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.

Disclosed herein is an antibody or antigen binding fragment thereof comprising (i) a heavy chain variable region (VH) and a light chain variable region (VL) or (ii) a VHH domain, wherein: (a) 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; (b) 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; or (c) 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.

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 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. 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); $(GGGGS)_n$ 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); LRQKDGGGSERP (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.

Disclosed herein is 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 CD3δ, CD3ε, CD3γ, or CD3ζ.

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 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.

Disclosed herein is a chimeric antigen 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 CD8β hinge, a CD8α 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.

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.

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, CD3δ, CD3ε, CD3γ, CD3ζ, CD4, CD5, CD8α, CD9, CD16, CD22, CD27, CD28, CD33, CD37, CD45, CD64, CD80, CD86, CD134, CD137, CD152, CD154, CD278, amnionless (AMN), and programmed cell death 1 (PDCD1).

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 consisting of FcRγ, FcRβ, CD3γ, CD3δ, CD3ε, CD3ζ, CD22, CD79a, CD79b, and CD66d.

In some embodiments, the one or more intracellular signaling domains comprises a primary signaling domain isolated from CD3ζ.

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 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 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 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.

In various embodiments, the disclosure contemplates, in part, a CAR comprising the 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 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 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.

Disclosed herein is 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.

Disclosed herein is a vector comprising the polynucleotide contemplated herein.

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.

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 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 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 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 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.

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.

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.

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.

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,

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 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 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 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 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.

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,

a paramyxovirus vector, a morbillovirus 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 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 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 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.

Disclosed herein is an RNA comprising: (a) 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: 910, 912, and 921; optionally a WPRE; a 3′ LTR comprising U3 and R regions; a polyadenylation signal, and optionally a poly(A) tail; or (b) 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: 930, 932, and 941; 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 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 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 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.

Disclosed herein is a recombinant lentivirus comprising one or more copies of a lentiviral vector or an RNA contemplated herein.

Disclosed herein is a composition comprising an antibody or antigen binding fragment thereof, a bispecific antibody, an antibody conjugate, a CAR, a polynucleotide, a vector, an RNA, or a recombinant lentivirus contemplated herein.

Disclosed herein is a pharmaceutical composition comprising a pharmaceutically acceptable carrier and the antibody or antigen binding fragment thereof, a bispecific antibody, an antibody conjugate, a CAR, a polynucleotide, a vector, an RNA, a recombinant lentivirus, or a composition 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 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 encoding a CD8α 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 encoding an MNDU3 promoter operably linked to a polynucleotide encoding a CD8α 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 encoding an MNDU3 promoter operably linked to a polynucleotide encoding a CD8α 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 IFNγ 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 operably linked to a polynucleotide encoding a CD8α 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, IFNγ 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 SFFV promoter, or an EF1α promoter operably linked to a polynucleotide encoding a CD8α 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 EF1α promoter operably linked to a polynucleotide encoding a CD8α 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 IFNγ 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 IFNγ 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 EF1α 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 EF1α 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 CD8α 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 EF1α 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 EF1α 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 EF1α 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 EF1α 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 EF1α 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 x 10^8 IU) or an EF1α promoter and no WPRE (5.6 x 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.

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.

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.

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.

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.

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 (IFNγ) 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 ± 15%, ± 10%, ± 9%, ± 8%, ± 7%, ± 6%, ± 5%, ± 4%, ± 3%, ± 2%, or ± 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 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.

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 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).

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 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 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); $(GGGGS)_n$ 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); LRQKDGGGSERP (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

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 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 (MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNA ILWTCLGLSLIISLAVFVLMFLLRKINSEPLKDEFKNTGSGLLGMANIDLEKSRTGD EIILPRGLEYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSL PAALSATEIEKSISAR).

An antibody or antigen binding fragment thereof "specifically binds" a BCMA polypeptide if it binds with an affinity or $K_a \geq 10^5\ M^{-1}$, while not significantly binding other components present in a test sample. An antibody or antigen binding fragment thereof may 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 $10^5\ M^{-1}$. 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-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 CDRLl, 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 Honegger 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 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 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 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. 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, 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, 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 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 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 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 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	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPG KALEWLALIYWNDEKRYSPSLKSRLTITKDTSKNQVVLTMTNMD PVDTAVYYCARDEYGGFDIWGQGTMVTVSS
	12	CDRH1	TSGVGVG
	13	CDRH2	LIYWNDEKRYSPSLKS
	14	CDRH3	DEYGGFDI
	15	VL	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAP RLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYC QQRVVYPITFGGGTKVEIK
	16	CDRL1	RASQSVSSYLA
	17	CDRL2	DASNRAT
	18	CDRL3	QQRVVYPIT
	19	scFv	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPG KALEWLALIYWNDEKRYSPSLKSRLTITKDTSKNQVVLTMTNMD PVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGGGG SGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQ

			KPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPED FAVYYCQQRVVYPITFGGGTKVEIK
	20	scFv	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAP RLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYC QQRVVYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQITLK ESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW LALIYWNDEKRYSPSLKSRLTITKDTSKNQVVLTMTNMDPVDTA VYYCARDEYGGFDIWGQGTMVTVSS
BCMA.2	21	VH	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPG KALEWLALIYWNDDKRYSPSLKSRLTITKDTSKNQVVLTMTNMD PVDTAVYYCARDEYGGFDIWGQGTMVTVSS
	22	CDRH1	TSGVGVG
	23	CDRH2	LIYWNDDKRYSPSLKS
	24	CDRH3	DEYGGFDI
	25	VL	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAP RLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYC QQRFDYPITFGGGTKVEIK
	26	CDRL1	RASQSVSSYLA
	27	CDRL2	DASNRAT
	28	CDRL3	QQRFDYPIT
	29	scFv	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPG KALEWLALIYWNDDKRYSPSLKSRLTITKDTSKNQVVLTMTNMD PVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGGGG SGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQ KPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPED FAVYYCQQRFDYPITFGGGTKVEIK
	30	scFv	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAP RLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYC QQRFDYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQITLK ESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW LALIYWNDDKRYSPSLKSRLTITKDTSKNQVVLTMTNMDPVDTA VYYCARDEYGGFDIWGQGTMVTVSS
BCMA.3	31	VH	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKG LEWVAVISYEGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRA EDTAVYYCARELGDGMDVWGQGTTVTVSS
	32	CDRH1	SYGMH
	33	CDRH2	VISYEGSNKYYADSVKG
	34	CDRH3	ELGDGMDV
	35	VL	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAP RLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYC QQRVDLWTFGGGTKVEIK
	36	CDRL1	RASQSVSSYLA
	37	CDRL2	DASNRAT
	38	CDRL3	QQRVDLWT
	39	scFv-ok	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKG LEWVAVISYEGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRA EDTAVYYCARELGDGMDVWGQGTTVTVSSGGGGSGGGGSGGGGS GGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQK PGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDF AVYYCQQRVDLWTFGGGTKVEIK
	40	scFv	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAP RLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYC QQRVDLWTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLVE SGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAV ISYEGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YCARELGDGMDVWGQGTTVTVSS
BCMA.4	41	VH	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKG LEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRA

			EDTAVYYCARDQGNYGVDVWGQGTTVTVSS
	42	CDRH1	DYYMS
	43	CDRH2	YISSSGSTIYYADSVKG
	44	CDRH3	DQGNYGVDV
	45	VL	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAP KLLIYDASSLESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYC QQVSSLPPTFGGGTKVEIK
	46	CDRL1	RASQSISSWLA
	47	CDRL2	DASSLES
	48	CDRL3	QQVSSLPPT
	49	scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKG LEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRA EDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGGGG SGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQ KPGKAPKLLIYDASSLESGVPSRFSGSGSGTEFTLTISSLQPDD FATYYCQQVSSLPPTFGGGTKVEIK
	50	scFv	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAP KLLIYDASSLESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYC QQVSSLPPTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLV ESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVS YISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAV YYCARDQGNYGVDVWGQGTTVTVSS
BCMA.5	51	VH	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKG LEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRA EDTAVYYCARDQGNYGVDVWGQGTTVTVSS
	52	CDRH1	DYYMS
	53	CDRH2	YISSSGSTIYYADSVKG
	54	CDRH3	DQGNYGVDV
	55	VL	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAP KLLIYEASSLESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYC QQSDSHPITFGGGTKVEIK
	56	CDRL1	RASQSISSWLA
	57	CDRL2	EASSLES
	58	CDRL3	QQSDSHPIT
	59	scFv-ok	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKG LEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRA EDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGGGG SGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQ KPGKAPKLLIYEASSLESGVPSRFSGSGSGTEFTLTISSLQPDD FATYYCQQSDSHPITFGGGTKVEIK
	60	scFv	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAP KLLIYEASSLESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYC QQSDSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQLV ESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVS YISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAV YYCARDQGNYGVDVWGQGTTVTVSS
	61	VH	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKG LEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRA EDTAVYYCARDQGNYGVDVWGQGTTVTVSS
	62	CDRH1	DYYMS
	63	CDRH2	YISSSGSTIYYADSVKG
	64	CDRH3	DQGNYGVDV
BCMA.6	65	VL	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAP KLLIYEASSLESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYC QQANSHPITFGGGTKVEIK
	66	CDRL1	RASQSISSWLA
	67	CDRL2	EASSLES
	68	CDRL3	QQANSHPIT

	69	scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKG LEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRA EDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGGGG SGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQ KPGKAPKLLIYEASSLESGVPSRFSGSGSGTEFTLTISSLQPDD FATYYCQQANSHPITFGGGTKVEIK
	70	scFv-ok	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAP KLLIYEASSLESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYC QQANSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLV ESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVS YISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAV YYCARDQGNYGVDVWGQGTTVTVSS
BCMA.7	71	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKG LEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRA EDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSS
	72	CDRH1	NYAMS
	73	CDRH2	AISGSGGSTYYADSVKG
	74	CDRH3	PGDGYYEGVYFDY
	75	VL	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAP KLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC QQAHSSPITFGGGTKVEIK
	76	CDRL1	RASQSISSYLN
	77	CDRL2	AASSLQS
	78	CDRL3	QQAHSSPIT
	79	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKG LEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRA EDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSGGGGSGGGGS GGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQAHSSPITFGGGTKVEIK
	80	scFv	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAP KLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC QQAHSSPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQLL ESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVS AISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV YYCARPGDGYYEGVYFDYWGQGTLVTVSS
BCMA.8	81	VH	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPG KALEWLALIYWNDEKRYSPSLKSRLTITKDTSKNQVVLTMTNMD PVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSS
	82	CDRH1	TSGVGVG
	83	CDRH2	LIYWNDEKRYSPSLKS
	84	CDRH3	EGSHDYKSSNWFDP
	85	VL	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAP KLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYC QQHFNLPLTFGGGTKVEIK
	86	CDRL1	QASQDIANYLN
	87	CDRL2	DASNLET
	88	CDRL3	QQHFNLPLTF
	89	scFv	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPG KALEWLALIYWNDEKRYSPSLKSRLTITKDTSKNQVVLTMTNMD PVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSGGGGSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANY LNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTIS SLQPEDIATYYCQQHFNLPLTFGGGTKVEIK
	90	scFv-ok	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAP KLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYC QQHFNLPLTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQITLK ESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW LALIYWNDEKRYSPSLKSRLTITKDTSKNQVVLTMTNMDPVDTA

			VYYCAREGSHDYKSSNWFDPWGQGTLVTVSS
BCMA.9	91	VH	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKG LEWVSSISSSSSYIYYADSVKGRFTISRDNAKNSLYLQMNSLRA EDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSS
	92	CDRH1	SYSMN
	93	CDRH2	SISSSSSYIYYADSVKG
	94	CDRH3	AGDTYSAADYYYMDV
	95	VL	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQK PGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDV GVYYCMQALGLITFGGGTKVEIK
	96	CDRL1	RSSQSLLHSNGYNYLD
	97	CDRL2	LGSNRAS
	98	CDRL3	MQALGLIT
	99	scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKG LEWVSSISSSSSYIYYADSVKGRFTISRDNAKNSLYLQMNSLRA EDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSGGGGSGGG GSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSLLHS NGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDF TLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIK
	100	scFv	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQK PGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDV GVYYCMQALGLITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSE VQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGL EWVSSISSSSSYIYYADSVKGRFTISRDNAKNSLYLQMNSLRAE DTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSS
BCMA.10	101	VHH-ok	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKE RELVSAISGSGEVTYYADSVKGRFTISRDNSKNTLYLQMNSLRA EDTAVYYCQRLVEAKRHWGQGTQVTVSS
	102	CDRH1	SEAMS
	103	CDRH2	AISGSGEVTYYADSVKG
	104	CDRH3	LVEAKRH
BCMA.11	105	VHH	EVQLLESGGGLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKE RELVSVITSEGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAE DTAVYYCAHIEWETRLNWGQGTQVTVSS
	106	CDRH1	SEAMS
	107	CDRH2	VITSEGSTYYADSVKG
	108	CDRH3	IEWETRLN
BCMA.12	109	VHH	EVQLLESGGGLVQPGGSLRLSCAASGFTFDEYTMHWFRQAPGKE REFVSAISGGGSETYYADSVKGRFTISRDNSKNTLYLQMNSLRA EDTAVYYCAAGGEEAGVGYWGQGTQVTVSS
	110	CDRH1	EYTMH
	111	CDRH2	AISGGGSETYYADSVKG
	112	CDRH3	GGEEAGVGY
BCMA.13	113	VHH	EVQLLESGGGLVQPGGSLRLSCAASGFTFEDYAMSWFRQAPGKE REGVSAISGKGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRA EDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSS
	114	CDRH1	DYAMS
	115	CDRH2	AISGKGGSTYYADSVKG
	116	CDRH3	LDEEAGAEGGY
BCMA.14	117	VHH-ok	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKE REGVSAISTSGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRA EDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSS
	118	CDRH1	RYAMS
	119	CDRH2	AISTSGDSTYYADSVKG
	120	CDRH3	LDEEAGAEGGY
BCMA.15	121	VHH	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMSWYRQAPGKE RELVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRA EDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSS

	122	CDRH1	SDAMS
	123	CDRH2	AISGSGGSTYYADSVKG
	124	CDRH3	HDSGEAYLAFDY
BCMA.16	125	VHH	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKE RELVSAISGHGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRA EDTAVYYCTRISITTEWLAGDYWGQGTQVTVSS
	126	CDRH1	SYTMS
	127	CDRH2	AISGHGDSTYYADSVKG
	128	CDRH3	ISITTEWLAGDY
BCMA.17	129	VHH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWFRQAPGKE REFVSFISGSGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRA EDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSS
	130	CDRH1	SYAMS
	131	CDRH2	FISGSGDSTYYADSVKG
	132	CDRH3	WPYDFEEPSEPGVY
BCMA.18	133	VHH	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYDMSWYRQAPGKE RELVSVIHSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAE DTAVYYCAPGYYSDLSFDYYNFDYWGQGTQVTVSS
	134	CDRH1	DYDMS
	135	CDRH2	VIHSGGSTYYADSVKG
	136	CDRH3	GYYSDLSFDYYNFDY
BCMA.19	137	VHH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMHWFRQAPGKE RVLVSSIDSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAE DTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSS
	138	CDRH1	DYAMH
	139	CDRH2	SIDSGGSTYYADSVKG
	140	CDRH3	GFKGDHPHPKDAFDI
BCMA.20	141	VHH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKE RELVSAISGSGDHTYYADSVRGRFTISRDNSKNTLYLQMNSLRA EDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSS
	142	CDRH1	SEGMS
	143	CDRH2	AISGSGDHTYYADSVRG
	144	CDRH3	LEGGPTTAIQPGGPDY

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 amatoxin, 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.

1. 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.

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 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, 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) 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 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 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 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 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 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 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 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 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 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 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 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, 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 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 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 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 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, 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, 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 primary signaling domain.

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, CD8α, CD8β, 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 immunoglobin 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 CD8β hinge, a CD8α 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	IEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKP
147	SGQVLLESNIKVLPTWSTPVQP
148	ESKYGPPCPPCP
149	ESKYGPPCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFQSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF LYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK
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 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 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, 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 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	IISFFLALTSTALLFLLFFLTLRFSVV
153	FWVLVVVGGVLACYSLLVTVAFIIFWV
154	VAAILGLGLVLGLLGPLAILL
155	WLPIGCAAFVVVCILGCILICWL
156	VMSVATIVIVDICITGGLLLLVYYWS
157	MALIVLGGVAGLLLFIGLGIFF

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 on 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 FcRγ, FcRβ, CD3γ, CD3δ, CD3ε, CD3ζ, 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 FcRγ, FcRβ, CD3γ, CD3δ, CD3ε, CD3ζ, 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, 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 FcRγ, FcRβ, CD3γ, CD3δ, CD3ε, CD3ζ, CD22, CD79a, 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.

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	RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKP RRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR
159	COSTIM	KRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL
160	COSTIM	RSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRS
161	COSTIM	ALYLLRRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAKI
162	COSTIM	TKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTL
163	COSTIM	QRRKYRSNKGESPVEPAEPCHYSCPREEEGSTIPIQEDYRKPEPACSP
164	COSTIM	KKKPLCLQREAKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESSAS ALDRRAPTRNQPQAPGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIV NVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEECAFRSQL ETPETLLGSTEEKPLPLGVPDAGMKPS

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 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 CD8β hinge, a CD8α 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 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, 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,

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 CD3ζ, CD22, CD79a, CD79b, or 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 comprising a hinge domain or fragment thereof selected from the group consisting of a CD8α hinge, a CD28 hinge, an IgG1 hinge, and an IgG4 hinge; a CD8α or CD28 transmembrane domain; a CD134, CD137, or CD278 costimulatory domain; and a CD3ζ primary signaling domain.

In particular embodiments, a CAR comprises an antibody or antigen binding 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 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, 204, 205, 206, 207, 208, 209, 210, 211, and 212.

SEQ ID NO.	AMINO ACID SEQUENCE
165	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIF KQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
166	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSD YMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT

	YDALHMQALPPR
167	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHD PNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
168	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLL YIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA TKDTYDALHMQALPPR
169	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLL HSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT KDTYDALHMQALPPR
170	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSS VHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
171	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMR PVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH MQALPPR
172	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTP RRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
173	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYM FMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
174	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG

	IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQP FMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
175	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMN MTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
176	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNG EYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPE MGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQAL PPR
177	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
178	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVK FSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
179	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSAD APAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
180	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKESKYGPPCPPCPFWV LVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCE LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
181	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKESKYGPPCPPCPFWV LVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRS RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKD KMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
182	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG

	IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKESKYGPPCPPCPFWV LVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSR SADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAY SEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
183	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
184	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYR SRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
185	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFS RSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEA YSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
186	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEE GGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
187	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFA AYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
188	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
189	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIF KQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
190	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSD

	YMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR
191	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHD PNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
192	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLL YIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA TKDTYDALHMQALPPR
193	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLL HSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT KDTYDALHMQALPPR
194	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSS VHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
195	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMR PVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH MQALPPR
196	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTP RRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
197	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYM FMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
198	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS

	GSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQP FMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
199	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMN MTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
200	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNG EYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPE MGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQAL PPR
201	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
202	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVK FSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
203	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSAD APAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
204	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSESKYGPPCPPCPFWV LVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCE LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
205	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSESKYGPPCPPCPFWV LVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRS RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKD KMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
206	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS

	GSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSESKYGPPCPPCPFWV LVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSR SADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAY SEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
207	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
208	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYR SRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
209	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFS RSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEA YSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
210	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEE GGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
211	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFA AYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
212	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVVYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM 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: 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 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, 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	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIF KQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
214	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSD YMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR
215	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHD PNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
216	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLL YIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA TKDTYDALHMQALPPR
217	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLL HSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT KDTYDALHMQALPPR
218	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKTTTPAPRPPTPAPTI

	ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSS VHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
219	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMR PVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH MQALPPR
220	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTP RRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
221	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYM FMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
222	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQP FMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
223	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMN MTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
224	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNG EYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPE MGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQAL PPR
225	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
226	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSL

	KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVK FSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
227	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSAD APAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
228	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKESKYGPPCPPCPFWV LVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCE LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
229	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKESKYGPPCPPCPFWV LVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRS RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKD KMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
230	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKESKYGPPCPPCPFWV LVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSR SADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAY SEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
231	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
232	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYR SRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
233	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFS RSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEA YSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
234	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKLEPKSCDKTHTCPPC

	PFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEE GGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
235	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFA AYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
236	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSGGGGSGGGGSGG GGSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATG IPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
237	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIF KQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
238	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSD YMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR
239	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHD PNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
240	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLL YIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA TKDTYDALHMQALPPR
241	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLL HSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT KDTYDALHMQALPPR
242	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT

	LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSS VHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
243	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMR PVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH MQALPPR
244	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTP RRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
245	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYM FMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
246	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQP FMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
247	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMN MTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
248	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNG EYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPE MGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQAL PPR
249	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM

	AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
250	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVK FSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
251	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSAD APAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
252	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSESKYGPPCPPCPFWV LVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCE LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
253	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSESKYGPPCPPCPFWV LVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRS RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKD KMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
254	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSESKYGPPCPPCPFWV LVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSR SADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAY SEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
255	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
256	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYR SRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
257	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFS RSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEA YSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
258	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT

	LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEE GGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
259	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFA AYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
260	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRFDYPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCARDEYGGFDIWGQGTMVTVSSLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

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	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSGGGGSGGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI PARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKTTTPAPRPPTPAPTIAS QPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQ PFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLD KRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTY DALHMQALPPR
262	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSGGGGSGGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI PARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKTTTPAPRPPTPAPTIAS QPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYM NMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
263	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSGGGGSGGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI

	PARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKTTTPAPRPPTPAPTIAS QPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPN GEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQA LPPR
264	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSGGGGSGGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI PARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKTTTPAPRPPTPAPTIAS QPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYI FKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR
265	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSGGGGSGGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI PARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKTTTPAPRPPTPAPTIAS QPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHS DYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
266	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSGGGGSGGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI PARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKTTTPAPRPPTPAPTIAS QPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVH DPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH MQALPPR
267	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSGGGGSGGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI PARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKIEVMYPPPYLDNEKSNG TIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPV QTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRD PEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQ ALPPR
268	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSGGGGSGGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI PARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKIEVMYPPPYLDNEKSNG TIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRR PGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQA LPPR
269	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSGGGGSGGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI PARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKIEVMYPPPYLDNEKSNG TIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFM RAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKP RRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
270	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSGGGGSGGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI PARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKIEVMYPPPYLDNEKSNG TIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFM RPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRR GRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDAL

	HMQALPPR
271	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSGGGGSGGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI PARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKIEVMYPPPYLDNEKSNG TIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMT PRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH MQALPPR
272	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSGGGGSGGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI PARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKIEVMYPPPYLDNEKSNG TIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEY MFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPP R
273	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSGGGGSGGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI PARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKESKYGPPCPPCPIYIWA PLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKF SRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAE AYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
274	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSGGGGSGGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI PARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKESKYGPPCPPCPIYIWA PLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFS RSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEA YSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
275	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSGGGGSGGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI PARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKESKYGPPCPPCPIYIWA PLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAP AYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGM KGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
276	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSGGGGSGGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI PARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKESKYGPPCPPCPFWVLV VVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELR VKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
277	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSGGGGSGGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI PARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKESKYGPPCPPCPFWVLV VVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
278	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSGGGGSGGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI PARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKESKYGPPCPPCPFWVLV VVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSA DAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSE IGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

279	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSGGGGSGGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI PARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKLEPKSCDKTHTCPPCPI YIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKD KMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
280	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSGGGGSGGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI PARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKLEPKSCDKTHTCPPCPI YIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSR VKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
281	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSGGGGSGGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI PARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKLEPKSCDKTHTCPPCPI YIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRS ADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYS EIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
282	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSGGGGSGGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI PARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKLEPKSCDKTHTCPPCPF WVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGG CELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
283	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSGGGGSGGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI PARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKLEPKSCDKTHTCPPCPF WVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAY RSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
284	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSGGGGSGGGGSGGG GSGGGGSEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGI PARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKLEPKSCDKTHTCPPCPF WVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKF SRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAE AYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

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	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQL VESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSTTTPAPRPPTPAPTIAS QPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQ PFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLD KRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTY DALHMQALPPR
286	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQL VESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSTTTPAPRPPTPAPTIAS QPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYM NMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
287	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQL VESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSTTTPAPRPPTPAPTIAS QPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPN GEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQA LPPR
288	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQL VESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSTTTPAPRPPTPAPTIAS QPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYI FKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR
289	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQL VESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSTTTPAPRPPTPAPTIAS QPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHS DYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
290	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQL VESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSTTTPAPRPPTPAPTIAS QPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVH DPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH MQALPPR
291	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQL VESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSIEVMYPPPYLDNEKSNG TIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPV

	QTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRD PEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQ ALPPR
292	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQL VESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSIEVMYPPPYLDNEKSNG TIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRR PGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQA LPPR
293	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQL VESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSIEVMYPPPYLDNEKSNG TIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFM RAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKP RRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
294	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQL VESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSIEVMYPPPYLDNEKSNG TIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFM RPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRR GRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDAL HMQALPPR
295	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQL VESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSIEVMYPPPYLDNEKSNG TIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMT PRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH MQALPPR
296	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQL VESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSIEVMYPPPYLDNEKSNG TIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEY MFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPP R
297	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQL VESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSESKYGPPCPPCPIYIWA PLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKF SRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAE AYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
298	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQL VESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSESKYGPPCPPCPIYIWA PLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFS RSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEA YSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
299	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQL VESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT

	ISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSESKYGPPCPPCPIYIWA PLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAP AYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGM KGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
300	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQL VESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSESKYGPPCPPCPFWVLV VVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELR VKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
301	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQL VESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSESKYGPPCPPCPFWVLV VVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
302	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQL VESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSESKYGPPCPPCPFWVLV VVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSA DAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSE IGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
303	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQL VESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSLEPKSCDKTHTCPPCPI YIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKD KMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
304	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQL VESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSLEPKSCDKTHTCPPCPI YIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSR VKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
305	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQL VESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSLEPKSCDKTHTCPPCPI YIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRS ADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYS EIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
306	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQL VESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSLEPKSCDKTHTCPPCPF WVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGG CELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
307	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQL VESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSLEPKSCDKTHTCPPCPF WVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAY RSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ

	KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
308	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRVDLWTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQL VESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCARELGDGMDVWGQGTTVTVSSLEPKSCDKTHTCPPCPF WVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKF SRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAE AYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

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 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, 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	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIF KQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
310	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSD YMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR
311	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHD PNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
312	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK

	GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLL YIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA TKDTYDALHMQALPPR
313	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLL HSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT KDTYDALHMQALPPR
314	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSS VHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
315	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMR PVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH MQALPPR
316	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTP RRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
317	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYM FMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
318	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQP FMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
319	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMN

	MTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
320	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNG EYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPE MGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQAL PPR
321	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
322	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVK FSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
323	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSAD APAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
324	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKESKYGPPCPPCPFWV LVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCE LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
325	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKESKYGPPCPPCPFWV LVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRS RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKD KMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
326	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKESKYGPPCPPCPFWV LVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSR SADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAY SEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
327	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ

	KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
328	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYR SRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
329	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFS RSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEA YSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
330	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEE GGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
331	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFA AYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
332	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
333	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIF KQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
334	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSD YMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR
335	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHD PNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM

	QALPPR
336	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLL YIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA TKDTYDALHMQALPPR
337	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLL HSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT KDTYDALHMQALPPR
338	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSS VHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
339	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMR PVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH MQALPPR
340	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTP RRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
341	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYM FMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
342	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQP FMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
343	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF

	TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMN MTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
344	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNG EYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPE MGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQAL PPR
345	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
346	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVK FSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
347	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSAD APAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
348	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSESKYGPPCPPCPFWV LVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCE LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
349	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSESKYGPPCPPCPFWV LVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRS RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKD KMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
350	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSESKYGPPCPPCPFWV LVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSR SADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAY SEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
351	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPPC

	PIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
352	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYR SRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
353	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFS RSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEA YSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
354	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEE GGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
355	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFA AYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
356	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQVSSLPPTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

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	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIF KQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
358	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSD YMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR
359	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHD PNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
360	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLL YIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA TKDTYDALHMQALPPR
361	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLL HSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT KDTYDALHMQALPPR
362	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSS VHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
363	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMR PVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH MQALPPR
364	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG

	VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTP RRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
365	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYM FMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
366	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQP FMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
367	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMN MTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
368	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNG EYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPE MGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQAL PPR
369	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
370	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVK FSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
371	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSAD APAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
372	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG

	GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKESKYGPPCPPCPFWV LVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCE LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
373	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKESKYGPPCPPCPFWV LVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRS RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKD KMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
374	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKESKYGPPCPPCPFWV LVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSR SADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAY SEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
375	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
376	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYR SRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
377	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFS RSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEA YSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
378	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEE GGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
379	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFA AYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
380	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRV

	KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM 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: 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	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIF KQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
382	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSD YMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR
383	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHD PNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
384	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLL YIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA TKDTYDALHMQALPPR
385	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSTTTPAPRPPTPAPTI

	ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLL HSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT KDTYDALHMQALPPR
386	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSS VHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
387	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMR PVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH MQALPPR
388	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTP RRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
389	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYM FMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
390	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQP FMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
391	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMN MTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
392	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNG EYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPE MGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQAL PPR

393	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
394	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVK FSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
395	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSAD APAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
396	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSESKYGPPCPPCPFWV LVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCE LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
397	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSESKYGPPCPPCPFWV LVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRS RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKD KMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
398	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSESKYGPPCPPCPFWV LVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSR SADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAY SEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
399	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
400	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYR SRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
401	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF

	TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFS RSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEA YSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
402	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEE GGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
403	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFA AYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
404	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQSDSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM 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	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIF KQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
406	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSD

	YMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR
407	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHD PNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
408	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLL YIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA TKDTYDALHMQALPPR
409	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLL HSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT KDTYDALHMQALPPR
410	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSS VHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
411	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMR PVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH MQALPPR
412	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTP RRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
413	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYM FMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
414	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK

	GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQP FMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
415	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMN MTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
416	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNG EYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPE MGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQAL PPR
417	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
418	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVK FSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
419	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSAD APAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
420	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKESKYGPPCPPCPFWV LVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCE LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
421	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKESKYGPPCPPCPFWV LVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRS RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKD KMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
422	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK

	GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKESKYGPPCPPCPFWV LVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSR SADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAY SEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
423	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
424	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYR SRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
425	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFS RSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEA YSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
426	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEE GGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
427	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFA AYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
428	EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSGGGGSGGGGSGG GGSGGGGSDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESG VPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM 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	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIF KQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
430	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSD YMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR
431	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHD PNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
432	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLL YIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA TKDTYDALHMQALPPR
433	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLL HSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT KDTYDALHMQALPPR
434	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSS VHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR

	RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
435	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMR PVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH MQALPPR
436	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTP RRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
437	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYM FMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
438	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQP FMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
439	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMN MTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
440	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSIEVMYPPPYLDNEKS NGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNG EYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPE MGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQAL PPR
441	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
442	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF

	TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVK FSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
443	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSESKYGPPCPPCPIYI WAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSAD APAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
444	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSESKYGPPCPPCPFWV LVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCE LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
445	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSESKYGPPCPPCPFWV LVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRS RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKD KMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
446	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSESKYGPPCPPCPFWV LVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSR SADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAY SEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
447	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
448	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYR SRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
449	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPPC PIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFS RSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEA YSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
450	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEE GGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN

	ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
451	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFA AYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
452	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYEASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQANSHPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRF TISRDNAKNSLYLQMNSLRAEDTAVYYCARDQGNYGVDVWGQGTTVTVSSLEPKSCDKTHTCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM 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: 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 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, 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	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSGGGGSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKTTTPAPRPPTP APTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKL LYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLST ATKDTYDALHMQALPPR
454	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSGGGGSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKTTTPAPRPPTP APTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRL LHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA TKDTYDALHMQALPPR
455	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSGGGGSGGG

	GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKTTTPAPRPPTP APTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKYSS SVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
456	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSGGGGSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKTTTPAPRPPTP APTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVKRGR KKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLG RREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQG LSTATKDTYDALHMQALPPR
457	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSGGGGSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKTTTPAPRPPTP APTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVRSKR SRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGL STATKDTYDALHMQALPPR
458	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSGGGGSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKTTTPAPRPPTP APTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVTKKK YSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
459	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSGGGGSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKIEVMYPPPYLD NEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQ PFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLD KRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTY DALHMQALPPR
460	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSGGGGSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKIEVMYPPPYLD NEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYM NMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
461	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSGGGGSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKIEVMYPPPYLD NEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPN GEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQA LPPR
462	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSGGGGSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKIEVMYPPPYLD NEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYI

	FKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR
463	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSGGGGSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKIEVMYPPPYLD NEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHS DYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
464	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSGGGGSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKIEVMYPPPYLD NEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVH DPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH MQALPPR
465	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSGGGGSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKESKYGPPCPPC PIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
466	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSGGGGSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKESKYGPPCPPC PIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYR SRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
467	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSGGGGSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKESKYGPPCPPC PIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFS RSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEA YSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
468	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSGGGGSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKESKYGPPCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEE GGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
469	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSGGGGSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKESKYGPPCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFA AYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
470	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSGGGGSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKESKYGPPCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRV

	KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
471	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSGGGGSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKLEPKSCDKTHT CPPCPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEE EGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLY NELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
472	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSGGGGSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKLEPKSCDKTHT CPPCPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDF AAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
473	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSGGGGSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKLEPKSCDKTHT CPPCPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLR VKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
474	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSGGGGSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKLEPKSCDKTHT CPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFP EEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQE GLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
475	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSGGGGSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKLEPKSCDKTHT CPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPP RDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
476	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSGGGGSGGG GSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKLEPKSCDKTHT CPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDV TLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
477	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSTTTPAPRPPTP APTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKL LYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLST ATKDTYDALHMQALPPR
478	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSTTTPAPRPPTP APTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRL LHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA

	TKDTYDALHMQALPPR
479	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSTTTPAPRPPTP APTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKYSS SVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
480	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSTTTPAPRPPTP APTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVKRGR KKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLG RREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQG LSTATKDTYDALHMQALPPR
481	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSTTTPAPRPPTP APTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVRSKR SRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGL STATKDTYDALHMQALPPR
482	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSTTTPAPRPPTP APTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVTKKK YSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
483	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSIEVMYPPPYLD NEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQ PFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLD KRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTY DALHMQALPPR
484	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSIEVMYPPPYLD NEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYM NMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
485	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSIEVMYPPPYLD NEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPN GEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQA LPPR
486	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ

	LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSIEVMYPPPYLD NEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYI FKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR
487	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSIEVMYPPPYLD NEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHS DYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
488	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSIEVMYPPPYLD NEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVH DPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH MQALPPR
489	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSESKYGPPCPPC PIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
490	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSESKYGPPCPPC PIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYR SRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
491	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSESKYGPPCPPC PIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFS RSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEA YSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
492	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSESKYGPPCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEE GGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
493	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSESKYGPPCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFA AYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
494	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ

	LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSESKYGPPCPPC PFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
495	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSLEPKSCDKTHT CPPCPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEE EGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLY NELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
496	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSLEPKSCDKTHT CPPCPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDF AAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
497	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSLEPKSCDKTHT CPPCPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLR VKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
498	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSLEPKSCDKTHT CPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFP EEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQE GLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
499	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSLEPKSCDKTHT CPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPP RDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
500	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQAHSSPITFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSEVQ LLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRF TISRDNSKNTLYLQMNSLRAEDTAVYYCARPGDGYYEGVYFDYWGQGTLVTVSSLEPKSCDKTHT CPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDV TLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ 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	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSGGGGSG GGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRK KLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGL STATKDTYDALHMQALPPR
502	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSGGGGSG GGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRS RLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLS TATKDTYDALHMQALPPR
503	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSGGGGSG GGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKY SSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR
504	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSGGGGSG GGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVKR GRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELN LGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLY QGLSTATKDTYDALHMQALPPR
505	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSGGGGSG GGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVRS KRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNL GRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQ GLSTATKDTYDALHMQALPPR
506	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSGGGGSG GGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVTK KKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT KDTYDALHMQALPPR
507	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSGGGGSG

	GGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIF KQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
508	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSGGGGSG GGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSD YMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR
509	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSGGGGSG GGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHD PNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
510	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSGGGGSG GGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLL YIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA TKDTYDALHMQALPPR
511	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSGGGGSG GGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLL HSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT KDTYDALHMQALPPR
512	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSGGGGSG GGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSS VHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
513	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSGGGGSG GGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKESKYGPPCP PCPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEG GCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
514	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSGGGGSG GGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKESKYGPPCP PCPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAA YRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL

	QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
515	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSGGGGSG GGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKESKYGPPCP PCPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVK FSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
516	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSGGGGSG GGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKESKYGPPCP PCPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEE EEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGL YNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
517	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSGGGGSG GGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKESKYGPPCP PCPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRD FAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLY NELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
518	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSGGGGSG GGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKESKYGPPCP PCPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKD KMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
519	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSGGGGSG GGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKLEPKSCDKT HTCPPCPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPE EEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
520	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSGGGGSG GGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKLEPKSCDKT HTCPPCPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPR DFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGL YNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
521	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSGGGGSG GGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKLEPKSCDKT HTCPPCPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVT LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
522	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSGGGGSG GGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKLEPKSCDKT HTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCR FPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNP QEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
523	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSGGGGSG

	GGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKLEPKSCDKT HTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYA PPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ EGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
524	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSL KSRLTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSGGGGSG GGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDA SNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKLEPKSCDKT HTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLT DVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE 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	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGS GSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRK KLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGL STATKDTYDALHMQALPPR
526	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGS GSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRS RLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLS TATKDTYDALHMQALPPR
527	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGS GSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKY SSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR
528	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGS GSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT

	LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVKR GRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELN LGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLY QGLSTATKDTYDALHMQALPPR
529	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGS GSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVRS KRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNL GRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQ GLSTATKDTYDALHMQALPPR
530	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGS GSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVTK KKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT KDTYDALHMQALPPR
531	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGS GSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIF KQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
532	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGS GSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSD YMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR
533	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGS GSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHD PNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
534	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGS GSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLL YIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA TKDTYDALHMQALPPR
535	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGS GSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLL

	HSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT KDTYDALHMQALPPR
536	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGS GSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSS VHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
537	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGS GSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSESKYGPPCP PCPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEG GCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
538	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGS GSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSESKYGPPCP PCPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAA YRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
539	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGS GSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSESKYGPPCP PCPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVK FSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
540	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGS GSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSESKYGPPCP PCPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEE EEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGL YNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
541	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGS GSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSESKYGPPCP PCPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRD FAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLY NELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
542	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGS GSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSESKYGPPCP PCPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKD KMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
543	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGS GSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSLEPKSCDKT HTCPPCPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPE EEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG

	LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
544	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGS GSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSLEPKSCDKT HTCPPCPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPR DFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGL YNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
545	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGS GSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSLEPKSCDKT HTCPPCPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVT LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
546	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGS GSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSLEPKSCDKT HTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCR FPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNP QEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
547	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGS GSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSLEPKSCDKT HTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYA PPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ EGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
548	DIQMTQSPSSLSASVGDRVTITCQASQDIANYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGS GSGTDFTFTISSLQPEDIATYYCQQHFNLPLTFGGGTKVEIKGGGGSGGGGSGGGGSGGGGSQIT LKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWNDEKRYSPSLKSR LTITKDTSKNQVVLTMTNMDPVDTAVYYCAREGSHDYKSSNWFDPWGQGTLVTVSSLEPKSCDKT HTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLT DVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

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 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, 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	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSGGGGSG GGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQL LIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCK RGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNEL NLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGL YQGLSTATKDTYDALHMQALPPR
550	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSGGGGSG GGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQL LIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCR SKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELN LGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLY QGLSTATKDTYDALHMQALPPR
551	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSGGGGSG GGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQL LIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCT KKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA TKDTYDALHMQALPPR
552	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSGGGGSG GGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQL LIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIF WVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLY NELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGH DGLYQGLSTATKDTYDALHMQALPPR
553	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSGGGGSG GGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQL LIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIF WVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYN ELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHD GLYQGLSTATKDTYDALHMQALPPR
554	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSGGGGSG GGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQL LIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIF WVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGL STATKDTYDALHMQALPPR
555	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSGGGGSG GGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQL LIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKIEVMY PPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKL LYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLST ATKDTYDALHMQALPPR
556	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVK

	GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSGGGGSG GGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQL LIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKIEVMY PPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRL LHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA TKDTYDALHMQALPPR
557	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSGGGGSG GGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQL LIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKIEVMY PPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSS SVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
558	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSGGGGSG GGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQL LIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKIEVMY PPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGR KKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLG RREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQG LSTATKDTYDALHMQALPPR
559	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSGGGGSG GGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQL LIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKIEVMY PPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKR SRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGL STATKDTYDALHMQALPPR
560	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSGGGGSG GGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQL LIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKIEVMY PPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKK YSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
561	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSGGGGSG GGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQL LIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKESKYG PPCPPCPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPE EEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
562	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSGGGGSG GGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQL LIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKESKYG PPCPPCPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPR DFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGL YNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
563	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSGGGGSG GGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQL LIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKESKYG PPCPPCPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVT LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK

	DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
564	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSGGGGSG GGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQL LIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKESKYG PPCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCR FPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNP QEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
565	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSGGGGSG GGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQL LIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKESKYG PPCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYA PPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ EGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
566	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSGGGGSG GGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQL LIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKESKYG PPCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLT DVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
567	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSGGGGSG GGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQL LIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKLEPKS CDKTHTCPPCPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSC RFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKN PQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
568	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSGGGGSG GGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQL LIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKLEPKS CDKTHTCPPCPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPY APPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNP QEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
569	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSGGGGSG GGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQL LIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKLEPKS CDKTHTCPPCPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRL TDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
570	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSGGGGSG GGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQL LIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKLEPKS CDKTHTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDG CSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPR RKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
571	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSGGGGSG GGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQL LIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKLEPKS CDKTHTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHY QPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRR KNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
572	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVK GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSGGGGSG

	GGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQL LIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKLEPKS CDKTHTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKK SRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
573	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPD RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCK RGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNEL NLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGL YQGLSTATKDTYDALHMQALPPR
574	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPD RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCR SKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELN LGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLY QGLSTATKDTYDALHMQALPPR
575	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPD RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCT KKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA TKDTYDALHMQALPPR
576	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPD RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIF WVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLY NELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGH DGLYQGLSTATKDTYDALHMQALPPR
577	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPD RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIF WVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYN ELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHD GLYQGLSTATKDTYDALHMQALPPR
578	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPD RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIF WVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGL STATKDTYDALHMQALPPR
579	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPD RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSIEVMY PPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKL LYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRRE

	EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLST ATKDTYDALHMQALPPR
580	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPD RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSIEVMY PPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRL LHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA TKDTYDALHMQALPPR
581	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPD RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSIEVMY PPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSS SVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
582	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPD RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSIEVMY PPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGR KKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLG RREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQG LSTATKDTYDALHMQALPPR
583	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPD RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSIEVMY PPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKR SRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGL STATKDTYDALHMQALPPR
584	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPD RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSIEVMY PPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKK YSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
585	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPD RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSESKYG PPCPPCPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPE EEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
586	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPD RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSESKYG PPCPPCPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPR DFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGL YNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
587	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPD RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV

	KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSESKYG PPCPPCPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVT LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
588	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPD RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSESKYG PPCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCR FPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNP QEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
589	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPD RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSESKYG PPCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYA PPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ EGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
590	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPD RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSESKYG PPCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLT DVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
591	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPD RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSLEPKS CDKTHTCPPCPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSC RFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKN PQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
592	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPD RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSLEPKS CDKTHTCPPCPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPY APPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNP QEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
593	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPD RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSLEPKS CDKTHTCPPCPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRL TDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
594	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPD RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSLEPKS CDKTHTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDG CSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPR RKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
595	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPD RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSLEPKS CDKTHTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHY QPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRR

	KNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
596	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPD RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALGLITFGGGTKVEIKGGGGSGGGGSGGGGSGGGG SEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSV KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARAGDTYSAADYYYMDVWGKGTTVTVSSLEPKS CDKTHTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKK SRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

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 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, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, and 620.

SEQ ID NO.	AMINO ACID SEQUENCE
597	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYI FKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR
598	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHS DYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
599	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVH DPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH MQALPPR
600	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKL LYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLST ATKDTYDALHMQALPPR
601	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRL LHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA TKDTYDALHMQALPPR

602	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSS SVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
603	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSIEVMYPPPYLDNEK SNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFM RPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRR GRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDAL HMQALPPR
604	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSIEVMYPPPYLDNEK SNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMT PRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH MQALPPR
605	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSIEVMYPPPYLDNEK SNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEY MFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPP R
606	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSIEVMYPPPYLDNEK SNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQ PFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLD KRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTY DALHMQALPPR
607	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSIEVMYPPPYLDNEK SNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYM NMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
608	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSIEVMYPPPYLDNEK SNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPN GEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQA LPPR
609	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSESKYGPPCPPCPIY IWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELR VKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
610	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSESKYGPPCPPCPIY IWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
611	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSESKYGPPCPPCPIY IWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSA DAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSE IGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
612	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSESKYGPPCPPCPFW

	VLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
613	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSESKYGPPCPPCPFW VLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYR SRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
614	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSESKYGPPCPPCPFW VLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFS RSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEA YSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
615	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSLEPKSCDKTHTCPP CPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGG CELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
616	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSLEPKSCDKTHTCPP CPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAY RSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
617	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSLEPKSCDKTHTCPP CPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKF SRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAE AYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
618	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSLEPKSCDKTHTCPP CPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEE EGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLY NELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
619	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSLEPKSCDKTHTCPP CPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDF AAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
620	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSEAMSWVRQAPGKERELVSAISGSGEVTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCQRLVEAKRHWGQGTQVTVSSLEPKSCDKTHTCPP CPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLR 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: 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	EVQLLESGGGLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYI FKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR
622	EVQLLESGGGLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHS DYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
623	EVQLLESGGGLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVH DPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH MQALPPR
624	EVQLLESGGGLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKL LYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLST ATKDTYDALHMQALPPR
625	EVQLLESGGGLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRL LHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA TKDTYDALHMQALPPR
626	EVQLLESGGGLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSTTTPAPRPPTPAPT IASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSS SVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
627	EVQLLESGGGLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSIEVMYPPPYLDNEK SNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFM RPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRR GRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDAL HMQALPPR
628	EVQLLESGGGLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSIEVMYPPPYLDNEK SNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMT PRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALH MQALPPR
629	EVQLLESGGGLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSIEVMYPPPYLDNEK SNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEY MFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMG GKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPP

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630	EVQLLESGGGLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSIEVMYPPPYLDNEK SNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQ PFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLD KRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTY DALHMQALPPR
631	EVQLLESGGGLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSIEVMYPPPYLDNEK SNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYM NMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
632	EVQLLESGGGLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSIEVMYPPPYLDNEK SNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPN GEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDP EMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQA LPPR
633	EVQLLESGGGLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSESKYGPPCPPCPIY IWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELR VKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
634	EVQLLESGGGLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSESKYGPPCPPCPIY IWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
635	EVQLLESGGGLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSESKYGPPCPPCPIY IWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSA DAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSE IGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
636	EVQLLESGGGLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSESKYGPPCPPCPFW VLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
637	EVQLLESGGGLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSESKYGPPCPPCPFW VLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYR SRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
638	EVQLLESGGGLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSESKYGPPCPPCPFW VLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFS RSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEA YSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
639	EVQLLESGGGLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSLEPKSCDKTHTCPP CPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGG CELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
640	EVQLLESGGGLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSLEPKSCDKTHTCPP CPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAY RSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

641	EVQLLESGGGLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSLEPKSCDKTHTCPP CPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKF SRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAE AYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
642	EVQLLESGGGLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSLEPKSCDKTHTCPP CPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEE EGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLY NELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
643	EVQLLESGGGLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSLEPKSCDKTHTCPP CPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDF AAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
644	EVQLLESGGGLVQPGGSLRLSCAASGFTFESEAMSWYRQAPGKERELVSVITSEGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAHIEWETRLNWGQGTQVTVSSLEPKSCDKTHTCPP CPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLR 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	EVQLLESGGGLVQPGGSLRLSCAASGFTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSTTTPAPRPPTPA PTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLL YIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA TKDTYDALHMQALPPR
646	EVQLLESGGGLVQPGGSLRLSCAASGFTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSTTTPAPRPPTPA PTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLL HSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT KDTYDALHMQALPPR
647	EVQLLESGGGLVQPGGSLRLSCAASGFTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSTTTPAPRPPTPA PTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSS VHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR

648	EVQLLESGGGLVQPGGSLRLSCAASGFTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSTTTPAPRPPTPA PTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRK KLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGL STATKDTYDALHMQALPPR
649	EVQLLESGGGLVQPGGSLRLSCAASGFTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSTTTPAPRPPTPA PTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRS RLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLS TATKDTYDALHMQALPPR
650	EVQLLESGGGLVQPGGSLRLSCAASGFTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSTTTPAPRPPTPA PTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKY SSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR
651	EVQLLESGGGLVQPGGSLRLSCAASGFTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSIEVMYPPPYLDN EKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQP FMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
652	EVQLLESGGGLVQPGGSLRLSCAASGFTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSIEVMYPPPYLDN EKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMN MTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
653	EVQLLESGGGLVQPGGSLRLSCAASGFTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSIEVMYPPPYLDN EKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNG EYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPE MGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQAL PPR
654	EVQLLESGGGLVQPGGSLRLSCAASGFTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSIEVMYPPPYLDN EKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIF KQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
655	EVQLLESGGGLVQPGGSLRLSCAASGFTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSIEVMYPPPYLDN EKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSD YMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR
656	EVQLLESGGGLVQPGGSLRLSCAASGFTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSIEVMYPPPYLDN EKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHD PNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
657	EVQLLESGGGLVQPGGSLRLSCAASGFTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSESKYGPPCPPCP IYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCE LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

658	EVQLLESGGGLVQPGGSLRLSCAASGFTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSESKYGPPCPPCP IYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRS RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKD KMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
659	EVQLLESGGGLVQPGGSLRLSCAASGFTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSESKYGPPCPPCP IYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSR SADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAY SEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
660	EVQLLESGGGLVQPGGSLRLSCAASGFTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSESKYGPPCPPCP FWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEG GCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
661	EVQLLESGGGLVQPGGSLRLSCAASGFTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSESKYGPPCPPCP FWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAA YRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
662	EVQLLESGGGLVQPGGSLRLSCAASGFTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSESKYGPPCPPCP FWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVK FSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
663	EVQLLESGGGLVQPGGSLRLSCAASGFTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSLEPKSCDKTHTC PPCPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEE GGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
664	EVQLLESGGGLVQPGGSLRLSCAASGFTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSLEPKSCDKTHTC PPCPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFA AYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
665	EVQLLESGGGLVQPGGSLRLSCAASGFTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSLEPKSCDKTHTC PPCPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRV KFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
666	EVQLLESGGGLVQPGGSLRLSCAASGFTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSLEPKSCDKTHTC PPCPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPE EEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
667	EVQLLESGGGLVQPGGSLRLSCAASGFTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSLEPKSCDKTHTC PPCPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPR DFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGL YNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
668	EVQLLESGGGLVQPGGSLRLSCAASGFTFDEYTMHWFRQAPGKEREFVSAISGGGSETYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGEEAGVGYWGQGTQVTVSSLEPKSCDKTHTC PPCPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVT LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

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	EVQLLESGGGLVQPGGSLRLSCAASGFTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSTTTPAPRPPT PAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKK LLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLS TATKDTYDALHMQALPPR
670	EVQLLESGGGLVQPGGSLRLSCAASGFTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSTTTPAPRPPT PAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSR LLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLST ATKDTYDALHMQALPPR
671	EVQLLESGGGLVQPGGSLRLSCAASGFTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSTTTPAPRPPT PAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKYS SSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLD KRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTY DALHMQALPPR
672	EVQLLESGGGLVQPGGSLRLSCAASGFTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSTTTPAPRPPT PAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVKRG RKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNL GRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQ GLSTATKDTYDALHMQALPPR
673	EVQLLESGGGLVQPGGSLRLSCAASGFTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSTTTPAPRPPT PAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVRSK RSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLG RREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQG LSTATKDTYDALHMQALPPR
674	EVQLLESGGGLVQPGGSLRLSCAASGFTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSTTTPAPRPPT PAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVTKK KYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR
675	EVQLLESGGGLVQPGGSLRLSCAASGFTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSIEVMYPPPYL DNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFK QPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR

676	EVQLLESGGGLVQPGGSLRLSCAASGFTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSIEVMYPPPYL DNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDY MNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLD KRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTY DALHMQALPPR
677	EVQLLESGGGLVQPGGSLRLSCAASGFTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSIEVMYPPPYL DNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDP NGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRD PEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQ ALPPR
678	EVQLLESGGGLVQPGGSLRLSCAASGFTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSIEVMYPPPYL DNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLY IFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT KDTYDALHMQALPPR
679	EVQLLESGGGLVQPGGSLRLSCAASGFTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSIEVMYPPPYL DNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLH SDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR
680	EVQLLESGGGLVQPGGSLRLSCAASGFTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSIEVMYPPPYL DNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSV HDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRR GRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDAL HMQALPPR
681	EVQLLESGGGLVQPGGSLRLSCAASGFTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSESKYGPPCPP CPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGG CELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
682	EVQLLESGGGLVQPGGSLRLSCAASGFTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSESKYGPPCPP CPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAY RSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
683	EVQLLESGGGLVQPGGSLRLSCAASGFTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSESKYGPPCPP CPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKF SRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAE AYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
684	EVQLLESGGGLVQPGGSLRLSCAASGFTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSESKYGPPCPP CPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEE EGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLY NELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
685	EVQLLESGGGLVQPGGSLRLSCAASGFTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSESKYGPPCPP CPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDF AAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
686	EVQLLESGGGLVQPGGSLRLSCAASGFTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSESKYGPPCPP CPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLR VKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDK

	MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
687	EVQLLESGGGLVQPGGSLRLSCAASGFTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSLEPKSCDKTH TCPPCPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEE EEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGL YNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
688	EVQLLESGGGLVQPGGSLRLSCAASGFTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSLEPKSCDKTH TCPPCPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRD FAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLY NELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
689	EVQLLESGGGLVQPGGSLRLSCAASGFTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSLEPKSCDKTH TCPPCPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKD KMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
690	EVQLLESGGGLVQPGGSLRLSCAASGFTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSLEPKSCDKTH TCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRF PEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ EGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
691	EVQLLESGGGLVQPGGSLRLSCAASGFTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSLEPKSCDKTH TCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAP PRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQE GLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
692	EVQLLESGGGLVQPGGSLRLSCAASGFTFEDYAMSWFRQAPGKEREGVSAISGKGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSLEPKSCDKTH TCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTD VTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

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	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSTTTPAPRPPT PAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKK LLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLS TATKDTYDALHMQALPPR
694	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK

	GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSTTTPAPRPPT PAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRSR LLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLST ATKDTYDALHMQALPPR
695	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSTTTPAPRPPT PAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKYS SSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLD KRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTY DALHMQALPPR
696	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSTTTPAPRPPT PAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVKRG RKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNL GRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQ GLSTATKDTYDALHMQALPPR
697	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSTTTPAPRPPT PAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVRSK RSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLG RREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQG LSTATKDTYDALHMQALPPR
698	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSTTTPAPRPPT PAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVTKK KYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR
699	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSIEVMYPPPYL DNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFK QPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR
700	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSIEVMYPPPYL DNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDY MNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLD KRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTY DALHMQALPPR
701	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSIEVMYPPPYL DNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDP NGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRD PEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQ ALPPR
702	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSIEVMYPPPYL DNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLY IFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT KDTYDALHMQALPPR
703	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSIEVMYPPPYL DNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLH SDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR

704	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSIEVMYPPPYL DNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSV HDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRR GRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDAL HMQALPPR
705	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSESKYGPPCPP CPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGG CELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
706	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSESKYGPPCPP CPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAY RSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
707	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSESKYGPPCPP CPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKF SRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAE AYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
708	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSESKYGPPCPP CPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEE EGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLY NELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
709	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSESKYGPPCPP CPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDF AAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
710	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSESKYGPPCPP CPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLR VKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
711	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSLEPKSCDKTH TCPPCPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEE EEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGL YNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
712	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSLEPKSCDKTH TCPPCPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRD FAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLY NELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
713	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSLEPKSCDKTH TCPPCPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKD KMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
714	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSLEPKSCDKTH TCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRF PEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ EGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
715	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSLEPKSCDKTH TCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAP

	PRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQE GLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
716	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYAMSWFRQAPGKEREGVSAISTSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVLDEEAGAEGGYWGQGTQVTVSSLEPKSCDKTH TCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTD VTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

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 GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRK KLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGL STATKDTYDALHMQALPPR
718	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRS RLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLS TATKDTYDALHMQALPPR
719	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKY SSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR
720	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVKR GRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELN LGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLY QGLSTATKDTYDALHMQALPPR
721	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVRS KRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNL GRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQ GLSTATKDTYDALHMQALPPR
722	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK

	GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVTK KKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT KDTYDALHMQALPPR
723	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIF KQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
724	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSD YMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR
725	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHD PNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM QALPPR
726	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLL YIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA TKDTYDALHMQALPPR
727	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLL HSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT KDTYDALHMQALPPR
728	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSS VHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
729	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSESKYGPPCP PCPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEG GCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
730	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSESKYGPPCP PCPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAA YRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
731	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSESKYGPPCP PCPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVK FSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
732	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSESKYGPPCP PCPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEE

	EEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGL YNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
733	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSESKYGPPCP PCPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRD FAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLY NELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
734	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSESKYGPPCP PCPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKD KMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
735	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSLEPKSCDKT HTCPPCPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPE EEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
736	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSLEPKSCDKT HTCPPCPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPR DFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGL YNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
737	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSLEPKSCDKT HTCPPCPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVT LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
738	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSLEPKSCDKT HTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCR FPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNP QEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
739	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSLEPKSCDKT HTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYA PPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ EGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
740	EVQLLESGGGLVQPGGSLRLSCAASGFTFASDAMSWYRQAPGKERELVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAHDSGEAYLAFDYWGQGTQVTVSSLEPKSCDKT HTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLT DVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

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 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, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, and 764.

SEQ ID NO.	AMINO ACID SEQUENCE
741	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKERELVSAISGHGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRK KLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGL STATKDTYDALHMQALPPR
742	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKERELVSAISGHGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSKRS RLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLS TATKDTYDALHMQALPPR
743	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKERELVSAISGHGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKKKY SSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR
744	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKERELVSAISGHGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVKR GRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELN LGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLY QGLSTATKDTYDALHMQALPPR
745	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKERELVSAISGHGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVRS KRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNL GRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQ GLSTATKDTYDALHMQALPPR
746	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKERELVSAISGHGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVTK KKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT KDTYDALHMQALPPR
747	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKERELVSAISGHGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIF KQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
748	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKERELVSAISGHGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSD YMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR
749	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKERELVSAISGHGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHD PNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHM

	QALPPR
750	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKERELVSAISGHGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLL YIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA TKDTYDALHMQALPPR
751	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKERELVSAISGHGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLL HSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT KDTYDALHMQALPPR
752	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKERELVSAISGHGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSIEVMYPPPY LDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSS VHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDA LHMQALPPR
753	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKERELVSAISGHGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSESKYGPPCP PCPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEG GCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
754	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKERELVSAISGHGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSESKYGPPCP PCPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAA YRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
755	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKERELVSAISGHGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSESKYGPPCP PCPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVK FSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMA EAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
756	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKERELVSAISGHGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSESKYGPPCP PCPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEE EEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGL YNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
757	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKERELVSAISGHGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSESKYGPPCP PCPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRD FAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLY NELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
758	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKERELVSAISGHGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSESKYGPPCP PCPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTL RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKD KMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
759	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKERELVSAISGHGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSLEPKSCDKT HTCPPCPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPE EEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
760	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKERELVSAISGHGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSLEPKSCDKT HTCPPCPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPR DFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGL YNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

761	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKERELVSAISGHGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSLEPKSCDKT HTCPPCPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVT LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
762	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKERELVSAISGHGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSLEPKSCDKT HTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCR FPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNP QEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
763	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKERELVSAISGHGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSLEPKSCDKT HTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYA PPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ EGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
764	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYTMSWYRQAPGKERELVSAISGHGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRISITTEWLAGDYWGQGTQVTVSSLEPKSCDKT HTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLT DVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

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	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSTTTPAPR PPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRG RKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNL GRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQ GLSTATKDTYDALHMQALPPR
766	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSTTTPAPR PPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSK RSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLG RREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQG LSTATKDTYDALHMQALPPR
767	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSTTTPAPR PPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKK KYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR

768	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSTTTPAPR PPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWV KRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNE LNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDG LYQGLSTATKDTYDALHMQALPPR
769	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSTTTPAPR PPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWV RSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNEL NLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGL YQGLSTATKDTYDALHMQALPPR
770	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSTTTPAPR PPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWV TKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLST ATKDTYDALHMQALPPR
771	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSIEVMYPP PYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLY IFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT KDTYDALHMQALPPR
772	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSIEVMYPP PYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLH SDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR
773	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSIEVMYPP PYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSV HDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRR GRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDAL HMQALPPR
774	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSIEVMYPP PYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKK LLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLS TATKDTYDALHMQALPPR
775	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSIEVMYPP PYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSR LLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLST ATKDTYDALHMQALPPR
776	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSIEVMYPP PYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYS SSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLD KRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTY DALHMQALPPR
777	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSESKYGPP CPPCPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEE EGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLY NELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

778	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSESKYGPP CPPCPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDF AAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
779	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSESKYGPP CPPCPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLR VKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
780	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSESKYGPP CPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFP EEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQE GLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
781	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSESKYGPP CPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPP RDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
782	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSESKYGPP CPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDV TLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
783	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSLEPKSCD KTHTCPPCPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRF PEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ EGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
784	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSLEPKSCD KTHTCPPCPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAP PRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQE GLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
785	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSLEPKSCD KTHTCPPCPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTD VTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
786	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSLEPKSCD KTHTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCS CRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRK NPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
787	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSLEPKSCD KTHTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQP YAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKN PQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
788	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWFRQAPGKEREFVSFISGSGDSTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRWPYDFEEPSEPGVYWGQGTQVTVSSLEPKSCD KTHTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSR 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: 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	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYDMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAPGYYSDLSFDYYNFDYWGQGTQVTVSSTTTPAPR PPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRG RKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNL GRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQ GLSTATKDTYDALHMQALPPR
790	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYDMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAPGYYSDLSFDYYNFDYWGQGTQVTVSSTTTPAPR PPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSK RSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLG RREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQG LSTATKDTYDALHMQALPPR
791	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYDMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAPGYYSDLSFDYYNFDYWGQGTQVTVSSTTTPAPR PPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKK KYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR
792	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYDMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAPGYYSDLSFDYYNFDYWGQGTQVTVSSTTTPAPR PPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWV KRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNE LNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDG LYQGLSTATKDTYDALHMQALPPR
793	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYDMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAPGYYSDLSFDYYNFDYWGQGTQVTVSSTTTPAPR PPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWV RSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNEL NLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGL YQGLSTATKDTYDALHMQALPPR
794	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYDMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAPGYYSDLSFDYYNFDYWGQGTQVTVSSTTTPAPR PPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWV TKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLST ATKDTYDALHMQALPPR
795	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYDMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAPGYYSDLSFDYYNFDYWGQGTQVTVSSIEVMYPP PYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLY IFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT KDTYDALHMQALPPR

796	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYDMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAPGYYSDLSFDYYNFDYWGQGTQVTVSSIEVMYPP PYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLH SDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR
797	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYDMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAPGYYSDLSFDYYNFDYWGQGTQVTVSSIEVMYPP PYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSV HDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRR GRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDAL HMQALPPR
798	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYDMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAPGYYSDLSFDYYNFDYWGQGTQVTVSSIEVMYPP PYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKK LLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLS TATKDTYDALHMQALPPR
799	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYDMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAPGYYSDLSFDYYNFDYWGQGTQVTVSSIEVMYPP PYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSR LLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLST ATKDTYDALHMQALPPR
800	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYDMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAPGYYSDLSFDYYNFDYWGQGTQVTVSSIEVMYPP PYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYS SSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLD KRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTY DALHMQALPPR
801	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYDMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAPGYYSDLSFDYYNFDYWGQGTQVTVSSESKYGPP CPPCPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEE EGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLY NELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
802	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYDMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAPGYYSDLSFDYYNFDYWGQGTQVTVSSESKYGPP CPPCPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDF AAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
803	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYDMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAPGYYSDLSFDYYNFDYWGQGTQVTVSSESKYGPP CPPCPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLR VKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
804	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYDMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAPGYYSDLSFDYYNFDYWGQGTQVTVSSESKYGPP CPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFP EEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQE GLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
805	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYDMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAPGYYSDLSFDYYNFDYWGQGTQVTVSSESKYGPP CPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPP RDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
806	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYDMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAPGYYSDLSFDYYNFDYWGQGTQVTVSSESKYGPP CPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDV TLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ

	KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
807	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYDMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAPGYYSDLSFDYYNFDYWGQGTQVTVSSLEPKSCD KTHTCPPCPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRF PEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ EGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
808	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYDMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAPGYYSDLSFDYYNFDYWGQGTQVTVSSLEPKSCD KTHTCPPCPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAP PRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQE GLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
809	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYDMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAPGYYSDLSFDYYNFDYWGQGTQVTVSSLEPKSCD KTHTCPPCPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTD VTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
810	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYDMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAPGYYSDLSFDYYNFDYWGQGTQVTVSSLEPKSCD KTHTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCS CRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRK NPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
811	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYDMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAPGYYSDLSFDYYNFDYWGQGTQVTVSSLEPKSCD KTHTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQP YAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKN PQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
812	EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYDMSWYRQAPGKERELVSVIHSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAPGYYSDLSFDYYNFDYWGQGTQVTVSSLEPKSCD KTHTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSR 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	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSTTTPAPR PPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRG RKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNL GRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQ GLSTATKDTYDALHMQALPPR
814	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG

	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSTTTPAPR PPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCRSK RSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLG RREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQG LSTATKDTYDALHMQALPPR
815	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSTTTPAPR PPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCTKK KYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR
816	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSTTTPAPR PPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWV KRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNE LNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDG LYQGLSTATKDTYDALHMQALPPR
817	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSTTTPAPR PPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWV RSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNEL NLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGL YQGLSTATKDTYDALHMQALPPR
818	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSTTTPAPR PPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWV TKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLST ATKDTYDALHMQALPPR
819	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSIEVMYPP PYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLY IFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT KDTYDALHMQALPPR
820	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSIEVMYPP PYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLH SDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR
821	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSIEVMYPP PYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSV HDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRR GRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDAL HMQALPPR
822	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSIEVMYPP PYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKK LLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLS TATKDTYDALHMQALPPR
823	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSIEVMYPP PYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSR LLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLST ATKDTYDALHMQALPPR

824	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSIEVMYPP PYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYS SSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLD KRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTY DALHMQALPPR
825	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSESKYGPP CPPCPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEE EGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLY NELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
826	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSESKYGPP CPPCPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDF AAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
827	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSESKYGPP CPPCPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLR VKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDK MAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
828	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSESKYGPP CPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFP EEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQE GLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
829	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSESKYGPP CPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPP RDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
830	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSESKYGPP CPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDV TLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
831	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSLEPKSCD KTHTCPPCPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRF PEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ EGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
832	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSLEPKSCD KTHTCPPCPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAP PRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQE GLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
833	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSLEPKSCD KTHTCPPCPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTD VTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
834	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSLEPKSCD KTHTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCS CRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRK NPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
835	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSLEPKSCD KTHTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQP

	YAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKN PQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
836	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMHWFRQAPGKERVLVSSIDSGGSTYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCNAGFKGDHPHPKDAFDIWGQGTQVTVSSLEPKSCD KTHTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSR 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: 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 GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCK RGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNEL NLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGL YQGLSTATKDTYDALHMQALPPR
838	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCR SKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELN LGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLY QGLSTATKDTYDALHMQALPPR
839	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCT KKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA TKDTYDALHMQALPPR
840	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIF WVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLY NELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGH DGLYQGLSTATKDTYDALHMQALPPR
841	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIF WVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYN ELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHD GLYQGLSTATKDTYDALHMQALPPR
842	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR

	GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSTTTPA PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIF WVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGL STATKDTYDALHMQALPPR
843	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSIEVMY PPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKL LYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLST ATKDTYDALHMQALPPR
844	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSIEVMY PPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRL LHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTA TKDTYDALHMQALPPR
845	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSIEVMY PPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSS SVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYD ALHMQALPPR
846	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSIEVMY PPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGR KKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLG RREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQG LSTATKDTYDALHMQALPPR
847	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSIEVMY PPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKR SRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGL STATKDTYDALHMQALPPR
848	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSIEVMY PPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKK YSSSVHDPNGEYMFMRAVNTAKKSRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD TYDALHMQALPPR
849	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSESKYG PPCPPCPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPE EEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
850	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSESKYG PPCPPCPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPR DFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGL YNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
851	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSESKYG PPCPPCPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVT LRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
852	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSESKYG PPCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCR

	FPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNP QEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
853	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSESKYG PPCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYA PPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ EGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
854	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSESKYG PPCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLT DVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
855	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSLEPKS CDKTHTCPPCPIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSC RFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKN PQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
856	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSLEPKS CDKTHTCPPCPIYIWAPLAGTCGVLLLSLVITLYCRSKRSRLLHSDYMNMTPRRPGPTRKHYQPY APPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNP QEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
857	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSLEPKS CDKTHTCPPCPIYIWAPLAGTCGVLLLSLVITLYCTKKKYSSSVHDPNGEYMFMRAVNTAKKSRL TDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYN ELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
858	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSLEPKS CDKTHTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDG CSCRFPEEEEGGCELRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPR RKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
859	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSLEPKS CDKTHTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHY QPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRR KNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
860	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSEGMSWVRQAPGKERELVSAISGSGDHTYYADSVR GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNALEGGPTTAIQPGGPDYWGQGTQVTVSSLEPKS CDKTHTCPPCPFWVLVVVGGVLACYSLLVTVAFIIFWVTKKKYSSSVHDPNGEYMFMRAVNTAKK SRLTDVTLRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

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 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 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).

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 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 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.

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 ± 1); glutamate (+3.0 ± 1); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (-0.4); proline (-0.5 ± 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 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 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 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 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 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: $(GGGGS)_n$ 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 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: $(GGGGS)_n$ wherein n = 1, 2, 3, 4 or 5, GEGTSTGSGGSGGSGGAD, GSTSGSGKPGSGEGSTKG and variants thereof comprising an amino acid sequence 95% identical thereto.

In particular embodiments, 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	MALPVTALLLPLALLLHAARP
862	METDTLLLWVLLLWVPGSTG
863	MDMRVPAQLLGLLLLWLRGARC
864	MPLLLLLPLLWAGALA
865	MDAMKRGLCCVLLLCGAVFVSPS
866	MLLLLLLLGLRLQLSLG
867	MWLQSLLLLGTVACSIS
868	MGVKVLFALICIAVAEA
869	MLLLVTSLLLCELPHPAFLLIP
870	MSRSVALAVLALLSLSGLEA
871	MGHTRRQGTSPSKCPYLNFFQLLVLAGLSHFCSG
872	MWWRLWWLLLLLLLLWPMVWA
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.

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.

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).

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, picoma 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, 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.

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 Thosea asigna virus (TaV) 2A peptide, a porcine teschovirus-1 (PTV-1) 2A peptide, a Theilovirus 2A peptide, and an encephalomyocarditis virus 2A peptide.

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 (SEQ ID NO: 967); TLNFDLLKLAGDVESNPGP (SEQ ID NO: 968); NFDLLKLAGDVESNPGP (SEQ ID NO: 969); QLLNFDLLKLAGDVESNPGP (SEQ ID NO: 970); APVKQTLNFDLLKLAGDVESNPGP (SEQ ID NO: 971); VTELLYRMKRAETYCPRPLLAIHPTEARHKQKIVAPVKQT (SEQ ID NO: 972); LNFDLLKLAGDVESNPGP (SEQ ID NO: 973);

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, 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. 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 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 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 GAAAGAGCCACACTGAGCTGTAGAGCCAGCCAGAGCGTGTCCTCTTAC CTGGCCTGGTATCAGCAGAAGCCTGGACAGGCTCCCCGGCTGCTGATC TACGATGCCAGCAATAGAGCCACAGGCATCCCCGCCAGATTTTCTGGC AGCGGCTCTGGCACCGATTTCACCCTGACCATAAGCAGCCTGGAACCT GAGGACTTCGCCGTGTACTACTGCCAGCAGAGAGTGGTGTACCCCATC ACCTTTGGCGGAGGCACCAAGGTGGAAATCAAAGGCGGCGGAGGAAGC GGAGGCGGAGGATCTGGTGGTGGTGGATCTGGCGGAGGTGGCAGCCAG ATCACACTGAAAGAGTCTGGCCCCACACTGGTCAAGCCCACACAGACC CTGACACTGACCTGCACCTTCAGCGGCTTTAGCCTGAGCACATCTGGC

		GTCGGCGTTGGCTGGATTAGACAGCCTCCTGGAAAGGCCCTGGAATGG CTGGCCCTGATCTACTGGAACGACGAGAAGAGATACAGCCCCAGCCTG AAGTCCCGGCTGACCATCACCAAGGACACCAGCAAGAACCAGGTGGTG CTGACCATGACAAACATGGACCCCGTGGACACCGCCGTGTATTATTGC GCCAGAGATGAGTACGGCGGCTTCGACATTTGGGGCCAGGGCACAATG GTCACCGTGTCTAGT
875	30	GAGATCGTGCTGACCCAGTCCCCTGCTACCCTGAGCCTGTCTCCAGGC GAGCGGGCCACACTGAGCTGTAGAGCTTCTCAGAGCGTGTCCAGCTAC CTGGCCTGGTATCAGCAGAAACCTGGCCAGGCCCCTAGACTGCTGATC TACGACGCCAGCAACCGGGCCACCGGCATCCCCGCCAGATTCAGCGGA TCTGGCAGCGGCACAGATTTTACCCTCACCATCAGCAGCCTGGAACCT GAGGACTTCGCCGTCTACTACTGCCAGCAAAGATTCGACTACCCCATC ACCTTCGGCGGCGGAACAAAGGTGGAAATTAAGGGTGGTGGGGGCAGC GGTGGAGGTGGGAGCGGAGGCGGGGGTAGCGGAGGCGGGGGTAGCCAA ATCACACTGAAAGAGAGCGGCCCTACACTCGTGAAACCTACCCAGACC CTGACACTGACATGTACCTTCAGCGGCTTCTCCCTGAGCACCTCTGGC GTCGGCGTTGGATGGATCAGACAGCCTCCAGGCAAGGCCCTGGAATGG CTGGCTCTGATCTATTGGAACGACGACAAGCGGTACAGCCCCAGCCTG AAGTCTAGACTGACCATCACAAAGGACACCAGCAAGAACCAGGTGGTG CTGACCATGACAAATATGGACCCCGTGGACACCGCCGTGTACTACTGC GCCAGAGATGAGTACGGCGGATTTGATATCTGGGGCCAGGGCACCATG GTGACCGTGTCCAGC
876	39	CAAGTGCAGCTCGTGGAAAGCGGCGGCGGAGTGGTGCAGCCCGGCCGG AGCCTGAGACTGTCCTGCGCCGCTTCTGGATTTACCTTCAGCAGCTAC GGCATGCACTGGGTCAGACAGGCCCCTGGCAAAGGCCTGGAGTGGGTG GCCGTTATCAGCTACGAGGGCAGCAACAAGTATTACGCCGACAGCGTG AAGGGCCGCTTCACAATCTCTAGAGATAATAGCAAGAACACCCTGTAC CTGCAGATGAACAGCCTGCGGGCCGAAGATACCGCCGTGTACTACTGT GCTAGAGAGCTGGGCGACGGCATGGACGTGTGGGGACAGGGCACAACC GTGACCGTGTCCTCTGGTGGTGGGGGCAGCGGTGGAGGTGGGAGCGGA GGCGGGGGTAGCGGAGGCGGGGGTAGCGAGATCGTGCTGACCCAGTCC CCTGCTACACTGAGCCTGTCTCCAGGCGAGCGGGCCACACTGAGCTGT AGAGCTTCTCAGAGCGTGTCCAGCTATCTGGCCTGGTTCCAGCAGAAA CCTGGCCAGGCCCCTAGACTGCTGATCTACGACGCCAGCAACCGGGCC ACCGGCATCCCCGCCAGATTCAGCGGCTCTGGCAGCGGCACCGACTTC ACCCTCACCATCAGCAGCCTGGAACCCGAGGATTTTGCCGTCTACTAC TGCCAGCAAAGAGTGGACCTGTGGACCTTCGGCGGAGGAACAAAGGTG GAAATCAAG
877	45	GACATCCAGATGACCCAGAGCCCTTCGACCCTATCCGCTTCCGTGGGT GACCGTGTGACCATCACCTGTCGCGCGTCGCAGAGCATCTCCTCCTGG CTCGCGTGGTACCAACAGAAGCCTGGCAAGGCCCCCAAGCTGCTGATT TACGACGCCAGTTCCCTGGAGTCTGGCGTGCCATCCCGCTTCTCCGGC AGCGGCAGCGGTACCGAGTTCACCCTGACGATCAGCTCCCTGCAGCCG GATGACTTTGCTACCTACTACTGTCAGCAGGTCTCCTCCCTCCCCCCC ACCTTCGGTGGCGGTACCAAGGTGGAGATCAAGGGCGGCGGCGGCTCT GGTGGCGGAGGTTCTGGCGGGGGAGGTTCGGGGGGGGGGAGGCTCCGAG GTGCAACTGGTAGAGAGCGGCGGGGGACTGGTAAAACCCGGCGGCTCC CTGCGGCTGTCATGCGCTGCTAGCGGCTTCACGTTCAGCGATTACTAC ATGAGTTGGATCCGCCAGGCCCCCGGGAAGGGTTTGGAGTGGGTCTCG TATATCTCTTCCAGCGGATCTACCATTTACTATGCGGACAGCGTGAAG GGGCGCTTCACCATATCTCGGGACAACGCCAAGAACTCCCTGTACCTG CAGATGAATTCCCTGCGTGCCGAGGACACGGCCGTGTATTACTGTGCC CGCGACCAGGGCAACTACGGCGTCGACGTGTGGGGCCAGGGTACAACC GTCACCGTGTCCAGT
878	59	CAAGTGCAGCTGGTCGAGAGCGGAGGAGGCCTGGTTAAGCCCGGCGGA TCTCTCAGACTGAGCTGCGCCGCTAGCGGCTTTACATTCAGCGACTAC TACATGAGCTGGATCCGGCAGGCCCCTGGCAAGGGCCTGGAATGGGTG TCCTACATCAGCTCCTCCGGCAGCACCATCTACTACGCCGACAGCGTG AAAGGCAGATTCACAATCTCTAGAGATAATGCCAAGAACAGCCTGTAC

		CTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTATTGT GCTAGAGATCAGGGCAACTACGGCGTGGACGTGTGGGGCCAGGGCACC ACCGTGACCGTGTCTAGCGGTGGTGGGGGCAGCGGTGGAGGTGGGAGC GGAGGCGGGGGTAGCGGAGGCGGGGGTAGCGATATCCAGATGACCCAG TCCCCATCTACACTGAGCGCCTCTGTGGGCGACCGGGTGACCATTACA TGTAGAGCCAGCCAGAGCATCAGCAGCTGGCTGGCTTGGTATCAGCAG AAACCTGGCAAGGCCCCTAAGCTGCTGATCTACGAGGCCAGCAGCCTG GAAAGCGGCGTCCCCAGCAGATTCAGCGGCAGCGGCTCTGGAACAGAG TTCACCCTGACCATCTCCTCCCTGCAGCCTGACGACTTCGCCACCTAC TACTGCCAGCAATCTGATAGCCACCCCATCACCTTTGGCGGAGGCACC AAGGTGGAAATCAAG
879	70	GATATCCAGATGACCCAGTCCCCATCTACACTGAGCGCCTCTGTGGGC GACCGGGTGACAATTACCTGTAGAGCTAGCCAGAGCATCTCCTCCTGG CTGGCTTGGTACCAGCAAAAACCTGGCAAGGCCCCTAAGCTGCTGATC TACGAGGCCAGCAGCCTGGAAAGCGGCGTCCCCTCTAGATTCAGCGGC AGCGGCTCTGGAACCGAGTTCACCCTGACAATCAGCAGCCTGCAGCCT GACGACTTCGCCACCTATTACTGCCAGCAGGCCAACAGCCACCCCATC ACCTTTGGCGGAGGCACCAAGGTGGAAATCAAGGGTGGTGGGGGCAGC GGTGGAGGTGGGAGCGGAGGCGGGGGTAGCGGAGGCGGGGGTAGCGAG GTGCAGCTGGTGGAAAGCGGCGGAGGACTCGTTAAGCCCGGCGGCAGC CTGAGACTGAGCTGCGCCGCTAGCGGATTTACCTTCAGCGACTACTAC ATGAGCTGGATCCGGCAGGCCCCTGGCAAGGGCCTGGAATGGGTCAGC TACATCAGCTCCTCTGGCTCTACAATCTACTACGCCGACAGCGTGAAA GGCAGATTCACCATCTCTAGAGATAATGCCAAGAACAGCCTGTACCTG CAAATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTATTGTGCT AGAGATCAGGGCAACTACGGCGTGGACGTGTGGGGCCAGGGCACCACC GTGACAGTGTCCTCC
880	80	GACATCCAGATGACCCAGAGCCCTAGCTCCCTGAGCGCCAGCGTGGGC GATAGAGTGACCATTACCTGTAGAGCCTCTCAGAGCATCTCCTCCTAC CTGAACTGGTATCAGCAGAAACCCGGCAAGGCCCCTAAGCTGCTGATC TACGCCGCTAGCAGCCTGCAGTCTGGCGTCCCCAGCCGGTTCAGCGGC AGCGGATCTGGCACCGACTTCACCCTGACAATCAGCAGCCTGCAACCT GAGGACTTTGCTACATACTACTGCCAGCAGGCCCACAGCTCTCCAATC ACCTTCGGCGGCGGAACAAAGGTGGAAATCAAGGGTGGTGGGGGCAGC GGTGGAGGTGGGAGCGGAGGCGGGGGTAGCGGAGGCGGGGGTAGCGAG GTGCAGCTGCTGGAAAGCGGAGGCGGACTCGTTCAACCTGGCGGCAGC CTGAGACTGAGCTGCGCCGCTTCTGGATTTACCTTCAGCAACTACGCC ATGAGCTGGGTGCGGCAGGCCCCTGGCAAAGGCCTGGAATGGGTCTCC GCCATCAGCGGCTCTGGCGGCTCCACCTACTACGCCGACAGCGTGAAG GGCAGATTCACCATCTCTAGAGATAATAGCAAGAACACCCTGTACCTG CAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTATTGTGCT AGACCCGGAGATGGCTACTACGAGGGCGTGTACTTCGACTACTGGGGC CAGGGCACACTGGTGACAGTGTCCAGC
881	90	GATATTCAGATGACCCAGAGCCCATCTAGCCTGAGCGCCAGCGTGGGC GATAGAGTGACCATCACCTGTCAGGCCTCTCAGGACATCGCTAATTAC CTGAACTGGTATCAGCAGAAACCCGGCAAGGCCCCTAAGCTGCTGATC TACGACGCCTCCAACCTGGAAACCGGCGTGCCCAGCCGGTTCAGCGGC AGCGGATCTGGCACAGACTTCACCTTTACCATCAGCTCCCTCCAGCCT GAGGACATCGCCACATACTACTGCCAGCAACACTTCAACCTGCCTCTG ACCTTCGGCGGCGGAACAAAGGTCGAGATCAAGGGTGGTGGGGGCAGC GGTGGAGGTGGGAGCGGAGGCGGGGGTAGCGGAGGCGGGGGTAGCCAA ATCACCCTGAAAGAGAGCGGACCTACACTGGTCAAGCCTACCCAGACA CTGACCCTCACATGTACATTCAGCGGCTTTAGCCTGAGCACCTCCGGC GTGGGAGTGGGCTGGATCAGACAGCCCCCCGGCAAGGCCCTGGAATGG CTGGCTCTGATCTATTGGAATGACGAGAAGCGGTACAGCCCTAGCCTG AAATCTAGACTGACAATCACCAAGGACACCAGCAAGAACCAGGTGGTG CTGACCATGACCAACATGGATCCTGTGGATACCGCCGTGTACTACTGC GCCAGAGAAGGCTCTCACGACTACAAGAGCTCCAACTGGTTCGACCCA TGGGGCCAGGGCACCCTGGTTACAGTGTCTAGC

882	100	GATATCGTGATGACCCAATCTCCACTGAGCCTGCCTGTGACACCTGGC GAGCCTGCTTCTATCAGCTGTAGAAGCAGCCAGTCCCTGCTGCACAGC AACGGCTACAACTACCTGGACTGGTATCTGCAGAAACCCGGCCAGAGC CCCCAGCTGCTGATCTACCTCGGCTCTAATCGGGCCAGCGGAGTGCCT GATAGATTCAGCGGAAGCGGCTCCGGCACCGACTTCACCCTGAAGATC AGCAGAGTGGAAGCCGAGGACGTGGGCGTCTACTACTGCATGCAGGCC CTGGGCCTGATTACATTTGGCGGCGGAACCAAGGTGGAAATCAAGGGT GGTGGGGGCAGCGGTGGAGGTGGGAGCGGAGGCGGGGGTAGCGGAGGC GGGGGTAGCGAAGTGCAGCTGGTTGAGAGCGGCGGCGGACTGGTGAAG CCCGGAGGCAGCCTCAGACTGAGCTGTGCTGCTTCTGGCTTTACCTTC AGCTCTTATAGCATGAACTGGGTGCGGCAGGCCCCTGGCAAGGGCCTG GAATGGGTCAGCTCCATCAGCTCTTCTAGCAGCTACATCTACTACGCC GACAGCGTGAAGGGCAGATTCACCATCAGCAGAGATAACGCCAAGAAC AGCCTGTACCTGCAGATGAATAGCCTGCGGGCCGAGGACACCGCCGTG TACTACTGCGCCAGAGCCGGCGACACCTACAGCGCCGCCGATTACTAC TACATGGACGTGTGGGGCAAAGGAACAACCGTGACAGTGTCCTCC
883	101	GAAGTGCAACTGCTGGAAAGCGGCGGAGGCCTGGTCCAGCCCGGCGGC TCTCTGCGGCTCAGCTGCGCCGCTTCTGGATTTACCTTCGGCAGCGAG GCTATGAGCTGGGTGCGGCAGGCCCCTGGAAAAGAGAGAGAGCTGGTG TCCGCCATCAGCGGCAGCGGCGAGGTGACCTACTACGCCGACAGCGTG AAGGGCAGATTCACCATCTCTAGAGATAATAGCAAGAACACCCTGTAC CTGCAGATGAACAGCCTGAGAGCCGAGGACACCGCCGTGTACTATTGT CAGAGACTGGTGGAAGCCAAGCGGCACTGGGGCCAGGGCACACAGGTT ACAGTGTCCAGC
884	105	GAAGTGCAACTGCTGGAATCTGGCGGAGGACTGGTGCAGCCCGGCGGC AGCCTGCGGCTGAGCTGTGCTGCTTCTGGCTTTACCTTCGAGTCTGAG GCCATGAGCTGGTATAGACAGGCCCCTGGCAAGGAAAGAGAGCTGGTC AGCGTGATCACCAGCGAGGGCTCCACCTACTACGCCGACAGCGTGAAA GGCAGATTCACAATCAGCCGGGACAATAGCAAGAACACCCTGTACCTG CAGATGAACAGCCTGCGCGCCGAAGATACAGCCGTGTACTACTGCGCC CACATCGAGTGGGAGACAAGACTCAACTGGGGCCAGGGCACCCAGGTG ACCGTGTCCAGC
885	109	GAGGTGCAGCTGCTGGAAAGCGGAGGGGGCCTGGTCCAACCCGGCGGG TCTCTTCGCCTAAGCTGTGCCGCTTCTGGCTTCACCTTCGACGAGTAC ACCATGCACTGGTTCAGACAGGCCCCCGGCAAGGAGCGCGAGTTCGTC AGTGCAATCAGCGGAGGCGGTAGCGAGACTTATTACGCGGACTCCGTG AAGGGCCGCTTCACCATTAGCCGCGACAACTCCAAGAACACGCTGTAC CTGCAGATGAATTCGCTGCGCGCCGAAGATACGGCCGTGTACTACTGT GCCGCTGGTGGGGAGGAGGCTGGCGTGGGCTATTGGGGCCAGGGCACC CAGGTCACCGTGTCGTCC
886	113	GAGGTGCAGCTGCTGGAGAGCGGAGGCGGCCTCGTGCAGCCAGGAGGT TCCCTACGACTCTCCTGTGCCGCCAGCGGCTTCACCTTCGAGGACTAC GCCATGAGTTGGTTCCGCCAGGCCCCGGGGAAGGAGCGCGAGGGCGTG AGCGCGATTTCTGGAAAGGGCGGCTCCACCTATTACGCGGACTCCGTG AAGGGTCGCTTTACCATCTCTCGCGACAACTCCAAGAACACGCTGTAC CTGCAGATGAATAGCCTGCGCGCTGAGGACACTGCCGTGTACTACTGT GCTGTCTTGGACGAGGAGGCCGGCGCAGAGGGCGGCTATTGGGGCCAG GGTACCCAGGTCACCGTGTCGTCC
887	117	GAGGTGCAACTGCTGGAAAGCGGCGGTGGACTGGTGCAGCCCGGCGGC AGCCTGAGACTGTCTTGTGCTGCTTCTGGATTTACATTCGACAGATAC GCCATGAGCTGGTTCCGCCAGGCCCCTGGCAAAGAGCGGGAAGGCGTG TCCGCCATCTCCACAAGCGGAGATAGCACATACTATGCCGACAGCGTG AAGGGCAGATTCACCATCAGCAGAGATAATAGCAAGAACACCCTGTAC CTGCAGATGAACAGCCTCCGGGCCGAGGACACCGCCGTCTACTACTGC GCCGTGCTGGACGAGGAAGCCGGCGCCGAGGGCGGCTACTGGGGCCAG GGCACCCAGGTGACCGTGTCTAGC
888	121	GAGGTGCAACTGCTGGAAAGCGGCGGAGGACTCGTCCAGCCCGGCGGC AGCCTGCGGCTGAGCTGTGCTGCTTCTGGATTTACCTTCGCCAGCGAC GCCATGAGCTGGTATAGACAGGCCCCTGGCAAAGAGCGGGAACTGGTG

		TCCGCCATCAGCGGCTCTGGCGGCTCCACCTACTACGCCGATAGCGTG AAGGGCAGATTCACAATCTCTAGAGATAATAGCAAGAACACCCTGTAC CTGCAGATGAACAGCCTGAGAGCCGAGGACACCGCCGTGTACTACTGC GCCGCTCACGACAGCGGCGAGGCCTACCTGGCCTTCGACTACTGGGGC CAGGGCACACAGGTGACCGTGTCTAGC
889	125	GAGGTGCAACTGCTGGAAAGCGGCGGAGGACTCGTCCAGCCCGGCGGC AGCCTGAGGCTGAGCTGTGCTGCTTCTGGCTTTACCTTCGACTCCTAC ACAATGAGCTGGTATAGACAGGCCCCTGGCAAGGAGCGGGAACTGGTG TCCGCCATCAGCGGCCACGGCGACTCTACATACTACGCCGACAGCGTG AAAGGCAGATTCACAATCTCTAGAGATAATAGCAAGAACACCCTGTAC CTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGC ACCAGAATCAGCATCACCACCGAGTGGCTGGCCGGAGATTACTGGGGC CAGGGCACCCAGGTGACAGTGTCCAGC
890	129	GAGGTGCAGCTGCTGGAAAGCGGAGGAGGCCTGGTCCAACCTGGCGGC AGCCTGCGGCTGAGCTGCGCCGCTTCTGGCTTCACCTTCAGCAGCTAC GCCATGAGCTGGTTCCGGCAGGCCCCTGGCAAGGAAAGAGAGTTCGTG TCTTTTATCAGCGGATCTGGCGACTCCACCTACTACGCTGATAGCGTG AAAGGCAGATTTACCATCTCTAGAGATAATAGCAAGAACACCCTGTAC CTCCAGATGAACAGCCTGCGCGCCGAGGACACAGCCGTGTACTATTGT ACCAGATGGCCTTACGACTTCGAGGAACCAAGCGAGCCCGGCGTGTAC TGGGGCCAGGGCACACAGGTGACAGTGTCCTCC
891	133	GAGGTGCAGCTGCTGGAAAGCGGCGGAGGCCTGGTGCAACCTGGCGGA TCTCTCAGACTGAGCTGTGCTGCTTCTGGCTTCACATTCACCGACTAC GACATGAGCTGGTATAGACAGGCCCCTGGAAAAGAGCGGGAACTGGTC TCCGTGATCCACAGCGGCGGCTCCACCTACTACGCCGATAGCGTGAAG GGCAGATTCACCATCAGCAGAGATAATAGCAAGAACACCCTGTACCTG CAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCGCC CCCGGCTACTACAGCGACCTGTCTTTTGATTATTACAACTTCGACTAC TGGGGCCAGGGCACACAGGTGACAGTGTCCAGC
892	137	GAGGTGCAGCTGCTGGAGAGCGGTGGAGGGTTGGTGCAGCCCGGGGGT AGCCTGCGTCTGTCGTGCGCCGCTTCCGGCTTCACGTTCTCTGATTAC GCCATGCACTGGTTCCGGCAGGCCCCCGGTAAGGAGCGCGTGCTGGTG TCGTCTATTGACTCCGGCGGCTCCACTTACTACGCAGACAGTGTCAAG GGCCGTTTCACCATCAGCCGCGACAACAGCAAGAACACGCTGTACCTG CAGATGAACTCCCTTCGAGCAGAGGACACCGCGGTGTACTACTGTAAT GCGGGCTTCAAGGGCGATCACCCCCACCCCAAGGATGCCTTCGACATT TGGGGCCAGGGCACCCAGGTCACCGTGTCGTCC
893	141	GAGGTGCAACTGCTGGAATCCGGCGGAGGCCTGGTGCAGCCCGGCGGC AGCCTCAGACTGAGCTGTGCCGCTTCTGGCTTTACCTTCAGCAGCGAG GGCATGAGCTGGGTGCGGCAGGCCCCTGGCAAGGAAAGAGAGCTGGTC TCCGCCATCAGCGGATCTGGCGACCACACCTACTATGCCGATAGCGTG CGCGGAAGATTCACAATCTCTAGAGATAATAGCAAGAACACCCTGTAC CTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGC AACGCCCTGGAAGGCGGCCCTACAACAGCTATCCAGCCAGGAGGCCCT GACTACTGGGGCCAGGGCACCCAGGTGACCGTGTCCAGC

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, Mosl, Tcl/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 Dalgamo sequence or Kozak sequence), introns, polyadenylation signals, 5′ and 3′ untranslated regions, all of which may interact with host 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 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 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 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 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 (EFlα) short promoter (intronless), an EFlα 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	GCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGAC

	GTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTG GAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCC CTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGA CTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTCGAGGTGAGCCCC ACGTTCTGCTTCACTCTCCCCATCTCCCCCCCCTCCCCACCCCCAATTTTGTATTTATTTATTT TTTAATTATTTTGTGCAGCGATGGGGGCGGGGGGGGGGGGGGGCGCGCGCCAGGCGGGGCGGG GCGGGGCGAGGGGCGGGGCGGGGCGAGGCGGAGAGGTGCGGCGGCAGCCAATCAGAGCGGCGCG CTCCGAAAGTTTCCTTTTATGGCGAGGCGGCGGCGGCGGCGGCCCTATAAAAAGCGAAGCGCGC GGCGGGCG
949	CGTGAGGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCACAGTCCCCGAGAAGTTGGG GGGAGGGGTCGGCAATTGAACCGGTGCCTAGAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGAT GTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCG CCGTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGGTAAGTGCCGTGTGTGGTTC CCGCGGGCCTGGCCTCTTTACGGGTTATGGCCCTTGCGTGCCTTGAATTACTTCCACCTGGCTG CAGTACGTGATTCTTGATCCCGAGCTTCGGGTTGGAAGTGGGTGGGAGAGTTCGAGGCCTTGCG CTTAAGGAGCCCCTTCGCCTCGTGCTTGAGTTGAGGCCTGGCCTGGGCGCTGGGGCCGCCGCGT GCGAATCTGGTGGCACCTTCGCGCCTGTCTCGCTGCTTTCGATAAGTCTCTAGCCATTTAAAAT TTTTGATGACCTGCTGCGACGCTTTTTTTCTGGCAAGATAGTCTTGTAAATGCGGGCCAAGATC TGCACACTGGTATTTCGGTTTTTGGGGCCGCGGGCGGCGACGGGGCCCGTGCGTCCCAGCGCAC ATGTTCGGCGAGGCGGGGCCTGCGAGCGCGGCCACCGAGAATCGGACGGGGGTAGTCTCAAGCT GGCCGGCCTGCTCTGGTGCCTGGCCTCGCGCCGCCGTGTATCGCCCCGCCCTGGGCGGCAAGGC TGGCCCGGTCGGCACCAGTTGCGTGAGCGGAAAGATGGCCGCTTCCCGGCCCTGCTGCAGGGAG CTCAAAATGGAGGACGCGGCGCTCGGGAGAGCGGGCGGGTGAGTCACCCACACAAAGGAAAAGG GCCTTTCCGTCCTCAGCCGTCGCTTCATGTGACTCCACGGAGTACCGGGCGCCGTCCAGGCACC TCGATTAGTTCTCGAGCTTTTGGAGTACGTCGTCTTTAGGTTGGGGGGAGGGGTTTTATGCGAT GGAGTTTCCCCACACTGAGTGGGTGGAGACTGAAGTTAGGCCAGCTTGGCACTTGATGTAATTC TCCTTGGAATTTGCCCTTTTTGAGTTTGGATCTTGGTTCATTCTCAAGCCTCAGACAGTGGTTC AAAGTTTTTTTCTTCCATTTCAGGTGTCGTGA
950	AATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGGATCAAGGTTAGGAACAGAGAGACAGCAG AATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGT TGGAACAGCAGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGG CCAAGAACAGATGGTCCCCAGATGCGGTCCCGCCCTCAGCAGTTTCTAGAGAACCATCAGATGT TTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGC TTCTCGCTTCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACT CGGC
951	GGGTAGGGGAGGCGCTTTTCCCAAGGCAGTCTGGAGCATGCGCTTTAGCAGCCCCGCTGGGCAC TTGGCGCTACACAAGTGGCCTCTGGCCTCGCACACATTCCACATCCACCGGTAGGCGCCAACCG GCTCCGTTCTTTGGTGGCCCCTTCGCGCCACCTTCTACTCCTCCCCTAGTCAGGAAGTTCCCCC CCGCCCCGCAGCTCGCGTCGTGCAGGACGTGACAAATGGAAGTAGCACGTCTCACTAGTCTCGT GCAGATGGACAGCACCGCTGAGCAATGGAAGCGGGTAGGCCTTTGGGGCAGCGGCCAATAGCAG CTTTGCTCCTTCGCTTTCTGGGCTCAGAGGCTGGGAAGGGGTGGGTCCGGGGGCGGGCTCAGGG GCGGGCTCAGGGGCGGGGCGGGCGCCCGAAGGTCCTCCGGAGGCCCGGCATTCTGCACGCTTCA AAAGCGCACGTCTGCCGCGCTGTTCTCCTCTTCCTCATCTCCGGGCCTTTCG
952	TGAAAGACCCCACCTGTAGGTTTGGCAAGATAGCTGCAGTAACGCCATTTTGCAAGGCATGGAA AAATACCAAACCAAGAATAGAGAAGTTCAGATCAAGGGCGGGTACATGAAAATAGCTAACGTTG GGCCAAACAGGATATCTGCGGTGAGCAGTTTCGGCCCCGGCCCGGGGCCAAGAACAGATGGTCA CCGCAGTTTCGGCCCCGGCCCGAGGCCAAGAACAGATGGTCCCCAGATATGGCCCAACCCTCAG CAGTTTCTTAAGACCCATCAGATGTTTCCAGGCTCCCCCAAGGACCTGAAATGACCCTGCGCCT TATTTGAATTAACCAATCAGCCTGCTTCTCGCTTCTGTTCGCGCGCTTCTGCTTCCCGAGCTCT ATAAAAGAGCTCACAACCCCTCACTCGGCGCGCCAGTCCTCCGATTGACTGAGTCGCCC
953	GGCCTCCGCGCCGGGTTTTGGCGCCTCCCGCGGGCGCCCCCCTCCTCACGGCGAGCGCTGCCAC GTCAGACGAAGGGCGCAGCGAGCGTCCTGATCCTTCCGCCCGGACGCTCAGGACAGCGGCCCGC TGCTCATAAGACTCGGCCTTAGAACCCCAGTATCAGCAGAAGGACATTTTAGGACGGGACTTGG GTGACTCTAGGGCACTGGTTTTCTTTCCAGAGAGCGGAACAGGCGAGGAAAAGTAGTCCCTTCT CGGCGATTCTGCGGAGGGATCTCCGTGGGGCGGTGAACGCCGATGATTATATAAGGACGCGCCG GGTGTGGCACAGCTAGTTCCGTCGCAGCCGGGATTTGGGTCGCGGTTCTTGTTTGTGGATCGCT GTGATCGTCACTTGGTGAGTAGCGGGCTGCTGGGCTGGCCGGGGCTTTCGTGGCCGCCGGGCCG CTCGGTGGGACGGAAGCGTGTGGAGAGACCGCCAAGGGCTGTAGTCTGGGTCCGCGAGCAAGGT TGCCCTGAACTGGGGGTTGGGGGGAGCGCAGCAAAATGGCGGCTGTTCCCGAGTCTTGAATGGA

	AGACGCTTGTGAGGCGGGCTGTGAGGTCGTTGAAACAAGGTGGGGGGCATGGTGGGCGGCAAGA ACCCAAGGTCTTGAGGCCTTCGCTAATGCGGGAAAGCTCTTATTCGGGTGAGATGGGCTGGGGC ACCATCTGGGGACCCTGACGTGAAGTTTGTCACTGACTGGAGAACTCGGTTTGTCGTCTGTTGC GGGGGCGGCAGTTATGGCGGTGCCGTTGGGCAGTGCACCCGTACCTTTGGGAGCGCGCGCCCTC GTCGTGTCGTGACGTCACCCGTTCTGTTGGCTTATAATGCAGGGTGGGGCCACCTGCCGGTAGG TGTGCGGTAGGCTTTTCTCCGTCGCAGGACGCAGGGTTCGGGCCTAGGGTAGGCTCTCCTGAAT CGACAGGCGCCGGACCTCTGGTGAGGGGAGGGATAAGTGAGGCGTCAGTTTCTTTGGTCGGTTT TATGTACCTATCTTCTTAAGTAGCTGAAGCTCCGGTTTTGAACTATGCGCTCGGGGTTGGCGAG TGTGTTTTGTGAAGTTTTTTAGGCACCTTTTGAAATGTAATCATTTGGGTCAATATGTAATTTT CAGTGTTAGACTAGTAAATTGTCCGCTAAATTCTGGCCGTTTTTGGCTTTTTTGTTAGAC

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	AATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTC CTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTAT

	GGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTGCTGTCTCTTTATGAGGAGTTGTGG CCCGTTGTCAGGCAACGTGGCGTGGTGTGCACTGTGTTTGCTGACGCAACCCCCACTGGTT GGGGCATTGCCACCACCTGTCAGCTCCTTTCCGGGACTTTCGCTTTCCCCCTCCCTATTGC CACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGC ACTGACAATTCCGTGGTGTTGTCGGGGAAGCTGACGTCCTTTCCATGGCTGCTCGCCTGTG TTGCCACCTGGATTCTGCGCGGGACGTCCTTCTGCTACGTCCCTTCGGCCCTCAATCCAGC GGACCTTCCTTCCCGCGGCCTGCTGCCGGCTCTGCGGCCTCTTCCGCGTCTTCGCCTTCGC CCTCAGACGAGTCGGATCTCCCTTTGGGCCGCCTCCCCGCCTG
946	AATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTC CTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTAT GGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTGCTGTCTCTTTATGAGGAGTTGTGG CCCGTTGTCAGGCAACGTGGCGTGGTGTGCACTGTGTTTGCTGACGCAACCCCCACTGGTT GGGGCATTGCCACCACCTGTCAGCTCCTTTCCGGGACTTTCGCTTTCCCCCTCCCTATTGC CACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGC ACTGACAATTCCGTGGTGTTGTCGGGGAAGGTCTGCTGAGACTCGGGGCTGCTCGCCTGTG TTGCCACCTGGATTCTGCGCGGGACGTCCTTCTGCTACGTCCCTTCGGCCCTCAATCCAGC GGACCTTCCTTCCCGCGGCCTGCTGCCGGCTCTGCGGCCTCTTCCGCGTCTTCGCCTTCGC CCTCAGACGAGTCGGATCTCCCTTTGGGCCGCCTCCCCGCCTG
947	AATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGATATTCTTAACTATGTTGCTC CTTTTACGCTGTGTGGATATGCTGCTTTAATGCCTCTGTATCATGCTATTGCTTCCCGTAC GGCTTTCGTTTTCTCCTCCTTGTATAAATCCTGGTTGCTGTCTCTTTATGAGGAGTTGTGG CCCGTTGTCCGTCAACGTGGCGTGGTGTGCTCTGTGTTTGCTGACGCAACCCCCACTGGCT GGGGCATTGCCACCACCTGTCAACTCCTTTCTGGGACTTTCGCTTTCCCCCTCCCGATCGC CACGGCAGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTAGGTTGCTGGGC ACTGATAATTCCGTGGTGTTGTC

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.

In particular embodiments, a vector comprises or encodes (in the case of an RNA vector, *e.g.*, a retroviral vector) an EF1α 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, a vector comprises or encodes an EF1α 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 EF1α 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 EF1α 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 EF1α 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 EF1α 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 EF1α 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 EF1α 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 EF1α 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 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

hormone poly(A) signal (BGHpA), a rabbit β-globin poly(A) signal (rβgpA), 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 peptide isolated from a polypeptide selected from the group consisting of CD8α, murine IgGκ, human IgGk, 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 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 (ATGGCTCTTCCCGTAACAGCCCTTTTGTTGCCCCTTGCACTCCTTCTGCATGCA GCACGACCG).

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 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 phosphribosyltransferase (HPRT) gene, the cellular adenine phosphoribosyltransferase (APRT) gene, and bacterial cytosine deaminase.

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

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.

Table 9

SEQ ID NO.	AA SEQ ID NO.	NUCLEIC ACID SEQUENCE
894	145	ACCACAACACCTGCTCCAAGGCCCCCCACACCCGCTCCAACTATAGCCA GCCAACCATTGAGCCTCAGACCTGAAGCTTGCAGGCCCGCAGCAGGAGG CGCCGTCCATACGCGAGGCCTGGACTTCGCGTGTGAT
895	146	ATTGAAGTTATGTATCCTCCTCCTTACCTAGACAATGAGAAGAGCAATG GAACCATTATCCATGTGAAAGGGAAACACCTTTGTCCAAGTCCCCTATT TCCCGGACCTTCTAAGCCC
896	148	GAGTCCAAATATGGTCCCCCGTGCCCACCATGCCCA
897	150	CTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA
898	151	ATTTATATTTGGGCACCTTTGGCCGGAACATGTGGGGTGTTGCTTCTCT CCCTTGTGATCACTCTGTATTGT
899	153	TTTTGGGTGCTGGTGGTGGTTGGTGGAGTCCTGGCTTGCTATAGCTTGC TAGTAACAGTGGCCTTTATTATTTTCTGGGTG
900	159	AAGCGCGGGAGAAAGAAGCTCCTGTACATCTTCAAGCAGCCTTTTATGC GACCTGTGCAAACCACTCAGGAAGAAGATGGGTGTTCATGCCGCTTCCC CGAGGAGGAAGAAGGAGGGTGTGAACTG
901	160	AGGAGTAAGAGGAGCAGGCTCCTGCACAGTGACTACATGAACATGACTC CCCGCCGCCCCGGGCCCACCCGCAAGCATTACCAGCCCTATGCCCCACC ACGCGACTTCGCAGCCTATCGCTCC
902	162	ACAAAAAAGAAGTATTCATCCAGTGTGCACGACCCTAACGGTGAATACA TGTTCATGAGAGCAGTGAACACAGCCAAAAAATCTAGACTCACAGATGT GACCCTA
903	158	AGGGTGAAATTTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAGGGTC AGAATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAGAAGAGTACGA TGTTCTGGACAAAAGACGGGGCAGGGATCCCGAGATGGGGGGAAAGCCC CGGAGAAAAAATCCTCAGGAGGGGTTGTACAATGAGCTGCAGAAGGACA AGATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGAAAGACGCAG AGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTACAGCCACCAAG GACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCCCGC
904	861	ATGGCTCTTCCCGTAACAGCCCTTTTGTTGCCCCTTGCACTCCTTCTGC ATGCAGCACGACCG
905	189	GAGATCGTGCTGACACAGTCTCCCGCCACACTGTCACTGTCTCCAGGCG AAAGAGCCACACTGAGCTGTAGAGCCAGCCAGAGCGTGTCCTCTTACCT GGCCTGGTATCAGCAGAAGCCTGGACAGGCTCCCCGGCTGCTGATCTAC GATGCCAGCAATAGAGCCACAGGCATCCCCGCCAGATTTTCTGGCAGCG GCTCTGGCACCGATTTCACCCTGACCATAAGCAGCCTGGAACCTGAGGA CTTCGCCGTGTACTACTGCCAGCAGAGAGTGGTGTACCCCATCACCTTT GGCGGAGGCACCAAGGTGGAAATCAAAGGCGGCGGAGGAAGCGGAGGCG GAGGATCTGGTGGTGGTGGATCTGGCGGAGGTGGCAGCCAGATCACACT GAAAGAGTCTGGCCCCACACTGGTCAAGCCCACACAGACCCTGACACTG ACCTGCACCTTCAGCGGCTTTAGCCTGAGCACATCTGGCGTCGGCGTTG GCTGGATTAGACAGCCTCCTGGAAAGGCCCTGGAATGGCTGGCCCTGAT CTACTGGAACGACGAGAAGAGATACAGCCCCAGCCTGAAGTCCCGGCTG ACCATCACCAAGGACACCAGCAAGAACCAGGTGGTGCTGACCATGACAA ACATGGACCCCGTGGACACCGCCGTGTATTATTGCGCCAGAGATGAGTA CGGCGGCTTCGACATTTGGGGCCAGGGCACAATGGTCACCGTGTCTAGT ACCACAACACCTGCTCCAAGGCCCCCCACACCCGCTCCAACTATAGCCA

		GCCAACCATTGAGCCTCAGACCTGAAGCTTGCAGGCCCGCAGCAGGAGG CGCCGTCCATACGCGAGGCCTGGACTTCGCGTGTGATATTTATATTTGG GCACCTTTGGCCGGAACATGTGGGGTGTTGCTTCTCTCCCTTGTGATCA CTCTGTATTGTAAGCGCGGGAGAAAGAAGCTCCTGTACATCTTCAAGCA GCCTTTTATGCGACCTGTGCAAACCACTCAGGAAGAAGATGGGTGTTCA TGCCGCTTCCCCGAGGAGGAAGAAGGAGGGTGTGAACTGAGGGTGAAAT TTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAGGGTCAGAATCAGCT CTACAATGAATTGAATCTCGGCAGGCGAGAAGAGTACGATGTTCTGGAC AAAAGACGGGGCAGGGATCCCGAGATGGGGGGAAAGCCCCGGAGAAAAA ATCCTCAGGAGGGGTTGTACAATGAGCTGCAGAAGGACAAGATGGCTGA AGCCTATAGCGAGATCGGAATGAAAGGCGAAAGACGCAGAGGCAAGGGG CATGACGGTCTGTACCAGGGTCTCTCTACAGCCACCAAGGACACTTATG ATGCGTTGCATATGCAAGCCTTGCCACCCCGC
906	237	GAGATCGTGCTGACCCAGTCCCCTGCTACCCTGAGCCTGTCTCCAGGCG AGCGGGCCACACTGAGCTGTAGAGCTTCTCAGAGCGTGTCCAGCTACCT GGCCTGGTATCAGCAGAAACCTGGCCAGGCCCCTAGACTGCTGATCTAC GACGCCAGCAACCGGGCCACCGGCATCCCCGCCAGATTCAGCGGATCTG GCAGCGGCACAGATTTTACCCTCACCATCAGCAGCCTGGAACCTGAGGA CTTCGCCGTCTACTACTGCCAGCAAAGATTCGACTACCCCATCACCTTC GGCGGCGGAACAAAGGTGGAAATTAAGGGTGGTGGGGGCAGCGGTGGAG GTGGGAGCGGAGGCGGGGGTAGCGGAGGCGGGGGTAGCCAAATCACACT GAAAGAGAGCGGCCCTACACTCGTGAAACCTACCCAGACCCTGACACTG ACATGTACCTTCAGCGGCTTCTCCCTGAGCACCTCTGGCGTCGGCGTTG GATGGATCAGACAGCCTCCAGGCAAGGCCCTGGAATGGCTGGCTCTGAT CTATTGGAACGACGACAAGCGGTACAGCCCCAGCCTGAAGTCTAGACTG ACCATCACAAAGGACACCAGCAAGAACCAGGTGGTGCTGACCATGACAA ATATGGACCCCGTGGACACCGCCGTGTACTACTGCGCCAGAGATGAGTA CGGCGGATTTGATATCTGGGGCCAGGGCACCATGGTGACCGTGTCCAGC ACCACAACACCTGCTCCAAGGCCCCCCACACCCGCTCCAACTATAGCCA GCCAACCATTGAGCCTCAGACCTGAAGCTTGCAGGCCCGCAGCAGGAGG CGCCGTCCATACGCGAGGCCTGGACTTCGCGTGTGATATTTATATTTGG GCACCTTTGGCCGGAACATGTGGGGTGTTGCTTCTCTCCCTTGTGATCA CTCTGTATTGTAAGCGCGGGAGAAAGAAGCTCCTGTACATCTTCAAGCA GCCTTTTATGCGACCTGTGCAAACCACTCAGGAAGAAGATGGGTGTTCA TGCCGCTTCCCCGAGGAGGAAGAAGGAGGGTGTGAACTGAGGGTGAAAT TTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAGGGTCAGAATCAGCT CTACAATGAATTGAATCTCGGCAGGCGAGAAGAGTACGATGTTCTGGAC AAAAGACGGGGCAGGGATCCCGAGATGGGGGGAAAGCCCCGGAGAAAAA ATCCTCAGGAGGGGTTGTACAATGAGCTGCAGAAGGACAAGATGGCTGA AGCCTATAGCGAGATCGGAATGAAAGGCGAAAGACGCAGAGGCAAGGGG CATGACGGTCTGTACCAGGGTCTCTCTACAGCCACCAAGGACACTTATG ATGCGTTGCATATGCAAGCCTTGCCACCCCGC
907	261	CAAGTGCAGCTCGTGGAAAGCGGCGGCGGAGTGGTGCAGCCCGGCCGGA GCCTGAGACTGTCCTGCGCCGCTTCTGGATTTACCTTCAGCAGCTACGG CATGCACTGGGTCAGACAGGCCCCTGGCAAAGGCCTGGAGTGGGTGGCC GTTATCAGCTACGAGGGCAGCAACAAGTATTACGCCGACAGCGTGAAGG GCCGCTTCACAATCTCTAGAGATAATAGCAAGAACACCCTGTACCTGCA GATGAACAGCCTGCGGGCCGAAGATACCGCCGTGTACTACTGTGCTAGA GAGCTGGGCGACGGCATGGACGTGTGGGGACAGGGCACAACCGTGACCG TGTCCTCTGGTGGTGGGGGCAGCGGTGGAGGTGGGAGCGGAGGCGGGGG TAGCGGAGGCGGGGGTAGCGAGATCGTGCTGACCCAGTCCCCTGCTACA CTGAGCCTGTCTCCAGGCGAGCGGGCCACACTGAGCTGTAGAGCTTCTC AGAGCGTGTCCAGCTATCTGGCCTGGTTCCAGCAGAAACCTGGCCAGGC CCCTAGACTGCTGATCTACGACGCCAGCAACCGGGCCACCGGCATCCCC GCCAGATTCAGCGGCTCTGGCAGCGGCACCGACTTCACCCTCACCATCA GCAGCCTGGAACCCGAGGATTTTGCCGTCTACTACTGCCAGCAAAGAGT GGACCTGTGGACCTTCGGCGGAGGAACAAAGGTGGAAATCAAGACCACA ACACCTGCTCCAAGGCCCCCCACACCCGCTCCAACTATAGCCAGCCAAC CATTGAGCCTCAGACCTGAAGCTTGCAGGCCCGCAGCAGGAGGCGCCGT

		CCATACGCGAGGCCTGGACTTCGCGTGTGATATTTATATTTGGGCACCT TTGGCCGGAACATGTGGGGTGTTGCTTCTCTCCCTTGTGATCACTCTGT ATTGTAAGCGCGGGAGAAAGAAGCTCCTGTACATCTTCAAGCAGCCTTT TATGCGACCTGTGCAAACCACTCAGGAAGAAGATGGGTGTTCATGCCGC TTCCCCGAGGAGGAAGAAGGAGGGTGTGAACTGAGGGTGAAATTTTCTA GAAGCGCCGATGCTCCCGCATATCAGCAGGGTCAGAATCAGCTCTACAA TGAATTGAATCTCGGCAGGCGAGAAGAGTACGATGTTCTGGACAAAAGA CGGGGCAGGGATCCCGAGATGGGGGGAAAGCCCCGGAGAAAAAATCCTC AGGAGGGGTTGTACAATGAGCTGCAGAAGGACAAGATGGCTGAAGCCTA TAGCGAGATCGGAATGAAAGGCGAAAGACGCAGAGGCAAGGGGCATGAC GGTCTGTACCAGGGTCTCTCTACAGCCACCAAGGACACTTATGATGCGT TGCATATGCAAGCCTTGCCACCCCGC
908	333	GACATCCAGATGACCCAGAGCCCTTCGACCCTATCCGCTTCCGTGGGTG ACCGTGTGACCATCACCTGTCGCGCGTCGCAGAGCATCTCCTCCTGGCT CGCGTGGTACCAACAGAAGCCTGGCAAGGCCCCCAAGCTGCTGATTTAC GACGCCAGTTCCCTGGAGTCTGGCGTGCCATCCCGCTTCTCCGGCAGCG GCAGCGGTACCGAGTTCACCCTGACGATCAGCTCCCTGCAGCCGGATGA CTTTGCTACCTACTACTGTCAGCAGGTCTCCTCCCTCCCCCCCACCTTC GGTGGCGGTACCAAGGTGGAGATCAAGGGCGGCGGCGGCTCTGGTGGCG GAGGTTCTGGCGGGGGAGGTTCGGGGGGGGGAGGCTCCGAGGTGCAACT GGTAGAGAGCGGCGGGGGACTGGTAAAACCCGGCGGCTCCCTGCGGCTG TCATGCGCTGCTAGCGGCTTCACGTTCAGCGATTACTACATGAGTTGGA TCCGCCAGGCCCCCGGGAAGGGTTTGGAGTGGGTCTCGTATATCTCTTC CAGCGGATCTACCATTTACTATGCGGACAGCGTGAAGGGGCGCTTCACC ATATCTCGGGACAACGCCAAGAACTCCCTGTACCTGCAGATGAATTCCC TGCGTGCCGAGGACACGGCCGTGTATTACTGTGCCCGCGACCAGGGCAA CTACGGCGTCGACGTGTGGGGCCAGGGTACAACCGTCACCGTGTCCAGT ACCACAACACCTGCTCCAAGGCCCCCCACACCCGCTCCAACTATAGCCA GCCAACCATTGAGCCTCAGACCTGAAGCTTGCAGGCCCGCAGCAGGAGG CGCCGTCCATACGCGAGGCCTGGACTTCGCGTGTGATATTTATATTTGG GCACCTTTGGCCGGAACATGTGGGGTGTTGCTTCTCTCCCTTGTGATCA CTCTGTATTGTAAGCGCGGGAGAAAGAAGCTCCTGTACATCTTCAAGCA GCCTTTTATGCGACCTGTGCAAACCACTCAGGAAGAAGATGGGTGTTCA TGCCGCTTCCCCGAGGAGGAAGAAGGAGGGTGTGAACTGAGGGTGAAAT TTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAGGGTCAGAATCAGCT CTACAATGAATTGAATCTCGGCAGGCGAGAAGAGTACGATGTTCTGGAC AAAAGACGGGGCAGGGATCCCGAGATGGGGGGAAAGCCCCGGAGAAAAA ATCCTCAGGAGGGGTTGTACAATGAGCTGCAGAAGGACAAGATGGCTGA AGCCTATAGCGAGATCGGAATGAAAGGCGAAAGACGCAGAGGCAAGGGG CATGACGGTCTGTACCAGGGTCTCTCTACAGCCACCAAGGACACTTATG ATGCGTTGCATATGCAAGCCTTGCCACCCCGC
909	357	CAAGTGCAGCTGGTCGAGAGCGGAGGAGGCCTGGTTAAGCCCGGCGGAT CTCTCAGACTGAGCTGCGCCGCTAGCGGCTTTACATTCAGCGACTACTA CATGAGCTGGATCCGGCAGGCCCCTGGCAAGGGCCTGGAATGGGTGTCC TACATCAGCTCCTCCGGCAGCACCATCTACTACGCCGACAGCGTGAAAG GCAGATTCACAATCTCTAGAGATAATGCCAAGAACAGCCTGTACCTGCA GATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTATTGTGCTAGA GATCAGGGCAACTACGGCGTGGACGTGTGGGGCCAGGGCACCACCGTGA CCGTGTCTAGCGGTGGTGGGGGCAGCGGTGGAGGTGGGAGCGGAGGCGG GGGTAGCGGAGGCGGGGGTAGCGATATCCAGATGACCCAGTCCCCATCT ACACTGAGCGCCTCTGTGGGCGACCGGGTGACCATTACATGTAGAGCCA GCCAGAGCATCAGCAGCTGGCTGGCTTGGTATCAGCAGAAACCTGGCAA GGCCCCTAAGCTGCTGATCTACGAGGCCAGCAGCCTGGAAAGCGGCGTC CCCAGCAGATTCAGCGGCAGCGGCTCTGGAACAGAGTTCACCCTGACCA TCTCCTCCCTGCAGCCTGACGACTTCGCCACCTACTACTGCCAGCAATC TGATAGCCACCCCATCACCTTTGGCGGAGGCACCAAGGTGGAAATCAAG ACCACAACACCTGCTCCAAGGCCCCCCACACCCGCTCCAACTATAGCCA GCCAACCATTGAGCCTCAGACCTGAAGCTTGCAGGCCCGCAGCAGGAGG CGCCGTCCATACGCGAGGCCTGGACTTCGCGTGTGATATTTATATTTGG

		GCACCTTTGGCCGGAACATGTGGGGTGTTGCTTCTCTCCCTTGTGATCA CTCTGTATTGTAAGCGCGGGAGAAAGAAGCTCCTGTACATCTTCAAGCA GCCTTTTATGCGACCTGTGCAAACCACTCAGGAAGAAGATGGGTGTTCA TGCCGCTTCCCCGAGGAGGAAGAAGGAGGGTGTGAACTGAGGGTGAAAT TTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAGGGTCAGAATCAGCT CTACAATGAATTGAATCTCGGCAGGCGAGAAGAGTACGATGTTCTGGAC AAAAGACGGGGCAGGGATCCCGAGATGGGGGGAAAGCCCCGGAGAAAAA ATCCTCAGGAGGGGTTGTACAATGAGCTGCAGAAGGACAAGATGGCTGA AGCCTATAGCGAGATCGGAATGAAAGGCGAAAGACGCAGAGGCAAGGGG CATGACGGTCTGTACCAGGGTCTCTCTACAGCCACCAAGGACACTTATG ATGCGTTGCATATGCAAGCCTTGCCACCCCGC
910	429	GATATCCAGATGACCCAGTCCCCATCTACACTGAGCGCCTCTGTGGGCG ACCGGGTGACAATTACCTGTAGAGCTAGCCAGAGCATCTCCTCCTGGCT GGCTTGGTACCAGCAAAAACCTGGCAAGGCCCCTAAGCTGCTGATCTAC GAGGCCAGCAGCCTGGAAAGCGGCGTCCCCTCTAGATTCAGCGGCAGCG GCTCTGGAACCGAGTTCACCCTGACAATCAGCAGCCTGCAGCCTGACGA CTTCGCCACCTATTACTGCCAGCAGGCCAACAGCCACCCCATCACCTTT GGCGGAGGCACCAAGGTGGAAATCAAGGGTGGTGGGGGCAGCGGTGGAG GTGGGAGCGGAGGCGGGGGTAGCGGAGGCGGGGGTAGCGAGGTGCAGCT GGTGGAAAGCGGCGGAGGACTCGTTAAGCCCGGCGGCAGCCTGAGACTG AGCTGCGCCGCTAGCGGATTTACCTTCAGCGACTACTACATGAGCTGGA TCCGGCAGGCCCCTGGCAAGGGCCTGGAATGGGTCAGCTACATCAGCTC CTCTGGCTCTACAATCTACTACGCCGACAGCGTGAAAGGCAGATTCACC ATCTCTAGAGATAATGCCAAGAACAGCCTGTACCTGCAAATGAACAGCC TGCGGGCCGAGGACACCGCCGTGTACTATTGTGCTAGAGATCAGGGCAA CTACGGCGTGGACGTGTGGGGCCAGGGCACCACCGTGACAGTGTCCTCC ACCACAACACCTGCTCCAAGGCCCCCCACACCCGCTCCAACTATAGCCA GCCAACCATTGAGCCTCAGACCTGAAGCTTGCAGGCCCGCAGCAGGAGG CGCCGTCCATACGCGAGGCCTGGACTTCGCGTGTGATATTTATATTTGG GCACCTTTGGCCGGAACATGTGGGGTGTTGCTTCTCTCCCTTGTGATCA CTCTGTATTGTAAGCGCGGGAGAAAGAAGCTCCTGTACATCTTCAAGCA GCCTTTTATGCGACCTGTGCAAACCACTCAGGAAGAAGATGGGTGTTCA TGCCGCTTCCCCGAGGAGGAAGAAGGAGGGTGTGAACTGAGGGTGAAAT TTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAGGGTCAGAATCAGCT CTACAATGAATTGAATCTCGGCAGGCGAGAAGAGTACGATGTTCTGGAC AAAAGACGGGGCAGGGATCCCGAGATGGGGGGAAAGCCCCGGAGAAAAA ATCCTCAGGAGGGGTTGTACAATGAGCTGCAGAAGGACAAGATGGCTGA AGCCTATAGCGAGATCGGAATGAAAGGCGAAAGACGCAGAGGCAAGGGG CATGACGGTCTGTACCAGGGTCTCTCTACAGCCACCAAGGACACTTATG ATGCGTTGCATATGCAAGCCTTGCCACCCCGC
911	477	GACATCCAGATGACCCAGAGCCCTAGCTCCCTGAGCGCCAGCGTGGGCG ATAGAGTGACCATTACCTGTAGAGCCTCTCAGAGCATCTCCTCCTACCT GAACTGGTATCAGCAGAAACCCGGCAAGGCCCCTAAGCTGCTGATCTAC GCCGCTAGCAGCCTGCAGTCTGGCGTCCCCAGCCGGTTCAGCGGCAGCG GATCTGGCACCGACTTCACCCTGACAATCAGCAGCCTGCAACCTGAGGA CTTTGCTACATACTACTGCCAGCAGGCCCACAGCTCTCCAATCACCTTC GGCGGCGGAACAAAGGTGGAAATCAAGGGTGGTGGGGGCAGCGGTGGAG GTGGGAGCGGAGGCGGGGGTAGCGGAGGCGGGGGTAGCGAGGTGCAGCT GCTGGAAAGCGGAGGCGGACTCGTTCAACCTGGCGGCAGCCTGAGACTG AGCTGCGCCGCTTCTGGATTTACCTTCAGCAACTACGCCATGAGCTGGG TGCGGCAGGCCCCTGGCAAAGGCCTGGAATGGGTCTCCGCCATCAGCGG CTCTGGCGGCTCCACCTACTACGCCGACAGCGTGAAGGGCAGATTCACC ATCTCTAGAGATAATAGCAAGAACACCCTGTACCTGCAGATGAACAGCC TGCGGGCCGAGGACACCGCCGTGTACTATTGTGCTAGACCCGGAGATGG CTACTACGAGGGCGTGTACTTCGACTACTGGGGCCAGGGCACACTGGTG ACAGTGTCCAGCACCACAACACCTGCTCCAAGGCCCCCCACACCCGCTC CAACTATAGCCAGCCAACCATTGAGCCTCAGACCTGAAGCTTGCAGGCC CGCAGCAGGAGGCGCCGTCCATACGCGAGGCCTGGACTTCGCGTGTGAT ATTTATATTTGGGCACCTTTGGCCGGAACATGTGGGGTGTTGCTTCTCT

		CCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGAAAGAAGCTCCTGTA CATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAACCACTCAGGAAGAA GATGGGTGTTCATGCCGCTTCCCCGAGGAGGAAGAAGGAGGGTGTGAAC TGAGGGTGAAATTTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAGGG TCAGAATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAGAAGAGTAC GATGTTCTGGACAAAAGACGGGGCAGGGATCCCGAGATGGGGGGAAAGC CCCGGAGAAAAAATCCTCAGGAGGGGTTGTACAATGAGCTGCAGAAGGA CAAGATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGAAAGACGC AGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTACAGCCACCA AGGACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCCCGC
912	525	GATATTCAGATGACCCAGAGCCCATCTAGCCTGAGCGCCAGCGTGGGCG ATAGAGTGACCATCACCTGTCAGGCCTCTCAGGACATCGCTAATTACCT GAACTGGTATCAGCAGAAACCCGGCAAGGCCCCTAAGCTGCTGATCTAC GACGCCTCCAACCTGGAAACCGGCGTGCCCAGCCGGTTCAGCGGCAGCG GATCTGGCACAGACTTCACCTTTACCATCAGCTCCCTCCAGCCTGAGGA CATCGCCACATACTACTGCCAGCAACACTTCAACCTGCCTCTGACCTTC GGCGGCGGAACAAAGGTCGAGATCAAGGGTGGTGGGGGCAGCGGTGGAG GTGGGAGCGGAGGCGGGGGTAGCGGAGGCGGGGGTAGCCAAATCACCCT GAAAGAGAGCGGACCTACACTGGTCAAGCCTACCCAGACACTGACCCTC ACATGTACATTCAGCGGCTTTAGCCTGAGCACCTCCGGCGTGGGAGTGG GCTGGATCAGACAGCCCCCCGGCAAGGCCCTGGAATGGCTGGCTCTGAT CTATTGGAATGACGAGAAGCGGTACAGCCCTAGCCTGAAATCTAGACTG ACAATCACCAAGGACACCAGCAAGAACCAGGTGGTGCTGACCATGACCA ACATGGATCCTGTGGATACCGCCGTGTACTACTGCGCCAGAGAAGGCTC TCACGACTACAAGAGCTCCAACTGGTTCGACCCATGGGGCCAGGGCACC CTGGTTACAGTGTCTAGCACCACAACACCTGCTCCAAGGCCCCCCACAC CCGCTCCAACTATAGCCAGCCAACCATTGAGCCTCAGACCTGAAGCTTG CAGGCCCGCAGCAGGAGGCGCCGTCCATACGCGAGGCCTGGACTTCGCG TGTGATATTTATATTTGGGCACCTTTGGCCGGAACATGTGGGGTGTTGC TTCTCTCCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGAAAGAAGCT CCTGTACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAACCACTCAG GAAGAAGATGGGTGTTCATGCCGCTTCCCCGAGGAGGAAGAAGGAGGGT GTGAACTGAGGGTGAAATTTTCTAGAAGCGCCGATGCTCCCGCATATCA GCAGGGTCAGAATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAGAA GAGTACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCGAGATGGGGG GAAAGCCCCGGAGAAAAAATCCTCAGGAGGGGTTGTACAATGAGCTGCA GAAGGACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGAA AGACGCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTACAG CCACCAAGGACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCCCG C
913	573	GATATCGTGATGACCCAATCTCCACTGAGCCTGCCTGTGACACCTGGCG AGCCTGCTTCTATCAGCTGTAGAAGCAGCCAGTCCCTGCTGCACAGCAA CGGCTACAACTACCTGGACTGGTATCTGCAGAAACCCGGCCAGAGCCCC CAGCTGCTGATCTACCTCGGCTCTAATCGGGCCAGCGGAGTGCCTGATA GATTCAGCGGAAGCGGCTCCGGCACCGACTTCACCCTGAAGATCAGCAG AGTGGAAGCCGAGGACGTGGGCGTCTACTACTGCATGCAGGCCCTGGGC CTGATTACATTTGGCGGCGGAACCAAGGTGGAAATCAAGGGTGGTGGGG GCAGCGGTGGAGGTGGGAGCGGAGGCGGGGGTAGCGGAGGCGGGGGTAG CGAAGTGCAGCTGGTTGAGAGCGGCGGCGGACTGGTGAAGCCCGGAGGC AGCCTCAGACTGAGCTGTGCTGCTTCTGGCTTTACCTTCAGCTCTTATA GCATGAACTGGGTGCGGCAGGCCCCTGGCAAGGGCCTGGAATGGGTCAG CTCCATCAGCTCTTCTAGCAGCTACATCTACTACGCCGACAGCGTGAAG GGCAGATTCACCATCAGCAGAGATAACGCCAAGAACAGCCTGTACCTGC AGATGAATAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCGCCAG AGCCGGCGACACCTACAGCGCCGCCGATTACTACTACATGGACGTGTGG GGCAAAGGAACAACCGTGACAGTGTCCTCCACCACAACACCTGCTCCAA GGCCCCCCACACCCGCTCCAACTATAGCCAGCCAACCATTGAGCCTCAG ACCTGAAGCTTGCAGGCCCGCAGCAGGAGGCGCCGTCCATACGCGAGGC CTGGACTTCGCGTGTGATATTTATATTTGGGCACCTTTGGCCGGAACAT

		GTGGGGTGTTGCTTCTCTCCCTTGTGATCACTCTGTATTGTAAGCGCGG GAGAAAGAAGCTCCTGTACATCTTCAAGCAGCCTTTTATGCGACCTGTG CAAACCACTCAGGAAGAAGATGGGTGTTCATGCCGCTTCCCCGAGGAGG AAGAAGGAGGGTGTGAACTGAGGGTGAAATTTTCTAGAAGCGCCGATGC TCCCGCATATCAGCAGGGTCAGAATCAGCTCTACAATGAATTGAATCTC GGCAGGCGAGAAGAGTACGATGTTCTGGACAAAAGACGGGGCAGGGATC CCGAGATGGGGGGAAAGCCCCGGAGAAAAAATCCTCAGGAGGGGTTGTA CAATGAGCTGCAGAAGGACAAGATGGCTGAAGCCTATAGCGAGATCGGA ATGAAAGGCGAAAGACGCAGAGGCAAGGGGCATGACGGTCTGTACCAGG GTCTCTCTACAGCCACCAAGGACACTTATGATGCGTTGCATATGCAAGC CTTGCCACCCCGC
914	597	GAAGTGCAACTGCTGGAAAGCGGCGGAGGCCTGGTCCAGCCCGGCGGCT CTCTGCGGCTCAGCTGCGCCGCTTCTGGATTTACCTTCGGCAGCGAGGC TATGAGCTGGGTGCGGCAGGCCCCTGGAAAAGAGAGAGAGCTGGTGTCC GCCATCAGCGGCAGCGGCGAGGTGACCTACTACGCCGACAGCGTGAAGG GCAGATTCACCATCTCTAGAGATAATAGCAAGAACACCCTGTACCTGCA GATGAACAGCCTGAGAGCCGAGGACACCGCCGTGTACTATTGTCAGAGA CTGGTGGAAGCCAAGCGGCACTGGGGCCAGGGCACACAGGTTACAGTGT CCAGCACCACAACACCTGCTCCAAGGCCCCCCACACCCGCTCCAACTAT AGCCAGCCAACCATTGAGCCTCAGACCTGAAGCTTGCAGGCCCGCAGCA GGAGGCGCCGTCCATACGCGAGGCCTGGACTTCGCGTGTGATATTTATA TTTGGGCACCTTTGGCCGGAACATGTGGGGTGTTGCTTCTCTCCCTTGT GATCACTCTGTATTGTAAGCGCGGGAGAAAGAAGCTCCTGTACATCTTC AAGCAGCCTTTTATGCGACCTGTGCAAACCACTCAGGAAGAAGATGGGT GTTCATGCCGCTTCCCCGAGGAGGAAGAAGGAGGGTGTGAACTGAGGGT GAAATTTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAGGGTCAGAAT CAGCTCTACAATGAATTGAATCTCGGCAGGCGAGAAGAGTACGATGTTC TGGACAAAAGACGGGGCAGGGATCCCGAGATGGGGGGAAAGCCCCGGAG AAAAAATCCTCAGGAGGGGTTGTACAATGAGCTGCAGAAGGACAAGATG GCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGAAAGACGCAGAGGCA AGGGGCATGACGGTCTGTACCAGGGTCTCTCTACAGCCACCAAGGACAC TTATGATGCGTTGCATATGCAAGCCTTGCCACCCCGC
915	621	GAAGTGCAACTGCTGGAATCTGGCGGAGGACTGGTGCAGCCCGGCGGCA GCCTGCGGCTGAGCTGTGCTGCTTCTGGCTTTACCTTCGAGTCTGAGGC CATGAGCTGGTATAGACAGGCCCCTGGCAAGGAAAGAGAGCTGGTCAGC GTGATCACCAGCGAGGGCTCCACCTACTACGCCGACAGCGTGAAAGGCA GATTCACAATCAGCCGGGACAATAGCAAGAACACCCTGTACCTGCAGAT GAACAGCCTGCGCGCCGAAGATACAGCCGTGTACTACTGCGCCCACATC GAGTGGGAGACAAGACTCAACTGGGGCCAGGGCACCCAGGTGACCGTGT CCAGCACCACAACACCTGCTCCAAGGCCCCCCACACCCGCTCCAACTAT AGCCAGCCAACCATTGAGCCTCAGACCTGAAGCTTGCAGGCCCGCAGCA GGAGGCGCCGTCCATACGCGAGGCCTGGACTTCGCGTGTGATATTTATA TTTGGGCACCTTTGGCCGGAACATGTGGGGTGTTGCTTCTCTCCCTTGT GATCACTCTGTATTGTAAGCGCGGGAGAAAGAAGCTCCTGTACATCTTC AAGCAGCCTTTTATGCGACCTGTGCAAACCACTCAGGAAGAAGATGGGT GTTCATGCCGCTTCCCCGAGGAGGAAGAAGGAGGGTGTGAACTGAGGGT GAAATTTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAGGGTCAGAAT CAGCTCTACAATGAATTGAATCTCGGCAGGCGAGAAGAGTACGATGTTC TGGACAAAAGACGGGGCAGGGATCCCGAGATGGGGGGAAAGCCCCGGAG AAAAAATCCTCAGGAGGGGTTGTACAATGAGCTGCAGAAGGACAAGATG GCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGAAAGACGCAGAGGCA AGGGGCATGACGGTCTGTACCAGGGTCTCTCTACAGCCACCAAGGACAC TTATGATGCGTTGCATATGCAAGCCTTGCCACCCCGC
916	645	GAGGTGCAGCTGCTGGAAAGCGGAGGGGGCCTGGTCCAACCCGGCGGGT CTCTTCGCCTAAGCTGTGCCGCTTCTGGCTTCACCTTCGACGAGTACAC CATGCACTGGTTCAGACAGGCCCCCGGCAAGGAGCGCGAGTTCGTCAGT GCAATCAGCGGAGGCGGTAGCGAGACTTATTACGCGGACTCCGTGAAGG GCCGCTTCACCATTAGCCGCGACAACTCCAAGAACACGCTGTACCTGCA GATGAATTCGCTGCGCGCCGAAGATACGGCCGTGTACTACTGTGCCGCT

		GGTGGGGAGGAGGCTGGCGTGGGCTATTGGGGCCAGGGCACCCAGGTCA CCGTGTCGTCCACCACAACACCTGCTCCAAGGCCCCCCACACCCGCTCC AACTATAGCCAGCCAACCATTGAGCCTCAGACCTGAAGCTTGCAGGCCC GCAGCAGGAGGCGCCGTCCATACGCGAGGCCTGGACTTCGCGTGTGATA TTTATATTTGGGCACCTTTGGCCGGAACATGTGGGGTGTTGCTTCTCTC CCTTGTGATCACTCTGTATTGTAAGCGCGGGAGAAAGAAGCTCCTGTAC ATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAACCACTCAGGAAGAAG ATGGGTGTTCATGCCGCTTCCCCGAGGAGGAAGAAGGAGGGTGTGAACT GAGGGTGAAATTTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAGGGT CAGAATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAGAAGAGTACG ATGTTCTGGACAAAAGACGGGGCAGGGATCCCGAGATGGGGGGAAAGCC CCGGAGAAAAAATCCTCAGGAGGGGTTGTACAATGAGCTGCAGAAGGAC AAGATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGAAAGACGCA GAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTACAGCCACCAA GGACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCCCGC
917	669	GAGGTGCAGCTGCTGGAGAGCGGAGGCGGCCTCGTGCAGCCAGGAGGTT CCCTACGACTCTCCTGTGCCGCCAGCGGCTTCACCTTCGAGGACTACGC CATGAGTTGGTTCCGCCAGGCCCCGGGGAAGGAGCGCGAGGGCGTGAGC GCGATTTCTGGAAAGGGCGGCTCCACCTATTACGCGGACTCCGTGAAGG GTCGCTTTACCATCTCTCGCGACAACTCCAAGAACACGCTGTACCTGCA GATGAATAGCCTGCGCGCTGAGGACACTGCCGTGTACTACTGTGCTGTC TTGGACGAGGAGGCCGGCGCAGAGGGCGGCTATTGGGGCCAGGGTACCC AGGTCACCGTGTCGTCCACCACAACACCTGCTCCAAGGCCCCCCACACC CGCTCCAACTATAGCCAGCCAACCATTGAGCCTCAGACCTGAAGCTTGC AGGCCCGCAGCAGGAGGCGCCGTCCATACGCGAGGCCTGGACTTCGCGT GTGATATTTATATTTGGGCACCTTTGGCCGGAACATGTGGGGTGTTGCT TCTCTCCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGAAAGAAGCTC CTGTACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAACCACTCAGG AAGAAGATGGGTGTTCATGCCGCTTCCCCGAGGAGGAAGAAGGAGGGTG TGAACTGAGGGTGAAATTTTCTAGAAGCGCCGATGCTCCCGCATATCAG CAGGGTCAGAATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAGAAG AGTACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCGAGATGGGGGG AAAGCCCCGGAGAAAAAATCCTCAGGAGGGGTTGTACAATGAGCTGCAG AAGGACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGAAA GACGCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTACAGC CACCAAGGACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCCCGC
918	693	GAGGTGCAACTGCTGGAAAGCGGCGGTGGACTGGTGCAGCCCGGCGGCA GCCTGAGACTGTCTTGTGCTGCTTCTGGATTTACATTCGACAGATACGC CATGAGCTGGTTCCGCCAGGCCCCTGGCAAAGAGCGGGAAGGCGTGTCC GCCATCTCCACAAGCGGAGATAGCACATACTATGCCGACAGCGTGAAGG GCAGATTCACCATCAGCAGAGATAATAGCAAGAACACCCTGTACCTGCA GATGAACAGCCTCCGGGCCGAGGACACCGCCGTCTACTACTGCGCCGTG CTGGACGAGGAAGCCGGCGCCGAGGGCGGCTACTGGGGCCAGGGCACCC AGGTGACCGTGTCTAGCACCACAACACCTGCTCCAAGGCCCCCCACACC CGCTCCAACTATAGCCAGCCAACCATTGAGCCTCAGACCTGAAGCTTGC AGGCCCGCAGCAGGAGGCGCCGTCCATACGCGAGGCCTGGACTTCGCGT GTGATATTTATATTTGGGCACCTTTGGCCGGAACATGTGGGGTGTTGCT TCTCTCCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGAAAGAAGCTC CTGTACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAACCACTCAGG AAGAAGATGGGTGTTCATGCCGCTTCCCCGAGGAGGAAGAAGGAGGGTG TGAACTGAGGGTGAAATTTTCTAGAAGCGCCGATGCTCCCGCATATCAG CAGGGTCAGAATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAGAAG AGTACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCGAGATGGGGGG AAAGCCCCGGAGAAAAAATCCTCAGGAGGGGTTGTACAATGAGCTGCAG AAGGACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGAAA GACGCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTACAGC CACCAAGGACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCCCGC
919	717	GAGGTGCAACTGCTGGAAAGCGGCGGAGGACTCGTCCAGCCCGGCGGCA GCCTGCGGCTGAGCTGTGCTGCTTCTGGATTTACCTTCGCCAGCGACGC

		CATGAGCTGGTATAGACAGGCCCCTGGCAAAGAGCGGGAACTGGTGTCC GCCATCAGCGGCTCTGGCGGCTCCACCTACTACGCCGATAGCGTGAAGG GCAGATTCACAATCTCTAGAGATAATAGCAAGAACACCCTGTACCTGCA GATGAACAGCCTGAGAGCCGAGGACACCGCCGTGTACTACTGCGCCGCT CACGACAGCGGCGAGGCCTACCTGGCCTTCGACTACTGGGGCCAGGGCA CACAGGTGACCGTGTCTAGCACCACAACACCTGCTCCAAGGCCCCCCAC ACCCGCTCCAACTATAGCCAGCCAACCATTGAGCCTCAGACCTGAAGCT TGCAGGCCCGCAGCAGGAGGCGCCGTCCATACGCGAGGCCTGGACTTCG CGTGTGATATTTATATTTGGGCACCTTTGGCCGGAACATGTGGGGTGTT GCTTCTCTCCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGAAAGAAG CTCCTGTACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAACCACTC AGGAAGAAGATGGGTGTTCATGCCGCTTCCCCGAGGAGGAAGAAGGAGG GTGTGAACTGAGGGTGAAATTTTCTAGAAGCGCCGATGCTCCCGCATAT CAGCAGGGTCAGAATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAG AAGAGTACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCGAGATGGG GGGAAAGCCCCGGAGAAAAAATCCTCAGGAGGGGTTGTACAATGAGCTG CAGAAGGACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCG AAAGACGCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTAC AGCCACCAAGGACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCC CGC
920	741	GAGGTGCAACTGCTGGAAAGCGGCGGAGGACTCGTCCAGCCCGGCGGCA GCCTGAGGCTGAGCTGTGCTGCTTCTGGCTTTACCTTCGACTCCTACAC AATGAGCTGGTATAGACAGGCCCCTGGCAAGGAGCGGGAACTGGTGTCC GCCATCAGCGGCCACGGCGACTCTACATACTACGCCGACAGCGTGAAAG GCAGATTCACAATCTCTAGAGATAATAGCAAGAACACCCTGTACCTGCA GATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCACCAGA ATCAGCATCACCACCGAGTGGCTGGCCGGAGATTACTGGGGCCAGGGCA CCCAGGTGACAGTGTCCAGCACCACAACACCTGCTCCAAGGCCCCCCAC ACCCGCTCCAACTATAGCCAGCCAACCATTGAGCCTCAGACCTGAAGCT TGCAGGCCCGCAGCAGGAGGCGCCGTCCATACGCGAGGCCTGGACTTCG CGTGTGATATTTATATTTGGGCACCTTTGGCCGGAACATGTGGGGTGTT GCTTCTCTCCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGAAAGAAG CTCCTGTACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAACCACTC AGGAAGAAGATGGGTGTTCATGCCGCTTCCCCGAGGAGGAAGAAGGAGG GTGTGAACTGAGGGTGAAATTTTCTAGAAGCGCCGATGCTCCCGCATAT CAGCAGGGTCAGAATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAG AAGAGTACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCGAGATGGG GGGAAAGCCCCGGAGAAAAAATCCTCAGGAGGGGTTGTACAATGAGCTG CAGAAGGACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCG AAAGACGCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTAC AGCCACCAAGGACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCC CGC
921	765	GAGGTGCAGCTGCTGGAAAGCGGAGGAGGCCTGGTCCAACCTGGCGGCA GCCTGCGGCTGAGCTGCGCCGCTTCTGGCTTCACCTTCAGCAGCTACGC CATGAGCTGGTTCCGGCAGGCCCCTGGCAAGGAAAGAGAGTTCGTGTCT TTTATCAGCGGATCTGGCGACTCCACCTACTACGCTGATAGCGTGAAAG GCAGATTTACCATCTCTAGAGATAATAGCAAGAACACCCTGTACCTCCA GATGAACAGCCTGCGCGCCGAGGACACAGCCGTGTACTATTGTACCAGA TGGCCTTACGACTTCGAGGAACCAAGCGAGCCCGGCGTGTACTGGGGCC AGGGCACACAGGTGACAGTGTCCTCCACCACAACACCTGCTCCAAGGCC CCCCACACCCGCTCCAACTATAGCCAGCCAACCATTGAGCCTCAGACCT GAAGCTTGCAGGCCCGCAGCAGGAGGCGCCGTCCATACGCGAGGCCTGG ACTTCGCGTGTGATATTTATATTTGGGCACCTTTGGCCGGAACATGTGG GGTGTTGCTTCTCTCCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGA AAGAAGCTCCTGTACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAA CCACTCAGGAAGAAGATGGGTGTTCATGCCGCTTCCCCGAGGAGGAAGA AGGAGGGTGTGAACTGAGGGTGAAATTTTCTAGAAGCGCCGATGCTCCC GCATATCAGCAGGGTCAGAATCAGCTCTACAATGAATTGAATCTCGGCA GGCGAGAAGAGTACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCGA

		GATGGGGGGAAAGCCCCGGAGAAAAAATCCTCAGGAGGGGTTGTACAAT GAGCTGCAGAAGGACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGA AAGGCGAAAGACGCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCT CTCTACAGCCACCAAGGACACTTATGATGCGTTGCATATGCAAGCCTTG CCACCCCGC
922	789	GAGGTGCAGCTGCTGGAAAGCGGCGGAGGCCTGGTGCAACCTGGCGGAT CTCTCAGACTGAGCTGTGCTGCTTCTGGCTTCACATTCACCGACTACGA CATGAGCTGGTATAGACAGGCCCCTGGAAAAGAGCGGGAACTGGTCTCC GTGATCCACAGCGGCGGCTCCACCTACTACGCCGATAGCGTGAAGGGCA GATTCACCATCAGCAGAGATAATAGCAAGAACACCCTGTACCTGCAGAT GAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCGCCCCCGGC TACTACAGCGACCTGTCTTTTGATTATTACAACTTCGACTACTGGGGCC AGGGCACACAGGTGACAGTGTCCAGCACCACAACACCTGCTCCAAGGCC CCCCACACCCGCTCCAACTATAGCCAGCCAACCATTGAGCCTCAGACCT GAAGCTTGCAGGCCCGCAGCAGGAGGCGCCGTCCATACGCGAGGCCTGG ACTTCGCGTGTGATATTTATATTTGGGCACCTTTGGCCGGAACATGTGG GGTGTTGCTTCTCTCCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGA AAGAAGCTCCTGTACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAA CCACTCAGGAAGAAGATGGGTGTTCATGCCGCTTCCCCGAGGAGGAAGA AGGAGGGTGTGAACTGAGGGTGAAATTTTCTAGAAGCGCCGATGCTCCC GCATATCAGCAGGGTCAGAATCAGCTCTACAATGAATTGAATCTCGGCA GGCGAGAAGAGTACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCGA GATGGGGGGAAAGCCCCGGAGAAAAAATCCTCAGGAGGGGTTGTACAAT GAGCTGCAGAAGGACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGA AAGGCGAAAGACGCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCT CTCTACAGCCACCAAGGACACTTATGATGCGTTGCATATGCAAGCCTTG CCACCCCGC
923	813	GAGGTGCAGCTGCTGGAGAGCGGTGGAGGGTTGGTGCAGCCCGGGGGTA GCCTGCGTCTGTCGTGCGCCGCTTCCGGCTTCACGTTCTCTGATTACGC CATGCACTGGTTCCGGCAGGCCCCCGGTAAGGAGCGCGTGCTGGTGTCG TCTATTGACTCCGGCGGCTCCACTTACTACGCAGACAGTGTCAAGGGCC GTTTCACCATCAGCCGCGACAACAGCAAGAACACGCTGTACCTGCAGAT GAACTCCCTTCGAGCAGAGGACACCGCGGTGTACTACTGTAATGCGGGC TTCAAGGGCGATCACCCCCACCCCAAGGATGCCTTCGACATTTGGGGCC AGGGCACCCAGGTCACCGTGTCGTCCACCACAACACCTGCTCCAAGGCC CCCCACACCCGCTCCAACTATAGCCAGCCAACCATTGAGCCTCAGACCT GAAGCTTGCAGGCCCGCAGCAGGAGGCGCCGTCCATACGCGAGGCCTGG ACTTCGCGTGTGATATTTATATTTGGGCACCTTTGGCCGGAACATGTGG GGTGTTGCTTCTCTCCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGA AAGAAGCTCCTGTACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAA CCACTCAGGAAGAAGATGGGTGTTCATGCCGCTTCCCCGAGGAGGAAGA AGGAGGGTGTGAACTGAGGGTGAAATTTTCTAGAAGCGCCGATGCTCCC GCATATCAGCAGGGTCAGAATCAGCTCTACAATGAATTGAATCTCGGCA GGCGAGAAGAGTACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCGA GATGGGGGGAAAGCCCCGGAGAAAAAATCCTCAGGAGGGGTTGTACAAT GAGCTGCAGAAGGACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGA AAGGCGAAAGACGCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCT CTCTACAGCCACCAAGGACACTTATGATGCGTTGCATATGCAAGCCTTG CCACCCCGC
924	837	GAGGTGCAACTGCTGGAATCCGGCGGAGGCCTGGTGCAGCCCGGCGGCA GCCTCAGACTGAGCTGTGCCGCTTCTGGCTTTACCTTCAGCAGCGAGGG CATGAGCTGGGTGCGGCAGGCCCCTGGCAAGGAAAGAGAGCTGGTCTCC GCCATCAGCGGATCTGGCGACCACACCTACTATGCCGATAGCGTGCGCG GAAGATTCACAATCTCTAGAGATAATAGCAAGAACACCCTGTACCTGCA GATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCAACGCC CTGGAAGGCGGCCCTACAACAGCTATCCAGCCAGGAGGCCCTGACTACT GGGGCCAGGGCACCCAGGTGACCGTGTCCAGCACCACAACACCTGCTCC AAGGCCCCCCACACCCGCTCCAACTATAGCCAGCCAACCATTGAGCCTC AGACCTGAAGCTTGCAGGCCCGCAGCAGGAGGCGCCGTCCATACGCGAG

		GCCTGGACTTCGCGTGTGATATTTATATTTGGGCACCTTTGGCCGGAAC ATGTGGGGTGTTGCTTCTCTCCCTTGTGATCACTCTGTATTGTAAGCGC GGGAGAAAGAAGCTCCTGTACATCTTCAAGCAGCCTTTTATGCGACCTG TGCAAACCACTCAGGAAGAAGATGGGTGTTCATGCCGCTTCCCCGAGGA GGAAGAAGGAGGGTGTGAACTGAGGGTGAAATTTTCTAGAAGCGCCGAT GCTCCCGCATATCAGCAGGGTCAGAATCAGCTCTACAATGAATTGAATC TCGGCAGGCGAGAAGAGTACGATGTTCTGGACAAAAGACGGGGCAGGGA TCCCGAGATGGGGGGAAAGCCCCGGAGAAAAAATCCTCAGGAGGGGTTG TACAATGAGCTGCAGAAGGACAAGATGGCTGAAGCCTATAGCGAGATCG GAATGAAAGGCGAAAGACGCAGAGGCAAGGGGCATGACGGTCTGTACCA GGGTCTCTCTACAGCCACCAAGGACACTTATGATGCGTTGCATATGCAA GCCTTGCCACCCCGC
925	861 + 189	ATGGCTCTTCCCGTAACAGCCCTTTTGTTGCCCCTTGCACTCCTTCTGC ATGCAGCACGACCGGAGATCGTGCTGACACAGTCTCCCGCCACACTGTC ACTGTCTCCAGGCGAAAGAGCCACACTGAGCTGTAGAGCCAGCCAGAGC GTGTCCTCTTACCTGGCCTGGTATCAGCAGAAGCCTGGACAGGCTCCCC GGCTGCTGATCTACGATGCCAGCAATAGAGCCACAGGCATCCCCGCCAG ATTTTCTGGCAGCGGCTCTGGCACCGATTTCACCCTGACCATAAGCAGC CTGGAACCTGAGGACTTCGCCGTGTACTACTGCCAGCAGAGAGTGGTGT ACCCCATCACCTTTGGCGGAGGCACCAAGGTGGAAATCAAAGGCGGCGG AGGAAGCGGAGGCGGAGGATCTGGTGGTGGTGGATCTGGCGGAGGTGGC AGCCAGATCACACTGAAAGAGTCTGGCCCCACACTGGTCAAGCCCACAC AGACCCTGACACTGACCTGCACCTTCAGCGGCTTTAGCCTGAGCACATC TGGCGTCGGCGTTGGCTGGATTAGACAGCCTCCTGGAAAGGCCCTGGAA TGGCTGGCCCTGATCTACTGGAACGACGAGAAGAGATACAGCCCCAGCC TGAAGTCCCGGCTGACCATCACCAAGGACACCAGCAAGAACCAGGTGGT GCTGACCATGACAAACATGGACCCCGTGGACACCGCCGTGTATTATTGC GCCAGAGATGAGTACGGCGGCTTCGACATTTGGGGCCAGGGCACAATGG TCACCGTGTCTAGTACCACAACACCTGCTCCAAGGCCCCCCACACCCGC TCCAACTATAGCCAGCCAACCATTGAGCCTCAGACCTGAAGCTTGCAGG CCCGCAGCAGGAGGCGCCGTCCATACGCGAGGCCTGGACTTCGCGTGTG ATATTTATATTTGGGCACCTTTGGCCGGAACATGTGGGGTGTTGCTTCT CTCCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGAAAGAAGCTCCTG TACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAACCACTCAGGAAG AAGATGGGTGTTCATGCCGCTTCCCCGAGGAGGAAGAAGGAGGGTGTGA ACTGAGGGTGAAATTTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAG GGTCAGAATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAGAAGAGT ACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCGAGATGGGGGGAAA GCCCCGGAGAAAAAATCCTCAGGAGGGGTTGTACAATGAGCTGCAGAAG GACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGAAAGAC GCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTACAGCCAC CAAGGACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCCCGC
926	861 + 237	ATGGCTCTTCCCGTAACAGCCCTTTTGTTGCCCCTTGCACTCCTTCTGC ATGCAGCACGACCGGAGATCGTGCTGACCCAGTCCCCTGCTACCCTGAG CCTGTCTCCAGGCGAGCGGGCCACACTGAGCTGTAGAGCTTCTCAGAGC GTGTCCAGCTACCTGGCCTGGTATCAGCAGAAACCTGGCCAGGCCCCTA GACTGCTGATCTACGACGCCAGCAACCGGGCCACCGGCATCCCCGCCAG ATTCAGCGGATCTGGCAGCGGCACAGATTTTACCCTCACCATCAGCAGC CTGGAACCTGAGGACTTCGCCGTCTACTACTGCCAGCAAAGATTCGACT ACCCCATCACCTTCGGCGGCGGAACAAAGGTGGAAATTAAGGGTGGTGG GGGCAGCGGTGGAGGTGGGAGCGGAGGCGGGGGTAGCGGAGGCGGGGGT AGCCAAATCACACTGAAAGAGAGCGGCCCTACACTCGTGAAACCTACCC AGACCCTGACACTGACATGTACCTTCAGCGGCTTCTCCCTGAGCACCTC TGGCGTCGGCGTTGGATGGATCAGACAGCCTCCAGGCAAGGCCCTGGAA TGGCTGGCTCTGATCTATTGGAACGACGACAAGCGGTACAGCCCCAGCC TGAAGTCTAGACTGACCATCACAAAGGACACCAGCAAGAACCAGGTGGT GCTGACCATGACAAATATGGACCCCGTGGACACCGCCGTGTACTACTGC GCCAGAGATGAGTACGGCGGATTTGATATCTGGGGCCAGGGCACCATGG TGACCGTGTCCAGCACCACAACACCTGCTCCAAGGCCCCCCACACCCGC

		TCCAACTATAGCCAGCCAACCATTGAGCCTCAGACCTGAAGCTTGCAGG CCCGCAGCAGGAGGCGCCGTCCATACGCGAGGCCTGGACTTCGCGTGTG ATATTTATATTTGGGCACCTTTGGCCGGAACATGTGGGGTGTTGCTTCT CTCCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGAAAGAAGCTCCTG TACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAACCACTCAGGAAG AAGATGGGTGTTCATGCCGCTTCCCCGAGGAGGAAGAAGGAGGGTGTGA ACTGAGGGTGAAATTTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAG GGTCAGAATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAGAAGAGT ACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCGAGATGGGGGGAAA GCCCCGGAGAAAAAATCCTCAGGAGGGGTTGTACAATGAGCTGCAGAAG GACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGAAAGAC GCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTACAGCCAC CAAGGACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCCCGC
927	861 + 261	ATGGCTCTTCCCGTAACAGCCCTTTTGTTGCCCCTTGCACTCCTTCTGC ATGCAGCACGACCGCAAGTGCAGCTCGTGGAAAGCGGCGGCGGAGTGGT GCAGCCCGGCCGGAGCCTGAGACTGTCCTGCGCCGCTTCTGGATTTACC TTCAGCAGCTACGGCATGCACTGGGTCAGACAGGCCCCTGGCAAAGGCC TGGAGTGGGTGGCCGTTATCAGCTACGAGGGCAGCAACAAGTATTACGC CGACAGCGTGAAGGGCCGCTTCACAATCTCTAGAGATAATAGCAAGAAC ACCCTGTACCTGCAGATGAACAGCCTGCGGGCCGAAGATACCGCCGTGT ACTACTGTGCTAGAGAGCTGGGCGACGGCATGGACGTGTGGGGACAGGG CACAACCGTGACCGTGTCCTCTGGTGGTGGGGGCAGCGGTGGAGGTGGG AGCGGAGGCGGGGGTAGCGGAGGCGGGGGTAGCGAGATCGTGCTGACCC AGTCCCCTGCTACACTGAGCCTGTCTCCAGGCGAGCGGGCCACACTGAG CTGTAGAGCTTCTCAGAGCGTGTCCAGCTATCTGGCCTGGTTCCAGCAG AAACCTGGCCAGGCCCCTAGACTGCTGATCTACGACGCCAGCAACCGGG CCACCGGCATCCCCGCCAGATTCAGCGGCTCTGGCAGCGGCACCGACTT CACCCTCACCATCAGCAGCCTGGAACCCGAGGATTTTGCCGTCTACTAC TGCCAGCAAAGAGTGGACCTGTGGACCTTCGGCGGAGGAACAAAGGTGG AAATCAAGACCACAACACCTGCTCCAAGGCCCCCCACACCCGCTCCAAC TATAGCCAGCCAACCATTGAGCCTCAGACCTGAAGCTTGCAGGCCCGCA GCAGGAGGCGCCGTCCATACGCGAGGCCTGGACTTCGCGTGTGATATTT ATATTTGGGCACCTTTGGCCGGAACATGTGGGGTGTTGCTTCTCTCCCT TGTGATCACTCTGTATTGTAAGCGCGGGAGAAAGAAGCTCCTGTACATC TTCAAGCAGCCTTTTATGCGACCTGTGCAAACCACTCAGGAAGAAGATG GGTGTTCATGCCGCTTCCCCGAGGAGGAAGAAGGAGGGTGTGAACTGAG GGTGAAATTTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAGGGTCAG AATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAGAAGAGTACGATG TTCTGGACAAAAGACGGGGCAGGGATCCCGAGATGGGGGGAAAGCCCCG GAGAAAAAATCCTCAGGAGGGGTTGTACAATGAGCTGCAGAAGGACAAG ATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGAAAGACGCAGAG GCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTACAGCCACCAAGGA CACTTATGATGCGTTGCATATGCAAGCCTTGCCACCCCGC
928	861 + 333	ATGGCTCTTCCCGTAACAGCCCTTTTGTTGCCCCTTGCACTCCTTCTGC ATGCAGCACGACCGGACATCCAGATGACCCAGAGCCCTTCGACCCTATC CGCTTCCGTGGGTGACCGTGTGACCATCACCTGTCGCGCGTCGCAGAGC ATCTCCTCCTGGCTCGCGTGGTACCAACAGAAGCCTGGCAAGGCCCCCA AGCTGCTGATTTACGACGCCAGTTCCCTGGAGTCTGGCGTGCCATCCCG CTTCTCCGGCAGCGGCAGCGGTACCGAGTTCACCCTGACGATCAGCTCC CTGCAGCCGGATGACTTTGCTACCTACTACTGTCAGCAGGTCTCCTCCC TCCCCCCCACCTTCGGTGGCGGTACCAAGGTGGAGATCAAGGGCGGCGG CGGCTCTGGTGGCGGAGGTTCTGGCGGGGGAGGTTCGGGGGGGGGAGGC TCCGAGGTGCAACTGGTAGAGAGCGGCGGGGGACTGGTAAAACCCGGCG GCTCCCTGCGGCTGTCATGCGCTGCTAGCGGCTTCACGTTCAGCGATTA CTACATGAGTTGGATCCGCCAGGCCCCCGGGAAGGGTTTGGAGTGGGTC TCGTATATCTCTTCCAGCGGATCTACCATTTACTATGCGGACAGCGTGA AGGGGCGCTTCACCATATCTCGGGACAACGCCAAGAACTCCCTGTACCT GCAGATGAATTCCCTGCGTGCCGAGGACACGGCCGTGTATTACTGTGCC CGCGACCAGGGCAACTACGGCGTCGACGTGTGGGGCCAGGGTACAACCG

		TCACCGTGTCCAGTACCACAACACCTGCTCCAAGGCCCCCCACACCCGC TCCAACTATAGCCAGCCAACCATTGAGCCTCAGACCTGAAGCTTGCAGG CCCGCAGCAGGAGGCGCCGTCCATACGCGAGGCCTGGACTTCGCGTGTG ATATTTATATTTGGGCACCTTTGGCCGGAACATGTGGGGTGTTGCTTCT CTCCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGAAAGAAGCTCCTG TACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAACCACTCAGGAAG AAGATGGGTGTTCATGCCGCTTCCCCGAGGAGGAAGAAGGAGGGTGTGA ACTGAGGGTGAAATTTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAG GGTCAGAATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAGAAGAGT ACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCGAGATGGGGGGAAA GCCCCGGAGAAAAAATCCTCAGGAGGGGTTGTACAATGAGCTGCAGAAG GACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGAAAGAC GCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTACAGCCAC CAAGGACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCCCGC
929	861 + 357	ATGGCTCTTCCCGTAACAGCCCTTTTGTTGCCCCTTGCACTCCTTCTGC ATGCAGCACGACCGCAAGTGCAGCTGGTCGAGAGCGGAGGAGGCCTGGT TAAGCCCGGCGGATCTCTCAGACTGAGCTGCGCCGCTAGCGGCTTTACA TTCAGCGACTACTACATGAGCTGGATCCGGCAGGCCCCTGGCAAGGGCC TGGAATGGGTGTCCTACATCAGCTCCTCCGGCAGCACCATCTACTACGC CGACAGCGTGAAAGGCAGATTCACAATCTCTAGAGATAATGCCAAGAAC AGCCTGTACCTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGT ACTATTGTGCTAGAGATCAGGGCAACTACGGCGTGGACGTGTGGGGCCA GGGCACCACCGTGACCGTGTCTAGCGGTGGTGGGGGCAGCGGTGGAGGT GGGAGCGGAGGCGGGGGTAGCGGAGGCGGGGGTAGCGATATCCAGATGA CCCAGTCCCCATCTACACTGAGCGCCTCTGTGGGCGACCGGGTGACCAT TACATGTAGAGCCAGCCAGAGCATCAGCAGCTGGCTGGCTTGGTATCAG CAGAAACCTGGCAAGGCCCCTAAGCTGCTGATCTACGAGGCCAGCAGCC TGGAAAGCGGCGTCCCCAGCAGATTCAGCGGCAGCGGCTCTGGAACAGA GTTCACCCTGACCATCTCCTCCCTGCAGCCTGACGACTTCGCCACCTAC TACTGCCAGCAATCTGATAGCCACCCCATCACCTTTGGCGGAGGCACCA AGGTGGAAATCAAGACCACAACACCTGCTCCAAGGCCCCCCACACCCGC TCCAACTATAGCCAGCCAACCATTGAGCCTCAGACCTGAAGCTTGCAGG CCCGCAGCAGGAGGCGCCGTCCATACGCGAGGCCTGGACTTCGCGTGTG ATATTTATATTTGGGCACCTTTGGCCGGAACATGTGGGGTGTTGCTTCT CTCCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGAAAGAAGCTCCTG TACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAACCACTCAGGAAG AAGATGGGTGTTCATGCCGCTTCCCCGAGGAGGAAGAAGGAGGGTGTGA ACTGAGGGTGAAATTTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAG GGTCAGAATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAGAAGAGT ACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCGAGATGGGGGGAAA GCCCCGGAGAAAAAATCCTCAGGAGGGGTTGTACAATGAGCTGCAGAAG GACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGAAAGAC GCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTACAGCCAC CAAGGACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCCCGC
930	861 + 429	ATGGCTCTTCCCGTAACAGCCCTTTTGTTGCCCCTTGCACTCCTTCTGC ATGCAGCACGACCGGATATCCAGATGACCCAGTCCCCATCTACACTGAG CGCCTCTGTGGGCGACCGGGTGACAATTACCTGTAGAGCTAGCCAGAGC ATCTCCTCCTGGCTGGCTTGGTACCAGCAAAAACCTGGCAAGGCCCCTA AGCTGCTGATCTACGAGGCCAGCAGCCTGGAAAGCGGCGTCCCCTCTAG ATTCAGCGGCAGCGGCTCTGGAACCGAGTTCACCCTGACAATCAGCAGC CTGCAGCCTGACGACTTCGCCACCTATTACTGCCAGCAGGCCAACAGCC ACCCCATCACCTTTGGCGGAGGCACCAAGGTGGAAATCAAGGGTGGTGG GGGCAGCGGTGGAGGTGGGAGCGGAGGCGGGGGTAGCGGAGGCGGGGGT AGCGAGGTGCAGCTGGTGGAAAGCGGCGGAGGACTCGTTAAGCCCGGCG GCAGCCTGAGACTGAGCTGCGCCGCTAGCGGATTTACCTTCAGCGACTA CTACATGAGCTGGATCCGGCAGGCCCCTGGCAAGGGCCTGGAATGGGTC AGCTACATCAGCTCCTCTGGCTCTACAATCTACTACGCCGACAGCGTGA AAGGCAGATTCACCATCTCTAGAGATAATGCCAAGAACAGCCTGTACCT GCAAATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTATTGTGCT

		AGAGATCAGGGCAACTACGGCGTGGACGTGTGGGGCCAGGGCACCACCG TGACAGTGTCCTCCACCACAACACCTGCTCCAAGGCCCCCCACACCCGC TCCAACTATAGCCAGCCAACCATTGAGCCTCAGACCTGAAGCTTGCAGG CCCGCAGCAGGAGGCGCCGTCCATACGCGAGGCCTGGACTTCGCGTGTG ATATTTATATTTGGGCACCTTTGGCCGGAACATGTGGGGTGTTGCTTCT CTCCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGAAAGAAGCTCCTG TACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAACCACTCAGGAAG AAGATGGGTGTTCATGCCGCTTCCCCGAGGAGGAAGAAGGAGGGTGTGA ACTGAGGGTGAAATTTTCTAGAAGCGCCGATGCTCCCGCATATCAGCAG GGTCAGAATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAGAAGAGT ACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCGAGATGGGGGGAAA GCCCCGGAGAAAAAATCCTCAGGAGGGGTTGTACAATGAGCTGCAGAAG GACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGAAAGAC GCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTACAGCCAC CAAGGACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCCCGC
931	861 + 477	ATGGCTCTTCCCGTAACAGCCCTTTTGTTGCCCCTTGCACTCCTTCTGC ATGCAGCACGACCGGACATCCAGATGACCCAGAGCCCTAGCTCCCTGAG CGCCAGCGTGGGCGATAGAGTGACCATTACCTGTAGAGCCTCTCAGAGC ATCTCCTCCTACCTGAACTGGTATCAGCAGAAACCCGGCAAGGCCCCTA AGCTGCTGATCTACGCCGCTAGCAGCCTGCAGTCTGGCGTCCCCAGCCG GTTCAGCGGCAGCGGATCTGGCACCGACTTCACCCTGACAATCAGCAGC CTGCAACCTGAGGACTTTGCTACATACTACTGCCAGCAGGCCCACAGCT CTCCAATCACCTTCGGCGGCGGAACAAAGGTGGAAATCAAGGGTGGTGG GGGCAGCGGTGGAGGTGGGAGCGGAGGCGGGGGTAGCGGAGGCGGGGGT AGCGAGGTGCAGCTGCTGGAAAGCGGAGGCGGACTCGTTCAACCTGGCG GCAGCCTGAGACTGAGCTGCGCCGCTTCTGGATTTACCTTCAGCAACTA CGCCATGAGCTGGGTGCGGCAGGCCCCTGGCAAAGGCCTGGAATGGGTC TCCGCCATCAGCGGCTCTGGCGGCTCCACCTACTACGCCGACAGCGTGA AGGGCAGATTCACCATCTCTAGAGATAATAGCAAGAACACCCTGTACCT GCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTATTGTGCT AGACCCGGAGATGGCTACTACGAGGGCGTGTACTTCGACTACTGGGGCC AGGGCACACTGGTGACAGTGTCCAGCACCACAACACCTGCTCCAAGGCC CCCCACACCCGCTCCAACTATAGCCAGCCAACCATTGAGCCTCAGACCT GAAGCTTGCAGGCCCGCAGCAGGAGGCGCCGTCCATACGCGAGGCCTGG ACTTCGCGTGTGATATTTATATTTGGGCACCTTTGGCCGGAACATGTGG GGTGTTGCTTCTCTCCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGA AAGAAGCTCCTGTACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAA CCACTCAGGAAGAAGATGGGTGTTCATGCCGCTTCCCCGAGGAGGAAGA AGGAGGGTGTGAACTGAGGGTGAAATTTTCTAGAAGCGCCGATGCTCCC GCATATCAGCAGGGTCAGAATCAGCTCTACAATGAATTGAATCTCGGCA GGCGAGAAGAGTACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCGA GATGGGGGGAAAGCCCCGGAGAAAAAATCCTCAGGAGGGGTTGTACAAT GAGCTGCAGAAGGACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGA AAGGCGAAAGACGCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCT CTCTACAGCCACCAAGGACACTTATGATGCGTTGCATATGCAAGCCTTG CCACCCCGC
932	861 + 525	ATGGCTCTTCCCGTAACAGCCCTTTTGTTGCCCCTTGCACTCCTTCTGC ATGCAGCACGACCGGATATTCAGATGACCCAGAGCCCATCTAGCCTGAG CGCCAGCGTGGGCGATAGAGTGACCATCACCTGTCAGGCCTCTCAGGAC ATCGCTAATTACCTGAACTGGTATCAGCAGAAACCCGGCAAGGCCCCTA AGCTGCTGATCTACGACGCCTCCAACCTGGAAACCGGCGTGCCCAGCCG GTTCAGCGGCAGCGGATCTGGCACAGACTTCACCTTTACCATCAGCTCC CTCCAGCCTGAGGACATCGCCACATACTACTGCCAGCAACACTTCAACC TGCCTCTGACCTTCGGCGGCGGAACAAAGGTCGAGATCAAGGGTGGTGG GGGCAGCGGTGGAGGTGGGAGCGGAGGCGGGGGTAGCGGAGGCGGGGGT AGCCAAATCACCCTGAAAGAGAGCGGACCTACACTGGTCAAGCCTACCC AGACACTGACCCTCACATGTACATTCAGCGGCTTTAGCCTGAGCACCTC CGGCGTGGGAGTGGGCTGGATCAGACAGCCCCCCGGCAAGGCCCTGGAA TGGCTGGCTCTGATCTATTGGAATGACGAGAAGCGGTACAGCCCTAGCC

		TGAAATCTAGACTGACAATCACCAAGGACACCAGCAAGAACCAGGTGGT GCTGACCATGACCAACATGGATCCTGTGGATACCGCCGTGTACTACTGC GCCAGAGAAGGCTCTCACGACTACAAGAGCTCCAACTGGTTCGACCCAT GGGGCCAGGGCACCCTGGTTACAGTGTCTAGCACCACAACACCTGCTCC AAGGCCCCCCACACCCGCTCCAACTATAGCCAGCCAACCATTGAGCCTC AGACCTGAAGCTTGCAGGCCCGCAGCAGGAGGCGCCGTCCATACGCGAG GCCTGGACTTCGCGTGTGATATTTATATTTGGGCACCTTTGGCCGGAAC ATGTGGGGTGTTGCTTCTCTCCCTTGTGATCACTCTGTATTGTAAGCGC GGGAGAAAGAAGCTCCTGTACATCTTCAAGCAGCCTTTTATGCGACCTG TGCAAACCACTCAGGAAGAAGATGGGTGTTCATGCCGCTTCCCCGAGGA GGAAGAAGGAGGGTGTGAACTGAGGGTGAAATTTTCTAGAAGCGCCGAT GCTCCCGCATATCAGCAGGGTCAGAATCAGCTCTACAATGAATTGAATC TCGGCAGGCGAGAAGAGTACGATGTTCTGGACAAAAGACGGGGCAGGGA TCCCGAGATGGGGGGAAAGCCCCGGAGAAAAAATCCTCAGGAGGGGTTG TACAATGAGCTGCAGAAGGACAAGATGGCTGAAGCCTATAGCGAGATCG GAATGAAAGGCGAAAGACGCAGAGGCAAGGGGCATGACGGTCTGTACCA GGGTCTCTCTACAGCCACCAAGGACACTTATGATGCGTTGCATATGCAA GCCTTGCCACCCCGC
933	861 + 573	ATGGCTCTTCCCGTAACAGCCCTTTTGTTGCCCCTTGCACTCCTTCTGC ATGCAGCACGACCGGATATCGTGATGACCCAATCTCCACTGAGCCTGCC TGTGACACCTGGCGAGCCTGCTTCTATCAGCTGTAGAAGCAGCCAGTCC CTGCTGCACAGCAACGGCTACAACTACCTGGACTGGTATCTGCAGAAAC CCGGCCAGAGCCCCCAGCTGCTGATCTACCTCGGCTCTAATCGGGCCAG CGGAGTGCCTGATAGATTCAGCGGAAGCGGCTCCGGCACCGACTTCACC CTGAAGATCAGCAGAGTGGAAGCCGAGGACGTGGGCGTCTACTACTGCA TGCAGGCCCTGGGCCTGATTACATTTGGCGGCGGAACCAAGGTGGAAAT CAAGGGTGGTGGGGGCAGCGGTGGAGGTGGGAGCGGAGGCGGGGGTAGC GGAGGCGGGGGTAGCGAAGTGCAGCTGGTTGAGAGCGGCGGCGGACTGG TGAAGCCCGGAGGCAGCCTCAGACTGAGCTGTGCTGCTTCTGGCTTTAC CTTCAGCTCTTATAGCATGAACTGGGTGCGGCAGGCCCCTGGCAAGGGC CTGGAATGGGTCAGCTCCATCAGCTCTTCTAGCAGCTACATCTACTACG CCGACAGCGTGAAGGGCAGATTCACCATCAGCAGAGATAACGCCAAGAA CAGCCTGTACCTGCAGATGAATAGCCTGCGGGCCGAGGACACCGCCGTG TACTACTGCGCCAGAGCCGGCGACACCTACAGCGCCGCCGATTACTACT ACATGGACGTGTGGGGCAAAGGAACAACCGTGACAGTGTCCTCCACCAC AACACCTGCTCCAAGGCCCCCCACACCCGCTCCAACTATAGCCAGCCAA CCATTGAGCCTCAGACCTGAAGCTTGCAGGCCCGCAGCAGGAGGCGCCG TCCATACGCGAGGCCTGGACTTCGCGTGTGATATTTATATTTGGGCACC TTTGGCCGGAACATGTGGGGTGTTGCTTCTCTCCCTTGTGATCACTCTG TATTGTAAGCGCGGGAGAAAGAAGCTCCTGTACATCTTCAAGCAGCCTT TTATGCGACCTGTGCAAACCACTCAGGAAGAAGATGGGTGTTCATGCCG CTTCCCCGAGGAGGAAGAAGGAGGGTGTGAACTGAGGGTGAAATTTTCT AGAAGCGCCGATGCTCCCGCATATCAGCAGGGTCAGAATCAGCTCTACA ATGAATTGAATCTCGGCAGGCGAGAAGAGTACGATGTTCTGGACAAAAG ACGGGGCAGGGATCCCGAGATGGGGGGAAAGCCCCGGAGAAAAAATCCT CAGGAGGGGTTGTACAATGAGCTGCAGAAGGACAAGATGGCTGAAGCCT ATAGCGAGATCGGAATGAAAGGCGAAAGACGCAGAGGCAAGGGGCATGA CGGTCTGTACCAGGGTCTCTCTACAGCCACCAAGGACACTTATGATGCG TTGCATATGCAAGCCTTGCCACCCCGC
934	861 + 597	ATGGCTCTTCCCGTAACAGCCCTTTTGTTGCCCCTTGCACTCCTTCTGC ATGCAGCACGACCGGAAGTGCAACTGCTGGAAAGCGGCGGAGGCCTGGT CCAGCCCGGCGGCTCTCTGCGGCTCAGCTGCGCCGCTTCTGGATTTACC TTCGGCAGCGAGGCTATGAGCTGGGTGCGGCAGGCCCCTGGAAAAGAGA GAGAGCTGGTGTCCGCCATCAGCGGCAGCGGCGAGGTGACCTACTACGC CGACAGCGTGAAGGGCAGATTCACCATCTCTAGAGATAATAGCAAGAAC ACCCTGTACCTGCAGATGAACAGCCTGAGAGCCGAGGACACCGCCGTGT ACTATTGTCAGAGACTGGTGGAAGCCAAGCGGCACTGGGGCCAGGGCAC ACAGGTTACAGTGTCCAGCACCACAACACCTGCTCCAAGGCCCCCCACA CCCGCTCCAACTATAGCCAGCCAACCATTGAGCCTCAGACCTGAAGCTT

		GCAGGCCCGCAGCAGGAGGCGCCGTCCATACGCGAGGCCTGGACTTCGC GTGTGATATTTATATTTGGGCACCTTTGGCCGGAACATGTGGGGTGTTG CTTCTCTCCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGAAAGAAGC TCCTGTACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAACCACTCA GGAAGAAGATGGGTGTTCATGCCGCTTCCCCGAGGAGGAAGAAGGAGGG TGTGAACTGAGGGTGAAATTTTCTAGAAGCGCCGATGCTCCCGCATATC AGCAGGGTCAGAATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAGA AGAGTACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCGAGATGGGG GGAAAGCCCCGGAGAAAAAATCCTCAGGAGGGGTTGTACAATGAGCTGC AGAAGGACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGA AAGACGCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTACA GCCACCAAGGACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCCC GC
935	861 + 621	ATGGCTCTTCCCGTAACAGCCCTTTTGTTGCCCCTTGCACTCCTTCTGC ATGCAGCACGACCGGAAGTGCAACTGCTGGAATCTGGCGGAGGACTGGT GCAGCCCGGCGGCAGCCTGCGGCTGAGCTGTGCTGCTTCTGGCTTTACC TTCGAGTCTGAGGCCATGAGCTGGTATAGACAGGCCCCTGGCAAGGAAA GAGAGCTGGTCAGCGTGATCACCAGCGAGGGCTCCACCTACTACGCCGA CAGCGTGAAAGGCAGATTCACAATCAGCCGGGACAATAGCAAGAACACC CTGTACCTGCAGATGAACAGCCTGCGCGCCGAAGATACAGCCGTGTACT ACTGCGCCCACATCGAGTGGGAGACAAGACTCAACTGGGGCCAGGGCAC CCAGGTGACCGTGTCCAGCACCACAACACCTGCTCCAAGGCCCCCCACA CCCGCTCCAACTATAGCCAGCCAACCATTGAGCCTCAGACCTGAAGCTT GCAGGCCCGCAGCAGGAGGCGCCGTCCATACGCGAGGCCTGGACTTCGC GTGTGATATTTATATTTGGGCACCTTTGGCCGGAACATGTGGGGTGTTG CTTCTCTCCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGAAAGAAGC TCCTGTACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAACCACTCA GGAAGAAGATGGGTGTTCATGCCGCTTCCCCGAGGAGGAAGAAGGAGGG TGTGAACTGAGGGTGAAATTTTCTAGAAGCGCCGATGCTCCCGCATATC AGCAGGGTCAGAATCAGCTCTACAATGAATTGAATCTCGGCAGGCGAGA AGAGTACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCGAGATGGGG GGAAAGCCCCGGAGAAAAAATCCTCAGGAGGGGTTGTACAATGAGCTGC AGAAGGACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGAAAGGCGA AAGACGCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTCTCTACA GCCACCAAGGACACTTATGATGCGTTGCATATGCAAGCCTTGCCACCCC GC
936	861 + 645	ATGGCTCTTCCCGTAACAGCCCTTTTGTTGCCCCTTGCACTCCTTCTGC ATGCAGCACGACCGGAGGTGCAGCTGCTGGAAAGCGGAGGGGGCCTGGT CCAACCCGGCGGGTCTCTTCGCCTAAGCTGTGCCGCTTCTGGCTTCACC TTCGACGAGTACACCATGCACTGGTTCAGACAGGCCCCCGGCAAGGAGC GCGAGTTCGTCAGTGCAATCAGCGGAGGCGGTAGCGAGACTTATTACGC GGACTCCGTGAAGGGCCGCTTCACCATTAGCCGCGACAACTCCAAGAAC ACGCTGTACCTGCAGATGAATTCGCTGCGCGCCGAAGATACGGCCGTGT ACTACTGTGCCGCTGGTGGGGAGGAGGCTGGCGTGGGCTATTGGGGCCA GGGCACCCAGGTCACCGTGTCGTCCACCACAACACCTGCTCCAAGGCCC CCCACACCCGCTCCAACTATAGCCAGCCAACCATTGAGCCTCAGACCTG AAGCTTGCAGGCCCGCAGCAGGAGGCGCCGTCCATACGCGAGGCCTGGA CTTCGCGTGTGATATTTATATTTGGGCACCTTTGGCCGGAACATGTGGG GTGTTGCTTCTCTCCCTTGTGATCACTCTGTATTGTAAGCGCGGGAGAA AGAAGCTCCTGTACATCTTCAAGCAGCCTTTTATGCGACCTGTGCAAAC CACTCAGGAAGAAGATGGGTGTTCATGCCGCTTCCCCGAGGAGGAAGAA GGAGGGTGTGAACTGAGGGTGAAATTTTCTAGAAGCGCCGATGCTCCCG CATATCAGCAGGGTCAGAATCAGCTCTACAATGAATTGAATCTCGGCAG GCGAGAAGAGTACGATGTTCTGGACAAAAGACGGGGCAGGGATCCCGAG ATGGGGGGAAAGCCCCGGAGAAAAAATCCTCAGGAGGGGTTGTACAATG AGCTGCAGAAGGACAAGATGGCTGAAGCCTATAGCGAGATCGGAATGAA AGGCGAAAGACGCAGAGGCAAGGGGCATGACGGTCTGTACCAGGGTCTC TCTACAGCCACCAAGGACACTTATGATGCGTTGCATATGCAAGCCTTGC CACCCCGC

937	861 + 669	ATGGCTCTTCCCGTAACAGCCCTTTTGTTGCCCCTTGCACTCCTTCTGC ATGCAGCACGACCGGAGGTGCAGCTGCTGGAGAGCGGAGGCGGCCTCGT GCAGCCAGGAGGTTCCCTACGACTCTCCTGTGCCGCCAGCGGCTTCACC TTCGAGGACTACGCCATGAGTTGGTTCCGCCAGGCCCCGGGGAAGGAGC GCGAGGGCGTGAGCGCGATTTCTGGAAAGGGCGGCTCCACCTATTACGC GGACTCCGTGAAGGGTCGCTTTACCATCTCTCGCGACAACTCCAAGAAC ACGCTGTACCTGCAGATGAATAGCCTGCGCGCTGAGGACACTGCCGTGT ACTACTGTGCTGTCTTGGACGAGGAGGCCGGCGCAGAGGGCGGCTATTG GGGCCAGGGTACCCAGGTCACCGTGTCGTCCACCACAACACCTGCTCCA AGGCCCCCCACACCCGCTCCAACTATAGCCAGCCAACCATTGAGCCTCA GACCTGAAGCTTGCAGGCCCGCAGCAGGAGGCGCCGTCCATACGCGAGG CCTGGACTTCGCGTGTGATATTTATATTTGGGCACCTTTGGCCGGAACA TGTGGGGTGTTGCTTCTCTCCCTTGTGATCACTCTGTATTGTAAGCGCG GGAGAAAGAAGCTCCTGTACATCTTCAAGCAGCCTTTTATGCGACCTGT GCAAACCACTCAGGAAGAAGATGGGTGTTCATGCCGCTTCCCCGAGGAG GAAGAAGGAGGGTGTGAACTGAGGGTGAAATTTTCTAGAAGCGCCGATG CTCCCGCATATCAGCAGGGTCAGAATCAGCTCTACAATGAATTGAATCT CGGCAGGCGAGAAGAGTACGATGTTCTGGACAAAAGACGGGGCAGGGAT CCCGAGATGGGGGGAAAGCCCCGGAGAAAAAATCCTCAGGAGGGGTTGT ACAATGAGCTGCAGAAGGACAAGATGGCTGAAGCCTATAGCGAGATCGG AATGAAAGGCGAAAGACGCAGAGGCAAGGGGCATGACGGTCTGTACCAG GGTCTCTCTACAGCCACCAAGGACACTTATGATGCGTTGCATATGCAAG CCTTGCCACCCCGC
938	861 + 693	ATGGCTCTTCCCGTAACAGCCCTTTTGTTGCCCCTTGCACTCCTTCTGC ATGCAGCACGACCGGAGGTGCAACTGCTGGAAAGCGGCGGTGGACTGGT GCAGCCCGGCGGCAGCCTGAGACTGTCTTGTGCTGCTTCTGGATTTACA TTCGACAGATACGCCATGAGCTGGTTCCGCCAGGCCCCTGGCAAAGAGC GGGAAGGCGTGTCCGCCATCTCCACAAGCGGAGATAGCACATACTATGC CGACAGCGTGAAGGGCAGATTCACCATCAGCAGAGATAATAGCAAGAAC ACCCTGTACCTGCAGATGAACAGCCTCCGGGCCGAGGACACCGCCGTCT ACTACTGCGCCGTGCTGGACGAGGAAGCCGGCGCCGAGGGCGGCTACTG GGGCCAGGGCACCCAGGTGACCGTGTCTAGCACCACAACACCTGCTCCA AGGCCCCCCACACCCGCTCCAACTATAGCCAGCCAACCATTGAGCCTCA GACCTGAAGCTTGCAGGCCCGCAGCAGGAGGCGCCGTCCATACGCGAGG CCTGGACTTCGCGTGTGATATTTATATTTGGGCACCTTTGGCCGGAACA TGTGGGGTGTTGCTTCTCTCCCTTGTGATCACTCTGTATTGTAAGCGCG GGAGAAAGAAGCTCCTGTACATCTTCAAGCAGCCTTTTATGCGACCTGT GCAAACCACTCAGGAAGAAGATGGGTGTTCATGCCGCTTCCCCGAGGAG GAAGAAGGAGGGTGTGAACTGAGGGTGAAATTTTCTAGAAGCGCCGATG CTCCCGCATATCAGCAGGGTCAGAATCAGCTCTACAATGAATTGAATCT CGGCAGGCGAGAAGAGTACGATGTTCTGGACAAAAGACGGGGCAGGGAT CCCGAGATGGGGGGAAAGCCCCGGAGAAAAAATCCTCAGGAGGGGTTGT ACAATGAGCTGCAGAAGGACAAGATGGCTGAAGCCTATAGCGAGATCGG AATGAAAGGCGAAAGACGCAGAGGCAAGGGGCATGACGGTCTGTACCAG GGTCTCTCTACAGCCACCAAGGACACTTATGATGCGTTGCATATGCAAG CCTTGCCACCCCGC
939	861 + 717	ATGGCTCTTCCCGTAACAGCCCTTTTGTTGCCCCTTGCACTCCTTCTGC ATGCAGCACGACCGGAGGTGCAACTGCTGGAAAGCGGCGGAGGACTCGT CCAGCCCGGCGGCAGCCTGCGGCTGAGCTGTGCTGCTTCTGGATTTACC TTCGCCAGCGACGCCATGAGCTGGTATAGACAGGCCCCTGGCAAAGAGC GGGAACTGGTGTCCGCCATCAGCGGCTCTGGCGGCTCCACCTACTACGC CGATAGCGTGAAGGGCAGATTCACAATCTCTAGAGATAATAGCAAGAAC ACCCTGTACCTGCAGATGAACAGCCTGAGAGCCGAGGACACCGCCGTGT ACTACTGCGCCGCTCACGACAGCGGCGAGGCCTACCTGGCCTTCGACTA CTGGGGCCAGGGCACACAGGTGACCGTGTCTAGCACCACAACACCTGCT CCAAGGCCCCCCACACCCGCTCCAACTATAGCCAGCCAACCATTGAGCC TCAGACCTGAAGCTTGCAGGCCCGCAGCAGGAGGCGCCGTCCATACGCG AGGCCTGGACTTCGCGTGTGATATTTATATTTGGGCACCTTTGGCCGGA ACATGTGGGGTGTTGCTTCTCTCCCTTGTGATCACTCTGTATTGTAAGC

		GCGGGAGAAAGAAGCTCCTGTACATCTTCAAGCAGCCTTTTATGCGACC TGTGCAAACCACTCAGGAAGAAGATGGGTGTTCATGCCGCTTCCCCGAG GAGGAAGAAGGAGGGTGTGAACTGAGGGTGAAATTTTCTAGAAGCGCCG ATGCTCCCGCATATCAGCAGGGTCAGAATCAGCTCTACAATGAATTGAA TCTCGGCAGGCGAGAAGAGTACGATGTTCTGGACAAAAGACGGGGCAGG GATCCCGAGATGGGGGGAAAGCCCCGGAGAAAAAATCCTCAGGAGGGGT TGTACAATGAGCTGCAGAAGGACAAGATGGCTGAAGCCTATAGCGAGAT CGGAATGAAAGGCGAAAGACGCAGAGGCAAGGGGCATGACGGTCTGTAC CAGGGTCTCTCTACAGCCACCAAGGACACTTATGATGCGTTGCATATGC AAGCCTTGCCACCCCGC
940	861 + 741	ATGGCTCTTCCCGTAACAGCCCTTTTGTTGCCCCTTGCACTCCTTCTGC ATGCAGCACGACCGGAGGTGCAACTGCTGGAAAGCGGCGGAGGACTCGT CCAGCCCGGCGGCAGCCTGAGGCTGAGCTGTGCTGCTTCTGGCTTTACC TTCGACTCCTACACAATGAGCTGGTATAGACAGGCCCCTGGCAAGGAGC GGGAACTGGTGTCCGCCATCAGCGGCCACGGCGACTCTACATACTACGC CGACAGCGTGAAAGGCAGATTCACAATCTCTAGAGATAATAGCAAGAAC ACCCTGTACCTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGT ACTACTGCACCAGAATCAGCATCACCACCGAGTGGCTGGCCGGAGATTA CTGGGGCCAGGGCACCCAGGTGACAGTGTCCAGCACCACAACACCTGCT CCAAGGCCCCCCACACCCGCTCCAACTATAGCCAGCCAACCATTGAGCC TCAGACCTGAAGCTTGCAGGCCCGCAGCAGGAGGCGCCGTCCATACGCG AGGCCTGGACTTCGCGTGTGATATTTATATTTGGGCACCTTTGGCCGGA ACATGTGGGGTGTTGCTTCTCTCCCTTGTGATCACTCTGTATTGTAAGC GCGGGAGAAAGAAGCTCCTGTACATCTTCAAGCAGCCTTTTATGCGACC TGTGCAAACCACTCAGGAAGAAGATGGGTGTTCATGCCGCTTCCCCGAG GAGGAAGAAGGAGGGTGTGAACTGAGGGTGAAATTTTCTAGAAGCGCCG ATGCTCCCGCATATCAGCAGGGTCAGAATCAGCTCTACAATGAATTGAA TCTCGGCAGGCGAGAAGAGTACGATGTTCTGGACAAAAGACGGGGCAGG GATCCCGAGATGGGGGGAAAGCCCCGGAGAAAAAATCCTCAGGAGGGGT TGTACAATGAGCTGCAGAAGGACAAGATGGCTGAAGCCTATAGCGAGAT CGGAATGAAAGGCGAAAGACGCAGAGGCAAGGGGCATGACGGTCTGTAC CAGGGTCTCTCTACAGCCACCAAGGACACTTATGATGCGTTGCATATGC AAGCCTTGCCACCCCGC
941	861 + 765	ATGGCTCTTCCCGTAACAGCCCTTTTGTTGCCCCTTGCACTCCTTCTGC ATGCAGCACGACCGGAGGTGCAGCTGCTGGAAAGCGGAGGAGGCCTGGT CCAACCTGGCGGCAGCCTGCGGCTGAGCTGCGCCGCTTCTGGCTTCACC TTCAGCAGCTACGCCATGAGCTGGTTCCGGCAGGCCCCTGGCAAGGAAA GAGAGTTCGTGTCTTTTATCAGCGGATCTGGCGACTCCACCTACTACGC TGATAGCGTGAAAGGCAGATTTACCATCTCTAGAGATAATAGCAAGAAC ACCCTGTACCTCCAGATGAACAGCCTGCGCGCCGAGGACACAGCCGTGT ACTATTGTACCAGATGGCCTTACGACTTCGAGGAACCAAGCGAGCCCGG CGTGTACTGGGGCCAGGGCACACAGGTGACAGTGTCCTCCACCACAACA CCTGCTCCAAGGCCCCCCACACCCGCTCCAACTATAGCCAGCCAACCAT TGAGCCTCAGACCTGAAGCTTGCAGGCCCGCAGCAGGAGGCGCCGTCCA TACGCGAGGCCTGGACTTCGCGTGTGATATTTATATTTGGGCACCTTTG GCCGGAACATGTGGGGTGTTGCTTCTCTCCCTTGTGATCACTCTGTATT GTAAGCGCGGGAGAAAGAAGCTCCTGTACATCTTCAAGCAGCCTTTTAT GCGACCTGTGCAAACCACTCAGGAAGAAGATGGGTGTTCATGCCGCTTC CCCGAGGAGGAAGAAGGAGGGTGTGAACTGAGGGTGAAATTTTCTAGAA GCGCCGATGCTCCCGCATATCAGCAGGGTCAGAATCAGCTCTACAATGA ATTGAATCTCGGCAGGCGAGAAGAGTACGATGTTCTGGACAAAAGACGG GGCAGGGATCCCGAGATGGGGGGAAAGCCCCGGAGAAAAAATCCTCAGG AGGGGTTGTACAATGAGCTGCAGAAGGACAAGATGGCTGAAGCCTATAG CGAGATCGGAATGAAAGGCGAAAGACGCAGAGGCAAGGGGCATGACGGT CTGTACCAGGGTCTCTCTACAGCCACCAAGGACACTTATGATGCGTTGC ATATGCAAGCCTTGCCACCCCGC
942	861 + 789	ATGGCTCTTCCCGTAACAGCCCTTTTGTTGCCCCTTGCACTCCTTCTGC ATGCAGCACGACCGGAGGTGCAGCTGCTGGAAAGCGGCGGAGGCCTGGT GCAACCTGGCGGATCTCTCAGACTGAGCTGTGCTGCTTCTGGCTTCACA

		TTCACCGACTACGACATGAGCTGGTATAGACAGGCCCCTGGAAAAGAGC GGGAACTGGTCTCCGTGATCCACAGCGGCGGCTCCACCTACTACGCCGA TAGCGTGAAGGGCAGATTCACCATCAGCAGAGATAATAGCAAGAACACC CTGTACCTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACT ACTGCGCCCCCGGCTACTACAGCGACCTGTCTTTTGATTATTACAACTT CGACTACTGGGGCCAGGGCACACAGGTGACAGTGTCCAGCACCACAACA CCTGCTCCAAGGCCCCCCACACCCGCTCCAACTATAGCCAGCCAACCAT TGAGCCTCAGACCTGAAGCTTGCAGGCCCGCAGCAGGAGGCGCCGTCCA TACGCGAGGCCTGGACTTCGCGTGTGATATTTATATTTGGGCACCTTTG GCCGGAACATGTGGGGTGTTGCTTCTCTCCCTTGTGATCACTCTGTATT GTAAGCGCGGGAGAAAGAAGCTCCTGTACATCTTCAAGCAGCCTTTTAT GCGACCTGTGCAAACCACTCAGGAAGAAGATGGGTGTTCATGCCGCTTC CCCGAGGAGGAAGAAGGAGGGTGTGAACTGAGGGTGAAATTTTCTAGAA GCGCCGATGCTCCCGCATATCAGCAGGGTCAGAATCAGCTCTACAATGA ATTGAATCTCGGCAGGCGAGAAGAGTACGATGTTCTGGACAAAAGACGG GGCAGGGATCCCGAGATGGGGGGAAAGCCCCGGAGAAAAAATCCTCAGG AGGGGTTGTACAATGAGCTGCAGAAGGACAAGATGGCTGAAGCCTATAG CGAGATCGGAATGAAAGGCGAAAGACGCAGAGGCAAGGGGCATGACGGT CTGTACCAGGGTCTCTCTACAGCCACCAAGGACACTTATGATGCGTTGC ATATGCAAGCCTTGCCACCCCGC
943	861 + 813	ATGGCTCTTCCCGTAACAGCCCTTTTGTTGCCCCTTGCACTCCTTCTGC ATGCAGCACGACCGGAGGTGCAGCTGCTGGAGAGCGGTGGAGGGTTGGT GCAGCCCGGGGGTAGCCTGCGTCTGTCGTGCGCCGCTTCCGGCTTCACG TTCTCTGATTACGCCATGCACTGGTTCCGGCAGGCCCCCGGTAAGGAGC GCGTGCTGGTGTCGTCTATTGACTCCGGCGGCTCCACTTACTACGCAGA CAGTGTCAAGGGCCGTTTCACCATCAGCCGCGACAACAGCAAGAACACG CTGTACCTGCAGATGAACTCCCTTCGAGCAGAGGACACCGCGGTGTACT ACTGTAATGCGGGCTTCAAGGGCGATCACCCCCACCCCAAGGATGCCTT CGACATTTGGGGCCAGGGCACCCAGGTCACCGTGTCGTCCACCACAACA CCTGCTCCAAGGCCCCCCACACCCGCTCCAACTATAGCCAGCCAACCAT TGAGCCTCAGACCTGAAGCTTGCAGGCCCGCAGCAGGAGGCGCCGTCCA TACGCGAGGCCTGGACTTCGCGTGTGATATTTATATTTGGGCACCTTTG GCCGGAACATGTGGGGTGTTGCTTCTCTCCCTTGTGATCACTCTGTATT GTAAGCGCGGGAGAAAGAAGCTCCTGTACATCTTCAAGCAGCCTTTTAT GCGACCTGTGCAAACCACTCAGGAAGAAGATGGGTGTTCATGCCGCTTC CCCGAGGAGGAAGAAGGAGGGTGTGAACTGAGGGTGAAATTTTCTAGAA GCGCCGATGCTCCCGCATATCAGCAGGGTCAGAATCAGCTCTACAATGA ATTGAATCTCGGCAGGCGAGAAGAGTACGATGTTCTGGACAAAAGACGG GGCAGGGATCCCGAGATGGGGGGAAAGCCCCGGAGAAAAAATCCTCAGG AGGGGTTGTACAATGAGCTGCAGAAGGACAAGATGGCTGAAGCCTATAG CGAGATCGGAATGAAAGGCGAAAGACGCAGAGGCAAGGGGCATGACGGT CTGTACCAGGGTCTCTCTACAGCCACCAAGGACACTTATGATGCGTTGC ATATGCAAGCCTTGCCACCCCGC
944	861 + 837	ATGGCTCTTCCCGTAACAGCCCTTTTGTTGCCCCTTGCACTCCTTCTGC ATGCAGCACGACCGGAGGTGCAACTGCTGGAATCCGGCGGAGGCCTGGT GCAGCCCGGCGGCAGCCTCAGACTGAGCTGTGCCGCTTCTGGCTTTACC TTCAGCAGCGAGGGCATGAGCTGGGTGCGGCAGGCCCCTGGCAAGGAAA GAGAGCTGGTCTCCGCCATCAGCGGATCTGGCGACCACACCTACTATGC CGATAGCGTGCGCGGAAGATTCACAATCTCTAGAGATAATAGCAAGAAC ACCCTGTACCTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGT ACTACTGCAACGCCCTGGAAGGCGGCCCTACAACAGCTATCCAGCCAGG AGGCCCTGACTACTGGGGCCAGGGCACCCAGGTGACCGTGTCCAGCACC ACAACACCTGCTCCAAGGCCCCCCACACCCGCTCCAACTATAGCCAGCC AACCATTGAGCCTCAGACCTGAAGCTTGCAGGCCCGCAGCAGGAGGCGC CGTCCATACGCGAGGCCTGGACTTCGCGTGTGATATTTATATTTGGGCA CCTTTGGCCGGAACATGTGGGGTGTTGCTTCTCTCCCTTGTGATCACTC TGTATTGTAAGCGCGGGAGAAAGAAGCTCCTGTACATCTTCAAGCAGCC TTTTATGCGACCTGTGCAAACCACTCAGGAAGAAGATGGGTGTTCATGC CGCTTCCCCGAGGAGGAAGAAGGAGGGTGTGAACTGAGGGTGAAATTTT

		CTAGAAGCGCCGATGCTCCCGCATATCAGCAGGGTCAGAATCAGCTCTA CAATGAATTGAATCTCGGCAGGCGAGAAGAGTACGATGTTCTGGACAAA AGACGGGGCAGGGATCCCGAGATGGGGGGAAAGCCCCGGAGAAAAAATC CTCAGGAGGGGTTGTACAATGAGCTGCAGAAGGACAAGATGGCTGAAGC CTATAGCGAGATCGGAATGAAAGGCGAAAGACGCAGAGGCAAGGGGCAT GACGGTCTGTACCAGGGTCTCTCTACAGCCACCAAGGACACTTATGATG CGTTGCATATGCAAGCCTTGCCACCCCGC

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.

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 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 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, Mosl, Tcl/mariner, Tol2, mini-Tol2, Tc3, MuA, Himar I, Frog Prince, and derivatives thereof.

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 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 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 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 tp carry large 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 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 purificationof 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.

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; 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 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 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, *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 epsilonretrovirus genome, a simiispumavirus genome, a bovispumavirus genome, 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, 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

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 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 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-Jinkins 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, 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.

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 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 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 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 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 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 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).

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.

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 or 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 "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 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.

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 (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 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, 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 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 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 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 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), 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 (Ig) B cell receptor, but usually express the surface markers CD16 (FcyRIII) 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 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 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 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 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.

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 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 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).

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.

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 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 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

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

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

(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 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.

Embodiment 3: The antibody or antigen binding fragment thereof of embodiment 1 or embodiment 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.

Embodiment 4: The antibody or antigen binding fragment thereof of any one of embodiments 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 and 976-

979); EGKSSGSGSESKVD (SEQ ID NO: 4); KESGSVSSEQLAQFRSLD (SEQ ID NO: 5); LRQRDGERP (SEQ ID NO: 6); LRQKDGGGSERP (SEQ ID NO: 7); LRQKD$(GGGS)_2$ERP (SEQ ID NO: 8), GEGTSTGSGGSGGSGGAD (SEQ ID NO: 9), 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, 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.

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, 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.

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 CD8β hinge, a CD8α 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.

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.

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, CD3δ, CD3ε, CD3γ, CD3ζ, CD4, CD5, CD8α, CD9, CD16, CD22, CD27, CD28, CD33, CD37, CD45, CD64, CD80, CD86, CD134, CD137, CD152, CD154, CD278, amnionless (AMN), and 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.

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 FcRγ, FcRβ, CD3γ, CD3δ, CD3ε, CD3ζ, 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 CD3ζ.

Embodiment 18: The CAR of embodiment 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.

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,

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 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 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.

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 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 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.

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, 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, 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.

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 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.

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: 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 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.

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 parvovirus vector, a rhabdovirus vector, a vesiculovirus vector, a paramyxovirus vector, a morbillovirus 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: 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 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

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 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 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.

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.

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.

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.

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.

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K. EXAMPLES

EXAMPLE 1

RECOMBINANT LENTIVIRUS DELIVERS FUNCTIONAL ANTI-BCMA CARS TO T CELLS

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 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 an MNDU3 promoter operably linked to a polynucleotide encoding a CD8α signal peptide and an anti-BCMA CAR and a WPRE element operably 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	CD8α	CD8α	CD137	CD3ζ
LV 2	237	scFv	CD8α	CD8α	CD137	CD3ζ
LV 3	261	scFv	CD8α	CD8α	CD137	CD3ζ
LV 4	333	scFv	CD8α	CD8α	CD137	CD3ζ
LV 5	357	scFv	CD8α	CD8α	CD137	CD3ζ
LV 6	429	scFv	CD8α	CD8α	CD137	CD3ζ
LV 7	477	scFv	CD8α	CD8α	CD137	CD3ζ
LV 8	525	scFv	CD8α	CD8α	CD137	CD3ζ
LV 9	597	VHH	CD8α	CD8α	CD137	CD3ζ
LV 10	621	VHH	CD8α	CD8α	CD137	CD3ζ
LV 11	645	VHH	CD8α	CD8α	CD137	CD3ζ
LV 12	669	VHH	CD8α	CD8α	CD137	CD3ζ
LV 13	693	VHH	CD8α	CD8α	CD137	CD3ζ
LV 14	717	VHH	CD8α	CD8α	CD137	CD3ζ
LV 15	741	VHH	CD8α	CD8α	CD137	CD3ζ
LV 16	789	VHH	CD8α	CD8α	CD137	CD3ζ
LV 17	813	VHH	CD8α	CD8α	CD137	CD3ζ
LV 18	837	VHH	CD8α	CD8α	CD137	CD3ζ

LV 19	NA	scFv	CD8α	CD8α	CD137	CD3ζ

Jurkat Functional Titer

1 x 10^5 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 10^5 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 10^4 PBMCs transduced with recombinant lentiviruses LV 1 to LV 19 were co-cultured with 5 x 10^4 high BCMA-expressing tumor cells (RPMI-8226) or 5 x 10^4 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 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 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 either an MNDU3 promoter (SEQ ID NO: 950), an SFFV promoter (SEQ ID NO: 952), or an EF1α promoter (SEQ ID NO: 949) operably linked to a polynucleotide encoding a CD8α 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 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	EF1α	wild-type
LV 3.8	261	EF1α	no PRE
LV 3.9	261	EF1α	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	EF1α	wild-type

LV 5.8	357	EF1α	no PRE
LV 5.9	357	EF1α	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	EF1α	wild-type
LV 6.8	429	EF1α	no PRE
LV 6.9	429	EF1α	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	EF1α	wild-type
LV 8.8	525	EF1α	no PRE
LV 8.9	525	EF1α	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	EF1α	wild-type
LV 9.8	597	EF1α	no PRE
LV 9.9	597	EF1α	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	EF1α	wild-type
LV 13.8	693	EF1α	no PRE
LV 13.9	693	EF1α	mutant WPRE
LV19		MNDU3	no PRE

Infectious Titer

1 x 10^5 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 x 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 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

5 x 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 EF1α promoter and no WPRE. PBMCs were transduced at an MOI of 1 (based on IU/mL determined in Jurkat cells), except for LV 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.

5 x 10^4 transduced PBMCs were co-cultured with 5 x 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 IFNγ and IL-2 levels using an MSD assay. IFNγ and IL-2 levels produced in co-culture were plotted against the percentage of anti-BCMA CAR positive cells. Figures 3C and 3D.

Antigen independent anti-BCMA CAR activity was assessed by culturing 5 x 10^4 transduced PBMCs in the absence of target cells for 24 hours. After 24 hours, the supernatants were harvested and IFNγ levels measures using an MSD assay. IFNγ 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 x 10^5 RPMI-8226 or 1 x 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 EF1α 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 CD8α 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 CD8α 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	EF1α	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	EF1α	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	EF1α	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	EF1α	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	EF1α	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	EF1α	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 CD8α 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 x 10^6 Daudi cells labeled with firefly luciferase. After four days, four out of five groups of mice were intravenously administered 1 x 10^6 human PBMCs. The next day mice that received the 1 x 10^6 human PBMCs were administered vehicle control (DMEM); or 2.2 x 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 x 10^6 *ex vivo* anti-BCMA CAR T cells. All groups of mice then received three doses of 2 x 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

NSG mice were intravenously injected with 2 x 10^6 Daudi cells labeled with firefly luciferase. After four days, eight out of nine groups of mice were intravenously administered 1 x 10^6 human PBMCs. The next day mice that received the 1 x 10^6 human PBMCs were administered vehicle control (DMEM); 1.25 x 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 x 10^7 IU of LV 6.8. Mice that were not administered PBMCs were administered 5 x 10^6 *ex vivo* anti-BCMA CAR T cells. All groups of mice then received three doses of 2 x 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 13.8 experienced durable tumor regression. Figure 4B.

Third Daudi Model Study

NSG mice were intravenously injected with 2 x 10^6 Daudi cells labeled with firefly luciferase. After four days, eight out of nine groups of mice were intravenously administered 1 x 10^6 human PBMCs. The next day mice that received the 1 x 10^6 human PBMCs were administered vehicle control (DMEM); 1.25 x 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 x 10^7 IU of LV 6.8. Mice that were not administered PBMCs were administered 5 x 10^6 *ex vivo* anti-BCMA CAR T cells. All groups of mice then received three doses of 2 x 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.

First RPMI Model Study

NOD scid gamma (NSG) mice were subcutaneously injected with 1 x 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 x 10^6 human PBMCs. The next day, mice that received the 1 x 10^6 human PBMCs were administered vehicle control (DMEM); 5.0 x 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 x 10^6 unmodified *ex vivo* anti-BCMA CAR T cells. All groups of mice then received three doses of 2 x 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 x 10^6 *ex vivo* anti-BCMA CAR T cells. All groups of mice then received three doses of 2 x 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 x 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 x 10^6 human PBMCs. The next day, mice that received the 1 x 10^6 human PBMCs were administered vehicle control (DMEM); 1.25 x 10^7 IU of LV 6.8, 5.0 x 10^7 IU of LV 6.8, or 1.25 x 10^8 IU of LV 6.8. The fifth group of mice was administered 2 x 10^6 unmodified *ex vivo* anti-BCMA CAR T cells. All groups of mice then received three doses of 2 x 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 x 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 x 10^6 human PBMCs. The next day, mice that received the 1 x 10^6 human PBMCs were administered vehicle control (DMEM); 5.0 x 10^7 IU of LV 6.3 or 1.25 x 10^8 IU of LV 6.3. The fourth group of mice was administered 2 x 10^6 unmodified *ex vivo* anti-BCMA CAR T cells. All groups of mice then received three doses of 2 x 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 x 10^6 Daudi cells labeled with firefly luciferase. After four days, four out of five groups of mice were intravenously administered 1 x 10^6 human PBMCs. The next day mice that received the 1 x 10^6 human PBMCs were administered vehicle control (DMEM); 1.25 x 10^8 IU of LV 6.1 or LV6.3; or 5.6 x 10^7 IU of LV 6.8. Mice that were not administered PBMCs were administered 5 x 10^6 *ex vivo* anti-BCMA CAR T cells. All groups of mice then received three doses of 2 x 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 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 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.

Table 13

SEQ ID NO:	NUCLEIC ACID SEQUENCE
954	DIVLTQSPPSLAMSLGKRATISCRASESVTILGSHLIHWYQQKPGQPPTLLIQLASNVQTG VPARFSGSGSRTDFTLTIDPVEEDDVAVYYCLQSRTIPRTFGGGTKLEIKGSTSGSGKPGS GEGSTKGQIQLVQSGPELKKPGETVKISCKASGYTFTDYSINWVKRAPGKGLKWMGWINTE TREPAYAYDFRGRFAFSLETSASTAYLQINNLKYEDTATYFCALDYSYAMDYWGQGTSVTV SSAAATTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTC GVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSR SADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKM AEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
955	QVKLEESGGGLVQAGRSLRLSCAASEHTFSSHVMGWFRQAPGKERESVAVIGWRDISTSYA DSVKGRFTISRDNAKKTLYLQMNSLKPEDTAVYYCAARRIDAADFDSWGQGTQVTVSSGGG GSEVQLVESGGGLVQAGGSLRLSCAASGRTFTMGWFRQAPGKEREFVAAISLSPTLAYYAE SVKGRFTISRDNAKNTVVLQMNSLKPEDTALYYCAADRKSVMSIRPDYWGQGTQVTVSSTS TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLL SLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAP 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	EF1α	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

NSG mice were intravenously injected with 2 x 10^6 Daudi cells labeled with firefly luciferase. After four days, four out of five groups of mice were intravenously administered 1 x 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 x 10^7 IU of LV 6.8, LV A, LV B, or LV 19 (GFP control). Tumor volume was measured by using a 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 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 x 10^6 Daudi cells labeled with firefly luciferase. After five days, three out of five groups of mice were intravenously administered 2 x 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 x 10^6 untransduced control human T cells (UTD) and mice that received the anti-BCMA CAR T cells were administered 2 x 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 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.

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

1. An antibody or antigen binding fragment thereof comprising (i) a heavy chain variable region (VH) and a light chain variable region (VL) or (ii) a VHH domain, wherein:

(a) 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;

(b) 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; or

(c) 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.

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

(a) 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;

(b) 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; or

(c) the VHH domain comprises the amino acid sequence set forth in SEQ ID NO: 129.

3. The antibody or antigen binding fragment thereof of claim 1 or claim 2, wherein the antibody or antigen binding fragment thereof further comprises a polypeptide linker, and 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); EGKSSGSGSESKVD (SEQ ID NO: 4); KESGSVSSEQLAQFRSLD (SEQ ID NO: 5); LRQRDGERP (SEQ ID NO: 6); LRQKDGGGSERP (SEQ ID NO: 7); $LRQKD(GGGS)_2ERP$ (SEQ ID NO: 8), GEGTSTGSGGSGGSGGAD (SEQ ID NO: 9), and GSTSGSGKPGSGEGSTKG (SEQ ID NO: 10) and variants thereof comprising an amino acid sequence at least 95% identical thereto.

4. The antibody or antigen binding fragment thereof of any one of claims 1 to 3, wherein the antibody or antigen binding fragment thereof comprises the amino acid sequence set forth in any one of SEQ ID NOs: 69, 70, 89, 90, and 129.

5. A bispecific antibody or an antibody conjugate, comprising the antibody or antigen binding fragment thereof of any one of claims 1 to 4.

6. The bispecific antibody or the antibody conjugate of claim 5, further comprising an anti-CD3 antibody that binds CD3δ, CD3ε, CD3γ, or CD3ζ.

7. A chimeric antigen receptor (CAR) comprising the antibody or antigen binding fragment thereof of any one of claims 1 to 4; a spacer domain; a transmembrane domain, and one or more intracellular signaling domains.

8. The CAR of claim 7, wherein:

(a) the spacer domain comprises a hinge domain or a fragment thereof selected from the group consisting of: a CD4 hinge, a CD8β hinge, a CD8α 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;

(b) the transmembrane domain is 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, CD64, CD80, CD86, CD134, CD137, CD152, CD154, CD278, amnionless (AMN), and programmed cell death 1 (PDCD1);

(c) the one or more intracellular signaling domains comprise a costimulatory signaling domain 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; and/or

(d) the one or more intracellular signaling domains comprise a primary signaling domain derived from a polypeptide selected from the group consisting of FcRγ, FcRβ, CD3γ, CD3δ, CD3ε, CD3ζ, CD22, CD79a, CD79b, and CD66d.

9. The CAR of claim 7 or claim 8, wherein

(a) 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;

(b) 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;

(c) the one or more intracellular signaling domains comprise 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; and/or

(d) 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.

10. The CAR of claim 7, wherein the CAR comprises an antibody or antigen binding fragment thereof comprising the amino acid sequence set forth in any one of SEQ ID NOs: 70, 90, or 129; 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; and 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.

11. The CAR of claim 10, wherein the CAR comprises:

(a) the amino acid sequence set forth in any one of SEQ ID NOs: 429 to 452;

(b) the amino acid sequence set forth in any one of SEQ ID NOs: 525 to 548; or

(c) the amino acid sequence set forth in any one of SEQ ID NOs: 765 to 788.

12. A polynucleotide encoding the antibody or antigen binding fragment thereof of any one of claims 1 to 4, the bispecific antibody or the antibody conjugate of claim 5 or claim 6, or the CAR of any one of claims 7 to 11.

13. The polynucleotide of claim 12, wherein the polynucleotide encodes a CAR comprising a polynucleotide sequence set forth in any one of SEQ ID NOs: 910, 912, 921, 930, 932, and 941.

14. A vector comprising the polynucleotide of claim 12 or claim 13.

15. The vector of claim 14, wherein:

(a) the vector encodes or comprises 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 sequence set forth in any one of SEQ ID NOs: 69, 70, 89, 90, and 129, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947;

(b) the vector encodes or comprises 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 sequence set forth in any one of SEQ ID NOs: 429, 525, and 765, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947;

(c) the vector encodes or comprises 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: 910, 912, and 921, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947; or

(d) the vector encodes or comprises 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: 930, 932, and 941, and optionally comprising a polynucleotide comprising a posttranscriptional regulatory element set forth in any one of SEQ ID NOs: 945-947.

16. The vector of claim 14 or claim 15, wherein:

(a) the vector is an expression vector, a transfer plasmid or a viral vector;

(b) 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 morbillovirus vector, a henipavirus vector, an alphavirus vector, a flavivirus vector, a retroviral vector, and a lentiviral vector (LVV);

(c) the vector is a lentiviral vector 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);

(d) the vector is 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: 910, 912, and 921; optionally a WPRE; a 3′ LTR comprising U3 and R regions; a polyadenylation signal, and a poly(A) tail; or

(e) the vector is 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: 930, 932, and 941; optionally a WPRE; a 3′ LTR comprising U3 and R regions; a polyadenylation signal, and a poly(A) tail.

17. An RNA comprising:

(a) 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: 910, 912, and 921; optionally a WPRE; a 3′ LTR comprising U3 and R regions; a polyadenylation signal, and optionally a poly(A) tail; or

(b) 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: 930, 932, and 941; optionally a WPRE; a 3′ LTR comprising U3 and R regions; a polyadenylation signal, and optionally a poly(A) tail.

18. A recombinant lentivirus comprising one or more copies of the lentiviral vector of claim 16 or the RNA of claim 17.

19. A composition comprising the antibody or antigen binding fragment thereof of any one of claims 1 to 4, the bispecific antibody or the antibody conjugate of claim 5 or claim 6, the CAR of any one of claims 7 to 11, the polynucleotide of claim 12 or claim 13, the vector of any one of claims 14 to 16, the RNA of claim 17, or the recombinant lentivirus of claim 18.

20. A pharmaceutical composition comprising a pharmaceutically acceptable carrier and the antibody or antigen binding fragment thereof of any one of claims 1 to 4, the bispecific antibody or the antibody conjugate of claim 5 or claim 6, the CAR of any one of claims 7 to 11, the polynucleotide of claim 12 or claim 13, the vector of any one of claims 14 to 16, the RNA of claim 17, the recombinant lentivirus of claim 18, or the composition of claim 19.