth in any one of SEQ ID NOs: 151, 152, 153, 154, 155, 156, and 157 or an amino acid sequence at least 95% identical thereto.

30 Embodiment 16: The CAR of any one of embodiments 11 to 15, wherein the one or more intracellular signaling domains comprises a primary signaling domain isolated or derived from a polypeptide selected from the group consisting of FcR γ , FcR β , CD3 γ , CD3 δ , CD3 ϵ , CD3 ζ , CD22, CD79a, CD79b, and CD66d.

Embodiment 17: The CAR of any one of embodiments 11 to 16, wherein the one or more intracellular signaling domains comprises a primary signaling domain isolated from CD3 ζ .

Embodiment 18: The CAR of embodiment 17, wherein the primary signaling domain
5 comprises an amino acid sequence set forth in SEQ ID NO: 158 or an amino acid sequence at least 95% identical thereto.

Embodiment 19: The CAR of any one of embodiments 11 to 18, wherein the one or more intracellular signaling domains comprises a costimulatory signaling domain isolated or derived from a polypeptide selected from the group consisting of TLR1, TLR2, TLR3, TLR4,
10 TLR5, TLR6, TLR7, TLR8, TLR9, TLR10, CARD11, CD2, CD7, CD27, CD28, CD30, CD40, ICAM, CD83, CD94, CD134 (OX40), CD137 (4-1BB), CD278 (ICOS), DAP10, LAT, SLP76, TRAT1, TNFR2, TNFRS14, TNFRS18, TNFRS25, and ZAP70.

Embodiment 20: The CAR of any one of embodiments 11 to 19, wherein the one or more intracellular signaling domains comprises a costimulatory signaling domain comprising
15 an amino acid sequence set forth in any one of SEQ ID NOs: 159, 160, 161, 162, 163, and 164 or an amino acid sequence at least 95% identical thereto.

Embodiment 21: A CAR comprising an antibody or antigen binding fragment thereof comprises the amino acid sequence set forth in any one of SEQ ID NOs: 39, 59, 70, 90, 101, or 117; a spacer domain comprising the amino acid sequence set forth in any one of SEQ ID
20 NOs: 145, 146, and 148 or an amino acid sequence at least 95% identical thereto; a transmembrane domain comprising the amino acid sequence set forth in SEQ ID NOs: 151 or 153; one or more intracellular signaling domains comprising a costimulatory signaling domain comprising an amino acid sequence set forth in any one of SEQ ID NOs: 159, 160, and 162 or an amino acid sequence at least 95% identical thereto and further comprising a
25 primary signaling domain comprising an amino acid sequence set forth in SEQ ID NO: 158 or an amino acid sequence at least 95% identical thereto.

Embodiment 22: A CAR comprising the amino acid sequence set forth in any one of SEQ ID NOs: 165-860.

Embodiment 23: A CAR comprising the amino acid sequence set forth in any one of
30 SEQ ID NOs: 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, and 283.

Embodiment 24: A CAR comprising the amino acid sequence set forth in any one of SEQ ID NOs: 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, and 380.

Embodiment 25: A CAR comprising the amino acid sequence set forth in any one of
5 SEQ ID NOs: 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, and 452.

Embodiment 26: A CAR comprising the amino acid sequence set forth in any one of SEQ ID NOs: 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, and 548.

10 Embodiment 27: A CAR comprising the amino acid sequence set forth in any one of SEQ ID NOs: 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, and 620.

Embodiment 28: A CAR comprising the amino acid sequence set forth in any one of SEQ ID NOs: 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707,
15 708, 709, 710, 711, 712, 713, 714, 715, and 716.

Embodiment 29: The CAR of any one of embodiments 11 to 28, further comprising a signal peptide.

Embodiment 30: The CAR of embodiment 29, wherein the signal peptide comprises an amino acid sequence set forth in any one of SEQ ID NOs: 861, 862, 863, 864, 865, 866,
20 867, 868, 869, 870, 871, 872, and 873.

Embodiment 31: A polynucleotide encoding a CAR, comprising a polynucleotide sequence set forth in any one of SEQ ID NOs: 905-924.

Embodiment 32: A polynucleotide encoding a signal peptide and a CAR comprising a polynucleotide sequence set forth in any one of SEQ ID NOs: 925-944.

25 Embodiment 33: A polynucleotide encoding the antibody or antigen binding fragment thereof of any one of embodiments 1 to 5, the bispecific antibody of embodiment 6 or embodiment 7, the antibody conjugate of any one of embodiments 8 to 10, or the CAR of any one of embodiments 11 to 30.

Embodiment 34: A polynucleotide encoding or comprising a promoter operably
30 linked to a polynucleotide of any one of embodiments 31 to 33.

Embodiment 35: The polynucleotide of embodiment 34, wherein the promoter comprises the polynucleotide sequence set forth in any one of SEQ ID NOs: 980, 981, 982, 983, 984, and 985.

Embodiment 36: The polynucleotide of embodiment 34 or embodiment 35, further comprising a post-transcriptional response element.

Embodiment 37: The polynucleotide of embodiment 36, wherein the post-transcriptional response element comprises the polynucleotide sequence set forth in any one of SEQ ID NOs: 945, 946, and 947.

Embodiment 38: A DNA comprising the polynucleotide sequence of any one of embodiments 31 to 37.

Embodiment 39: An RNA encoded by the polynucleotide sequence of any one of embodiments 31 to 37.

Embodiment 40: A vector comprising the polynucleotide of any one of embodiments 31 to 39.

Embodiment 41: A vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 950 operably linked to a polynucleotide encoding a signal peptide and a chimeric antigen receptor comprising an anti-BCMA antibody or antigen binding fragment thereof comprising an amino acid set forth in any one of SEQ ID NOs: 11-144, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

Embodiment 42: A vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 950 operably linked to a polynucleotide encoding a signal peptide and a chimeric antigen receptor comprising an anti-BCMA antibody or antigen binding fragment thereof comprising an amino acid set forth in any one of SEQ ID NOs: 20, 30, 39, 50, 59, 70, 80, 90, 100, 101, 105, 109, 113, 117, 121, 125, 129, 133, 137, and 141, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

Embodiment 43: A vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 950 operably linked to a polynucleotide encoding a signal peptide and a chimeric antigen receptor comprising an amino acid set forth in any one of SEQ ID NOs: 165-860, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

Embodiment 44: A vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 950 operably linked to a polynucleotide encoding a signal peptide and a chimeric antigen receptor comprising an amino acid set forth in any one of SEQ ID NOs: 189, 237, 261, 333, 357, 429, 477, 525, 573, 597, 621, 645, 669, 693, 717, 741, 765,

789, 813, and 837, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

Embodiment 45: A vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 950 operably linked to a polynucleotide comprising a polynucleotide sequence set forth in SEQ ID NO: 904 and a polynucleotide sequence set forth in any one of SEQ ID NOs: 905-924, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

Embodiment 46: A vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 950 operably linked to a polynucleotide comprising a polynucleotide sequence set forth in any one of SEQ ID NOs: 925-944, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

Embodiment 47: A vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 949 operably linked to a polynucleotide encoding a signal peptide and a chimeric antigen receptor comprising an anti-BCMA antibody or antigen binding fragment thereof comprising an amino acid set forth in any one of SEQ ID NOs: 11-144, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

Embodiment 48: A vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 949 operably linked to a polynucleotide encoding a signal peptide and a chimeric antigen receptor comprising an anti-BCMA antibody or antigen binding fragment thereof comprising an amino acid set forth in any one of SEQ ID NOs: 20, 30, 39, 50, 59, 70, 80, 90, 100, 101, 105, 109, 113, 117, 121, 125, 129, 133, 137, and 141, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

Embodiment 49: A vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 949 operably linked to a polynucleotide encoding a signal peptide and a chimeric antigen receptor comprising an amino acid set forth in any one of SEQ ID NOs: 165-860, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

Embodiment 50: A vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 949 operably linked to a polynucleotide encoding a signal peptide

and a chimeric antigen receptor comprising an amino acid set forth in any one of SEQ ID NOs: 189, 237, 261, 333, 357, 429, 477, 525, 573, 597, 621, 645, 669, 693, 717, 741, 765, 789, 813, and 837, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

5 Embodiment 51: A vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 949 operably linked to a polynucleotide comprising a polynucleotide sequence set forth in SEQ ID NO: 904 and a polynucleotide sequence set forth in any one of SEQ ID NOs: 905-924, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs:
10 945-947.

 Embodiment 52: A vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 949 operably linked to a polynucleotide comprising a polynucleotide sequence set forth in any one of SEQ ID NOs: 925-944, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in
15 any one of SEQ ID NOs: 945-947.

 Embodiment 53: The vector of embodiment any one of embodiments 40 to 52, wherein the vector is an expression vector.

 Embodiment 54: The vector of embodiment any one of embodiments 40 to 52, wherein the vector is a transfer plasmid or viral vector.

20 Embodiment 55: The vector of embodiment any one of embodiments 40 to 52, wherein the vector is a plasmid.

 Embodiment 56: The vector of embodiment any one of embodiments 40 to 54, wherein the vector is a viral vector selected from the group consisting of an adenoviral (Ad) vector, an adeno-associated virus (AAV) vector, a herpes simplex virus (HSV) vector, a
25 parvovirus vector, a rhabdovirus vector, a vesiculovirus vector, a paramyxovirus vector, a morbillivirus vector, a henipavirus vector, an alphavirus vector, a flavivirus vector, a retroviral vector, and a lentiviral vector (LVV).

 Embodiment 57: The vector of embodiment 56, wherein the lentiviral vector is engineered or derived from the genome of a lentivirus selected from the group consisting of:
30 HIV (HIV type 1 or HIV type 2); visna-maedi virus (VMV); caprine arthritis-encephalitis virus (CAEV); equine infectious anemia virus (EIAV); feline immunodeficiency virus (FIV); bovine immune deficiency virus (BIV); and simian immunodeficiency virus (SIV).

Embodiment 58: A lentiviral vector comprising: a 5' long terminal repeat (LTR) comprising R and U5 regions; a Psi (Ψ) packaging signal; a cPPT/FLAP; an export element; a polynucleotide encoding or comprising a promoter operably linked to a polynucleotide sequence set forth in SEQ ID NO: 904 and a polynucleotide sequence set forth in any one of
5 SEQ ID NOs: 905-924; optionally a WPRE; a 3' LTR comprising U3 and R regions; a polyadenylation signal, and a poly(A) tail.

Embodiment 59: A lentiviral vector comprising: a 5' long terminal repeat (LTR) comprising R and U5 regions; a Psi (Ψ) packaging signal; a cPPT/FLAP; an export element; a polynucleotide encoding or comprising a promoter operably linked to a polynucleotide
10 sequence set forth in any one of SEQ ID NOs: 925-944; optionally a WPRE; a 3' LTR comprising U3 and R regions; a polyadenylation signal, and a poly(A) tail.

Embodiment 60: An RNA comprising: a 5' long terminal repeat (LTR) comprising R and U5 regions; a Psi (Ψ) packaging signal; a cPPT/FLAP; an export element; a polynucleotide encoding a promoter operably linked to a polynucleotide sequence set forth
15 in SEQ ID NO: 904 and a polynucleotide sequence set forth in any one of SEQ ID NOs: 905-924; optionally a WPRE; a 3' LTR comprising U3 and R regions; a polyadenylation signal, and optionally a poly(A) tail.

Embodiment 61: An RNA comprising: a 5' long terminal repeat (LTR) comprising R and U5 regions; a Psi (Ψ) packaging signal; a cPPT/FLAP; an export element; a polynucleotide encoding a promoter operably linked to a polynucleotide sequence set forth
20 in any one of SEQ ID NOs: 925-944; optionally a WPRE; a 3' LTR comprising U3 and R regions; a polyadenylation signal, and optionally a poly(A) tail.

Embodiment 62: The lentiviral vector of embodiments 58 or 59, wherein the vector encodes a promoter sequence set forth in SEQ ID NO: 949 or 950.

25 Embodiment 63: The RNA of embodiments 60 or 61, wherein the RNA encodes a promoter sequence set forth in SEQ ID NO: 949 or 950.

Embodiment 64: A recombinant lentivirus comprising one or more copies of the lentiviral vector of any one of embodiments 58-60 or the RNA of any one of embodiments 61-63.

30 Embodiment 65: A composition comprising the antibody or antigen binding fragment thereof of any one of embodiments 1 to 5, the bispecific antibody of embodiment 6 or embodiment 7, the antibody conjugate of any one of embodiments 8 to 10, the CAR of any one of embodiments 11 to 30, the polynucleotide of any one of embodiments 31 to 39,

the vector of any one of embodiments 40 to 60, the RNA of any one of embodiments 61-63, or the recombinant lentivirus of embodiment 64.

5 All publications, patent applications, and issued patents cited in this specification are herein incorporated by reference as if each individual publication, patent application, or issued patent were specifically and individually indicated to be incorporated by reference.

10 Although the foregoing embodiments have been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to one of ordinary skill in the art in light of the teachings contemplated herein that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims. The following examples are provided by way of illustration only and not by way of limitation. Those of skill in the art will readily recognize a variety of noncritical parameters that could be changed or modified to yield essentially similar results.

15

K. EXAMPLES

EXAMPLE 1RECOMBINANT LENTIVIRUS DELIVERS
FUNCTIONAL ANTI-BCMA CARs TO T CELLS

5 Recombinant T cell specific lentiviral particles with a viral envelope expressing a mutated viral envelope glycoprotein(fusogen) and a non-viral membrane bound tropism molecule and harboring a lentiviral vector encoding an anti-BCMA CAR were generated. Figure 1.

HEK293T cells were transfected with plasmids encoding a non-viral membrane
10 bound tropism molecule comprising an anti-CD3 scFv fused to a CD8 α hinge and transmembrane domain; a mutant VSIV-G fusogen comprising K47Q and R354A amino acid substitutions; lentiviral GAG/POL; lentiviral REV; and a transfer plasmid encoding a lentiviral vector comprising an MNDU3 promoter operably linked to a polynucleotide encoding a CD8 α signal peptide and an anti-BCMA CAR and a WPRE element operably
15 linked to the 3' end of the polynucleotide encoding the anti-BCMA CAR.

Table 10 lists the recombinant lentivirus (LV) reference number and the corresponding SEQ ID NOs of the amino acid sequences of the anti-BCMA CARs and their CARchitectures.

Table 10

LV Ref.	SEQ ID NO.	anti-BCMA binding domain	Hinge	TM	Costim	Primary
LV 1	189	scFv	CD8 α	CD8 α	CD137	CD3 ζ
LV 2	237	scFv	CD8 α	CD8 α	CD137	CD3 ζ
LV 3	261	scFv	CD8 α	CD8 α	CD137	CD3 ζ
LV 4	333	scFv	CD8 α	CD8 α	CD137	CD3 ζ
LV 5	357	scFv	CD8 α	CD8 α	CD137	CD3 ζ
LV 6	429	scFv	CD8 α	CD8 α	CD137	CD3 ζ
LV 7	477	scFv	CD8 α	CD8 α	CD137	CD3 ζ
LV 8	525	scFv	CD8 α	CD8 α	CD137	CD3 ζ
LV 9	597	VHH	CD8 α	CD8 α	CD137	CD3 ζ
LV 10	621	VHH	CD8 α	CD8 α	CD137	CD3 ζ
LV 11	645	VHH	CD8 α	CD8 α	CD137	CD3 ζ
LV 12	669	VHH	CD8 α	CD8 α	CD137	CD3 ζ
LV 13	693	VHH	CD8 α	CD8 α	CD137	CD3 ζ
LV 14	717	VHH	CD8 α	CD8 α	CD137	CD3 ζ
LV 15	741	VHH	CD8 α	CD8 α	CD137	CD3 ζ
LV 16	789	VHH	CD8 α	CD8 α	CD137	CD3 ζ
LV 17	813	VHH	CD8 α	CD8 α	CD137	CD3 ζ
LV 18	837	VHH	CD8 α	CD8 α	CD137	CD3 ζ

LV 19	NA	scFv	CD8α	CD8α	CD137	CD3ζ
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Jurkat Functional Titer

1 x 10⁵ Jurkat cells were plated in each well of a 96-well plate. Cells were transduced with recombinant lentiviruses LV 1 to LV 18 that harbor novel anti-BCMA CARs and LV 19, which harbors a control anti-BCMA CAR obtained from the literature. Seven days post-transduction, Jurkat cells were harvested and stained with a recombinant, phycoerythrin (PE) labeled, BCMA extracellular domain-FC fusion protein (BCMA-PE) and analyzed by flow cytometry. Functional titer, expressed as the number of transducing units (TU) per mL, was determined by measuring the number of transduced Jurkat cells. Figure 2A.

Anti-BCMA CAR Expression

5 x 10⁵ human PBMCs were plated in each well of a 24-well plate. Cells were transduced with recombinant lentiviruses LV 1 to LV 19 at a MOI 2 based on the Jurkat functional titer, or a 0.5 mL volumetric transduction if MOI 2 was not achievable. Seven days post-transduction, PBMCs were harvested and stained with BCMA-PE and analyzed by flow cytometry to assess the percentage of anti-BCMA CAR expressing cells. Figure 2B.

Anti-BCMA CAR Activity

5 x 10⁴ PBMCs transduced with recombinant lentiviruses LV 1 to LV 19 were co-cultured with 5 x 10⁴ high BCMA-expressing tumor cells (RPMI-8226) or 5 x 10⁴ low BCMA-expressing tumor cells (Daudi) for 24 hours. Anti-BCMA CAR activity was assessed by harvesting co-culture supernatants and measuring IFNγ levels using a Meso Scale Discovery (MSD®) assay. The percentage of anti-BCMA CAR positive cells was plotted against IFNγ levels produced in co-culture. Figure 2D.

Summary

These data indicate that the recombinant T cell specific lentiviral particles harboring anti-BCMA CARs (LV 1 to LV 18) are able to transduce CD3 expressing cells, that anti-BCMA CARs are expressed on PBMCs transduced with LV 1 to LV 18 and that the transduced PBMCs express anti-BCMA CARs that recognize high or low BCMA-expressing cells and produce IFNγ in response to binding antigen.

EXAMPLE 2

LENTIVIRAL VECTOR ARCHITECTURE AND ANTI-BCMA CAR EXPRESSION AND
FUNCTION

Recombinant T cell specific lentiviral particles with a viral envelope expressing a
5 mutated viral envelope glycoprotein(fusogen) and a non-viral membrane bound tropism
molecule and harboring a lentiviral vector encoding various promoters, anti-BCMA CARs,
and either no posttranscriptional response element (PRE) or a wild-type WPRE, or a mutated
WPRE.

HEK293T cells were transfected with plasmids encoding a non-viral membrane
10 bound tropism molecule comprising an anti-CD3 scFv fused to a CD8 α hinge and
transmembrane domain; a mutant VSIV-G fusogen comprising K47Q and R354A amino
acid substitutions; lentiviral GAG/POL; lentiviral REV; and a transfer plasmid encoding a
lentiviral vector comprising either an MNDU3 promoter (SEQ ID NO: 950), an SFFV
promoter (SEQ ID NO: 952), or an EF1 α promoter (SEQ ID NO: 949) operably linked to a
15 polynucleotide encoding a CD8 α signal peptide and an anti-BCMA CAR and either no
posttranscriptional response element or a wild-type WPRE (SEQ ID NO: 945) or a mutated
WPRE (SEQ ID NO: 946) operably linked to the 3' end of the polynucleotide encoding the
anti-BCMA CAR.

Table 11 lists the recombinant lentivirus reference number and the corresponding
20 SEQ ID NOs of the amino acid sequences of the anti-BCMA CARs and the different
lentiviral vector architectures.

Table 11

Ref.	SEQ ID NO.	Promoter	WPRE
LV 3.1	261	MNDU3	wild-type
LV 3.2	261	MNDU3	no PRE
LV 3.3	261	MNDU3	mutant WPRE
LV 3.4	261	SFFV	wild-type
LV 3.5	261	SFFV	no PRE
LV 3.6	261	SFFV	mutant WPRE
LV 3.7	261	EF1 α	wild-type
LV 3.8	261	EF1 α	no PRE
LV 3.9	261	EF1 α	mutant WPRE
LV 5.1	357	MNDU3	wild-type
LV 5.2	357	MNDU3	no PRE
LV 5.3	357	MNDU3	mutant WPRE
LV 5.4	357	SFFV	wild-type
LV 5.5	357	SFFV	no PRE
LV 5.6	357	SFFV	mutant WPRE
LV 5.7	357	EF1 α	wild-type

LV 5.8	357	EF1 α	no PRE
LV 5.9	357	EF1 α	mutant WPRE
LV 6.1	429	MNDU3	wild-type
LV 6.2	429	MNDU3	no PRE
LV 6.3	429	MNDU3	mutant WPRE
LV 6.4	429	SFFV	wild-type
LV 6.5	429	SFFV	no PRE
LV 6.6	429	SFFV	mutant WPRE
LV 6.7	429	EF1 α	wild-type
LV 6.8	429	EF1 α	no PRE
LV 6.9	429	EF1 α	mutant WPRE
LV 8.1	525	MNDU3	wild-type
LV 8.2	525	MNDU3	no PRE
LV 8.3	525	MNDU3	mutant WPRE
LV 8.4	525	SFFV	wild-type
LV 8.5	525	SFFV	no PRE
LV 8.6	525	SFFV	mutant WPRE
LV 8.7	525	EF1 α	wild-type
LV 8.8	525	EF1 α	no PRE
LV 8.9	525	EF1 α	mutant WPRE
LV 9.1	597	MNDU3	wild-type
LV 9.2	597	MNDU3	no PRE
LV 9.3	597	MNDU3	mutant WPRE
LV 9.4	597	SFFV	wild-type
LV 9.5	597	SFFV	no PRE
LV 9.6	597	SFFV	mutant WPRE
LV 9.7	597	EF1 α	wild-type
LV 9.8	597	EF1 α	no PRE
LV 9.9	597	EF1 α	mutant WPRE
LV 13.1	693	MNDU3	wild-type
LV 13.2	693	MNDU3	no PRE
LV 13.3	693	MNDU3	mutant WPRE
LV 13.4	693	SFFV	wild-type
LV 13.5	693	SFFV	no PRE
LV 13.6	693	SFFV	mutant WPRE
LV 13.7	693	EF1 α	wild-type
LV 13.8	693	EF1 α	no PRE
LV 13.9	693	EF1 α	mutant WPRE
LV19		MNDU3	no PRE

Infectious Titer

1 x 10⁵ Jurkat cells were plated in each well of a 96-well plate and transduced with the recombinant lentiviruses listed in Table 11 including LV 19, which harbors a lentiviral vector encoding a control anti-BCMA CAR obtained from the literature. Three days post-transduction, the cells were passaged. Seven days post-transduction the cells were harvested. Genomic DNA was isolated and purified from the harvested cells and used in a quantitative PCR (qPCR) assay to determine vector copy number (VCN) and subsequently, IU/mL. Figure 3A.

All lentiviral vector architectures examined produced infectious titers and were subsequently used to transduce PBMCs.

VCN and Anti-BCMA CAR Expression

5 5×10^5 human PBMCs were plated in each well of a 24-well plate and transduced with volume matched recombinant lentiviruses listed in Table 11.

Four days post-transduction, PBMCs were passaged to a 24-well GREX plate. Seven days post-transduction, PBMCs were harvested, one aliquot of cells was stained with BCMA-PE and analyzed by flow cytometry to assess the percentage of anti-BCMA CAR expressing cells and another aliquot was used to isolate and purify genomic DNA for a
10 quantitative PCR (qPCR) assay to determine vector copy number (VCN). Figure 3B.

These data show that different lentiviral vector architectures tested in combination with different anti-BCMA CARs result in a spectrum of transduction and anti-BCMA CAR expression.

Anti-BCMA CAR Activity

15 5×10^5 human PBMCs were plated in each well of a 24-well plate and transduced with recombinant lentiviruses listed in Table 11 that have the following lentiviral vector architectures: MNDU3 promoter and wild-type WPRE, MNDU3 promoter and a mutated WPRE, SFFV promoter and a mutated WPRE, and EF1 α promoter and no WPRE. PBMCs were transduced at an MOI of 1 (based on IU/mL determined in Jurkat cells), except for LV
20 3.6, LV 3.8, LV 9.8, and LV 13.8, in which volume matched lentivirus was used. Four days post-transduction, PBMCs were passaged to a 24-well GREX plate. Seven days post-transduction, PBMCs were harvested, one aliquot of cells was stained with BCMA-PE and analyzed by flow cytometry to assess the number of anti-BCMA CAR expressing cells and another aliquot was used in co-culture assays to assess anti-BCMA CAR function.

25 5×10^4 transduced PBMCs were co-cultured with 5×10^4 RPMI-8226 cells for 24 hours. Anti-BCMA CAR activity was assessed by harvesting PBMC/RPMI-8226 cell co-culture supernatants and measuring IFN γ and IL-2 levels using an MSD assay. IFN γ and IL-2 levels produced in co-culture were plotted against the percentage of anti-BCMA CAR positive cells. Figures 3C and 3D.

30 Antigen independent anti-BCMA CAR activity was assessed by culturing 5×10^4 transduced PBMCs in the absence of target cells for 24 hours. After 24 hours, the supernatants were harvested and IFN γ levels measured using an MSD assay. IFN γ levels

were plotted against lentiviral architectures used to express the anti-BCMA CARs. Figure 3E.

These data indicate that combinations of different lentiviral architectures and anti-BCMA CARs can be selected to modulate anti-BCMA CAR expression and activity. Further, the data show that PBMCs expressing the anti-BCMA CARs set forth in SEQ ID NOs: 259, 263, 266, 270, 273, and 277 show comparable or increased cell expansion and comparable or increased activity compared to the control anti-BCMA CAR and that only three combinations showed high levels of antigen independent (tonic) signaling.

Off-Target Transduction

Off-target transduction of multiple myeloma cells was evaluated in two BCMA-expressing multiple myeloma cell lines, RPMI-8226 cells and KMS-11 cells. 1×10^5 RPMI-8226 or 1×10^5 KMS-11 cells were plated in each well of a 96-well plate and treated at an MOI of 1 with recombinant lentiviruses listed in Table 11 that have the following lentiviral vector architectures, MNDU3 promoter and wild-type WPRE, MNDU3 promoter and a mutated WPRE, SFFV promoter and a mutated WPRE, and EF1 α promoter and no WPRE; LV 19; and with LV 20. LV 20 is a recombinant lentiviral particle comprising a viral envelope that expresses a non-viral membrane bound tropism molecule comprising an anti-CD3 scFv fused to a CD8 α hinge and transmembrane domain; a mutant VSIV-G fusogen comprising K47Q and R354A amino acid substitutions; and a lentiviral vector comprising an MNDU3 promoter (SEQ ID NO: 950), operably linked to a polynucleotide encoding a CD8 α signal peptide and GFP and a wild-type WPRE (SEQ ID NO: 945) operably linked to the 3' end of the polynucleotide encoding GFP.

Three days post-treatment, the cells were passaged. Seven days post-treatment, the cells were harvested and genomic DNA was isolated and purified for a qPCR assay to determine vector integration using VCN. VCN values for anti-BCMA CARs were normalized to VCN for LV 20, which expresses GFP rather than an anti-BCMA CAR.

The data show that differences in off-target multiple myeloma transduction were largely driven by the particular anti-BCMA CAR being expressed, rather than any particular lentiviral vector architecture. Several architectures used to express the anti-BCMA CARs in LV 3, LV 5, LV 6, LV 8, and LV 9 showed low levels of off-target transduction that were comparable to or less than LV 19, which expresses a control anti-BCMA CAR. In contrast,

LV 13 exhibited the highest rates of off-target transduction compared to other LVs. Figure 3F.

EXAMPLE 3

IN VIVO ADMINISTERED LENTIVIRUS DEMONSTRATES ANTI-TUMOR EFFICACY
IN A MULTIPLE MYELOMA MOUSE MODEL

The anti-tumor efficacy of *in vivo* administered recombinant lentiviral particles comprising an envelope that expresses an anti-CD3-based tropism molecule and a mutant VSIV-G fusogen and a lentiviral vector encoding an anti-BCMA CAR was investigated in multiple myeloma mouse models.

Recombinant lentivirus for *in vivo* administration was produced by transient transfection of HEK293T cells with plasmids encoding a non-viral membrane bound tropism molecule comprising an anti-CD3 scFv fused to a CD8α hinge and transmembrane domain; a mutant VSIV-G fusogen comprising K47Q and R354A amino acid substitutions; lentiviral GAG/POL; lentiviral REV; and a transfer plasmid encoding a lentiviral vector comprising:

(i) an MNDU3 promoter (SEQ ID NO: 950) operably linked to a polynucleotide encoding a CD8α signal peptide and an anti-BCMA CAR, and a wild-type WPRE (SEQ ID NO: 945) operably linked to the 3' end of the polynucleotide encoding the anti-BCMA CAR; (ii) an MNDU3 promoter (SEQ ID NO: 950) operably linked to a polynucleotide encoding a CD8α signal peptide and an anti-BCMA CAR, and a mutated WPRE (SEQ ID NO: 946) operably linked to the 3' end of the polynucleotide encoding the anti-BCMA CAR; (iii) an SFFV promoter (SEQ ID NO: 952) operably linked to a polynucleotide encoding a CD8α signal peptide and an anti-BCMA CAR, and a mutated WPRE (SEQ ID NO: 946) operably linked to the 3' end of the polynucleotide encoding the anti-BCMA CAR; or (iv) an EF1α promoter (SEQ ID NO: 949) operably linked to a polynucleotide encoding a CD8α signal peptide and an anti-BCMA CAR without a PRE.

The recombinant lentivirus reference number, the SEQ ID NO of the anti-BCMA CAR polypeptide and the corresponding lentiviral architectures shown in Table 12 were used in this Example.

Table 12

Ref.	SEQ ID NO.	Promoter	WPRE
LV 3.1	261	MNDU3	wild-type
LV 3.3	261	MNDU3	mutant WPRE

LV 3.6	261	SFFV	mutant WPRE
LV 3.8	261	EF1 α	no PRE
LV 5.1	357	MNDU3	wild-type
LV 5.3	357	MNDU3	mutant WPRE
LV 5.6	357	SFFV	mutant WPRE
LV 5.8	357	EF1 α	no PRE
LV 6.1	429	MNDU3	wild-type
LV 6.3	429	MNDU3	mutant WPRE
LV 6.6	429	SFFV	mutant WPRE
LV 6.8	429	EF1 α	no PRE
LV 8.1	525	MNDU3	wild-type
LV 8.3	525	MNDU3	mutant WPRE
LV 8.6	525	SFFV	mutant WPRE
LV 8.8	525	EF1 α	no PRE
LV 9.1	597	MNDU3	wild-type
LV 9.3	597	MNDU3	mutant WPRE
LV 9.6	597	SFFV	mutant WPRE
LV 9.8	597	EF1 α	no PRE
LV 13.1	693	MNDU3	wild-type
LV 13.3	693	MNDU3	mutant WPRE
LV 13.6	693	SFFV	mutant WPRE
LV 13.8	693	EF1 α	no PRE

Ex vivo anti-BCMA CAR T cells were also prepared. Briefly, HEK293T cells were transiently transfected with plasmids encoding a wild-type VSIV-G fusogen; lentiviral GAG/POL; lentiviral REV; and a transfer plasmid encoding a lentiviral vector comprising an MNDU3 promoter operable linked to a CD8 α signal peptide and a control anti-BCMA CAR obtained from the literature (SEQ ID NO: 954), and a wild-type WPRE (SEQ ID NO: 945) operably linked to the 3' end of the polynucleotide encoding the anti-BCMA CAR. PBMCs were then transduced with the recombinant lentivirus and cultured for 7 days to generate anti-BCMA CAR T cells.

First Daudi Model Study

NSG mice were intravenously injected with 2×10^6 Daudi cells labeled with firefly luciferase. After four days, four out of five groups of mice were intravenously administered 1×10^6 human PBMCs. The next day mice that received the 1×10^6 human PBMCs were administered vehicle control (DMEM); or 2.2×10^8 IU of LV 3.1, LV 6.1, LV 8.1, or LV 13.1. Mice that were not administered PBMCs were administered 5×10^6 *ex vivo* anti-BCMA CAR T cells. All groups of mice then received three doses of 2×10^5 IU recombinant human IL-2 at 6, 24, and 48 hours post LV administration. Tumor volume was measured by using a bioluminescence imaging system.

Tumor size increased in mice treated with vehicle. Mice treated with *ex vivo* anti-BCMA CAR T cells and *in vivo* with LV anti-BCMA CAR experienced tumor regression. Figure 4A.

Second Daudi Model Study

5 NSG mice were intravenously injected with 2×10^6 Daudi cells labeled with firefly luciferase. After four days, eight out of nine groups of mice were intravenously administered 1×10^6 human PBMCs. The next day mice that received the 1×10^6 human PBMCs were administered vehicle control (DMEM); 1.25×10^8 IU of LV 3.1, LV 6.1, LV 6.3, LV 8.1, LV 9.3, LV 9.6, or LV 13.8; or 5.6×10^7 IU of LV 6.8. Mice that were not administered PBMCs
10 were administered 5×10^6 *ex vivo* anti-BCMA CAR T cells. All groups of mice then received three doses of 2×10^5 IU recombinant human IL-2 at 6, 24, and 48 hours post LV administration. Tumor volume was measured by using a bioluminescence imaging system.

Tumor size increased in mice treated with vehicle. Mice treated with *ex vivo* anti-BCMA CAR T cells and *in vivo* with some LV anti-BCMA CARs experienced mild control
15 of tumor growth, whereas LV 6.8 and LV 13.8 experienced durable tumor regression. Figure 4B.

Third Daudi Model Study

NSG mice were intravenously injected with 2×10^6 Daudi cells labeled with firefly luciferase. After four days, eight out of nine groups of mice were intravenously administered
20 1×10^6 human PBMCs. The next day mice that received the 1×10^6 human PBMCs were administered vehicle control (DMEM); 1.25×10^8 IU of LV 3.3, LV 3.6, LV 8.3, LV 8.6, LV 8.8, LV 13.3, or LV 13.6; or 5.6×10^7 IU of LV 6.8. Mice that were not administered PBMCs were administered 5×10^6 *ex vivo* anti-BCMA CAR T cells. All groups of mice then received
25 three doses of 2×10^5 IU recombinant human IL-2 at 6, 24, and 48 hours post LV administration. Tumor volume was measured by using a bioluminescence imaging system.

Tumor size increased in mice treated with vehicle. Mice treated with *ex vivo* anti-BCMA CAR T cells and *in vivo* with some LV anti-BCMA CARs experienced mild control
of tumor growth, whereas LV 6.8 and LV 8.8 experienced durable tumor regression. Figure 4C.

30 *First RPMI Model Study*

NOD scid gamma (NSG) mice were subcutaneously injected with 1×10^6 RPMI-8226 cells (a BCMA positive tumor cell line). Tumors were allowed to grow to a size of about 110mm^3 to 140mm^3 (about two and a half weeks).

Five out of six groups of mice were then intravenously administered 1×10^6 human PBMCs. The next day, mice that received the 1×10^6 human PBMCs were administered vehicle control (DMEM); 5.0×10^7 IU of LV 6.3, LV 6.8, LV 8.3, or LV 8.8. The sixth group of mice was administered 2×10^6 unmodified *ex vivo* anti-BCMA CAR T cells. All groups of mice then received three doses of 2×10^5 IU recombinant human IL-2 at 6, 24, and 48 hours post LV administration. Tumor volume was measured externally using calipers and mice were euthanized at pre-determined humane endpoints based on tumor size and body condition.

Tumor size increased in mice treated with vehicle control. Mice treated with LV 6.3 experienced moderate tumor regression, whereas mice treated with *ex vivo* anti-BCMA CAR T cells or *in vivo* with LV 6.8, LV 8.3, or LV 8.8 experienced complete and durable tumor regression. Figure 4D.

Mice that were not administered PBMCs were administered 5×10^6 *ex vivo* anti-BCMA CAR T cells. All groups of mice then received three doses of 2×10^5 IU recombinant human IL-2 at 6, 24, and 48 hours post LV administration.

Second RPMI Model Study

NOD scid gamma (NSG) mice were subcutaneously injected with 1×10^6 RPMI-8226 cells (a BCMA positive tumor cell line). Tumors were allowed to grow to a size of about 110mm^3 to 140mm^3 (about two and a half weeks).

Four out of five groups of mice were then intravenously administered 1×10^6 human PBMCs. The next day, mice that received the 1×10^6 human PBMCs were administered vehicle control (DMEM); 1.25×10^7 IU of LV 6.8, 5.0×10^7 IU of LV 6.8, or 1.25×10^8 IU of LV 6.8. The fifth group of mice was administered 2×10^6 unmodified *ex vivo* anti-BCMA CAR T cells. All groups of mice then received three doses of 2×10^5 IU recombinant human IL-2 at 6, 24, and 48 hours post LV administration. Tumor volume was measured externally using calipers and mice were euthanized at pre-determined humane endpoints based on tumor size and body condition.

Tumor size increased in mice treated with vehicle control. Mice treated with all three doses of LV 6.8 experienced dose-dependent but complete and durable tumor regression.

Mice treated with *ex vivo* anti-BCMA CAR T cells also experienced complete and durable tumor regression. Figure 4E.

Third RPMI Model Study

NOD scid gamma (NSG) mice were subcutaneously injected with 1×10^6 RPMI-8226 cells (a BCMA positive tumor cell line). Tumors were allowed to grow to a size of about 110mm^3 to 140mm^3 (about two and a half weeks).

Three out of four groups of mice were then intravenously administered 1×10^6 human PBMCs. The next day, mice that received the 1×10^6 human PBMCs were administered vehicle control (DMEM); 5.0×10^7 IU of LV 6.3 or 1.25×10^8 IU of LV 6.3. The fourth group of mice was administered 2×10^6 unmodified *ex vivo* anti-BCMA CAR T cells. All groups of mice then received three doses of 2×10^5 IU recombinant human IL-2 at 6, 24, and 48 hours post LV administration. Tumor volume was measured externally using calipers and mice were euthanized at pre-determined humane endpoints based on tumor size and body condition.

Tumor size increased in mice treated with vehicle control. Mice treated with both doses of LV 6.3 experienced dose-dependent tumor regression. Mice treated with *ex vivo* anti-BCMA CAR T cells experienced complete and durable tumor regression. Figure 4F.

Fourth Daudi Model Study

NSG mice were intravenously injected with 2×10^6 Daudi cells labeled with firefly luciferase. After four days, four out of five groups of mice were intravenously administered 1×10^6 human PBMCs. The next day mice that received the 1×10^6 human PBMCs were administered vehicle control (DMEM); 1.25×10^8 IU of LV 6.1 or LV6.3; or 5.6×10^7 IU of LV 6.8. Mice that were not administered PBMCs were administered 5×10^6 *ex vivo* anti-BCMA CAR T cells. All groups of mice then received three doses of 2×10^5 IU recombinant human IL-2 at 6, 24, and 48 hours post LV administration. Tumor volume was measured by using a bioluminescence imaging system.

Tumor size increased in mice treated with vehicle. Mice treated with *ex vivo* anti-BCMA CAR T cells and *in vivo* with LV 6.1 and LV 6.3 experienced mild control of tumor growth, whereas LV 6.8 experienced complete and durable tumor regression. Figure 4G.

EXAMPLE 4

COMPARATIVE ANTI-TUMOR EFFICACY IN A MULTIPLE MYELOMA MOUSE MODEL
IN BOTH *IN VIVO* AND *EX VIVO* FORMATS

The anti-tumor efficacy of recombinant lentiviral particles comprising an envelope
5 that expresses an anti-CD3-based tropism molecule and a mutant VSIV-G fusogen and a
lentiviral vector encoding various anti-BCMA CARs was investigated in multiple myeloma
mouse models. The recombinant lentiviruses were formulated as *in vivo* administered
lentiviral particles and were also used to manufacture *ex vivo* anti-BCMA CAR T cells.

Recombinant lentivirus was produced by transient transfection of HEK293T cells
10 with plasmids encoding a non-viral membrane bound tropism molecule comprising an anti-
CD3 scFv fused to a CD8α hinge and transmembrane domain; a mutant VSIV-G fusogen
comprising K47Q and R354A amino acid substitutions; lentiviral GAG/POL; lentiviral
REV; and a transfer plasmid encoding a lentiviral vector encoding an anti-BCMA CAR set
forth in SEQ ID NO: 429, SEQ ID NO: 954, or SEQ ID NO: 955 or a GFP control.

15 Table 13

SEQ ID NO:	NUCLEIC ACID SEQUENCE
954	DIVLTQSPPSLAMSLGKRATISCRASESVTILGSHLIHWYQOKPGQPPTLLIQLASNVQTG VPAFSGSGSRTDFTLTIDPVEEDDVAVYYCQSRTPRTFGGGTKLEIKGSTSGSGKPGS GEGSTKGQIQLVQSGPELKKPGETVKISCKASGYTFTDYSINWVKRAPGKGLKWMGWINTE TREPAYAYDFRGRFAFSLETSASTAYLQINNLYEDTATYFCALDYSYAMDYWGQTSVTV SSAAATTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTC GVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPPEEEEGGCELRVKFSR SADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
955	QVKLEESGGGLVQAGRSLRLSCAASEHTFSSHVMGWFRQAPGKERESVAVIGWRDISTSYA DSVKGRFTISRDNAKKTLYLQMNLSKPEDTAVYYCAARRIDAADFDSWGQGTQVTVSSGGG GSEVQLVESGGGLVQAGGSLRLSCAASGRTFTMGWFRQAPGKEREFVAAISLSPTLAYYAE SVKGRFTISRDNAKNTVVLQMNLSKPEDTALYYCAADRKSVMISIRPDYWGQGTQVTVSSSTS TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLS SLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPPEEEEGGCELRVKFSRSADAP AYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYS EIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

The recombinant lentivirus reference number, the SEQ ID NO of the anti-BCMA
CAR polypeptide and the corresponding lentiviral architectures shown in Table 12 were used
in this Example.

Table 14

Ref.	SEQ ID NO.	Promoter	WPRE
LV 6.8	429	EF1α	none
LV A	954	MNDU3	WT WPRE

LV B	955	EF1 α	none
LV19	GFP	MNDU3	none

Ex vivo anti-BCMA CAR T cells were also prepared by transducing PBMCs with the recombinant lentivirus and culturing the transduced cell for 7 days to generate anti-BCMA CAR T cells.

In vivo Daudi Model Study

5 NSG mice were intravenously injected with 2×10^6 Daudi cells labeled with firefly luciferase. After four days, four out of five groups of mice were intravenously administered 1×10^6 human PBMCs. The next day, mice that did not receive PBMCs were administered vehicle control (DMEM) and mice that received the PBMCs were administered 5.0×10^7 IU of LV 6.8, LV A, LV B, or LV 19 (GFP control). Tumor volume was measured by using a
10 bioluminescence imaging system.

Tumor size increased in mice treated with vehicle, mice treated with the GFP control, and mice treated with a lentivirus expressing an anti-BCMA CAR comprising the binding domain used in idecabtagene vicleucel. Mice treated with a lentivirus expressing an anti-BCMA CAR comprising the binding domains like those used in ciltacabtagene autoleucel
15 experienced suppression of tumor growth. Only mice treated with an anti-BCMA CAR comprising SEQ ID NO: 429 experienced tumor regression. Figure 5A.

Ex vivo Daudi Model Study

NSG mice were intravenously injected with 2×10^6 Daudi cells labeled with firefly luciferase. After five days, three out of five groups of mice were intravenously administered
20 2×10^6 human anti-BCMA CAR T cells. Mice that did not receive anti-BCMA CAR T cells were administered vehicle control (DMEM) or 2×10^6 untransduced control human T cells (UTD) and mice that received the anti-BCMA CAR T cells were administered 2×10^6 anti-BCMA CAR T cells expressing the CAR encoded by SEQ ID NO: 429, SEQ ID NO: 954 or SEQ ID NO: 955. Tumor volume was measured by using a bioluminescence imaging
25 system.

Tumor size increased in mice treated with vehicle and with untransduced control T cells. Mice treated with CAR T cells expressing an anti-BCMA CAR comprising the binding domain used in idecabtagene vicleucel showed a transient decrease in tumor burden whereas mice treated with CAR T cells expressing an anti-BCMA CAR comprising SEQ ID NO: 429

or an anti-BCMA CAR comprising the binding domains like those used in ciltacabtagene autoleucel experienced comparable and complete tumor regression. Figure 5B.

- 5 In general, in the following claims, the terms used should not be construed to limit the claims to the specific embodiments disclosed in the specification and the claims but should be construed to include all possible embodiments along with the full scope of equivalents to which such claims are entitled. Accordingly, the claims are not limited by the disclosure.

CLAIMS

What is claimed is:

1. An antibody or antigen binding fragment thereof comprising:
 - (a) a heavy chain variable region (VH) comprising a CDRH1, a CDRH2, and a CDRH3 of an antibody or antigen binding fragment thereof set forth in Table 1; a polypeptide linker; and a light chain variable region (VL) comprising a CDRL1, a CDRL2, and a CDRL3 of an antibody or antigen binding fragment thereof set forth in Table 1; or
 - (b) a VHH domain comprising a CDRH1, a CDRH2, and a CDRH3 of an antibody or antigen binding fragment thereof set forth in Table 1.
2. The antibody or antigen binding fragment thereof of claim 1, wherein:
 - (a) the VH comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 12, 13, and 14 and the VL comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 16, 17, and 18;
 - (b) the VH comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 22, 23, and 24 and the VL comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 26, 27, and 28;
 - (c) the VH comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 32, 33, and 34 and the VL comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 36, 37, and 38;
 - (d) the VH comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 42, 43, and 44 and the VL comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 46, 47, and 48;
 - (e) the VH comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 52, 53, and 54 and the VL comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 56, 57, and 58;

(f) the VH comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 62, 63, and 64 and the VL comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 66, 67, and 68;

(g) the VH comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 72, 73, and 74 and the VL comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 76, 77, and 78;

(h) the VH comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 82, 83, and 84 and the VL comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 86, 87, and 88;

(i) the VH comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 92, 93, and 94 and the VL comprises a CDRL1, a CDRL2, and a CDRL3 comprising the amino acid sequences set forth in SEQ ID NOs: 96, 97, and 98;

(j) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 102, 103, and 104;

(k) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 106, 107, and 108;

(l) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 110, 111, and 112;

(m) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 114, 115, and 116;

(n) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 118, 119, and 120;

(o) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 122, 123, and 124;

(p) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 126, 127, and 128;

(q) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 130, 131, and 132;

(r) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 134, 135, and 136;

(s) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 138, 139, and 140; or

(t) the VHH domain comprises a CDRH1, a CDRH2, and a CDRH3 comprising the amino acid sequences set forth in SEQ ID NOs: 142, 143, and 144.

3. The antibody or antigen binding fragment thereof of claim 1 or claim 2, wherein:

(a) the VH comprises the amino acid sequence set forth in SEQ ID NO: 11 and the VL comprises the amino acid sequence set forth in SEQ ID NO: 15;

(b) the VH comprises the amino acid sequence set forth in SEQ ID NO: 21 and the VL comprises the amino acid sequence set forth in SEQ ID NO: 25;

(c) the VH comprises the amino acid sequence set forth in SEQ ID NO: 31 and the VL comprises the amino acid sequence set forth in SEQ ID NO: 35;

(d) the VH comprises the amino acid sequence set forth in SEQ ID NO: 41 and the VL comprises the amino acid sequence set forth in SEQ ID NO: 45;

(e) the VH comprises the amino acid sequence set forth in SEQ ID NO: 51 and the VL comprises the amino acid sequence set forth in SEQ ID NO: 55;

(f) the VH comprises the amino acid sequence set forth in SEQ ID NO: 61 and the VL comprises the amino acid sequence set forth in SEQ ID NO: 65;

(g) the VH comprises the amino acid sequence set forth in SEQ ID NO: 71 and the VL comprises the amino acid sequence set forth in SEQ ID NO: 75;

(h) the VH comprises the amino acid sequence set forth in SEQ ID NO: 81 and the VL comprises the amino acid sequence set forth in SEQ ID NO: 85;

(i) the VH comprises the amino acid sequence set forth in SEQ ID NO: 91 and the VL comprises the amino acid sequence set forth in SEQ ID NO: 95; or

(a) the VHH domain comprises the amino acid sequence set forth in any one of SEQ ID NOs: 101, 105, 109, 113, 117, 121, 125, 129, 133, 137, and 141.

4. The antibody or antigen binding fragment thereof of any one of claims 1 to 3, wherein the polypeptide linker is selected from the group consisting of: TGEKP (SEQ ID NO: 2); (GGGGS)_n wherein n = 1, 2, 3, 4 or 5 (SEQ ID NOs: 3, 976-979);

EGKSSSGSGSESKVD (SEQ ID NO: 4); KESGSVSSEQLAQFRSLD (SEQ ID NO: 5); LRQRDGERP (SEQ ID NO: 6); LRQKDGGGGERP (SEQ ID NO: 7); LRQKD(GGGS)₂ERP (SEQ ID NO: 8), GEGTSTGSGGSGGGGAD (SEQ ID NO: 9), and GSTSGSGKPGSGEGSTKG (SEQ ID NO: 10) and variants thereof comprising an amino acid sequence 95% identical thereto.

5. The antibody or antigen binding fragment thereof of any one of claims 1 to 4, wherein the antibody or antigen binding fragment thereof comprises the amino acid sequence set forth in any one of SEQ ID NOs: 19, 20, 29, 30, 39, 40, 49, 50, 59, 60, 69, 70, 79, 80, 89, 90, 99, 100, 101, 105, 109, 113, 117, 121, 125, 129, 133, 137, and 141.

6. A bispecific antibody comprising the antibody or antigen binding fragment thereof of any one of claims 1 to 5.

7. The bispecific antibody of claim 6, further comprising an anti-CD3 antibody that binds CD3 δ , CD3 ϵ , CD3 γ , or CD3 ζ .

8. An antibody conjugate comprising the antibody or antigen binding fragment thereof of any one of claims 1 to 5.

9. The antibody conjugate of claim 8, wherein the antigen or antigen binding fragment thereof is conjugated to a cytotoxic agent.

10. The antibody conjugate of claim 8 or claim 9, wherein:

(a) the cytotoxic agent is a toxin selected from the group consisting of: saporin, diphtheria toxin, pseudomonas exotoxin A, Ricin A chain derivatives, a small molecule toxin, and combinations thereof;

(b) the cytotoxic agent is a radioisotope selected from the group consisting of: ¹³¹I, ⁹⁰Y, ¹⁷⁷Lu, ¹⁸⁸Re, ⁶⁷Cu, ²¹³Bi, ²¹¹At, and ²²⁷Ac;

(c) the cytotoxic agent is an RNA polymerase II inhibitor and/or RNA polymerase III inhibitor selected from the group consisting of: an amatoxin, α -amanitin, β -amanitin, γ -amanitin, ϵ -amanitin, amanin, amaninamide, amanullin, amanullinic acid and any functional fragments, derivatives or analogs thereof; or

(d) the cytotoxic agent is a DNA-damaging agent selected from the group consisting of: an antitubulin agent, a DNA crosslinking agent, a DNA alkylating agent and a mitotic disrupting agent.

11. A chimeric antigen receptor (CAR) comprising the antibody or antigen binding fragment thereof of any one of claims 1 to 5; a spacer domain; a transmembrane domain, and one or more intracellular signaling domains.

12. The CAR of claim 11, wherein the spacer domain comprises a hinge domain or fragment thereof selected from the group consisting of: a CD4 hinge, a CD8 β hinge, a CD8 α hinge, a CD28 hinge, a CD134 hinge, a CD137 hinge, a CD152 hinge, a CD278 hinge, an IgG1 hinge, an IgG2 hinge, an IgG3 hinge, and an IgG4 hinge.

13. The CAR of claim 11 or claim 12, wherein the spacer domain comprises an amino acid sequence set forth in any one of SEQ ID NOs: 145, 146, 147, 148, 149, and 150 or an amino acid sequence at least 95% identical thereto.

14. The CAR of any one of claims 11 to 13, wherein the transmembrane domain is isolated or derived from a polypeptide selected from the group consisting of an alpha, beta, gamma, or delta chain of the T-cell receptor, CD3 δ , CD3 ϵ , CD3 γ , CD3 ζ , CD4, CD5, CD8 α , CD9, CD16, CD22, CD27, CD28, CD33, CD37, CD45, CD64, CD80, CD86, CD134, CD137, CD152, CD154, CD278, amnionless (AMN), and programmed cell death 1 (PDCD1).

15. The CAR of any one of claims 11 to 14, wherein the transmembrane domain comprises an amino acid sequence set forth in any one of SEQ ID NOs: 151, 152, 153, 154, 155, 156, and 157 or an amino acid sequence at least 95% identical thereto.

16. The CAR of any one of claims 11 to 15, wherein the one or more intracellular signaling domains comprises a primary signaling domain isolated or derived from a polypeptide selected from the group consisting of FcR γ , FcR β , CD3 γ , CD3 δ , CD3 ϵ , CD3 ζ , CD22, CD79a, CD79b, and CD66d.

17. The CAR of any one of claims 11 to 16, wherein the one or more intracellular signaling domains comprises a primary signaling domain isolated from CD3 ζ .

18. The CAR of claim 17, wherein the primary signaling domain comprises an amino acid sequence set forth in SEQ ID NO: 158 or an amino acid sequence at least 95% identical thereto.

19. The CAR of any one of claims 11 to 18, wherein the one or more intracellular signaling domains comprises a costimulatory signaling domain isolated or derived from a polypeptide selected from the group consisting of TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9, TLR10, CARD11, CD2, CD7, CD27, CD28, CD30, CD40, ICAM, CD83, CD94, CD134 (OX40), CD137 (4-1BB), CD278 (ICOS), DAP10, LAT, SLP76, TRAT1, TNFR2, TNFRS14, TNFRS18, TNFRS25, and ZAP70.

20. The CAR of any one of claims 11 to 19, wherein the one or more intracellular signaling domains comprises a costimulatory signaling domain comprising an amino acid sequence set forth in any one of SEQ ID NOs: 159, 160, 161, 162, 163, and 164 or an amino acid sequence at least 95% identical thereto.

21. A CAR comprising an antibody or antigen binding fragment thereof comprises the amino acid sequence set forth in any one of SEQ ID NOs: 39, 59, 70, 90, 101, or 117; a spacer domain comprising the amino acid sequence set forth in any one of SEQ ID NOs: 145, 146, and 148 or an amino acid sequence at least 95% identical thereto; a transmembrane domain comprising the amino acid sequence set forth in SEQ ID NOs: 151 or 153; one or more intracellular signaling domains comprising a costimulatory signaling domain comprising an amino acid sequence set forth in any one of SEQ ID NOs: 159, 160, and 162 or an amino acid sequence at least 95% identical thereto and further comprising a primary signaling domain comprising an amino acid sequence set forth in SEQ ID NO: 158 or an amino acid sequence at least 95% identical thereto.

22. A CAR comprising the amino acid sequence set forth in any one of SEQ ID NOs: 165-860.

23. A CAR comprising the amino acid sequence set forth in any one of SEQ ID NOs: 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, and 283.

24. A CAR comprising the amino acid sequence set forth in any one of SEQ ID NOs: 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, and 380.

25. A CAR comprising the amino acid sequence set forth in any one of SEQ ID NOs: 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, and 452.

26. A CAR comprising the amino acid sequence set forth in any one of SEQ ID NOs: 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, and 548.

27. A CAR comprising the amino acid sequence set forth in any one of SEQ ID NOs: 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, and 620.

28. A CAR comprising the amino acid sequence set forth in any one of SEQ ID NOs: 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, and 716.

29. The CAR of any one of claims 11 to 28, further comprising a signal peptide.

30. The CAR of claim 29, wherein the signal peptide comprises an amino acid sequence set forth in any one of SEQ ID NOs: 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, and 873.

31. A polynucleotide encoding a CAR, comprising a polynucleotide sequence set forth in any one of SEQ ID NOs: 905-924.

32. A polynucleotide encoding a signal peptide and a CAR comprising a polynucleotide sequence set forth in any one of SEQ ID NOs: 925-944.

33. A polynucleotide encoding the antibody or antigen binding fragment thereof of any one of claims 1 to 5, the bispecific antibody of claim 6 or claim 7, the antibody conjugate of any one of claims 8 to 10, or the CAR of any one of claims 11 to 30.

34. A polynucleotide encoding or comprising a promoter operably linked to a polynucleotide of any one of claims 31 to 33.
35. The polynucleotide of claim 34, wherein the promoter comprises the polynucleotide sequence set forth in any one of SEQ ID NOs: 980, 981, 982, 983, 984, and 985.
36. The polynucleotide of claim 34 or claim 35, further comprising a post-transcriptional response element.
37. The polynucleotide of claim 36, wherein the post-transcriptional response element comprises the polynucleotide sequence set forth in any one of SEQ ID NOs: 945, 946, and 947.
38. A DNA comprising the polynucleotide sequence of any one of claims 31 to 37.
39. An RNA encoded by the polynucleotide sequence of any one of claims 31 to 37.
40. A vector comprising the polynucleotide of any one of claims 31 to 39.
41. A vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 950 operably linked to a polynucleotide encoding a signal peptide and a chimeric antigen receptor comprising an anti-BCMA antibody or antigen binding fragment thereof comprising an amino acid set forth in any one of SEQ ID NOs: 11-144, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.
42. A vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 950 operably linked to a polynucleotide encoding a signal peptide and a chimeric antigen receptor comprising an anti-BCMA antibody or antigen binding fragment thereof comprising an amino acid set forth in any one of SEQ ID NOs: 20, 30, 39, 50, 59, 70, 80, 90, 100, 101, 105, 109, 113, 117, 121, 125, 129, 133, 137, and 141, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

43. A vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 950 operably linked to a polynucleotide encoding a signal peptide and a chimeric antigen receptor comprising an amino acid set forth in any one of SEQ ID NOs: 165-860, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

44. A vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 950 operably linked to a polynucleotide encoding a signal peptide and a chimeric antigen receptor comprising an amino acid set forth in any one of SEQ ID NOs: 189, 237, 261, 333, 357, 429, 477, 525, 573, 597, 621, 645, 669, 693, 717, 741, 765, 789, 813, and 837, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

45. A vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 950 operably linked to a polynucleotide comprising a polynucleotide sequence set forth in SEQ ID NO: 904 and a polynucleotide sequence set forth in any one of SEQ ID NOs: 905-924, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

46. A vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 950 operably linked to a polynucleotide comprising a polynucleotide sequence set forth in any one of SEQ ID NOs: 925-944, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

47. A vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 949 operably linked to a polynucleotide encoding a signal peptide and a chimeric antigen receptor comprising an anti-BCMA antibody or antigen binding fragment thereof comprising an amino acid set forth in any one of SEQ ID NOs: 11-144, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

48. A vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 949 operably linked to a polynucleotide encoding a signal peptide and a chimeric antigen receptor comprising an anti-BCMA antibody or antigen binding fragment

thereof comprising an amino acid set forth in any one of SEQ ID NOs: 20, 30, 39, 50, 59, 70, 80, 90, 100, 101, 105, 109, 113, 117, 121, 125, 129, 133, 137, and 141, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

49. A vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 949 operably linked to a polynucleotide encoding a signal peptide and a chimeric antigen receptor comprising an amino acid set forth in any one of SEQ ID NOs: 165-860, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

50. A vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 949 operably linked to a polynucleotide encoding a signal peptide and a chimeric antigen receptor comprising an amino acid set forth in any one of SEQ ID NOs: 189, 237, 261, 333, 357, 429, 477, 525, 573, 597, 621, 645, 669, 693, 717, 741, 765, 789, 813, and 837, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

51. A vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 949 operably linked to a polynucleotide comprising a polynucleotide sequence set forth in SEQ ID NO: 904 and a polynucleotide sequence set forth in any one of SEQ ID NOs: 905-924, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

52. A vector encoding or comprising a promoter comprising a sequence set forth in SEQ ID NO: 949 operably linked to a polynucleotide comprising a polynucleotide sequence set forth in any one of SEQ ID NOs: 925-944, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

53. The vector of any one of claims 40 to 52, wherein the vector is an expression vector.

54. The vector of any one of claims 40 to 52, wherein the vector is a transfer plasmid or viral vector.

55. The vector of any one of claims 40 to 52, wherein the vector is a plasmid.

56. The vector of any one of claims 40 to 54, wherein the vector is a viral vector selected from the group consisting of an adenoviral (Ad) vector, an adeno-associated virus (AAV) vector, a herpes simplex virus (HSV) vector, a parvovirus vector, a rhabdovirus vector, a vesiculovirus vector, a paramyxovirus vector, a morbillivirus vector, a henipavirus vector, an alphavirus vector, a flavivirus vector, a retroviral vector, and a lentiviral vector (LVV).

57. The vector of claim 56, wherein the lentiviral vector is engineered or derived from the genome of a lentivirus selected from the group consisting of: HIV (HIV type 1 or HIV type 2); visna-maedi virus (VMV); caprine arthritis-encephalitis virus (CAEV); equine infectious anemia virus (EIAV); feline immunodeficiency virus (FIV); bovine immune deficiency virus (BIV); and simian immunodeficiency virus (SIV).

58. A lentiviral vector comprising: a 5' long terminal repeat (LTR) comprising R and U5 regions; a Psi (Ψ) packaging signal; a cPPT/FLAP; an export element; a polynucleotide encoding or comprising a promoter operably linked to a polynucleotide sequence set forth in SEQ ID NO: 904 and a polynucleotide sequence set forth in any one of SEQ ID NOs: 905-924; optionally a WPRE; a 3' LTR comprising U3 and R regions; a polyadenylation signal, and a poly(A) tail.

59. A lentiviral vector comprising: a 5' long terminal repeat (LTR) comprising R and U5 regions; a Psi (Ψ) packaging signal; a cPPT/FLAP; an export element; a polynucleotide encoding or comprising a promoter operably linked to a polynucleotide sequence set forth in any one of SEQ ID NOs: 925-944; optionally a WPRE; a 3' LTR comprising U3 and R regions; a polyadenylation signal, and a poly(A) tail.

60. The lentiviral vector of claim 58 or claim 59, wherein the lentiviral vector encodes a promoter comprising a polynucleotide sequence set forth in SEQ ID NO: 949 or 950.

61. An RNA comprising: a 5' long terminal repeat (LTR) comprising R and U5 regions; a Psi (Ψ) packaging signal; a cPPT/FLAP; an export element; a polynucleotide encoding a promoter operably linked to a polynucleotide sequence set forth in SEQ ID NO:

904 and a polynucleotide sequence set forth in any one of SEQ ID NOs: 905-924; optionally a WPRE; a 3' LTR comprising U3 and R regions; a polyadenylation signal, and optionally a poly(A) tail.

62. An RNA comprising: a 5' long terminal repeat (LTR) comprising R and U5 regions; a Psi (Ψ) packaging signal; a cPPT/FLAP; an export element; a polynucleotide encoding a promoter operably linked to a polynucleotide sequence set forth in any one of SEQ ID NOs: 925-944; optionally a WPRE; a 3' LTR comprising U3 and R regions; a polyadenylation signal, and optionally a poly(A) tail.

63. The RNA of claim 61 or claim 62, wherein the lentiviral vector encodes a promoter comprising a polynucleotide sequence set forth in SEQ ID NO: 949 or 950.

64. A recombinant lentivirus comprising one or more copies of the lentiviral vector of any one of claims 58-60 or the RNA of any one of claims 61-63.

65. A composition comprising the antibody or antigen binding fragment thereof of any one of claims 1 to 5, the bispecific antibody of claim 6 or claim 7, the antibody conjugate of any one of claims 8 to 10, the CAR of any one of claims 11 to 30, the polynucleotide of any one of claims 31 to 39, the vector of any one of claims 40 to 60, the RNA of any one of claims 61-63, or the recombinant lentivirus of claim 64.