CD79A CHIMERIC ANTIGEN RECEPTORS

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims the benefit under 35 U.S.C. § 119(e) of U.S. Provisional Application No. 62/685,078, filed June 14, 2018, which is incorporated by reference herein in its entirety.

STATEMENT REGARDING SEQUENCE LISTING

The Sequence Listing associated with this application is provided in text format in lieu of a paper copy and is hereby incorporated by reference into the specification. The name of the text file containing the Sequence Listing is BLBD_100_01WO_ST25.txt. The text file is 64 KB, created on June 14, 2019, and is being submitted electronically via EFS-Web, concurrent with the filing of the specification.

BACKGROUND

Technical Field

The present invention relates to improved compositions and methods for treating cancer. More particularly, the invention relates to improved anti-CD79A chimeric antigen receptors (CARs), genetically modified immune effector cells, and use of these compositions to effectively treat CD79A expressing cancers.

Description of the Related Art

Cancer is a significant health problem throughout the world. Based on rates from 2008-2010, 40.76% of men and women born today will be diagnosed with some form of cancer at some time during their lifetime. 20.37% of men will develop cancer between their 50th and 70th birthdays compared to 15.30% for women. On January 1, 2010, in the United States there were approximately 13,027,914 men and women alive who had a history of cancer -- 6,078,974 men and 6,948,940 women. It is estimated that 1,660,290 men and women (854,790 men and 805,500 women) in the United States will be diagnosed with and 580,350 men and women will die of cancer of all sites in 2013. Howlader *et al*. 2013.

Malignant transformation of B cells leads to cancers including, but not limited to lymphomas, e.g., multiple myeloma and non-Hodgkins' lymphoma. The large majority of patients having B cell malignancies, including non-Hodgkin's lymphoma (NHL) and multiple myeloma (MM), are significant contributors to cancer mortality. The response of B cell malignancies to various forms of treatment is mixed. Traditional methods of treating B cell malignancies, including chemotherapy and radiotherapy, have limited utility due to toxic side effects. Immunotherapy with anti-CD19, anti-CD20, anti-CD22, anti-CD23, anti-CD52, anti-CD80, and anti-HLA-DR therapeutic antibodies have provided limited success, due in part to poor pharmacokinetic profiles, rapid elimination of antibodies by serum proteases and filtration at the glomerulus, and limited penetration into the tumor site and expression levels of the target antigen on cancer cells. Attempts to use genetically modified cells expressing chimeric antigen receptors (CARs) have also met with limited success. In addition, the therapeutic efficacy of a given antigen binding domain used in a particular CAR can be unpredictable: if the antigen binding domain binds too strongly, the CAR T cells may induce massive cytokine release resulting in a potentially fatal immune reaction deemed a "cytokine storm," and if the antigen binding domain binds too weakly, the CAR T cells may not display sufficient therapeutic efficacy in clearing cancer cells.

BRIEF SUMMARY

The invention generally provides improved vectors for generating adoptive cell therapies and methods of using the same. More particularly, the invention provides anti-CD79A CAR molecules and their use in treating, preventing, or ameliorating cancers that express CD79A.

In various embodiments, a chimeric antigen receptor (CAR) is provided comprising: an extracellular domain that comprises: a) an anti-CD79A antibody or antigen binding fragment thereof that binds one or more epitopes of a human CD79A polypeptide, wherein the anti-CD79A antibody or antigen binding fragment thereof comprises a variable light chain sequence comprising CDRL1-CDRL3 sequences set forth in SEQ ID NOs: 1-3, 9-11, or 17-19, and/or and a variable heavy chain sequence comprising CDRH1-CDRH3 sequences set forth in SEQ ID NOs: 4-6, 12-14, or 20-22; b) a transmembrane domain; c) one or more intracellular co-stimulatory signaling domains; and/or d) a primary signaling domain.

Disclosed herein is a chimeric antigen receptor (CAR) comprising: a) an extracellular

domain that comprises an anti-CD79A antibody or antigen binding fragment thereof that binds one or more epitopes of a human CD79A polypeptide, wherein the anti-CD79A antibody or antigen binding fragment thereof comprises a variable light chain sequence comprising CDRL1-CDRL3 sequences set forth in SEQ ID NOs: 1-3 and a variable heavy chain sequence comprising CDRH1-CDRH3 sequences set forth in SEQ ID NOs: 4-6; b) a transmembrane domain; c) one or more intracellular co-stimulatory signaling domains; and d) a primary signaling domain.

Disclosed herein is a chimeric antigen receptor (CAR) comprising: a) an extracellular domain that comprises an anti-CD79A antibody or antigen binding fragment thereof that binds one or more epitopes of a human CD79A polypeptide, wherein the anti-CD79A antibody or antigen binding fragment thereof comprises a variable light chain sequence comprising CDRL1-CDRL3 sequences set forth in SEQ ID NOs: 9-11 and a variable heavy chain sequence comprising CDRH1-CDRH3 sequences set forth in SEQ ID NOs: 12-14; b) a transmembrane domain; c) one or more intracellular co-stimulatory signaling domains; and d) a primary signaling domain.

Disclosed herein is a chimeric antigen receptor (CAR) comprising: a) an extracellular domain that comprises an anti-CD79A antibody or antigen binding fragment thereof that binds one or more epitopes of a human CD79A polypeptide, wherein the anti-CD79A antibody or antigen binding fragment thereof comprises a variable light chain sequence comprising CDRL1-CDRL3 sequences set forth in SEQ ID NOs: 17-19 and a variable heavy chain sequence comprising CDRH1-CDRH3 sequences set forth in SEQ ID NOs: 20-22; b) a transmembrane domain; c) one or more intracellular co-stimulatory signaling domains; and d) a primary signaling domain.

In particular embodiments, the anti-CD79A antibody or antigen binding fragment that binds the human CD79A polypeptide is selected from the group consisting of: a Fab' fragment, a F(ab')2 fragment, a bispecific Fab dimer (Fab2), a trispecific Fab trimer (Fab3), an Fv, an 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, Nanobody).

In certain embodiments, the anti-CD79A antibody or antigen binding fragment that binds the human CD79A polypeptide is an scFv.

In particular embodiments, the anti-CD79A antibody or antigen binding fragment thereof comprises one or more light chain CDRs as set forth in any one of SEQ ID NOs: 1-3 and/or one or more heavy chain CDRs as set forth in any one of SEQ ID NOs: 4-6.

In some embodiments, the anti-CD79A antibody or antigen binding fragment thereof comprises one or more light chain CDRs as set forth in any one of SEQ ID NOs: 9-11 and/or one or more heavy chain CDRs as set forth in any one of SEQ ID NOs: 12-14.

In some embodiments, the anti-CD79A antibody or antigen binding fragment thereof comprises one or more light chain CDRs as set forth in any one of SEQ ID NOs: 17-19 and/or one or more heavy chain CDRs as set forth in any one of SEQ ID NOs: 20-22.

In some embodiments, the anti-CD79A antibody or antigen binding fragment thereof comprises a variable light chain sequence as set forth in any one of SEQ ID NOs: 7, 15, or 23 and/or a variable heavy chain sequence as set forth in any one of SEQ ID NOs: 8, 16, or 24.

In certain embodiments, the anti-CD79A antibody or antigen binding fragment thereof comprises a variable light chain sequence with at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% amino acid identity to the amino acid sequence set forth in any one of SEQ ID NOs: 7, 15, or 23 and/or a variable heavy chain sequence with at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% amino acid identity to the amino acid sequence set forth in any one of SEQ ID NOs: 8, 16, or 24.

In further embodiments, the anti-CD79A antibody or antigen binding fragment thereof comprises a variable light chain sequence as set forth in SEQ ID NO: 7 and/or a variable heavy chain sequence as set forth in SEQ ID NO: 8.

In further embodiments, the anti-CD79A antibody or antigen binding fragment thereof comprises a variable light chain sequence as set forth in SEQ ID NO: 15 and/or a variable heavy chain sequence as set forth in SEQ ID NO: 16.

In further embodiments, the anti-CD79A antibody or antigen binding fragment thereof comprises a variable light chain sequence as set forth in SEQ ID NO: 23 and/or a variable heavy chain sequence as set forth in SEQ ID NO: 24.

In further embodiments, the transmembrane domain is from a polypeptide selected from the group consisting of: alpha or beta chain of the T-cell receptor, CDδ, CD3ε, CDγ,

CD3ζ, CD4, CD5, CD8α, CD9, CD 16, CD22, CD27, CD28, CD33, CD37, CD45, CD64, CD80, CD86, CD 134, CD137, CD152, CD154, and PD1.

In additional embodiments, the transmembrane domain is from a polypeptide selected from the group consisting of: CD8α, CD28, CD4, CD45, PD1, and CD152.

In some embodiments, the transmembrane domain is from CD8α.

In further embodiments, the one or more co-stimulatory signaling domains are from a co-stimulatory molecule selected from the group consisting of: TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9, TLR10, CARD11, CD2, CD7, CD27, CD28, CD30, CD40, CD54 (ICAM), CD83, CD134 (OX40), CD137 (4-1BB), CD278 (ICOS), DAP10, LAT, NKD2C, SLP76, TRIM, and ZAP70.

In certain embodiments, the one or more co-stimulatory signaling domains are from a co-stimulatory molecule selected from the group consisting of: CD28, CD134, and CD137.

In some embodiments, the one or more co-stimulatory signaling domains is from CD137.

In particular embodiments, the primary signaling domain is isolated from a polypeptide selected from the group consisting of: FcRγ, FcRβ, CD3γ, CD3δ, CD3ε, CD3ζ, CD22, CD79a, CD79b, and CD66d.

In particular embodiments, the primary signaling domain is isolated from CD3ζ.

In additional embodiments, the CAR further comprises a hinge region polypeptide.

In certain embodiments, the hinge region polypeptide comprises a hinge region of CD8α.

In additional embodiments, the CAR further comprises a spacer region.

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

In particular embodiments, the signal peptide comprises an IgG1 heavy chain signal polypeptide, a CD8α signal polypeptide, or a human GM-CSF receptor alpha signal polypeptide.

In particular embodiments, a CAR comprises an amino acid sequence set forth in any one of SEQ ID NOs: 25 to 30.

In particular embodiments, a CAR comprises an amino acid sequence set forth in SEQ ID NO: 25.

In particular embodiments, a CAR comprises an amino acid sequence set forth in SEQ ID NO: 26.

In particular embodiments, a CAR comprises an amino acid sequence set forth in SEQ ID NO: 27.

In particular embodiments, a CAR comprises an amino acid sequence set forth in SEQ ID NO: 28.

In particular embodiments, a CAR comprises an amino acid sequence set forth in SEQ ID NO: 29.

In particular embodiments, a CAR comprises an amino acid sequence set forth in SEQ ID NO: 30.

In various embodiments, a polypeptide comprising the amino acid sequence of the CAR contemplated herein is provided.

Disclosed herein is a polypeptide comprising the CAR as defined herein, wherein the polypeptide further comprises a signal peptide.

In various embodiments, a polynucleotide encoding a CAR contemplated herein is provided.

In particular embodiments, a polynucleotide encoding a CAR contemplated herein comprises the sequence set forth in any one of SEQ ID NOs: 31-36.

Disclosed herein is a polynucleotide encoding a CAR as defined herein, or the sequence set forth in any one of SEQ ID NOs: 31-36.

In various embodiments, a vector comprising a polynucleotide encoding a CAR contemplated herein is provided.

Disclosed herein is a vector comprising the polynucleotide as defined herein.

In certain embodiments, the vector is an expression vector.

In particular embodiments, the vector is an episomal vector.

In further embodiments, the vector is a viral vector.

In further embodiments, the vector is a retroviral vector.

In particular embodiments, the vector is a lentiviral vector.

In further embodiments, the lentiviral vector is selected from the group consisting essentially of: human immunodeficiency virus 1 (HIV-1); human immunodeficiency virus 2 (HIV-2), visna-maedi virus (VMV) virus; 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, the vector comprises a left (5') retroviral LTR, a Psi (Ψ) packaging signal, a central polypurine tract/DNA flap (cPPT/FLAP), a retroviral export element; a promoter operably linked to the polynucleotide; and a right (3') retroviral LTR.

In further embodiments, the vector further comprises a heterologous polyadenylation sequence.

In particular embodiments, the vector further comprises a hepatitis B virus posttranscriptional regulatory element (HPRE) or woodchuck post-transcriptional regulatory element (WPRE).

In additional embodiments, the promoter of the 5' LTR is replaced with a heterologous promoter.

In further embodiments, the heterologous promoter is a cytomegalovirus (CMV) promoter, a Rous Sarcoma Virus (RSV) promoter, or a Simian Virus 40 (SV40) promoter.

In some embodiments, the 5' LTR or 3' LTR is a lentivirus LTR.

In certain embodiments, the 3' LTR comprises one or more modifications.

In certain embodiments, the 3' LTR comprises one or more deletions.

In particular embodiments, the 3' LTR is a self-inactivating (SIN) LTR.

In particular embodiments, the polyadenylation sequence is a bovine growth hormone polyadenylation or signal rabbit β-globin polyadenylation sequence.

In additional embodiments, the polynucleotide comprises an optimized Kozak sequence.

In additional embodiments, the promoter operably linked to the polynucleotide is selected from the group consisting of: a cytomegalovirus immediate early gene promoter (CMV), an elongation factor 1 alpha promoter (EF1-α), a phosphoglycerate kinase-1 promoter (PGK), a ubiquitin-C promoter (UBQ-C), a cytomegalovirus enhancer/chicken beta-actin promoter (CAG), polyoma enhancer/herpes simplex thymidine kinase promoter (MC1), a beta actin promoter (β-ACT), a simian virus 40 promoter (SV40), and a myeloproliferative sarcoma virus enhancer, negative control region deleted, dl587rev primer-binding site substituted (MND) promoter.

Disclosed herein is an immune effector cell comprising a vector encoding a CAR contemplated herein.

In particular embodiments, the immune effector cell is selected from the group consisting of: a T lymphocyte, a natural killer (NK) cell, and an NKT cell.

In some embodiments, the immune effector cell is transduced with a vector contemplated herein and is activated and stimulated in the presence of an inhibitor of the PI3K pathway, thereby maintaining proliferation of the transduced immune effector cells compared to the proliferation of transduced immune effector cells that were activated and stimulated in the absence of the inhibitor of the PI3K pathway.

In particular embodiments, the immune effector cell activated and stimulated in the presence of the inhibitor of PI3K pathway has increased expression of i) one or more markers selected from the group consisting of: CD62L, CD127, CD197, and CD38 or ii) all of the markers CD62L, CD127, CD197, and CD38 compared to an immune effector cell activated and stimulated in the absence of the inhibitor of PI3K pathway.

In particular embodiments, the immune effector cell activated and stimulated in the presence of the inhibitor of PI3K pathway has increased expression of i) one or more markers selected from the group consisting of: CD62L, CD127, CD27, and CD8 or ii) all of the markers CD62L, CD127, CD27, and CD8 compared to an immune effector cell activated and stimulated in the absence of the inhibitor of PI3K pathway.

In one embodiment, the PI3K inhibitor is ZSTK474.

Disclosed herein is a composition comprising the immune effector cell contemplated herein and a physiologically acceptable excipient.

In various embodiments, a method of generating a population of immune effector cells comprising a CAR contemplated herein is provided comprising introducing into a population of immune effector cells a vector encoding a CAR contemplated herein.

In particular embodiments, the method further comprises stimulating the immune effector cells and inducing the cells to proliferate by contacting the cells with antibodies that bind CD3 and antibodies that bind to CD28; thereby generating an expanded population of immune effector cells.

In certain embodiments, the immune effector cells are stimulated and induced to proliferate before introducing the vector.

In additional embodiments, the population of immune effector cells comprises T cells.

In some embodiments, the population of immune effector cells comprises NK cells.

In particular embodiments, the cells are the activated and stimulated in the presence of an inhibitor of the PI3K pathway, thereby maintaining proliferation of the transduced immune effector cells compared to the proliferation of immune effector cells that are activated and stimulated in the absence of the inhibitor of the PI3K pathway.

In some embodiments, the immune effector cells activated and stimulated in the presence of the inhibitor of PI3K pathway have increased expression of i) one or more markers selected from the group consisting of: CD62L, CD127, CD197, and CD38 or ii) all of the markers CD62L, CD127, CD197, and CD38 compared to immune effector cells activated and stimulated in the absence of the inhibitor of PI3K pathway.

In particular embodiments, the immune effector cell activated and stimulated in the presence of the inhibitor of PI3K pathway has increased expression of i) one or more markers selected from the group consisting of: CD62L, CD127, CD27, and CD8 or ii) all of the markers CD62L, CD127, CD27, and CD8 compared to an immune effector cell activated and stimulated in the absence of the inhibitor of PI3K pathway.

In one embodiment, the PI3K inhibitor is ZSTK474.

In various embodiments, method for increasing the cytotoxicity in cancer cells that express CD79A in a subject is provided, comprising administering to the subject an amount of a composition contemplated herein sufficient to increase the cytotoxicity in cancer cells that express CD79A compared to the cytotoxicity of the cancer cells that express CD79A prior to the administration.

In various embodiments, a method for decreasing the number of cancer cells expressing CD79A in a subject is provided, comprising administering to the subject an amount of a composition contemplated herein sufficient to decrease the number of cancer cells that express CD79A compared to the number of the cancer cells that express CD79A prior to the administration.

In various embodiments, a method of treating a cancer in a subject in need thereof, is provided comprising administering to the subject a therapeutically effect amount of a composition contemplated herein.

Disclosed herein is a composition as defined herein for use in treating a cancer in a

subject in need thereof.

Disclosed herein is the use of the composition as defined herein in the manufacture of a medicament for treating cancer.

In certain embodiments, the cancer is a liquid cancer.

In some embodiments, the cancer is a hematological malignancy.

In further embodiments, the cancer is lung cancer, breast cancer, pancreatic cancer, ovarian cancer, prostate cancer, adrenal cancer, melanoma, uterine cancer, testicular cancer, or bladder cancer, non-Hodgkin's lymphoma, acute lymphocytic leukemia (ALL), chronic lymphocytic leukemia (CLL), hairy cell leukemia (HCL), multiple myeloma (MM), acute myeloid leukemia (AML), or chronic myeloid leukemia (CML).

In particular embodiments, the non-Hodgkin's lymphoma is small lymphocytic lymphoma (SLL), diffuse large B cell lymphoma (DLBCL), follicular lymphoma (FL), mantle cell lymphoma (MCL), or marginal zone lymphoma (MZL).

In certain embodiments, the cancer is acute lymphocytic leukemia (ALL), chronic lymphocytic leukemia (CLL), hairy cell leukemia (HCL), multiple myeloma (MM), acute myeloid leukemia (AML), or chronic myeloid leukemia (CML).

In particular embodiments, the cancer is diffuse large B cell lymphoma (DLBCL).

In particular embodiments, the cancer is a MM selected from the group consisting of: overt multiple myeloma, smoldering multiple myeloma, plasma cell leukemia, non-secretory myeloma, IgD myeloma, osteosclerotic myeloma, solitary plasmacytoma of bone, and extramedullary plasmacytoma

In various embodiments, a method for ameliorating at one or more symptoms associated with a cancer expressing CD79A in a subject is provided, comprising administering to the subject an amount of a composition contemplated herein sufficient to ameliorate at least one symptom associated with cancer cells that express CD79A.

In particular embodiments, the one or more symptoms ameliorated are selected from the group consisting of: weakness, fatigue, shortness of breath, easy bruising and bleeding, frequent infections, enlarged lymph nodes, distended or painful abdomen, bone or joint pain, fractures, unplanned weight loss, poor appetite, night sweats, persistent mild fever, and decreased urination.

BRIEF DESCRIPTION OF SEVERAL VIEWS OF THE DRAWINGS

Figure 1 shows CD79A expression on target cells, CAR expression, and anti-CD79A CAR T cell antigen dependent activity in the presence of CD79A expressing target cells. A) This panel shows CD79A expression on Pfeiffer and Daudi cells, but not K562 cells. B) This panel shows representative anti-CD79A CAR expression on T cells measured using flow cytometry. C) This panel shows IFNγ secretion of anti-CD79A CAR T cells co-cultured in the absence of target cells or with K562 cells (CD79A-), Daudi cells (CD79A+, high expression), or Pfeiffer cells (CD79A+, low expression).

Figure 2 shows CAR expression, CD79A expression on target cells, and anti-CD79A CAR T cell antigen dependent activity in the presence of CD79A expressing target cells. A) This panel shows CD79A receptor density on Daudi, NU-DUL-1, SU-DHL-2, and Pfeiffer cells. B) This panel shows representative anti-CD79A CAR expression on T cells measured using flow cytometry. C) This panel shows IFNγ secretion of anti-CD79A CAR T cells co-cultured in the absence of target cells or with Huh7 cells (CD79A-), Huh7.CD79a cells (CD79A+), Daudi cells (CD79A+), NU-DUL-1 (CD79A+), SU-DHL-2 (CD79A+) or Pfeiffer cells (CD79A+).

BRIEF DESCRIPTION OF THE SEQUENCE IDENTIFIERS

SEQ ID NOs: 1-24 set forth amino acid sequences of exemplary light chain CDR sequences, heavy chain CDR sequences, variable domain light chains, and variable domain heavy chains for anti-CD79A CARs contemplated herein.

SEQ ID NOs: 25-30 set forth the amino acid sequences of exemplary anti-CD79A CARs.

SEQ ID NOs: 31-36 set forth the nucleic acid sequences of exemplary anti-CD79A CARs.

SEQ ID NOs: 37-38 set forth the amino acid sequences of exemplary human CD79A polypeptides.

SEQ ID NOs: 39-49 set forth the amino acid sequences of various linkers.

SEQ ID NOs: 50-74 set forth the amino acid sequences of protease cleavage sites and self-cleaving polypeptide cleavage sites.

DETAILED DESCRIPTION

A. OVERVIEW

The invention generally relates to improved compositions and methods for preventing or treating cancers that express CD79A or preventing, treating, or ameliorating at least one symptom associated with an CD79A expressing cancer. In particular embodiments, the invention relates to improved adoptive cell therapy of cancers that express CD79A using genetically modified immune effector cells. Genetic approaches offer a potential means to enhance immune recognition and elimination of cancer cells. One promising strategy is to genetically engineer immune effector cells to express chimeric antigen receptors (CAR) that redirect cytotoxicity toward cancer cells.

The improved compositions and methods of adoptive cell therapy contemplated herein, provide genetically modified immune effector cells that can readily be expanded, exhibit long-term persistence *in vivo*, and demonstrate antigen dependent cytotoxicity to cells expressing CD79A, also known as B cell antigen receptor complex-associated protein alpha chain, Membrane-Bound Immunoglobulin-Associated Protein (MB1, MB-1), surface IgM-associated protein, and Ig-alpha (IGA). Illustrative examples of polynucleotide sequences encoding CD79a include, but are not limited to: NM_001783.3, NM_021601.3, ENST00000221972 (uc002orv.3), ENST00000597454 (uc060zdj.1), ENST00000444740 (uc002oru.4), Hs.631567, and AK223371. Illustrative examples of polypeptide sequences encoding CD79a include, but are not limited to: P11912-1, P11912-2, ENSP00000400605 ENSP00000468922, ENSP00000221972, NP_001774.1, and NP_067612.1.

CD79 consist of two proteins, namely CD79A and CD79B. CD79A is located at chromosome 19q13.2 and encodes a 226-amino-acid glycoprotein of approximately 47 kDa. The exact molecular weight depends on the extent of glycosylation. CD79B is located at chromosome 17q23 and encodes a 229-amino-acid glycoprotein of approximately 37 kDa. CD79A and CD79B share an exon-intron structure, both contain a single IgSF Ig domain (111-residue C-type for CD79A and 129-residue V-type for CD79B). Each also contains a highly conserved transmembrane domain and a 61 (CD79A) or 48 (CD79B) amino acid cytoplasmic tail that also exhibits striking amino acid evolutionary conservation. CD79A and CD79B are expressed by the earliest committed B-cell progenitors. The CD79A/B heterodimer has also been observed on the surface of early B-cell progenitors in the absence of μ heavy chain, although neither protein is required for progenitors to commit to the B-cell

lineage. Later in development, CD79A and CD79B are coexpressed together with Ig of all isotypes on the surface of B cells as a mature BCR complex. The CD79 proteins are specific to the B lineage and are expressed throughout B lymphopoiesis. CD79A and CD79B can be used markers for the identification of B-cell neoplasms, including DLBCL, the majority of acute leukemias of precursor B cell type, in B cell lines, B cell lymphomas, and in some myelomas.

In various embodiments, CARs comprising anti-CD79A antibody sequences are highly efficacious; undergo robust *in vivo* expansion; and recognize cancer cells expressing CD79A and show cytotoxic activity against the CD79A expressing cancer cells.

In one embodiment, a CAR comprising an anti-CD79A antibody or antigen binding fragment, a transmembrane domain, and one or more intracellular signaling domains is provided.

In one embodiment, an immune effector cell is genetically modified to express a CAR. T cells expressing a CAR are referred to herein as CAR T cells or CAR modified T cells.

In various embodiments, genetically modified immune effector cells are administered to a subject with cancer cells expressing CD79A including, but not limited to liquid tumors and hematological malignancies. In one embodiment, anti-CD79A CAR T cells are administered to a subject that has DLBCL.

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*, 3d 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; 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 andCC 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. Additional definitions are set forth throughout this disclosure.

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 thereof of the alternatives.

The term "and/or" should be understood to mean either one, 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% about 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. By "consisting essentially of" is meant including any elements listed after the phrase, and limited to 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.

C. CHIMERIC ANTIGEN RECEPTORS

In various embodiments, genetically engineered receptors that redirect cytotoxicity of immune effector cells toward cancer cells expressing CD79A are provided. These genetically engineered receptors referred to herein as chimeric antigen receptors (CARs). CARs are molecules that combine antibody-based specificity for a desired antigen (*e.g.,* CD79A) with a T cell receptor-activating intracellular domain to generate a chimeric protein that exhibits a specific anti-CD79A cellular immune activity. As used herein, the term, "chimeric," describes being composed of parts of different proteins or DNAs from different origins.

In particular embodiments, CARs comprise an extracellular domain (also referred to as a binding domain or antigen-specific binding domain) that binds to CD79A, a transmembrane domain, and an intracellular signaling domain. Engagement of the anti-CD79A antigen binding domain of the CAR with CD79A on the surface of a target cell results in clustering of the CAR and delivers an activation stimulus to the CAR-containing cell. The main characteristic of CARs is their ability 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, exploiting the cell specific targeting abilities of monoclonal antibodies, soluble ligands or cell specific co-receptors.

In various embodiments, a CAR comprises an extracellular binding domain that comprises an CD79A-specific binding domain; a transmembrane domain; and one or more intracellular co-stimulatory signaling domains and/or a primary signaling domain.

In particular embodiments, a CAR comprises an extracellular binding domain that comprises an anti-CD79A antibody or antigen binding fragment thereof; one or more hinge domains or spacer domains; a transmembrane domain including; and one or more intracellular co-stimulatory signaling domains and/or a primary signaling domain.

1. BINDING DOMAIN

In particular embodiments, CARs comprise an extracellular binding domain that comprises an anti-CD79A antibody or antigen binding fragment thereof that specifically binds to a human CD79A polypeptide expressed on a target cell, *e.g.,* a cancer cell. As used herein, the terms, "binding domain," "extracellular domain," "extracellular binding domain," "antigen-specific binding domain," and "extracellular antigen specific binding domain," are used interchangeably and provide a CAR with the ability to specifically bind to the target antigen of interest, *e.g.,* CD79A. The binding domain may be derived either from a natural, synthetic, semi-synthetic, or recombinant source.

The terms "specific binding affinity" or "specifically binds" or "specifically bound" or "specific binding" or "specifically targets" as used herein, describe binding of an anti-CD79A antibody or antigen binding fragment thereof (or a CAR comprising the same) to CD79A at greater binding affinity than background binding. A binding domain (or a CAR comprising a binding domain or a fusion protein containing a binding domain) "specifically binds" to an CD79A polypeptide if it binds to or associates with CD79A with an affinity or K_a (*i.e.*, an equilibrium association constant of a particular binding interaction with units of 1/M) of, for example, greater than or equal to about 10^5 M^{-1}. In certain embodiments, a binding domain (or a fusion protein thereof) binds to a target with a K_a greater than or equal to about 10^6 M^{-1}, 10^7 M^{-1}, 10^8 M^{-1}, 10^9 M^{-1}, 10^{10} M^{-1}, 10^{11} M^{-1}, 10^{12} M^{-1}, or 10^{13} M^{-1}. "High affinity" binding domains (or single chain fusion proteins thereof) refers to those binding domains 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}, at least 10^{13} M^{-1}, or greater.

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, or less). Affinities of binding domain polypeptides and CAR proteins according to the present disclosure can be

readily determined using conventional techniques, *e.g.,* by competitive ELISA (enzyme-linked immunosorbent assay), or by binding association, or displacement assays using labeled ligands, or using a surface-plasmon resonance device such as the Biacore T100, which is available from Biacore, Inc., Piscataway, NJ, or optical biosensor technology such as the EPIC system or EnSpire that are available from Corning and Perkin Elmer respectively (*see also*, *e.g.,* Scatchard *et al.* (1949) Ann. N.Y. Acad. Sci. 51:660; and U.S. Patent Nos. 5,283,173; 5,468,614, or the equivalent) .

In one embodiment, the affinity of specific binding is about 2 times greater than background binding, about 5 times greater than background binding, about 10 times greater than background binding, about 20 times greater than background binding, about 50 times greater than background binding, about 100 times greater than background binding, or about 1000 times greater than background binding or more.

In particular embodiments, the extracellular binding domain of a CAR comprises an antibody or antigen binding fragment thereof. An "antibody" refers to a binding agent that is a polypeptide comprising at least a light chain or heavy chain immunoglobulin variable region which specifically recognizes and binds an epitope of an antigen, such as a peptide, lipid, polysaccharide, or nucleic acid containing an antigenic determinant, such as those recognized by an immune cell. An "isolated antibody or antigen binding fragment thereof" is one which has been identified and separated and/or recovered from a component of its natural environment.

An "antigen (Ag)" refers to a compound, composition, or substance that can stimulate the production of antibodies or a T cell response in an animal, including compositions (such as one that includes a cancer-specific protein) that are injected or absorbed into an animal. An antigen reacts with the products of specific humoral or cellular immunity, including those induced by heterologous antigens, such as the disclosed antigens. In particular embodiments, the target antigen is an epitope of an CD79A polypeptide.

An "epitope" or "antigenic determinant" refers to the region of an antigen to which a binding agent binds. Epitopes can be formed both from contiguous amino acids or noncontiguous amino acids juxtaposed by tertiary folding of a protein. Epitopes formed from contiguous amino acids are typically retained on exposure to denaturing solvents whereas epitopes formed by tertiary folding are typically lost on treatment with denaturing solvents. An epitope typically includes at least 3, and more usually, at least 5, about 9, or about 8-10 amino acids in a unique spatial conformation.

Antibodies include antigen binding fragments thereof, such as Camel Ig, Ig NAR, Fab fragments, Fab' fragments, F(ab')2 fragments, bispecific Fab dimers (Fab2), trispecific Fab trimers (Fab3), Fv, single chain Fv proteins ("scFv"), bis-scFv, (scFv)2, minibodies, diabodies, triabodies, tetrabodies, disulfide stabilized Fv proteins ("dsFv"), and single-domain antibody (sdAb, Nanobody) and portions of full length antibodies responsible for antigen binding. The term also includes genetically engineered forms such as chimeric antibodies (for example, humanized murine antibodies), heteroconjugate antibodies (such as, bispecific antibodies) and antigen binding fragments thereof. See also, Pierce Catalog and Handbook, 1994-1995 (Pierce Chemical Co., Rockford, IL); Kuby, J., Immunology, 3rd Ed., W. H. Freeman & Co., New York, 1997.

As would be understood by the skilled person and as described elsewhere herein, a complete antibody comprises two heavy chains and two light chains. Each heavy chain consists of a variable region and a first, second, and third constant region, while each light chain consists of a variable region and a constant region. Mammalian heavy chains are classified as α, δ, ε, γ, and μ. Mammalian light chains are classified as λ or κ. Immunoglobulins comprising the α, δ, ε, γ, and μ heavy chains are classified as immunoglobulin (Ig)A, IgD, IgE, IgG, and IgM. The complete antibody forms a "Y" shape. The stem of the Y consists of the second and third constant regions (and for IgE and IgM, the fourth constant region) of two heavy chains bound together and disulfide bonds (inter-chain) are formed in the hinge. Heavy chains γ, α and δ have a constant region composed of three tandem (in a line) Ig domains, and a hinge region for added flexibility; heavy chains μ and ε have a constant region composed of four immunoglobulin domains. The second and third constant regions are referred to as "CH2 domain" and "CH3 domain", respectively. Each arm of the Y includes the variable region and first constant region of a single heavy chain bound to the variable and constant regions of a single light chain. The variable regions of the light and heavy chains are responsible for antigen binding.

Light and heavy chain variable regions contain a "framework" region interrupted by three hypervariable regions, also called "complementarity-determining regions" or "CDRs." The CDRs can be defined or identified by conventional methods, such as by sequence according to Kabat *et al.* (Wu, TT and Kabat, E. A., *J Exp Med.* 132(2):211-50, (1970); Borden, P. and Kabat E. A., *PNAS*, 84: 2440-2443 (1987); (see, Kabat *et al.*, *Sequences of Proteins of Immunological Interest,* U.S. Department of Health and Human Services, 1991,

which is hereby incorporated by reference), or by structure according to Chothia *et al* (Chothia, C. and Lesk, A.M., *J Mol. Biol*., 196(4): 901-917 (1987), Chothia, C. *et al*, *Nature*, 342: 877 - 883 (1989)).

Illustrative examples of rules for predicting light chain CDRs include: CDR-L1 starts at about residue 24, is preceded by a Cys, is about 10-17 residues, and is followed by a Trp (typically Trp-Tyr-Gln, but also, Trp-Leu-Gln, Trp-Phe-Gln, Trp-Tyr-Leu); CDR-L2 starts about 16 residues after the end of CDR-L1, is generally preceded by Ile-Tyr, but also, Val-Tyr, Ile-Lys, Ile-Phe, and is 7 residues; and CDR-L3 starts about 33 residues after the end of CDR-L2, is preceded by a Cys, is 7-11 residues, and is followed by Phe-Gly-XXX-Gly (SEQ ID NO: 76) (XXX is any amino acid).

Illustrative examples of rules for predicting heavy chain CDRs include: CDR-H1 starts at about residue 26, is preceded by Cys-XXX-XXX-XXX (SEQ ID NO: 77), is 10-12 residues and is followed by a Trp (typically Trp-Val, but also, Trp-Ile, Trp-Ala); CDR-H2 starts about 15 residues after the end of CDR-H1, is generally preceded by Leu-Glu-Trp-Ile-Gly (SEQ ID NO: 78), or a number of variations, is 16-19 residues, and is followed by Lys/Arg-Leu/Ile/Val/Phe/Thr/Ala-Thr/Ser/Ile/Ala; and CDR-H3 starts about 33 residues after the end of CDR-H2, is preceded by Cys-XXX-XXX (typically Cys-Ala-Arg), is 3 to 25 residues, and is followed by Trp-Gly-XXX-Gly (SEQ ID NO: 79).

In one embodiment, light chain CDRs and the heavy chain CDRs are determined according to the Kabat method

In one embodiment, light chain CDRs and the heavy chain CDR2 and CDR3 are determined according to the Kabat method, and heavy chain CDR1 is determined according to the AbM method, which is a comprise between the Kabat and Clothia methods, *see e.g.,* Whitelegg N & Rees AR, *Protein Eng.* 2000 Dec;13(12):819-24 and *Methods Mol Biol.* 2004;248:51-91. Programs for predicting CDRs are publicly available, *e.g.,* AbYsis (www.bioinf.org.uk/abysis/).

The sequences of the framework regions of different light or heavy chains are relatively conserved within a species, such as humans. The framework region of an antibody, that is the combined framework regions of the constituent light and heavy chains, serves to position and align the CDRs in three-dimensional space. The CDRs are primarily responsible for binding to an epitope of an antigen. The CDRs of each chain are typically referred to as CDR1, CDR2, and CDR3, numbered sequentially starting from the N-terminus, and are also typically identified by the chain in which the particular CDR is located. Thus, the CDRs

located in the variable domain of the heavy chain of the antibody are referred to as CDRH1, CDRH2, and CDRH3, whereas the CDRs located in the variable domain of the light chain of the antibody are referred to as CDRL1, CDRL2, and CDRL3. Antibodies with different specificities (*i.e.,* different combining sites for different antigens) have different CDRs. Although it is the CDRs that vary from antibody to antibody, only a limited number of amino acid positions within the CDRs are directly involved in antigen binding. These positions within the CDRs are called specificity determining residues (SDRs). Illustrative examples of light chain CDRs that are suitable for constructing anti-CD79A CARs contemplated in particular embodiments include, but are not limited to the CDR sequences set forth in SEQ ID NOs: 1-3, 9-11, and 17-19. Illustrative examples of heavy chain CDRs that are suitable for constructing anti-CD79A CARs contemplated in particular embodiments include, but are not limited to the CDR sequences set forth in SEQ ID NOs: 4-6, 12-14, and 20-22.

References to "V_L" or "VL" refer to the variable region of an immunoglobulin light chain, including that of an antibody, Fv, scFv, dsFv, Fab, or other antibody fragment as contemplated herein. Illustrative examples of light chain variable regions that are suitable for constructing anti-CD79A CARs contemplated in particular embodiments include, but are not limited to the light chain variable region sequences set forth in SEQ ID NOs: 7, 15, and 23.

References to "V_H" or "VH" refer to the variable region of an immunoglobulin heavy chain, including that of an antibody, Fv, scFv, dsFv, Fab, or other antibody fragment as contemplated herein. Illustrative examples of heavy chain variable regions that are suitable for constructing anti-CD79A CARs contemplated in particular embodiments include, but are not limited to the heavy chain variable region sequences set forth in SEQ ID NOs: 8, 16, and 24.

A "monoclonal antibody" is an antibody produced by a single clone of B lymphocytes or by a cell into which the light and heavy chain genes of a single antibody have been transfected. Monoclonal antibodies are produced by methods known to those of skill in the art, for instance by making hybrid antibody-forming cells from a fusion of myeloma cells with immune spleen cells. Monoclonal antibodies include humanized monoclonal antibodies.

A "chimeric antibody" has framework residues from one species, such as human, and CDRs (which generally confer antigen binding) from another species, such as a mouse. In particular preferred embodiments, a CAR comprises antigen-specific binding domain that is a chimeric antibody or antigen binding fragment thereof.

In preferred embodiments, the antibody is a human antibody (such as a human monoclonal antibody) or fragment thereof that specifically binds to a human CD79A polypeptide. Human antibodies can be constructed by combining Fv clone variable domain sequence(s) selected from human-derived phage display libraries with known human constant domain sequences(s) as described above. Alternatively, human monoclonal antibodies may be made by the hybridoma method. Human myeloma and mouse-human heteromyeloma cell lines for the production of human monoclonal antibodies have been described, for example, by Kozbor *J. Immunol.*, 133: 3001 (1984); Brodeur *et al.*, *Monoclonal Antibody Production Techniques and Applications*, pp. 51-63 (Marcel Dekker, Inc., New York, 1987); and Boerner *et al.*, *J. Immunol.*, 147: 86 (1991). In addition, transgenic animals (*e.g.,* mice) can be used to produce a full repertoire of human antibodies in the absence of endogenous immunoglobulin production. See, *e.g.,* Jakobovits *et al.*, *PNAS USA*, 90: 2551 (1993); Jakobovits *et al.*, *Nature*, 362: 255 (1993); Bruggermann *et al.*, *Year in Immunol.*, 7: 33 (1993). Gene shuffling can also be used to derive human antibodies from non-human, *e.g.,* rodent antibodies, where the human antibody has similar affinities and specificities to the starting non-human antibody. (*See* PCT WO 93/06213 published Apr. 1, 1993). Unlike traditional humanization of non-human antibodies by CDR grafting, this technique provides completely human antibodies, which have no FR or CDR residues of non-human origin.

In one embodiment, a CAR comprises a "humanized" antibody. A humanized antibody is an immunoglobulin including a human framework region and one or more CDRs from a non-human (for example a mouse, rat, or synthetic) immunoglobulin. The non-human immunoglobulin providing the CDRs is termed a "donor," and the human immunoglobulin providing the framework is termed an "acceptor." In one embodiment, all the CDRs are from the donor immunoglobulin in a humanized immunoglobulin. Constant regions need not be present, but if they are, they must be substantially identical to human immunoglobulin constant regions, *i.e.*, at least about 85-90%, such as about 95% or more identical. Hence, all parts of a humanized immunoglobulin, except possibly the CDRs, are substantially identical to corresponding parts of natural human immunoglobulin sequences. Humanized or other monoclonal antibodies can have additional conservative amino acid substitutions, which have substantially no effect on antigen binding or other immunoglobulin functions. Humanized antibodies can be constructed by means of genetic engineering (see for example, U.S. Patent No. 5,585,089).

In particular embodiments, an anti-CD79A antibody or antigen binding fragment thereof, includes but is not limited to a Camel Ig (a camelid antibody (VHH)), Ig NAR, Fab fragments, Fab' fragments, F(ab')2 fragments, bispecific Fab dimers (Fab2), trispecific Fab trimers (Fab3), Fv, single chain Fv antibody ("scFv"), bis-scFv, (scFv)2, minibody, diabody, triabody, tetrabody, disulfide stabilized Fv protein ("dsFv"), and single-domain antibody (sdAb, Nanobody).

"Camel Ig" or "camelid VHH" as used herein refers to the smallest known antigen-binding unit of a heavy chain antibody (Koch-Nolte, *et al*, FASEB J., 21: 3490-3498 (2007)). A "heavy chain antibody" or a "camelid antibody" refers to an antibody that contains two VH domains and no light chains (Riechmann L. *et al*, J. Immunol. Methods 231:25–38 (1999); WO94/04678; WO94/25591; U.S. Patent No. 6,005,079).

"IgNAR" of "immunoglobulin new antigen receptor" refers to class of antibodies from the shark immune repertoire that consist of homodimers of one variable new antigen receptor (VNAR) domain and five constant new antigen receptor (CNAR) domains. IgNARs represent some of the smallest known immunoglobulin-based protein scaffolds and are highly stable and possess efficient binding characteristics. The inherent stability can be attributed to both (i) the underlying Ig scaffold, which presents a considerable number of charged and hydrophilic surface exposed residues compared to the conventional antibody VH and VL domains found in murine antibodies; and (ii) stabilizing structural features in the complementary determining region (CDR) loops including inter-loop disulphide bridges, and patterns of intra-loop hydrogen bonds.

Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, whose name reflects its ability to crystallize readily. Pepsin treatment yields an F(ab′)2 fragment that has two antigen-combining sites and is still capable of cross-linking antigen.

"Fv" is the minimum antibody fragment which contains a complete antigen-binding site. In one embodiment, a two-chain Fv species consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. In a single-chain Fv (scFv) species, one heavy- and one light-chain variable domain can be covalently linked by a flexible peptide linker such that the light and heavy chains can associate in a "dimeric" structure analogous to that in a two-chain Fv species. It is in this configuration that the three hypervariable regions (HVRs) of each variable domain interact to define an antigen-binding site on the surface of the VH-VL dimer. Collectively, the six HVRs confer antigen-binding

specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three HVRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

The Fab fragment contains the heavy- and light-chain variable domains and also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab′ fragments differ from Fab fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab′-SH is the designation herein for Fab′ in which the cysteine residue(s) of the constant domains bear a free thiol group. F(ab′)2 antibody fragments originally were produced as pairs of Fab′ fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known. Bispecific Fab dimers (Fab2) have two Fab′ fragments, each binding a different antigen. Trispecific Fab trimers (Fab3) have three Fab′ fragments, each binding a different antigen.

The term "diabodies" refers to antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain (VH) connected to a light-chain variable domain (VL) in the same polypeptide chain (VH-VL). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies may be bivalent or bispecific. Diabodies are described more fully in, for example, EP 404,097; WO 1993/01161; Hudson *et al.*, *Nat. Med*. 9:129-134 (2003); and Hollinger *et al.*, *PNAS USA* 90: 6444-6448 (1993). Triabodies and tetrabodies are also described in Hudson *et al.*, *Nat. Med.* 9:129-134 (2003).

"Single domain antibody" or "sdAb" or "nanobody" refers to an antibody fragment that consists of the variable region of an antibody heavy chain (VH domain) or the variable region of an antibody light chain (VL domain) (Holt, L., *et al*, T*rends in Biotechnology*, 21(11): 484-490).

"Single-chain Fv" or "scFv" antibody fragments comprise the VH and VL domains of 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. For a review of scFv, see, *e.g.,* Pluckthün, in *The Pharmacology of Monoclonal Antibodies*, vol. 113, Rosenburg and Moore eds., (Springer-Verlag, New York, 1994), pp. 269-315.

In preferred embodiments, the anti-CD79A antigen binding fragment is an scFv. In particular embodiments, the scFv is a murine, human or humanized scFv. Single chain antibodies may be cloned form the V region genes of a hybridoma specific for a desired target. The production of such hybridomas has become routine. A technique which can be used for cloning the variable region heavy chain (V_H) and variable region light chain (V_L) has been described, for example, in Orlandi *et al., PNAS,* 1989; 86: 3833-3837.

In various embodiments, an anti-CD79A antibody or antigen binding fragment thereof comprises a variable light chain sequence comprising CDRL1-CDRL3 sequences set forth in SEQ ID NOs: 1-3, 9-11, or 17-19 and/or a variable heavy chain sequence comprising CDRH1-CDRH3 sequences set forth in SEQ ID NOs: 4-6, 12-14. In some embodiments, the anti-CD79A antibody or antigen binding fragment thereof comprises a variable light chain sequence as set forth in any one of SEQ ID NOs: 7, 15, or 23 and/or a variable heavy chain sequence as set forth in any one of SEQ ID NOs: 8, 16, or 24.

In particular embodiments, the antigen-specific binding domain is an scFv that binds a human CD79A polypeptide.

An exemplary CD79A-specific binding domain is an immunoglobulin variable region specific for CD79A that comprises at least one human framework region. A "human framework region" refers to a wild type (*i.e.*, naturally occurring) framework region of a human immunoglobulin variable region, an altered framework region of a human immunoglobulin variable region with less than about 50% (*e.g.,* preferably less than about 45%, 40%, 30%, 25%, 20%, 15%, 10%, 5%, or 1%) of the amino acids in the region are deleted or substituted (*e.g.,* with one or more amino acid residues of a nonhuman immunoglobulin framework region at corresponding positions), or an altered framework region of a nonhuman immunoglobulin variable region with less than about 50% (*e.g.,* less than 45%, 40%, 30%, 25%, 20%, 15%, 10%, or 5%) of the amino acids in the region deleted or substituted (*e.g.,* at positions of exposed residues and/or with one or more amino acid residues of a human immunoglobulin framework region at corresponding positions) so that, in one aspect, immunogenicity is reduced.

In certain embodiments, a human framework region is a wild type framework region of a human immunoglobulin variable region. In certain other embodiments, a human framework region is an altered framework region of a human immunoglobulin variable region with amino acid deletions or substitutions at one, two, three, four, five, six, seven, eight, nine, ten or more positions. In other embodiments, a human framework region is an

altered framework region of a non-human immunoglobulin variable region with amino acid deletions or substitutions at one, two, three, four, five, six, seven, eight, nine, ten or more positions.

In particular embodiments, an CD79A-specific binding domain comprises at least one, two, three, four, five, six, seven or eight human framework regions (FR) selected from human light chain FR1, human heavy chain FR1, human light chain FR2, human heavy chain FR2, human light chain FR3, human heavy chain FR3, human light chain FR4, and human heavy chain FR4.

Human FRs that may be present in an CD79A-specific binding domains also include variants of the exemplary FRs provided herein in which one, two, three, four, five , six, seven, eight, nine, ten or more amino acids of the exemplary FRs have been substituted or deleted.

In certain embodiments, an CD79A-specific binding domain comprises (a) a humanized light chain variable region that comprises a human light chain FR1, a human light chain FR2, a human light chain FR3, and a human light chain FR4, and (b) a humanized heavy chain variable region that comprises a human heavy chain FR1, a human heavy chain FR2, a human heavy chain FR3, and a human heavy chain FR4.

CD79A-specific binding domains provided herein also comprise one, two, three, four, five, or six CDRs. Such CDRs may be nonhuman CDRs or altered nonhuman CDRs selected from CDRL1, CDRL2 and CDRL3 of the light chain and CDRH1, CDRH2 and CDRH3 of the heavy chain. In certain embodiments, an CD79A-specific binding domain comprises (a) a light chain variable region that comprises a light chain CDRL1, a light chain CDRL2, and a light chain CDRL3, and (b) a heavy chain variable region that comprises a heavy chain CDRH1, a heavy chain CDRH2, and a heavy chain CDRH3.

In some embodiments, an anti-CD79A antibody or antigen binding fragment thereof comprises a variable light chain sequence comprising CDRL1-CDRL3 sequences with at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% amino acid identity to the amino acid sequences set forth in SEQ ID NOs: 1-3, 9-11, or 17-19 and/or a variable heavy chain sequence comprising CDRH1-CDRH3 sequences with at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% amino acid identity to the amino acid sequence set forth in SEQ ID NOs: 4-6, 12-14 or 20-22.

In one embodiment, an CD79A-specific binding domain comprises light chain CDR sequences set forth in SEQ ID NOs: 1-3, 9-11, or 17-19. In a particular embodiment, an

CD79A-specific binding domain comprises light chain CDR sequences with at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% amino acid identity to the light chain CDR sequences set forth in SEQ ID NOs: 1-3, 9-11, or 17-19.

In one embodiment, an CD79A-specific binding domain comprises heavy chain CDR sequences set forth in SEQ ID NOs: 4-6, 12-14 or 20-22. In a particular embodiment, an CD79A-specific binding domain comprises heavy chain CDR sequences with at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% amino acid identity to the heavy chain CDR sequences set forth in SEQ ID NOs: 4-6, 12-14 or 20-22.

In some embodiments, the anti-idiotype antibody or antigen binding fragment thereof comprises a variable light chain sequence with at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% amino acid identity to the amino acid sequence set forth in any one of SEQ ID NOs: 7, 15, or 23 and/or a variable heavy chain sequence with at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% amino acid identity to the amino acid sequence set forth in any one of SEQ ID NOs: 8, 16, or 24.

2. LINKERS

In certain embodiments, anti-CD79A CARs comprise linker residues between the various domains, *e.g.,* added for appropriate spacing and conformation of the molecule. In particular embodiments the linker is a variable region linking sequence. A "variable region linking sequence," is an amino acid sequence that connects the V_H and V_L domains 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 heavy chain variable regions. In particular embodiments, CARs comprise one, two, three, four, or five or more linkers. In particular embodiments, the length of a linker is about 1 to about 25 amino acids, about 5 to about 20 amino acids, or about 10 to about 20 amino acids, or any intervening length of amino acids. In some embodiments, the linker is 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, or more amino acids long.

Illustrative examples of linkers include glycine polymers $(G)_n$; glycine-serine polymers $(G_{1-5}S_{1-5})_n$, where n is an integer of at least one, two, three, four, or five; glycine-alanine polymers; alanine-serine polymers; and other flexible linkers known in the art. Glycine and glycine-serine polymers are relatively unstructured, and therefore may be able

to serve as a neutral tether between domains of fusion proteins such as the CARs described herein. Glycine accesses significantly more phi-psi space than even alanine, and is much less restricted than residues with longer side chains (*see* Scheraga, *Rev. Computational Chem.* 11173-142 (1992)). The ordinarily skilled artisan will recognize that design of a CAR in particular embodiments can include linkers that are all or partially flexible, such that the linker can include a flexible linker as well as one or more portions that confer less flexible structure to provide for a desired CAR structure.

Other exemplary linkers include, but are not limited to the following amino acid sequences: DGGGS (SEQ ID NO: 39); TGEKP (SEQ ID NO: 40) (see, *e.g.,* Liu *et al.*, PNAS 5525-5530 (1997)); GGRR (SEQ ID NO: 41) (Pomerantz *et al.* 1995, supra); $(GGGGS)_n$ wherein = 1, 2, 3, 4 or 5 (SEQ ID NO: 42) (Kim *et al.*, PNAS 93, 1156-1160 (1996.); EGKSSGSGSESKVD (SEQ ID NO: 43) (Chaudhary *et al.*, 1990, Proc. Natl. Acad. Sci. U.S.A. 87:1066-1070); KESGSVSSEQLAQFRSLD (SEQ ID NO: 44) (Bird *et al.*, 1988, Science 242:423-426), GGRRGGGS (SEQ ID NO: 45); LRQRDGERP (SEQ ID NO: 46); LRQKDGGGSERP (SEQ ID NO: 47); LRQKD$(GGGS)_2$ ERP (SEQ ID NO: 48). Alternatively, flexible linkers can be rationally designed using a computer program capable of modeling both DNA-binding sites and the peptides themselves (Desjarlais & Berg, *PNAS* 90:2256-2260 (1993), *PNAS* 91:11099-11103 (1994) or by phage display methods. In one embodiment, the linker comprises the following amino acid sequence: GSTSGSGKPGSGEGSTKG (SEQ ID NO: 49) (Cooper *et al., Blood*, 101(4): 1637-1644 (2003)).

3. SPACER DOMAIN

In particular embodiments, the binding domain of an anti-CD79A CAR is followed by one or more "spacer domains," which refers to the region that moves the antigen binding domain away from the effector cell surface to enable proper cell/cell contact, antigen binding and activation (Patel *et al.*, *Gene Therapy*, 1999; 6: 412-419). The hinge domain may be derived either from a natural, synthetic, semi-synthetic, or recombinant source. In certain embodiments, a spacer domain is a portion of an immunoglobulin, including, but not limited to, one or more heavy chain constant regions, *e.g.,* CH2 and CH3. The spacer domain can include the amino acid sequence of a naturally occurring immunoglobulin hinge region or an altered immunoglobulin hinge region.

In one embodiment, the spacer domain comprises the CH2 and CH3 of IgG1, IgG4, or IgD.

4. HINGE DOMAIN

The binding domain of an anti-CD79A CAR is generally followed by one or more "hinge domains," which plays a role in positioning the antigen binding domain away from the effector cell surface to enable proper cell/cell contact, antigen binding and activation. A an anti-CD79A CAR generally comprises one or more hinge domains between the binding domain and the transmembrane domain (TM). The hinge domain may be derived either from a natural, synthetic, semi-synthetic, or recombinant source. The hinge domain can include the amino acid sequence of a naturally occurring immunoglobulin hinge region or an altered immunoglobulin hinge region.

An "altered hinge region" refers to (a) a naturally occurring hinge region with up to 30% amino acid changes (*e.g.,* up to 25%, 20%, 15%, 10%, or 5% amino acid substitutions or deletions), (b) a portion of a naturally occurring hinge region that is at least 10 amino acids (*e.g.,* at least 12, 13, 14 or 15 amino acids) in length with up to 30% amino acid changes (*e.g.,* up to 25%, 20%, 15%, 10%, or 5% amino acid substitutions or deletions), or (c) a portion of a naturally occurring hinge region that comprises the core hinge region (which may be 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15, or at least 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 amino acids in length). In certain embodiments, one or more cysteine residues in a naturally occurring immunoglobulin hinge region may be substituted by one or more other amino acid residues (*e.g.,* one or more serine residues). An altered immunoglobulin hinge region may alternatively or additionally have a proline residue of a wild type immunoglobulin hinge region substituted by another amino acid residue (*e.g.,* a serine residue).

Illustrative hinge domains suitable for use in the CARs described herein include the hinge region derived from the extracellular regions of type 1 membrane proteins such as CD8α, and CD4, which may be wild-type hinge regions from these molecules or may be altered. In one embodiment, the hinge is a PD-1 hinge or CD152 hinge In another embodiment, the hinge domain comprises a CD8α hinge region.

5. TRANSMEMBRANE (TM) DOMAIN

The "transmembrane domain" is the portion of an anti-CD79A CAR that fuses the extracellular binding portion and intracellular signaling domain and anchors the CAR to the

plasma membrane of the immune effector cell. The TM domain may be derived either from a natural, synthetic, semi-synthetic, or recombinant source. The TM domain may be derived from (*i.e.*, comprise at least the transmembrane region(s) of the alpha or beta chain of the T-cell receptor, CDδ, CD3ε, CDγ, CD3ζ, CD4, CD5, CD8α, CD9, CD 16, CD22, CD27, CD28, CD33, CD37, CD45, CD64, CD80, CD86, CD 134, CD137, CD152, CD154, and PD1. In a particular embodiment, the TM domain is synthetic and predominantly comprises hydrophobic residues such as leucine and valine.

In one embodiment, the CARs comprise a TM domain derived from, PD1, CD152, CD28, or CD8α. In another embodiment, a CAR comprises a TM domain derived from, PD1, CD152, CD28, or CD8α and a short oligo- or polypeptide linker, preferably between 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acids in length that links the TM domain and the intracellular signaling domain of the CAR. A glycine-serine based linker provides a particularly suitable linker.

6. INTRACELLULAR SIGNALING DOMAIN

In particular embodiments, anti-CD79A CARs comprise one or more intracellular signaling domains. An "intracellular signaling domain," refers to the part of a CAR that participates in transducing the message of effective anti-CD79A CAR binding to a human CD79A polypeptide into the interior of the immune effector cell to elicit effector cell function, *e.g.,* activation, cytokine production, proliferation and cytotoxic activity, including the release of cytotoxic factors to the CAR-bound target cell, or other cellular responses elicited with antigen binding to the extracellular CAR domain.

The term "effector function" refers to a specialized function of an immune effector cell. Effector function of the T cell, for example, may be cytolytic activity or help or activity including the secretion of a cytokine. Thus, the term "intracellular signaling domain" refers to the portion of a protein which transduces the effector function signal and that directs the cell to perform a specialized function. While usually the entire intracellular signaling domain can be employed, in many cases it is not necessary to use the entire domain. To the extent that a truncated portion of an intracellular signaling domain is used, such truncated portion may be used in place of the entire domain as long as it transduces the effector function signal. The term intracellular signaling domain is meant to include any truncated portion of the intracellular signaling domain sufficient to transducing effector function signal.

It is known that signals generated through the TCR alone are insufficient for full activation of the T cell and that a secondary or co-stimulatory signal is also required. Thus, 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 co-stimulatory signaling domains that act in an antigen-independent manner to provide a secondary or co-stimulatory signal. In preferred embodiments, a CAR comprises an intracellular signaling domain that comprises one or more "co-stimulatory signaling domain" and a "primary signaling domain."

Primary signaling domains regulate 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.

Illustrative examples of ITAM containing primary signaling domains that are useful in particular embodiments include those derived from FcRγ, FcRβ, CD3γ, CD3δ, CD3ε, CD3ζ, CD22, CD79a, CD79b, and CD66d. In particular preferred embodiments, an anti-CD79A CAR comprises a CD3ζ primary signaling domain and one or more co-stimulatory signaling domains. The intracellular primary signaling and co-stimulatory signaling domains may be linked in any order in tandem to the carboxyl terminus of the transmembrane domain.

In particular embodiments, CARs comprise one or more co-stimulatory signaling domains to enhance the efficacy and expansion of T cells expressing CAR receptors. As used herein, the term, "co-stimulatory signaling domain," or "co-stimulatory domain", refers to an intracellular signaling domain of a co-stimulatory molecule. Co-stimulatory 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. Illustrative examples of such co-stimulatory molecules include TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9, TLR10, CARD11, CD2, CD7, CD27, CD28, CD30, CD40, CD54 (ICAM), CD83, CD134 (OX40), CD137 (4-1BB), CD278 (ICOS), DAP10, LAT, NKD2C, SLP76, TRIM, and ZAP70. In one embodiment, a CAR comprises one or more co-stimulatory signaling domains selected from the group consisting of CD28, CD137, and CD134, and a CD3ζ primary signaling domain.

In another embodiment, a CAR comprises CD28 and CD137 co-stimulatory signaling domains and a CD3ζ primary signaling domain.

In yet another embodiment, a CAR comprises CD28 and CD134 co-stimulatory signaling domains and a CD3ζ primary signaling domain.

In one embodiment, a CAR comprises CD137 and CD134 co-stimulatory signaling domains and a CD3ζ primary signaling domain.

In one embodiment, a CAR comprises a CD137 co-stimulatory signaling domain and a CD3ζ primary signaling domain.

In one embodiment, a CAR comprises a CD134 co-stimulatory signaling domain and a CD3ζ primary signaling domain.

In one embodiment, a CAR comprises a CD28 co-stimulatory signaling domain and a CD3ζ primary signaling domain.

In particular embodiments, CARs comprise an anti-CD79A antibody or antigen binding fragment thereof that specifically binds to an CD79A polypeptide expressed on a cancer cell.

In one embodiment, a CAR comprises an anti-CD79A scFv that binds an CD79A polypeptide; a transmembrane domain derived from a polypeptide selected from the group consisting of: alpha or beta chain of the T-cell receptor, CDδ, CD3ε, CDγ, CD3ζ, CD4, CD5, CD8α, CD9, CD 16, CD22, CD27, CD28, CD33, CD37, CD45, CD64, CD80, CD86, CD 134, CD137, CD152, CD154, AMN1, and PD1; and one or more intracellular co-stimulatory signaling domains from a co-stimulatory molecule selected from the group consisting of: TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9, TLR10, CARD11, CD2, CD7, CD27, CD28, CD30, CD40, CD54 (ICAM), CD83, CD134 (OX40), CD137 (4-1BB), CD278 (ICOS), DAP10, LAT, NKD2C, SLP76, TRIM, and ZAP70; and a primary signaling domain from FcRγ, FcRβ, CD3γ, CD3δ, CD3ε, CD3ζ, CD22, CD79a, CD79b, and CD66d.

In one embodiment, a CAR comprises an anti-CD79A scFv that binds an CD79A polypeptide; a hinge domain selected from the group consisting of: IgG1 hinge/CH2/CH3, IgG4 hinge/CH2/CH3, a PD1 hinge, a CD152 hinge, and a CD8α hinge; a transmembrane domain derived from a polypeptide selected from the group consisting of: alpha or beta chain of the T-cell receptor, CDδ, CD3ε, CDγ, CD3ζ, CD4, CD5, CD8α, CD9, CD 16, CD22, CD27, CD28, CD33, CD37, CD45, CD64, CD80, CD86, CD 134, CD137, CD152, CD154, AMN1, and PD1; and one or more intracellular co-stimulatory signaling domains from a co-stimulatory molecule selected from the group consisting of: TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9, TLR10, CARD11, CD2, CD7, CD27, CD28,

CD30, CD40, CD54 (ICAM), CD83, CD134 (OX40), CD137 (4-1BB), CD278 (ICOS), DAP10, LAT, NKD2C, SLP76, TRIM, and ZAP70; and a primary signaling domain from FcRγ, FcRβ, CD3γ, CD3δ, CD3ε, CD3ζ, CD22, CD79a, CD79b, and CD66d.

In one embodiment, a CAR comprises an anti-CD79A scFv that binds an CD79A polypeptide; a hinge domain selected from the group consisting of: IgG1 hinge/CH2/CH3, IgG4 hinge/CH2/CH3, a PD1 hinge, a CD152 hinge, and a CD8α hinge; a transmembrane domain derived from a polypeptide selected from the group consisting of: alpha or beta chain of the T-cell receptor, CDδ, CD3ε, CDγ, CD3ζ, CD4, CD5, CD8α, CD9, CD 16, CD22, CD27, CD28, CD33, CD37, CD45, CD64, CD80, CD86, CD 134, CD137, CD152, CD154, AMN1, and PD1; a short oligo- or polypeptide linker, preferably between 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acids in length that links the TM domain to the intracellular signaling domain of the CAR; and one or more intracellular co-stimulatory signaling domains from a co-stimulatory molecule selected from the group consisting of: TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9, TLR10, CARD11, CD2, CD7, CD27, CD28, CD30, CD40, CD54 (ICAM), CD83, CD134 (OX40), CD137 (4-1BB), CD278 (ICOS), DAP10, LAT, NKD2C, SLP76, TRIM, and ZAP70; and a primary signaling domain from FcRγ, FcRβ, CD3γ, CD3δ, CD3ε, CD3ζ, CD22, CD79a, CD79b, and CD66d.

In a particular embodiment, a CAR comprises an anti-CD79A scFv that binds an CD79A polypeptide; a hinge domain comprising an IgG1 hinge/CH2/CH3 polypeptide and a CD8α polypeptide; a CD8α transmembrane domain comprising a polypeptide linker of about 3 to about 10 amino acids; a CD137 intracellular co-stimulatory signaling domain; and a CD3ζ primary signaling domain.

In a particular embodiment, a CAR comprises an anti-CD79A scFv that binds an CD79A polypeptide; a hinge domain comprising a CD8α polypeptide; a CD8α transmembrane domain comprising a polypeptide linker of about 3 to about 10 amino acids; a CD134 intracellular co-stimulatory signaling domain; and a CD3ζ primary signaling domain.

In a particular embodiment, a CAR comprises an anti-CD79A scFv that binds an CD79A polypeptide; a hinge domain comprising a CD8α polypeptide; a CD8α transmembrane domain comprising a polypeptide linker of about 3 to about 10 amino acids; a CD28 intracellular co-stimulatory signaling domain; and a CD3ζ primary signaling domain.

The design of the CARs contemplated in particular embodiments enable improved expansion, long-term persistence, and cytotoxic properties in T cells expressing the CARs compared to non-modified T cells or T cells modified to express other CARs.

D. POLYPEPTIDES

Various polypeptides, fusion polypeptides, and polypeptide variants are contemplated herein, including, but not limited to, CAR polypeptides and fragments thereof. In preferred embodiments, a polypeptide comprising one or more CARs is provided. In particular embodiments, the CAR is an anti-CD79A CAR comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 25-30.

"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. Polypeptides are not limited to a specific length, *e.g.,* they may comprise a full-length polypeptide or a polypeptide fragment, and may include one or more post-translational modifications of the polypeptide, for example, glycosylations, acetylations, phosphorylations and the like, as well as other modifications known in the art, both naturally occurring and non-naturally occurring. In various embodiments, the CAR polypeptides comprise a signal (or leader) sequence at the N-terminal end of the protein, which co-translationally or post-translationally directs transfer of the protein. Illustrative examples of suitable signal sequences useful in CARs contemplated in particular embodiments include, but are not limited to the IgG1 heavy chain signal polypeptide, a CD8α signal polypeptide, or a human GM-CSF receptor alpha signal polypeptide. Polypeptides can be prepared using any of a variety of well-known recombinant and/or synthetic techniques. Polypeptides contemplated herein, encompass the CARs of the present disclosure, or sequences that have deletions from, additions to, and/or substitutions of one or more amino acid of a CAR contemplated herein.

An "isolated polypeptide" and the like, as used herein, refer to in vitro synthesis, isolation, and/or purification of a peptide or 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. In particular embodiments, an isolated polypeptide is a synthetic polypeptide, a semi-synthetic polypeptide, or a polypeptide obtained or derived from a recombinant source.

Polypeptides include "polypeptide variants." Polypeptide variants may differ from a naturally occurring polypeptide in one or more substitutions, deletions, additions and/or

insertions. Such variants may be naturally occurring or may be synthetically generated, for example, by modifying one or more of the above polypeptide sequences. For example, in particular embodiments, it may be desirable to improve the binding affinity and/or other biological properties of the CARs by introducing one or more substitutions, deletions, additions and/or insertions into a binding domain, hinge, TM domain, co-stimulatory signaling domain or primary signaling domain of a CAR polypeptide. In particular embodiments, polypeptides include polypeptides 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 of the reference sequences contemplated herein, typically where the variant maintains at least one biological activity of the reference sequence. In particular embodiments, the biological activity is binding affinity. In particular embodiments, the biological activity is cytolytic activity.

Polypeptides include "polypeptide fragments." Polypeptide fragments refer to a polypeptide, which can be monomeric or multimeric that has an amino-terminal deletion, a carboxyl-terminal deletion, and/or an internal deletion or substitution of a naturally-occurring or recombinantly-produced polypeptide. Illustrative examples of biologically active polypeptide fragments include antibody fragments. As used herein, the term "biologically active fragment" or "minimal biologically active fragment" refers to a polypeptide fragment 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. In preferred embodiments, the biological activity is binding affinity to an idiotype. In certain embodiments, a polypeptide fragment can comprise an amino acid chain 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, or 450 amino acids long. Particularly useful polypeptide fragments include functional domains, including antigen-binding domains or fragments of antibodies. In the case of an anti-CD79A antibody, useful fragments include, but are not limited to: a CDR region, a CDR3 region of the heavy or light chain; a variable region of a heavy or light chain; a portion of an antibody chain or variable region including two CDRs; and the like.

The polypeptide may also be fused in-frame or conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.,* poly-His), or to enhance binding of the polypeptide to a solid support.

As noted above, in particular embodiments, polypeptides may be altered in various ways including amino acid substitutions, deletions, truncations, and insertions. Methods for such manipulations are generally known in the art. For example, amino acid sequence variants of a reference polypeptide can be prepared by mutations in the DNA. Methods for mutagenesis and nucleotide sequence alterations are well known in the art. See, for example, Kunkel (1985, *Proc. Natl. Acad. Sci. USA*. 82: 488-492), Kunkel *et al.*, (1987, *Methods in Enzymol*, 154: 367-382), 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.*, (1978) *Atlas of Protein Sequence and Structure* (Natl. Biomed. Res. Found., Washington, D.C.).

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, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. Modifications may be made in the structure of the polynucleotides and polypeptides contemplated in particular embodiments and still obtain a functional molecule that encodes a variant or derivative polypeptide with desirable characteristics. When it is desired to alter the amino acid sequence of a polypeptide to create an equivalent, or even an improved, variant polypeptide, one skilled in the art, for example, can change one or more of the codons of the encoding DNA sequence, *e.g.,* according to Table 1.

TABLE 1- Amino Acid Codons

Amino Acids	**One letter code**	**Three letter code**	**Codons**			
Alanine	A	Ala	GCA	GCC	GCG	GCU
Cysteine	C	Cys	UGC	UGU		

Aspartic acid	D	Asp	GAC	GAU				
Glutamic acid	E	Glu	GAA	GAG				
Phenylalanine	F	Phe	UUC	UUU				
Glycine	G	Gly	GGA	GGC	GGG	GGU		
Histidine	H	His	CAC	CAU				
Isoleucine	I	Iso	AUA	AUC	AUU			
Lysine	K	Lys	AAA	AAG				
Leucine	L	Leu	UUA	UUG	CUA	CUC	CUG	CUU
Methionine	M	Met	AUG					
Asparagine	N	Asn	AAC	AAU				
Proline	P	Pro	CCA	CCC	CCG	CCU		
Glutamine	Q	Gln	CAA	CAG				
Arginine	R	Arg	AGA	AGG	CGA	CGC	CGG	CGU
Serine	S	Ser	AGC	AGU	UCA	UCC	UCG	UCU
Threonine	T	Thr	ACA	ACC	ACG	ACU		
Valine	V	Val	GUA	GUC	GUG	GUU		
Tryptophan	W	Trp	UGG					
Tyrosine	Y	Tyr	UAC	UAU				

Guidance in determining which amino acid residues can be substituted, inserted, or deleted without abolishing biological activity can be found using computer programs well known in the art, such as DNASTAR, DNA Strider, Geneious, Mac Vector, or Vector NTI software. Preferably, amino acid changes in the protein variants disclosed herein are conservative amino acid changes, *i.e.,* substitutions of similarly charged or uncharged amino acids. A conservative amino acid change involves substitution of one of a family of amino acids which are related in their side chains. 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 a peptide or protein, suitable conservative substitutions of amino acids are known to those of skill in this art and generally can be made without altering a biological activity of a resulting molecule. 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).

As outlined above, amino acid substitutions may be based on the relative similarity of the amino acid side-chain substituents, for example, their hydrophobicity, hydrophilicity, charge, size, and the like.

Polypeptide variants further include glycosylated forms, aggregative conjugates with other molecules, and covalent conjugates with unrelated chemical moieties (*e.g.,* pegylated molecules). Covalent variants can be prepared by linking functionalities to groups which are found in the amino acid chain or at the N- or C-terminal residue, as is known in the art. Variants also include allelic variants, species variants, and muteins. Truncations or deletions of regions which do not affect functional activity of the proteins are also variants.

In one embodiment, where expression of two or more polypeptides is desired, the polynucleotide sequences encoding them can be separated by and IRES sequence as discussed elsewhere herein. In another embodiment, two or more polypeptides can be expressed as a fusion protein that comprises one or more self-cleaving polypeptide sequences.

Polypeptides contemplated in particular embodiments include fusion polypeptides. In preferred embodiments, fusion polypeptides and polynucleotides encoding fusion polypeptides are provided, *e.g.,* CARs. Fusion polypeptides and fusion proteins refer to a polypeptide having at least two, three, four, five, six, seven, eight, nine, or ten or more polypeptide segments. Fusion 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. The polypeptides of the fusion protein can be in any order or a specified order. Fusion polypeptides or fusion proteins can also include conservatively modified variants, polymorphic variants, alleles, mutants, subsequences, and interspecies homologs, so long as the desired transcriptional activity of the fusion polypeptide is preserved. Fusion polypeptides may be produced by chemical synthetic methods or by chemical linkage between the two moieties or may generally be prepared using other standard techniques. Ligated DNA sequences comprising the fusion polypeptide are operably linked to suitable transcriptional or translational control elements as discussed elsewhere herein.

In one embodiment, a fusion partner comprises a sequence that assists in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Other fusion partners may be selected so as to increase the solubility of the protein or to enable the protein to be targeted to desired intracellular compartments or to facilitate transport of the fusion protein through the cell membrane.

Fusion polypeptides may further comprise a polypeptide cleavage signal between each of the polypeptide domains described herein. In addition, a polypeptide cleavage site can be put into any linker peptide sequence. Exemplary polypeptide cleavage signals include polypeptide cleavage recognition sites such as protease cleavage sites, nuclease cleavage sites (*e.g.,* rare restriction enzyme recognition sites, self-cleaving ribozyme recognition sites), and self-cleaving viral oligopeptides (see deFelipe and Ryan, 2004. *Traffic*, 5(8); 616-26).

Suitable protease cleavages sites and self-cleaving peptides are known to the skilled person (*see, e.g.,* in Ryan *et al.*, 1997. *J. Gener. Virol.* 78, 699-722; 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), potyvirus HC proteases, potyvirus P1 (P35) proteases, byovirus NIa proteases, byovirus RNA-2-encoded proteases, aphthovirus L proteases, enterovirus 2A proteases, rhinovirus 2A proteases, picorna 3C proteases, comovirus 24K proteases, nepovirus 24K proteases, RTSV (rice tungro spherical virus) 3C-like protease, PYVF (parsnip yellow fleck virus) 3C-like protease, heparin, thrombin, factor Xa and enterokinase. Due to its high cleavage stringency, TEV (tobacco etch virus) protease cleavage sites are preferred in one embodiment, *e.g.,* EXXYXQ(G/S) (SEQ ID NO: 50), for example, ENLYFQG (SEQ ID NO: 51) and ENLYFQS (SEQ ID NO: 52), wherein X represents any amino acid (cleavage by TEV occurs between Q and G or Q and S).

In particular embodiments, the polypeptide cleavage signal is a viral self-cleaving peptide or ribosomal skipping sequence.

Illustrative examples of ribosomal skipping sequences include, but are not limited to: a 2A or 2A-like site, sequence or domain (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 2A sites are provided in Table 2.

TABLE 2

SEQ ID NO: 53	GSGATNFSLLKQAGDVEENPGP

SEQ ID NO: 54	ATNFSLLKQAGDVEENPGP
SEQ ID NO: 55	LLKQAGDVEENPGP
SEQ ID NO: 56	GSGEGRGSLLTCGDVEENPGP
SEQ ID NO: 57	EGRGSLLTCGDVEENPGP
SEQ ID NO: 58	LLTCGDVEENPGP
SEQ ID NO: 59	GSGQCTNYALLKLAGDVESNPGP
SEQ ID NO: 60	QCTNYALLKLAGDVESNPGP
SEQ ID NO: 61	LLKLAGDVESNPGP
SEQ ID NO: 62	GSGVKQTLNFDLLKLAGDVESNPGP
SEQ ID NO: 63	VKQTLNFDLLKLAGDVESNPGP
SEQ ID NO: 64	LLKLAGDVESNPGP
SEQ ID NO: 65	LLNFDLLKLAGDVESNPGP
SEQ ID NO: 66	TLNFDLLKLAGDVESNPGP
SEQ ID NO: 67	LLKLAGDVESNPGP
SEQ ID NO: 68	NFDLLKLAGDVESNPGP
SEQ ID NO: 69	QLLNFDLLKLAGDVESNPGP
SEQ ID NO: 70	APVKQTLNFDLLKLAGDVESNPGP
SEQ ID NO: 71	VTELLYRMKRAETYCPRPLLAIHPTEARHKQKIVAPVKQT
SEQ ID NO: 72	LNFDLLKLAGDVESNPGP
SEQ ID NO: 73	LLAIHPTEARHKQKIVAPVKQTLNFDLLKLAGDVESNPGP
SEQ ID NO: 74	EARHKQKIVAPVKQTLNFDLLKLAGDVESNPGP

In preferred embodiments, a polypeptide comprises an anti-CD79A CAR polypeptide.

E. POLYNUCLEOTIDES

In preferred embodiments, a polynucleotide encoding one or more CAR polypeptides is provided. 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, genomic DNA (gDNA), 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.* In particular embodiments, polynucleotides or 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.

Illustrative examples of polynucleotides include, but are not limited to SEQ ID NOs: 31-36 and polynucleotides encoding SEQ ID NOs: 1-30.

As used herein, "isolated polynucleotide" refers to a polynucleotide that has been purified from the sequences which flank it in a naturally-occurring state, *e.g.,* a DNA fragment that has been removed from the sequences that are normally adjacent to the fragment. In particular embodiments, an "isolated polynucleotide" also refers to a complementary DNA (cDNA), a recombinant DNA, or other polynucleotide that does not exist in nature and that has been made by the hand of man. In particular embodiments, an isolated polynucleotide is a synthetic polynucleotide, a semi-synthetic polynucleotide, or a polynucleotide obtained or derived from a recombinant source.

In various embodiments, a polynucleotide comprises an mRNA encoding a polypeptide contemplated herein. In certain embodiments, the mRNA comprises a cap, one or more nucleotides, and a poly(A) tail.

In particular embodiments, polynucleotides may be codon-optimized. As used herein, the term "codon-optimized" refers to substituting codons in a polynucleotide encoding a polypeptide in order to increase the expression, stability and/or activity of the polypeptide. 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.

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 include polynucleotides in which one or more nucleotides have been added or deleted, or replaced with different nucleotides compared to a reference polynucleotide. 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.

Polynucleotide variants include polynucleotide fragments that encode 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.

The recitations "sequence identity" or, for example, comprising a "sequence 50% identical to," as used herein, 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. Thus, 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. Included are nucleotides and polypeptides having 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, typically where the polypeptide variant maintains at least one biological activity of the reference polypeptide.

Terms used to describe sequence relationships between two or more polynucleotides or polypeptides include "reference sequence," "comparison window," "sequence identity," "percentage of sequence identity," and "substantial identity". A "reference sequence" is at least 12 but frequently 15 to 18 and often at least 25 monomer units, inclusive of nucleotides and amino acid residues, in length. Because two polynucleotides may each comprise (1) a sequence (*i.e*., only a portion of the complete polynucleotide sequence) that is similar between the two polynucleotides, and (2) a sequence that is divergent between the two polynucleotides, sequence comparisons between two (or more) polynucleotides are typically performed by comparing sequences of the two polynucleotides over a "comparison window" to identify and compare local regions of sequence similarity. A "comparison window" refers to a conceptual segment of at least 6 contiguous positions, usually about 50 to about 100, more usually about 100 to about 150 in which a sequence is compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. The comparison window may comprise additions or deletions (*i.e.,* gaps) of about 20% or less as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. Optimal alignment of sequences for aligning a comparison window may be conducted by computerized implementations of algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package Release 7.0, Genetics Computer Group, 575 Science Drive Madison, WI, USA) or by inspection and the best alignment (*i.e*., resulting in the highest percentage homology over the comparison window) generated by any of the various methods selected. Reference also may be made to the BLAST family of programs as for example disclosed by Altschul *et al.*, 1997, Nucl. Acids Res. 25:3389. A detailed discussion of sequence analysis can be found in Unit 19.3 of Ausubel *et al.*, Current Protocols in Molecular Biology, John Wiley & Sons Inc, 1994-1998, Chapter 15.

Terms that describe the orientation of polynucleotides include: 5' (normally the end of the polynucleotide having a free phosphate group) and 3' (normally the end of the polynucleotide having a free hydroxyl (OH) group). Polynucleotide sequences can be annotated in the 5' to 3' orientation or the 3' to 5' orientation. For DNA and mRNA, the 5' to 3' strand is designated the "sense," "plus," or "coding" strand because its sequence is identical to the sequence of the premessenger (premRNA) [except for uracil (U) in RNA, instead of thymine (T) in DNA]. For DNA and mRNA, the complementary 3' to 5' strand which is the strand transcribed by the RNA polymerase is designated as "template," "antisense," "minus," or "non-coding" strand. As used herein, the term "reverse orientation" refers to a 5' to 3' sequence written in the 3' to 5' orientation or a 3' to 5' sequence written in the 5' to 3' orientation.

The terms "complementary" and "complementarity" refer to polynucleotides *(i.e.,* a sequence of nucleotides) related by the base-pairing rules. For example, the complementary strand of the DNA sequence 5' A G T C A T G 3' is 3' T C A G T A C 5'. The latter sequence is often written as the reverse complement with the 5' end on the left and the 3' end on the right, 5' C A T G A C T 3'. A sequence that is equal to its reverse complement is said to be a palindromic sequence. Complementarity can be "partial," in which only some of the nucleic acids' bases are matched according to the base pairing rules. Or, there can be "complete" or "total" complementarity between the nucleic acids.

Moreover, it will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide, or fragment of variant thereof, as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated in particular embodiments, for example polynucleotides that are optimized for human and/or primate codon selection. Further, alleles of the genes comprising the polynucleotide sequences provided herein may also be used. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides.

The term "nucleic acid cassette" or "expression cassette" as used herein refers to genetic sequences within the vector which can express an RNA, and subsequently a polypeptide. In one embodiment, the nucleic acid cassette contains a gene(s)-of-interest, *e.g.*, a polynucleotide(s)-of-interest. In another embodiment, the nucleic acid cassette contains one or more expression

control sequences, *e.g.*, a promoter, enhancer, poly(A) sequence, and a gene(s)-of-interest, *e.g.,* a polynucleotide(s)-of-interest. Vectors may comprise 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 or more nucleic acid cassettes. The nucleic acid cassette is positionally and sequentially oriented within the vector such that the nucleic acid in the cassette can be transcribed into RNA, and when necessary, translated into a protein or a polypeptide, undergo appropriate post-translational modifications required for activity in the transformed cell, and be translocated to the appropriate compartment for biological activity by targeting to appropriate intracellular compartments or secretion into extracellular compartments. Preferably, the cassette has its 3´ and 5´ ends adapted for ready insertion into a vector, *e.g.*, it has restriction endonuclease sites at each end. In a preferred embodiment, the nucleic acid cassette contains the sequence of a chimeric antigen receptor used to increase the cytotoxicity of cancer cells that express CD79A. The cassette can be removed and inserted into a plasmid or viral vector as a single unit.

Polynucleotides include polynucleotide(s)-of-interest. As used herein, the term "polynucleotide-of-interest" refers to a polynucleotide encoding a polypeptide, polypeptide variant, or fusion polypeptide. A vector may comprise 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 polynucleotides-of-interest. In certain embodiments, the polynucleotide-of-interest encodes a polypeptide that provides a therapeutic effect in the treatment or prevention of a disease or disorder. Polynucleotides-of-interest, and polypeptides encoded therefrom, include both polynucleotides that encode wild-type polypeptides, as well as functional variants and fragments thereof. In particular embodiments, a functional variant has at least 80%, at least 90%, at least 95%, or at least 99% identity to a corresponding wild-type reference polynucleotide or polypeptide sequence. In certain embodiments, a functional variant or fragment has at least 50%, at least 60%, at least 70%, at least 80%, or at least 90% of a biological activity of a corresponding wild-type polypeptide.

The polynucleotides contemplated herein, regardless of the length of the coding sequence itself, may be combined with other DNA sequences, such as promoters and/or enhancers, untranslated regions (UTRs), signal sequences, Kozak sequences, polyadenylation signals, additional restriction enzyme sites, multiple cloning sites, internal ribosomal entry sites (IRES), recombinase recognition sites (*e.g.,* LoxP, FRT, and Att sites), termination codons, transcriptional termination signals, and polynucleotides encoding self-cleaving polypeptides, epitope tags, as disclosed elsewhere herein or as known in the art, such that their overall length may vary considerably. It is therefore contemplated that a polynucleotide fragment of almost any length may be employed in particular embodiments, with the total

length preferably being limited by the ease of preparation and use in the intended recombinant DNA protocol.

Polynucleotides can be prepared, manipulated and/or expressed 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 appropriate vector.

Illustrative examples of vectors include, but are not limited to plasmid, autonomously replicating sequences, and transposable elements, *e.g.,* piggyBac, Sleeping Beauty, Mos1, Tc1/mariner, Tol2, mini-Tol2, Tc3, MuA, Himar I, Frog Prince, and derivatives thereof.

Additional Illustrative examples of vectors include, without limitation, plasmids, phagemids, cosmids, artificial chromosomes such as yeast artificial chromosome (YAC), bacterial artificial chromosome (BAC), or P1-derived artificial chromosome (PAC), bacteriophages such as lambda phage or M13 phage, and animal viruses.

Illustrative examples of viruses useful as vectors include, without limitation, retrovirus (including lentivirus), adenovirus, adeno-associated virus, herpesvirus (*e.g.,* herpes simplex virus), poxvirus, baculovirus, papillomavirus, and papovavirus (*e.g.,* SV40).

Illustrative examples of expression vectors include, but are not limited to, pClneo vectors (Promega) for expression in mammalian cells; pLenti4/V5-DEST™, pLenti6/V5-DEST™, and pLenti6.2/V5-GW/lacZ (Invitrogen) for lentivirus-mediated gene transfer and expression in mammalian cells. In particular embodiments, coding sequences of polypeptides disclosed herein can be ligated into such expression vectors for the expression of the polypeptides in mammalian cells.

In particular embodiments, the vector is an episomal vector or a vector that is maintained extrachromosomally. As used herein, the term "episomal" refers to a vector that is able to replicate without integration into host's chromosomal DNA and without gradual loss from a dividing host cell also meaning that said vector replicates extrachromosomally or episomally.

The "control elements" or "regulatory sequences" present in an expression vector are those non-translated regions of the vector—origin of replication, selection cassettes, promoters, enhancers, translation initiation signals (Shine Dalgarno sequence or Kozak sequence) introns, a polyadenylation sequence, 5' and 3' untranslated regions—which interact with host cellular proteins to carry out transcription and translation. Such elements may vary in their strength and specificity. Depending on the vector system and host utilized, any

number of suitable transcription and translation elements, including ubiquitous promoters and inducible promoters may be used.

In particular embodiments, vectors include, but are not limited to expression vectors and viral vectors, will include exogenous, endogenous, or heterologous control sequences such as promoters and/or enhancers. An "endogenous" control sequence is one which is naturally linked with a given gene in the genome. An "exogenous" control sequence is one which is placed in juxtaposition to a gene by means of genetic manipulation (*i.e.*, molecular biological techniques) such that transcription of that gene is directed by the linked enhancer/promoter. A "heterologous" control sequence is an exogenous sequence that is from a different species than the cell being genetically manipulated.

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 a nucleic acid expression control sequence (such as a promoter, and/or enhancer) and a second polynucleotide sequence, *e.g.,* a polynucleotide-of-interest, wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

As used herein, the term "constitutive expression control sequence" refers to a promoter, enhancer, or promoter/enhancer that continually or continuously allows for transcription of an operably linked sequence. A constitutive expression control sequence may be a "ubiquitous" promoter, enhancer, or promoter/enhancer that allows expression in a

wide variety of cell and tissue types or a "cell specific," "cell type specific," "cell lineage specific," or "tissue specific" promoter, enhancer, or promoter/enhancer that allows expression in a restricted variety of cell and tissue types, respectively.

Illustrative ubiquitous expression control sequences suitable for use in particular embodiments include, but are not limited to, a cytomegalovirus (CMV) immediate early promoter, a viral simian virus 40 (SV40) (*e.g.,* early or late), a Moloney murine leukemia virus (MoMLV) LTR promoter, a Rous sarcoma virus (RSV) LTR, a herpes simplex virus (HSV) (thymidine kinase) promoter, H5, P7.5, and P11 promoters from vaccinia virus, an elongation factor 1-alpha (EF1a) promoter, early growth response 1 (EGR1), ferritin H (FerH), ferritin L (FerL), Glyceraldehyde 3-phosphate dehydrogenase (GAPDH), eukaryotic translation initiation factor 4A1 (EIF4A1), heat shock 70kDa protein 5 (HSPA5), heat shock protein 90kDa beta, member 1 (HSP90B1), heat shock protein 70kDa (HSP70), β-kinesin (β-KIN), the human ROSA 26 locus (Irions *et al.*, *Nature Biotechnology* 25, 1477 - 1482 (2007)), a Ubiquitin C promoter (UBC), a phosphoglycerate kinase-1 (PGK) promoter, a cytomegalovirus enhancer/chicken β-actin (CAG) promoter, a β-actin 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).

In one embodiment, a vector comprises an MNDU3 promoter.

In one embodiment, a vector comprises an EF1a promoter comprising the first intron of the human EF1a gene.

In one embodiment, a vector comprises an EF1a promoter that lacks the first intron of the human EF1a gene.

In a particular embodiment, it may be desirable to express a polynucleotide comprising a CAR from a T cell specific promoter.

As used herein, "conditional expression" may refer to any type of conditional expression including, but not limited to, inducible expression; repressible expression; expression in cells or tissues having a particular physiological, biological, or disease state, *etc.* This definition is not intended to exclude cell type or tissue specific expression. Certain embodiments provide conditional expression of a polynucleotide-of-interest*, e.g.,* expression is controlled by subjecting a cell, tissue, organism, *etc.*, to a treatment or condition that causes the polynucleotide to be expressed or that causes an increase or decrease in expression of the polynucleotide encoded by the polynucleotide-of-interest.

Illustrative examples of inducible promoters/systems include, but are not limited to, steroid-inducible promoters such as promoters for genes encoding glucocorticoid or estrogen receptors (inducible by treatment with the corresponding hormone), metallothionine promoter (inducible by treatment with various heavy metals), MX-1 promoter (inducible by interferon), the "GeneSwitch" mifepristone-regulatable system (Sirin *et al.*, 2003, *Gene*, 323:67), the cumate inducible gene switch (WO 2002/088346), tetracycline-dependent regulatory systems, *etc.*

Conditional expression can also be achieved by using a site-specific DNA recombinase. According to certain embodiments the vector comprises at least one (typically two) site(s) for recombination mediated by a site-specific recombinase. As used herein, the terms "recombinase" or "site specific recombinase" include excisive or integrative proteins, enzymes, co-factors or associated proteins that are involved in recombination reactions involving one or more recombination sites (*e.g.,* two, three, four, five, seven, ten, twelve, fifteen, twenty, thirty, fifty, *etc.*), which may be wild-type proteins (*see* Landy, *Current Opinion in Biotechnology* 3:699-707 (1993)), or mutants, derivatives (*e.g.,* fusion proteins containing the recombination protein sequences or fragments thereof), fragments, and variants thereof. Illustrative examples of recombinases suitable for use in particular embodiments include, but are not limited to: Cre, Int, IHF, Xis, Flp, Fis, Hin, Gin, ΦC31, Cin, Tn3 resolvase, TndX, XerC, XerD, TnpX, Hjc, Gin, SpCCE1, and ParA.

The vectors may comprise one or more recombination sites for any of a wide variety of site specific recombinases. It is to be understood that the target site for a site-specific recombinase is in addition to any site(s) required for integration of a vector, *e.g.,* a retroviral vector or lentiviral vector. As used herein, the terms "recombination sequence," "recombination site," or "site specific recombination site" refer to a particular nucleic acid sequence to which a recombinase recognizes and binds.

For example, one recombination site for Cre recombinase is loxP which is a 34 base pair sequence comprising two 13 base pair inverted repeats (serving as the recombinase binding sites) flanking an 8 base pair core sequence (see FIG. 1 of Sauer, B., *Current Opinion in Biotechnology* 5:521-527 (1994)). Other exemplary loxP sites include, but are not limited to: lox511 (Hoess *et al.*, 1996; Bethke and Sauer, 1997), lox5171 (Lee and Saito, 1998), lox2272 (Lee and Saito, 1998), m2 (Langer *et al.*, 2002), lox71 (Albert *et al.*, 1995), and lox66 (Albert *et al.*, 1995).

Suitable recognition sites for the FLP recombinase include, but are not limited to: FRT (McLeod, *et al.*, 1996), F_1, F_2, F_3 (Schlake and Bode, 1994), F_4, F_5 (Schlake and Bode, 1994), FRT(LE) (Senecoff *et al.*, 1988), FRT(RE) (Senecoff *et al.*, 1988).

Other examples of recognition sequences are the attB, attP, attL, and attR sequences, which are recognized by the recombinase enzyme λ Integrase, *e.g.,* phi-c31. The φC31 SSR mediates recombination only between the heterotypic sites attB (34 bp in length) and attP (39 bp in length) (Groth *et al.*, 2000). attB and attP, named for the attachment sites for the phage integrase on the bacterial and phage genomes, respectively, both contain imperfect inverted repeats that are likely bound by φC31 homodimers (Groth *et al.*, 2000). The product sites, attL and attR, are effectively inert to further φC31-mediated recombination (Belteki *et al.*, 2003), making the reaction irreversible. For catalyzing insertions, it has been found that attB-bearing DNA inserts into a genomic attP site more readily than an attP site into a genomic attB site (Thyagarajan *et al.*, 2001; Belteki *et al.*, 2003). Thus, typical strategies position by homologous recombination an attP-bearing "docking site" into a defined locus, which is then partnered with an attB-bearing incoming sequence for insertion.

As used herein, an "internal ribosome entry site" or "IRES" refers to an element that promotes direct internal ribosome entry to the initiation codon, such as ATG, of a cistron (a protein encoding region), thereby leading to the cap-independent translation of the gene. *See, e.g.,* Jackson *et al.*, 1990. *Trends Biochem Sci* 15(12):477-83) and Jackson and Kaminski. 1995. *RNA* 1(10):985-1000. In particular embodiments, vectors include one or more polynucleotides-of-interest that encode one or more polypeptides. In particular embodiments, to achieve efficient translation of each of the plurality of polypeptides, the polynucleotide sequences can be separated by one or more IRES sequences or polynucleotide sequences encoding self-cleaving polypeptides. In one embodiment, the IRES used in polynucleotides contemplated herein is an EMCV IRES.

As used herein, the term "Kozak sequence" refers to a short nucleotide 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 (SEQ ID NO: 75), where R is a purine (A or G) (Kozak, 1986. *Cell*. 44(2):283-92, and Kozak, 1987. *Nucleic Acids Res*. 15(20):8125-48). In particular embodiments, the vectors comprise polynucleotides that have a consensus Kozak sequence and that encode a desired polypeptide, *e.g.,* a CAR.

Elements directing the efficient termination and polyadenylation of the heterologous nucleic acid transcripts increases heterologous gene expression. Transcription termination signals are generally found downstream of the polyadenylation signal. In particular embodiments, vectors comprise a polyadenylation sequence 3′ of a polynucleotide encoding a polypeptide to be expressed. The term "polyA site" or "polyA sequence" as used herein denotes a DNA sequence which directs both the termination and polyadenylation of the nascent RNA transcript by RNA polymerase II. Polyadenylation sequences can promote mRNA stability by addition of a polyA tail to the 3′ end of the coding sequence and thus, contribute to increased translational efficiency. Cleavage and polyadenylation is directed by a poly(A) sequence in the RNA. The core poly(A) sequence 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) sequence is an ideal polyA sequence (e.g., AATAAA, ATTAAA, AGTAAA). In particular embodiments, the poly(A) sequence is an SV40 polyA sequence, a bovine growth hormone polyA sequence (BGHpA), a rabbit β-globin polyA sequence (rβgpA), variants thereof, or another suitable heterologous or endogenous polyA sequence known in the art.

In some embodiments, a polynucleotide or cell harboring the polynucleotide utilizes a suicide gene, including an inducible suicide gene to reduce the risk of direct toxicity and/or uncontrolled proliferation. In specific aspects, the suicide gene is not immunogenic to the host harboring the polynucleotide or cell. A certain example of a suicide gene that may be used is caspase-9 or caspase-8 or cytosine deaminase. Caspase-9 can be activated using a specific chemical inducer of dimerization (CID).

In particular embodiments, one or more polynucleotides encoding an anti-CD79A CAR are introduced into a cell (*e.g.,* an immune effector cell) by non-viral or viral vectors.

The term "vector" is used herein to refer to a nucleic acid molecule capable transferring or transporting another nucleic acid molecule. The transferred nucleic acid is generally linked to, *e.g.,* inserted into, the vector nucleic acid molecule. A vector may include sequences that direct autonomous replication in a cell, or may include sequences sufficient to allow integration into host cell DNA. In particular embodiments, non-viral vectors are used to deliver one or more polynucleotides contemplated herein to a T cell. In one embodiment, the vector is an *in vitro* synthesized or synthetically prepared mRNA encoding an anti-CD79A CAR.

Illustrative examples of non-viral vectors include, but are not limited to mRNA, plasmids (*e.g.,* DNA plasmids or RNA plasmids), transposons, cosmids, and bacterial artificial chromosomes.

Illustrative methods of non-viral delivery of polynucleotides contemplated in particular embodiments include, but are not limited to: electroporation, sonoporation, lipofection, microinjection, biolistics, virosomes, liposomes, immunoliposomes, nanoparticles, polycation or lipid:nucleic acid conjugates, naked DNA, artificial virions, DEAE-dextran-mediated transfer, gene gun, and heat-shock.

Illustrative examples of polynucleotide delivery systems suitable for use in particular embodiments contemplated in particular embodiments include, but are not limited to those provided by Amaxa Biosystems, Maxcyte, Inc., BTX Molecular Delivery Systems, and Copernicus Therapeutics Inc. Lipofection reagents are sold commercially (*e.g.,* Transfectam™ and Lipofectin™). Cationic and neutral lipids that are suitable for efficient receptor-recognition lipofection of polynucleotides have been described in the literature. See *e.g.,* Liu *et al.* (2003) *Gene Therapy.* 10:180–187; and Balazs *et al.* (2011) *Journal of Drug Delivery.* 2011:1-12. Antibody-targeted, bacterially derived, non-living nanocell-based delivery is also contemplated in particular embodiments.

In various embodiments, the polynucleotide is an mRNA that is introduced into a cell in order to transiently express a desired polypeptide. As used herein, "transient" refers to expression of a non-integrated transgene for a period of hours, days or weeks, wherein the period of time of expression is less than the period of time for expression of the polynucleotide if integrated into the genome or contained within a stable plasmid replicon in the cell.

In particular embodiments, the mRNA encoding a polypeptide is an *in vitro* transcribed mRNA. As used herein, "*in vitro* transcribed RNA" refers to RNA, preferably mRNA that has been synthesized *in vitro*. Generally, the *in vitro* transcribed RNA is generated from an *in vitro* transcription vector. The *in vitro* transcription vector comprises a template that is used to generate the *in vitro* transcribed RNA.

In particular embodiments, mRNAs may further comprise a comprise a 5' cap or modified 5' cap and/or a poly(A) sequence. As used herein, a 5' cap (also termed an RNA cap, an RNA 7-methylguanosine cap or an RNA m^{7G} cap) is a modified guanine nucleotide that has been added to the "front" or 5' end of a eukaryotic messenger RNA shortly after the start of transcription. The 5' cap comprises a terminal group which is linked to the first

transcribed nucleotide and recognized by the ribosome and protected from RNases. The capping moiety can be modified to modulate functionality of mRNA such as its stability or efficiency of translation. In a particular embodiment, the mRNA comprises a poly(A) sequence of between about 50 and about 5000 adenines. In one embodiment, the mRNA comprises a poly(A) sequence of between about 100 and about 1000 bases, between about 200 and about 500 bases, or between about 300 and about 400 bases. In one embodiment, the mRNA comprises a poly(A) sequence of about 65 bases, about 100 bases, about 200 bases, about 300 bases, about 400 bases, about 500 bases, about 600 bases, about 700 bases, about 800 bases, about 900 bases, or about 1000 or more bases. poly(A) sequences can be modified chemically or enzymatically to modulate mRNA functionality such as localization, stability or efficiency of translation.

Viral vectors comprising polynucleotides contemplated in particular embodiments can be delivered *in vivo* by administration to an individual patient, typically by systemic administration (*e.g.,* intravenous, intraperitoneal, intramuscular, subdermal, or intracranial infusion) or topical application, as described below. Alternatively, vectors can be delivered to cells *ex vivo*, such as cells explanted from an individual patient (*e.g.,* mobilized peripheral blood, lymphocytes, bone marrow aspirates, tissue biopsy, *etc.*) or universal donor hematopoietic stem cells, followed by reimplantation of the cells into a patient.

In one embodiment, a viral vector comprising a polynucleotide encoding an anti-CD79A CAR is administered directly to an organism for transduction of cells *in vivo*. Alternatively, naked DNA can be administered. Administration is by any of the routes normally used for introducing a molecule into ultimate contact with blood or tissue cells including, but not limited to, injection, infusion, topical application and electroporation. Suitable methods of administering such nucleic acids are available and well known to those of skill in the art, and, although more than one route can be used to administer a particular composition, a particular route can often provide a more immediate and more effective reaction than another route.

Illustrative examples of viral vector systems suitable for use in particular embodiments contemplated herein include but are not limited to adeno-associated virus (AAV), retrovirus, herpes simplex virus, adenovirus, and vaccinia virus vectors.

In various embodiments, one or more polynucleotides encoding an anti-CD79A CAR are introduced into an immune effector cell, *e.g.,* a T cell, by transducing the cell with a recombinant adeno-associated virus (rAAV), comprising the one or more polynucleotides.

AAV is a small (~26 nm) replication-defective, primarily episomal, non-enveloped virus. AAV can infect both dividing and non-dividing cells and may incorporate its genome into that of the host cell. Recombinant AAV (rAAV) are typically composed of, at a minimum, a transgene and its regulatory sequences, and 5´ and 3´ AAV inverted terminal repeats (ITRs). The ITR sequences are about 145 bp in length. In particular embodiments, the rAAV comprises ITRs and capsid sequences isolated from AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, or AAV10.

In some embodiments, a chimeric rAAV is used the ITR sequences are isolated from one AAV serotype and the capsid sequences are isolated from a different AAV serotype. For example, a rAAV with ITR sequences derived from AAV2 and capsid sequences derived from AAV6 is referred to as AAV2/AAV6. In particular embodiments, the rAAV vector may comprise ITRs from AAV2, and capsid proteins from any one of AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, or AAV10. In a preferred embodiment, the rAAV comprises ITR sequences derived from AAV2 and capsid sequences derived from AAV6. In a preferred embodiment, the rAAV comprises ITR sequences derived from AAV2 and capsid sequences derived from AAV2.

In some embodiments, engineering and selection methods can be applied to AAV capsids to make them more likely to transduce cells of interest.

Construction of rAAV vectors, production, and purification thereof 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 various embodiments, one or more polynucleotides encoding an anti-CD79A CAR are introduced into an immune effector cell, by transducing the cell with a retrovirus, *e.g.,* lentivirus, comprising the one or more polynucleotides.

As used herein, the term "retrovirus" refers to an RNA virus that reverse transcribes its genomic RNA into a linear double-stranded DNA copy and subsequently covalently integrates its genomic DNA into a host genome. Illustrative retroviruses suitable for use in particular embodiments, include, but are not limited to: Moloney murine leukemia virus (M-MuLV), Moloney murine sarcoma virus (MoMSV), Harvey murine sarcoma virus (HaMuSV), murine mammary tumor virus (MuMTV), gibbon ape leukemia virus (GaLV), feline leukemia virus (FLV), spumavirus, Friend murine leukemia virus, Murine Stem Cell Virus (MSCV) and Rous Sarcoma Virus (RSV)) and lentivirus.

As used herein, the term "lentivirus" refers to a group (or genus) of complex retroviruses. Illustrative lentiviruses include, but are not limited to: HIV (human immunodeficiency virus; including HIV type 1, and HIV 2); visna-maedi virus (VMV) virus; the 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 one embodiment, HIV based vector backbones (*i.e.,* HIV cis-acting sequence elements) are preferred.

In various embodiments, a lentiviral vector contemplated herein comprises one or more LTRs, and one or more, or all, of the following accessory elements: a cPPT/FLAP, a Psi (Ψ) packaging signal, an export element, poly (A) sequences, and may optionally comprise a WPRE or HPRE, an insulator element, a selectable marker, and a cell suicide gene, as discussed elsewhere herein.

In particular embodiments, lentiviral vectors contemplated herein may be integrative or non-integrating or integration defective lentivirus. 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 genome into the genome of the host cells. 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 the HIV-1 pol gene suitable to reduce integrase activity include, but are not limited to: H12N, H12C, H16C, H16V, S81 R, D41A, K42A, H51A, Q53C, D55V, D64E, D64V, E69A, K71A, E85A, E87A, D116N, D1161, D116A, N120G, N1201, N120E, E152G, E152A, D35E, K156E, K156A, E157A, K159E, K159A, K160A, R166A, D167A, E170A, H171A, K173A, K186Q, K186T, K188T, E198A, R199c, R199T, R199A, D202A, K211A, Q214L, Q216L, Q221 L, W235F, W235E, K236S, K236A, K246A, G247W, D253A, R262A, R263A and K264H.

In one embodiment, the HIV-1 integrase deficient pol gene comprises a D64V, D116I, D116A, E152G, or E152A mutation; D64V, D116I, and E152G mutations; or D64V, D116A, and E152A mutations.

In one embodiment, the HIV-1 integrase deficient pol gene comprises a D64V mutation.

The term "long terminal repeat (LTR)" refers to domains of base pairs located at the ends of retroviral DNAs which, in their natural sequence context, are direct repeats and contain U3, R and U5 regions.

As used herein, the term "FLAP element" or "cPPT/FLAP" refers to a nucleic acid whose sequence includes the central polypurine tract and central termination sequences (cPPT and CTS) of a retrovirus, *e.g.,* HIV-1 or HIV-2. Suitable FLAP elements are described in U.S. Pat. No. 6,682,907 and in Zennou, *et al.,* 2000, *Cell*, 101:173. In another embodiment, a lentiviral vector contains a FLAP element with one or more mutations in the cPPT and/or CTS elements. In yet another embodiment, a lentiviral vector comprises either a cPPT or CTS element. In yet another embodiment, a lentiviral vector does not comprise a cPPT or CTS element.

As used herein, the term "packaging signal" or "packaging sequence" refers to psi [Ψ] 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.

The term "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), and the hepatitis B virus post-transcriptional regulatory element (HPRE).

In particular embodiments, expression of heterologous sequences in viral vectors is increased by incorporating posttranscriptional regulatory elements, efficient polyadenylation sites, 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.,* woodchuck hepatitis virus posttranscriptional regulatory element (WPRE; Zufferey *et al.*, 1999, *J. Virol*., 73:2886); the posttranscriptional regulatory element present in hepatitis B virus (HPRE) (Huang *et al., Mol. Cell. Biol*., 5:3864); and the like (Liu *et al.,* 1995, *Genes Dev*., 9:1766).

Lentiviral vectors preferably contain several safety enhancements as a result of modifying the LTRs. "Self-inactivating" (SIN) vectors refers to replication-defective vectors, *e.g.,* 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. 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 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.

The terms "pseudotype" or "pseudotyping" as used herein, refer to a virus that has viral envelope proteins that have been substituted with those of another virus possessing preferable characteristics. For example, HIV can be pseudotyped with vesicular stomatitis virus G-protein (VSV-G) envelope proteins, which allows HIV to infect a wider range of cells because HIV envelope proteins (encoded by the env gene) normally target the virus to $CD4^+$ presenting cells.

In certain embodiments, lentiviral vectors are produced according to known methods. *See e.g.,* Kutner *et al., BMC Biotechnol.* 2009;9:10. doi: 10.1186/1472-6750-9-10; Kutner *et al. Nat. Protoc.* 2009;4(4):495–505. doi: 10.1038/nprot.2009.22.

According to certain specific embodiments contemplated herein, most or all of the viral vector backbone sequences are derived from a lentivirus, *e.g.,* HIV-1. However, it is to be understood that many different sources of retroviral and/or lentiviral sequences can be used, or combined and numerous substitutions and alterations in certain of the lentiviral sequences may be accommodated without impairing the ability of a transfer vector to perform the functions described herein. Moreover, a variety of lentiviral vectors are known in the art, *see* Naldini *et al.,* (1996a, 1996b, and 1998); Zufferey *et al.*, (1997); Dull *et al.*, 1998, U.S. Pat. Nos. 6,013,516; and 5,994,136, many of which may be adapted to produce a viral vector or transfer plasmid contemplated herein.

In various embodiments, one or more polynucleotides encoding an anti-CD79A CAR are introduced into an immune effector cell by transducing the cell with an adenovirus comprising the one or more polynucleotides.

Adenoviral based vectors are capable of very high transduction efficiency in many cell types and do not require cell division. With such vectors, high titer and high levels of expression have been obtained. This vector can be produced in large quantities in a relatively simple system. Most adenovirus vectors are engineered such that a transgene replaces the Ad E1a, E1b, and/or E3 genes; subsequently the replication defective vector is propagated in human 293 cells that supply deleted gene function in trans. Ad vectors can transduce multiple types of tissues *in vivo*, including non-dividing, differentiated cells such as those found in liver, kidney and muscle. Conventional Ad vectors have a large carrying capacity.

Generation and propagation of the current adenovirus vectors, which are replication deficient, may utilize a unique helper cell line, designated 293, which was transformed from

human embryonic kidney cells by Ad5 DNA fragments and constitutively expresses E1 proteins (Graham *et al.*, 1977). Since the E3 region is dispensable from the adenovirus genome (Jones & Shenk, 1978), the current adenovirus vectors, with the help of 293 cells, carry foreign DNA in either the E1, the D3 or both regions (Graham & Prevec, 1991). Adenovirus vectors have been used in eukaryotic gene expression (Levrero *et al.*, 1991; Gomez-Foix *et al.*, 1992) and vaccine development (Grunhaus & Horwitz, 1992; Graham & Prevec, 1992). Studies in administering recombinant adenovirus to different tissues include trachea instillation (Rosenfeld *et al.*, 1991; Rosenfeld *et al.,* 1992), muscle injection (Ragot *et al.*, 1993), peripheral intravenous injections (Herz & Gerard, 1993) and stereotactic inoculation into the brain (Le Gal La Salle *et al.*, 1993). An example of the use of an Ad vector in a clinical trial involved polynucleotide therapy for antitumor immunization with intramuscular injection (Sterman *et al., Hum. Gene Ther*. 7:1083-9 (1998)).

In various embodiments, one or more polynucleotides encoding an anti-CD79A CAR are introduced into an immune effector cell by transducing the cell with a herpes simplex virus, *e.g.,* HSV-1, HSV-2, comprising the one or more polynucleotides.

The mature HSV virion consists of an enveloped icosahedral capsid with a viral genome consisting of a linear double-stranded DNA molecule that is 152 kb. In one embodiment, the HSV based viral vector is deficient in one or more essential or non-essential HSV genes. In one embodiment, the HSV based viral vector is replication deficient. Most replication deficient HSV vectors contain a deletion to remove one or more intermediate-early, early, or late HSV genes to prevent replication. For example, the HSV vector may be deficient in an immediate early gene selected from the group consisting of: ICP4, ICP22, ICP27, ICP47, and a combination thereof. 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.

F. GENETICALLY MODIFIED CELLS

In various embodiments, cells genetically modified to express the CARs contemplated herein, for use in the treatment of cancer are provided. As used herein, the term "genetically engineered" or "genetically modified" refers to the addition of extra genetic material in the

form of DNA or RNA into the total genetic material in a cell. The terms, "genetically modified cells," "modified cells," and, "redirected cells," are used interchangeably. As used herein, the term "gene therapy" refers to the introduction of extra genetic material in the form of DNA or RNA into the total genetic material in a cell that restores, corrects, or modifies expression of a gene, or for the purpose of expressing a therapeutic polypeptide, *e.g.,* a CAR.

In particular embodiments, anti-CD79A CARs contemplated herein are introduced and expressed in immune effector cells so as to redirect their specificity to a target antigen of interest, *e.g.,* an CD79A polypeptide. 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 immune effector cells contemplated herein are T lymphocytes, including but not limited to cytotoxic T cells (CTLs; $CD8^+$ T cells), TILs, and helper T cells (HTLs; $CD4^+$ T cells. In a particular embodiment, the cells comprise αβ T cells. In a particular embodiment, the cells comprise γδ T cells. In one embodiment, immune effector cells include natural killer (NK) cells. In one embodiment, immune effector cells include natural killer T (NKT) cells.

Immune effector cells can be autologous/autogeneic ("self") or non-autologous ("non-self," *e.g.,* allogeneic, syngeneic or xenogeneic). "Autologous," as used herein, refers to cells from the same subject. "Allogeneic," as used herein, refers to cells of the same species that differ genetically to the cell in comparison. "Syngeneic," as used herein, refers to cells of a different subject that are genetically identical to the cell in comparison. "Xenogeneic," as used herein, refers to cells of a different species to the cell in comparison. In preferred embodiments, the cells are allogeneic.

Illustrative immune effector cells used with the anti-CD79A CARs contemplated in particular embodiments include T lymphocytes. The terms "T cell" or "T lymphocyte" are art-recognized and are intended to include thymocytes, immature T lymphocytes, mature T lymphocytes, resting T lymphocytes, or activated T lymphocytes. A T cell can be a T helper (Th) cell, for example a T helper 1 (Th1) or a T helper 2 (Th2) cell. The T cell can be a helper T cell (HTL; $CD4^+$ T cell) $CD4^+$ T cell, a cytotoxic T cell (CTL; $CD8^+$ T cell), $CD4^+CD8^+$ T cell, $CD4^-CD8^-$ T cell, or any other subset of T cells. Other illustrative populations of T cells suitable for use in particular embodiments include naïve T cells (T_N), T memory stem cells (T_{SCM}), central memory T cells (T_{CM}), effector memory T cells (T_{EM}), and effector T cells (T_{EFF}).

As would be understood by the skilled person, other cells may also be used as immune effector cells with the anti-CD79A CARs as contemplated herein. In particular, immune effector cells also include NK cells, NKT cells, neutrophils, and macrophages. Immune effector cells also include progenitors of effector cells wherein such progenitor cells can be induced to differentiate into an immune effector cells *in vivo* or *in vitro*. Thus, in particular embodiments, immune effector cell includes progenitors of immune effectors cells such as hematopoietic stem cells (HSCs) contained within the $CD34^+$ population of cells derived from cord blood, bone marrow or mobilized peripheral blood which upon administration in a subject differentiate into mature immune effector cells, or which can be induced *in vitro* to differentiate into mature immune effector cells.

As used herein, immune effector cells genetically engineered to contain a CD79A-specific CAR may be referred to as, "CD79A-specific redirected immune effector cells."

The term, "$CD34^+$ cell," as used herein refers to a cell expressing the CD34 protein on its cell surface. "CD34," as used herein refers to a cell surface glycoprotein (*e.g.,* sialomucin protein) that often acts as a cell-cell adhesion factor and is involved in T cell entrance into lymph nodes. The $CD34^+$ cell population contains hematopoietic stem cells (HSC), which upon administration to a patient differentiate and contribute to all hematopoietic lineages, including T cells, NK cells, NKT cells, neutrophils and cells of the monocyte/macrophage lineage.

Methods for making the immune effector cells which express an anti-CD79A CAR contemplated herein are provided in particular embodiments. In one embodiment, the method comprises transfecting or transducing immune effector cells isolated from an individual such that the immune effector cells express one or more anti-CD79A CARs contemplated herein. In certain embodiments, the immune effector cells are isolated from an individual and genetically modified without further manipulation *in vitro*. Such cells can then be directly re-administered into the individual. In further embodiments, the immune effector cells are first activated and stimulated to proliferate *in vitro* prior to being genetically modified to express an anti-CD79A CAR. In this regard, the immune effector cells may be cultured before and/or after being genetically modified (*i.e.,* transduced or transfected to express an anti-CD79A CAR contemplated herein).

In particular embodiments, prior to *in vitro* manipulation or genetic modification of the immune effector cells described herein, the source of cells is obtained from a subject. In particular embodiments, CAR-modified immune effector cells comprise T cells.

In particular embodiments, PBMCs may be directly genetically modified to express anti-CD79A CARs using methods contemplated herein. In certain embodiments, after isolation of PBMC, T lymphocytes are further isolated and in certain embodiments, both cytotoxic and helper T lymphocytes can be sorted into naïve, memory, and effector T cell subpopulations either before or after genetic modification and/or expansion.

The immune effector cells, such as T cells, can be genetically modified following isolation using known methods, or the immune effector cells can be activated and expanded (or differentiated in the case of progenitors) *in vitro* prior to being genetically modified. In a particular embodiment, the immune effector cells, such as T cells, are genetically modified with the chimeric antigen receptors contemplated herein (*e.g.,* transduced with a viral vector comprising a nucleic acid encoding an anti-CD79A CAR) and then are activated and expanded *in vitro*. In various embodiments, T cells can be activated and expanded before or after genetic modification to express a CAR, using methods as described, for example, in U.S. Patents 6,352,694; 6,534,055; 6,905,680; 6,692,964; 5,858,358; 6,887,466; 6,905,681; 7,144,575; 7,067,318; 7, 172,869; 7,232,566; 7, 175,843; 5,883,223; 6,905,874; 6,797,514; 6,867,041; and U.S. Patent Application Publication No. 20060121005.

In one embodiment, $CD34^+$ cells are transduced with a nucleic acid construct contemplated herein. In certain embodiments, the transduced $CD34^+$ cells differentiate into mature immune effector cells *in vivo* following administration into a subject, generally the subject from whom the cells were originally isolated. In another embodiment, $CD34^+$ cells may be stimulated *in vitro* prior to exposure to or after being genetically modified with a CAR as described herein, with one or more of the following cytokines: Flt-3 ligand (FLT3), stem cell factor (SCF), megakaryocyte growth and differentiation factor (TPO), IL-3 and IL-6 according to the methods described previously (Asheuer *et al.*, 2004; Imren, *et al.*, 2004).

In particular embodiments, a population of modified immune effector cells for the treatment of cancer comprises a CAR as contemplated herein. For example, a population of modified immune effector cells are prepared from peripheral blood mononuclear cells (PBMCs) obtained from a patient diagnosed with B cell malignancy described herein (autologous donors). The PBMCs form a heterogeneous population of T lymphocytes that can be $CD4^+$, $CD8^+$, or $CD4^+$ and $CD8^+$.

The PBMCs also can include other cytotoxic lymphocytes such as NK cells or NKT cells. An expression vector carrying the coding sequence of a CAR contemplated in particular embodiments is introduced into a population of human donor T cells, NK cells or

NKT cells. In particular embodiments, successfully transduced T cells that carry the expression vector can be sorted using flow cytometry to isolate CD3 positive T cells and then further propagated to increase the number of these CAR protein expressing T cells in addition to cell activation using anti-CD3 antibodies and or anti-CD28 antibodies and IL-2 or any other methods known in the art as described elsewhere herein. Standard procedures are used for cryopreservation of T cells expressing the CAR protein T cells for storage and/or preparation for use in a human subject. In one embodiment, the *in vitro* transduction, culture and/or expansion of T cells are performed in the absence of non-human animal derived products such as fetal calf serum and fetal bovine serum. Since a heterogeneous population of PBMCs is genetically modified, the resultant transduced cells are a heterogeneous population of modified cells comprising an anti-CD79A CAR as contemplated herein.

In a further embodiment, a mixture of, *e.g.,* one, two, three, four, five or more, different expression vectors can be used in genetically modifying a donor population of immune effector cells wherein each vector encodes a different chimeric antigen receptor protein as contemplated herein. The resulting modified immune effector cells forms a mixed population of modified cells, with a proportion of the modified cells expressing more than one different CAR proteins.

G. T CELL MANUFACTURING METHODS

In various embodiments, genetically modified T cells are expanded by contact with an agent that stimulates a CD3 TCR complex associated signal and a ligand that stimulates a co-stimulatory molecule on the surface of the T cells.

In particular embodiments, PBMCs or isolated T cells are contacted with a stimulatory agent and costimulatory agent, such as soluble anti-CD3 and anti-CD28 antibodies, or antibodies attached to a bead or other surface, in a culture medium with appropriate cytokines, such as IL-2, IL-7, and/or IL-15.

In particular embodiments, PBMCs or isolated T cells are contacted with a stimulatory agent and costimulatory agent, such as soluble anti-CD3 and anti-CD28 antibodies, or antibodies attached to a bead or other surface, in a culture medium with appropriate cytokines, such as IL-2, IL-7, and/or IL-15 and/or one or more agents that modulate a PI3K/Akt/mTOR cell signaling pathway.

In preferred embodiments, the T cells manufactured by the methods contemplated herein provide improved adoptive immunotherapy compositions. Without wishing to be bound to any

particular theory, it is believed that the T cell compositions manufactured by the methods in particular embodiments contemplated herein are imbued with superior properties, including increased survival, expansion in the relative absence of differentiation, and persistence *in vivo*. In one embodiment, a method of manufacturing T cells comprises contacting the cells with one or more agents that modulate a PI3K cell signaling pathway. In one embodiment, a method of manufacturing T cells comprises contacting the cells with one or more agents that modulate a PI3K/Akt/mTOR cell signaling pathway. In various embodiments, the T cells may be obtained from any source and contacted with the agent during the activation and/or expansion phases of the manufacturing process. The resulting T cell compositions are enriched in developmentally potent T cells that have the ability to proliferate and express one or more of the following biomarkers: CD62L, CCR7, CD28, CD27, CD122, CD127, CD197, CD38, and CD8. In one embodiment, populations of cell comprising T cells, that have been treated with one or more PI3K inhibitors is enriched for a population of $CD8^+$ T cells co-expressing one or more or, or all of, the following biomarkers: CD62L, CD127, CD197, and CD38.

In one embodiment, populations of cell comprising T cells, that have been treated with one or more PI3K inhibitors is enriched for a population of $CD8^+$ T cells co-expressing one or more or, or all of, the following biomarkers: CD62L, CD127, CD27, and CD8.

In one embodiment, modified T cells comprising maintained levels of proliferation and decreased differentiation are manufactured. In a particular embodiment, T cells are manufactured by stimulating T cells to become activated and to proliferate in the presence of one or more stimulatory signals and an agent that is an inhibitor of a PI3K cell signaling pathway.

The T cells can then be modified to express an anti-CD79A CARs. In one embodiment, the T cells are modified by transducing the T cells with a viral vector comprising an anti-CD79A CAR contemplated herein. In a certain embodiment, the T cells are modified prior to stimulation and activation in the presence of an inhibitor of a PI3K cell signaling pathway. In another embodiment, T cells are modified after stimulation and activation in the presence of an inhibitor of a PI3K cell signaling pathway. In a particular embodiment, T cells are modified within 12 hours, 24 hours, 36 hours, or 48 hours of stimulation and activation in the presence of an inhibitor of a PI3K cell signaling pathway.

After T cells are activated, the cells are cultured to proliferate. T cells may be cultured for at least 1, 2, 3, 4, 5, 6, or 7 days, at least 2 weeks, at least 1, 2, 3, 4, 5, or 6 months or more with 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 or more rounds of expansion.

In various embodiments, T cell compositions are manufactured in the presence of one or more inhibitors of a PI3K/Akt/mTOR cell signaling pathway. The inhibitors may target one or more activities in the pathway or a single activity. Without wishing to be bound to any particular theory, it is contemplated that treatment or contacting T cells with one or more inhibitors of the PI3K pathway during the stimulation, activation, and/or expansion phases of the manufacturing process preferentially increases young T cells, thereby producing superior therapeutic T cell compositions.

In a particular embodiment, a method for increasing the proliferation of T cells expressing an engineered T cell receptor is provided. Such methods may comprise, for example, harvesting a source of T cells from a subject, stimulating and activating the T cells in the presence of one or more inhibitors of the PI3K pathway, modification of the T cells to express an anti-CD79A CAR, and expanding the T cells in culture.

In a certain embodiment, a method for producing populations of T cells enriched for expression of one or more of the following biomarkers: CD62L, CCR7, CD28, CD27, CD122, CD127, CD197, CD38, and CD8 is contemplated. In one embodiment, young T cells comprise one or more of, or all of the following biological markers: CD62L, CD127, CD197, and CD38.

In one embodiment, young T cells comprise one or more of, or all of the following biological markers: CD62L, CD127, CD27, and CD8.

In one embodiment, the young T cells lack expression of CD57, CD244, CD160, PD-1, CTLA4, TIM3, and LAG3 are provided. As discussed elsewhere herein, the expression levels young T cell biomarkers is relative to the expression levels of such markers in more differentiated T cells or immune effector cell populations.

In one embodiment, peripheral blood mononuclear cells (PBMCs) are used as the source of T cells in the T cell manufacturing methods contemplated herein. PBMCs form a heterogeneous population of T lymphocytes that can be $CD4^+$, $CD8^+$, or $CD4^+$ and $CD8^+$ and can include other mononuclear cells such as monocytes, B cells, NK cells and NKT cells. An expression vector comprising a polynucleotide encoding an engineered TCR or CAR contemplated in particular embodiments are introduced into a population of human donor T cells, NK cells or NKT cells. In a particular embodiment, successfully transduced T cells that carry the expression vector can be sorted using flow cytometry to isolate CD3 positive T cells and then further propagated to increase the number of the modified T cells in addition to cell activation using anti-CD3 antibodies and or anti-CD28 antibodies and IL-2, IL-7, and/or IL-15.

Manufacturing methods contemplated herein may further comprise cryopreservation of modified T cells for storage and/or preparation for use in a human subject. In one embodiment, a method of storing genetically modified murine, human or humanized CAR protein expressing immune effector cells which target an CD79A expressing cell, comprises cryopreserving the immune effector cells such that the cells remain viable upon thawing. A fraction of the immune effector cells expressing the CAR proteins can be cryopreserved by methods known in the art to provide a permanent source of such cells for the future treatment of patients afflicted with an CD79A expressing cancer cell. T cells are cryopreserved such that the cells remain viable upon thawing. When needed, the cryopreserved transformed immune effector cells can be thawed, grown and expanded for more such cells. As used herein, "cryopreserving," refers to the preservation of cells by cooling to sub-zero temperatures, such as (typically) 77 K or −196° C. (the boiling point of liquid nitrogen). Cryoprotective agents are often used at sub-zero temperatures to prevent the cells being preserved from damage due to freezing at low temperatures or warming to room temperature. Cryopreservative agents and optimal cooling rates can protect against cell injury. Cryoprotective agents which can be used include but are not limited to dimethyl sulfoxide (DMSO) (Lovelock and Bishop, *Nature*, 1959; 183: 1394-1395; Ashwood-Smith, *Nature*, 1961; 190: 1204-1205), glycerol, polyvinylpyrrolidine (Rinfret, *Ann. N.Y. Acad. Sci*., 1960; 85: 576), and polyethylene glycol (Sloviter and Ravdin, *Nature*, 1962; 196: 48). The preferred cooling rate is 1° to 3° C/minute. After at least two hours, the T cells have reached a temperature of −80° C and can be placed directly into liquid nitrogen (−196° C) for permanent storage such as in a long-term cryogenic storage vessel.

1. T CELLS

The manufacture of improved CAR T cell compositions is provided in particular embodiments. T cells used for CAR T cell production may be autologous/autogeneic ("self") or non-autologous ("non-self," *e.g.,* allogeneic, syngeneic or xenogeneic). In preferred embodiments, the T cells are obtained from a mammalian subject. In a more preferred embodiment, the T cells are obtained from a primate subject. In the most preferred embodiment, the T cells are obtained from a human subject.

T cells can be obtained from a number of sources including, but not limited to, peripheral blood mononuclear cells, bone marrow, lymph nodes tissue, cord blood, thymus issue, tissue from a site of infection, ascites, pleural effusion, spleen tissue, and tumors. In certain embodiments, T cells can be obtained from a unit of blood collected from a subject using any

number of techniques known to the skilled person, such as sedimentation, *e.g.,* FICOLL™ separation. In one embodiment, cells from the circulating blood of an individual are obtained by apheresis. The apheresis product typically contains lymphocytes, including T cells, monocytes, granulocytes, B cells, other nucleated white blood cells, red blood cells, and platelets. In one embodiment, the cells collected by apheresis may be washed to remove the plasma fraction and to place the cells in an appropriate buffer or media for subsequent processing. The cells can be washed with PBS or with another suitable solution that lacks calcium, magnesium, and most, if not all other, divalent cations. As would be appreciated by those of ordinary skill in the art, a washing step may be accomplished by methods known to those in the art, such as by using a semiautomated flowthrough centrifuge. For example, the Cobe 2991 cell processor, the Baxter CytoMate, or the like. After washing, the cells may be resuspended in a variety of biocompatible buffers or other saline solution with or without buffer. In certain embodiments, the undesirable components of the apheresis sample may be removed in the cell directly resuspended culture media.

In particular embodiments, a population of cells comprising T cells, *e.g.,* PBMCs, is used in the manufacturing methods contemplated herein. In other embodiments, an isolated or purified population of T cells is used in the manufacturing methods contemplated herein. Cells can be isolated from peripheral blood mononuclear cells (PBMCs) by lysing the red blood cells and depleting the monocytes, for example, by centrifugation through a PERCOLL™ gradient. In some embodiments, after isolation of PBMC, both cytotoxic and helper T lymphocytes can be sorted into naïve, memory, and effector T cell subpopulations either before or after activation, expansion, and/or genetic modification.

In particular embodiments, a population of cells comprising T cells, *e.g.,* PBMCs, is used in the manufacturing methods contemplated herein. In other embodiments, an isolated or purified population of T cells is used in the manufacturing methods contemplated herein. Cells can be isolated from peripheral blood mononuclear cells (PBMCs) by lysing the red blood cells and depleting the monocytes, for example, by centrifugation through a PERCOLL™ gradient. In some embodiments, after isolation of PBMC, both cytotoxic and helper T lymphocytes can be sorted into naïve, memory, and effector T cell subpopulations either before or after activation, expansion, and/or genetic modification.

In particular embodiments, the population of immune effector cells is manufactured from PBMC that are genetically modified to express CARs using methods contemplated herein, but that are not subjected to positive or negative selection. In certain embodiments, after isolation of

PBMC, T lymphocytes are further isolated and in certain embodiments, both cytotoxic and helper T lymphocytes can be sorted into naïve, memory, and effector T cell subpopulations either before or after genetic modification and/or expansion.

In certain embodiments, specific subpopulation of T cells, expressing one or more of the following markers: CD3, CD4, CD8, CD28, CD45RA, CD45RO, CD62, CD127, and HLA-DR can be further isolated by positive or negative selection techniques. In one embodiment, a specific subpopulation of T cells, expressing one or more of the markers selected from the group consisting of i) CD62L, CCR7, CD28, CD27, CD122, CD127, CD197; ii) CD62L, CD127, CD197, and CD38 or iii) CD62L, CD127, CD27, and CD8, is further isolated by positive or negative selection techniques. In various embodiments, the manufactured T cell compositions do not express or do not substantially express one or more of the following markers: CD57, CD244, CD160, PD-1, CTLA4, TIM3, and LAG3.

In one embodiment, expression of one or more of the markers selected from the group consisting of i) CD62L, CD127, CD197, and CD38 or ii) CD62L, CD127, CD27, and CD8, is increased at least 1.5 fold, at least 2 fold, at least 3 fold, at least 4 fold, at least 5 fold, at least 6 fold, at least 7 fold, at least 8 fold, at least 9 fold, at least 10 fold, at least 25 fold, or more compared to a population of T cells activated and expanded without a PI3K inhibitor. In one embodiment, the T cells comprise $CD8^+$ T cells.

In one embodiment, expression of one or more of the markers selected from the group consisting of CD57, CD244, CD160, PD-1, CTLA4, TIM3, and LAG3 is decreased at least 1.5 fold, at least 2 fold, at least 3 fold, at least 4 fold, at least 5 fold, at least 6 fold, at least 7 fold, at least 8 fold, at least 9 fold, at least 10 fold, at least 25 fold, or more compared to a population of T cells activated and expanded with a PI3K inhibitor. In one embodiment, the T cells comprise $CD8^+$ T cells.

In one embodiment, the manufacturing methods contemplated herein increase the number of CAR T cells comprising one or more markers of naïve or developmentally potent T cells. Without wishing to be bound to any particular theory, the present inventors believe that treating a population of cells comprising T cells with one or more PI3K inhibitors results in an increase an expansion of developmentally potent T cells and provides a more robust and efficacious adoptive CAR T cell immunotherapy compared to existing CAR T cell therapies.

Illustrative examples of markers of naïve or developmentally potent T cells increased in T cells manufactured using the methods contemplated in particular embodiments include, but are not limited to i) CD62L, CD127, CD197, and CD38 or ii) CD62L, CD127, CD27, and CD8. In

particular embodiments, naïve T cells do not express do not express or do not substantially express one or more of the following markers: CD57, CD244, CD160, PD-1, BTLA, CD45RA, CTLA4, TIM3, and LAG3.

With respect to T cells, the T cell populations resulting from the various expansion methodologies contemplated herein may have a variety of specific phenotypic properties, depending on the conditions employed. In various embodiments, expanded T cell populations comprise one or more of the following phenotypic markers: CD62L, CD27, CD127, CD197, CD38, CD8, and HLA-DR.

In one embodiment, such phenotypic markers include enhanced expression of one or more of, or all of CD62L, CD127, CD197, and CD38. In particular embodiments, $CD8^+$ T lymphocytes characterized by the expression of phenotypic markers of naive T cells including CD62L, CD127, CD197, and CD38 are expanded.

In one embodiment, such phenotypic markers include enhanced expression of one or more of, or all of CD62L, CD127, CD27, and CD8. In particular embodiments, $CD8^+$ T lymphocytes characterized by the expression of phenotypic markers of naive T cells including CD62L, CD127, CD27, and CD8 are expanded.

In particular embodiments, T cells characterized by the expression of phenotypic markers of central memory T cells including CD45RO, CD62L, CD127, CD197, and CD38 and negative for granzyme B are expanded. In some embodiments, the central memory T cells are $CD45RO^+$, $CD62L^+$, $CD8^+$ T cells.

In certain embodiments, $CD4^+$ T lymphocytes characterized by the expression of phenotypic markers of naïve $CD4^+$ cells including CD62L and negative for expression of CD45RA and/or CD45RO are expanded. In some embodiments, $CD4^+$ cells characterized by the expression of phenotypic markers of central memory $CD4^+$ cells including CD62L and CD45RO positive. In some embodiments, effector $CD4^+$ cells are CD62L positive and CD45RO negative.

In certain embodiments, the T cells are isolated from an individual and activated and stimulated to proliferate *in vitro* prior to being genetically modified to express an anti-CD79A CAR. In this regard, the T cells may be cultured before and/or after being genetically modified (*i.e.,* transduced or transfected to express an anti-CD79A CAR contemplated herein).

2. ACTIVATION AND EXPANSION

In order to achieve sufficient therapeutic doses of T cell compositions, T cells are often subject to one or more rounds of stimulation, activation and/or expansion. T cells can be

activated and expanded generally using methods as described, for example, in U.S. Patents 6,352,694; 6,534,055; 6,905,680; 6,692,964; 5,858,358; 6,887,466; 6,905,681; 7,144,575; 7,067,318; 7,172,869; 7,232,566; 7,175,843; 5,883,223; 6,905,874; 6,797,514; and 6,867,041, each of which is incorporated herein by reference in its entirety. T cells modified to express an anti-CD79A CAR can be activated and expanded before and/or after the T cells are modified. In addition, T cells may be contacted with one or more agents that modulate a PI3K/Akt/mTOR cell signaling pathway before, during, and/or after activation and/or expansion. In one embodiment, T cells manufactured by the methods contemplated herein undergo one, two, three, four, or five or more rounds of activation and expansion, each of which may include one or more agents that modulate a PI3K/Akt/mTOR cell signaling pathway.

Artificial antigen presenting cells (aAPCs) support *ex vivo* growth and long-term expansion of functional human $CD8^+$ T cells without requiring the addition of exogenous cytokines, in contrast to the use of natural APCs. In particular embodiments, PBMCs or isolated T cells are contacted with a stimulatory agent and costimulatory agent, such as anti-CD3 and anti-CD28 antibodies, generally attached to a bead or other surface, in a culture medium with appropriate cytokines, such as IL-2, IL-7, and/or IL-15.

In other embodiments, artificial APC (aAPC) made by engineering K562, U937, 721.221, T2, and C1R cells to direct the stable expression and secretion, of a variety of costimulatory molecules and cytokines. In a particular embodiment, K32 or U32 aAPCs are used to direct the display of one or more antibody-based stimulatory molecules on the AAPC cell surface. Populations of T cells can be expanded by aAPCs expressing a variety of costimulatory molecules including, but not limited to, CD137L (4-1BBL), CD134L (OX40L), and/or CD80 or CD86. The aAPCs provide an efficient platform to expand genetically modified T cells and to maintain CD28 expression on $CD8^+$ T cells. aAPCs provided in WO 03/057171 and US2003/0147869 are hereby incorporated by reference in their entirety.

In one embodiment, a costimulatory ligand is presented on an antigen presenting cell (*e.g.,* an aAPC, dendritic cell, B cell, and the like) that specifically binds a cognate costimulatory molecule on a T cell, thereby providing a signal which, in addition to the primary signal provided by, for instance, binding of a TCR/CD3 complex, mediates a desired T cell response. Suitable costimulatory ligands include, but are not limited to, CD7, B7-1 (CD80), B7-2 (CD86), 4-1BBL, OX40L, inducible costimulatory ligand (ICOS-L), intercellular adhesion molecule (ICAM), CD30L, CD40, CD70, CD83, HLA-G, MICA, MICB, HVEM, lymphotoxin beta receptor, ILT3,

ILT4, an agonist or antibody that binds Toll ligand receptor, and a ligand that specifically binds with B7-H3.

In a particular embodiment, a costimulatory ligand comprises an antibody or antigen binding fragment thereof that specifically binds to a costimulatory molecule present on a T cell, including but not limited to, CD27, CD28, 4-1BB, OX40, CD30, CD40, ICOS, lymphocyte function-associated antigen-1 (LFA-1), CD7, LIGHT, NKG2C, B7-H3, and a ligand that specifically binds with CD83.

Suitable costimulatory ligands further include target antigens, which may be provided in soluble form or expressed on APCs or aAPCs that bind engineered TCRs or CARs expressed on modified T cells.

In various embodiments, a method for manufacturing T cells contemplated herein comprises activating a population of cells comprising T cells and expanding the population of T cells. T cell activation can be accomplished by providing a primary stimulation signal through the T cell TCR/CD3 complex or via stimulation of the CD2 surface protein and by providing a secondary costimulation signal through an accessory molecule, *e.g,* CD28.

The TCR/CD3 complex may be stimulated by contacting the T cell with a suitable CD3 binding agent, *e.g.,* a CD3 ligand or an anti-CD3 monoclonal antibody. Illustrative examples of CD3 antibodies include, but are not limited to, OKT3, G19-4, BC3, and 64.1.

In another embodiment, a CD2 binding agent may be used to provide a primary stimulation signal to the T cells. Illustrative examples of CD2 binding agents include, but are not limited to, CD2 ligands and anti-CD2 antibodies, *e.g.,* the T11.3 antibody in combination with the T11.1 or T11.2 antibody (Meuer, S. C. *et al.* (1984) *Cell* 36:897-906) and the 9.6 antibody (which recognizes the same epitope as TI 1.1) in combination with the 9-1 antibody (Yang, S. Y. *et al.* (1986) *J. Immunol*. 137:1097-1100). Other antibodies which bind to the same epitopes as any of the above described antibodies can also be used. Additional antibodies, or combinations of antibodies, can be prepared and identified by standard techniques as disclosed elsewhere herein.

In addition to the primary stimulation signal provided through the TCR/CD3 complex, or via CD2, induction of T cell responses requires a second, costimulatory signal. In particular embodiments, a CD28 binding agent can be used to provide a costimulatory signal. Illustrative examples of CD28 binding agents include but are not limited to: natural CD 28 ligands, *e.g.,* a natural ligand for CD28 (*e.g.,* a member of the B7 family of proteins, such as B7-1(CD80) and B7-2 (CD86); and anti-CD28 monoclonal antibody or fragment thereof capable of crosslinking

the CD28 molecule, *e.g.,* monoclonal antibodies 9.3, B-T3, XR-CD28, KOLT-2, 15E8, 248.23.2, and EX5.3D10.

In one embodiment, the molecule providing the primary stimulation signal, for example a molecule which provides stimulation through the TCR/CD3 complex or CD2, and the costimulatory molecule are coupled to the same surface.

In certain embodiments, binding agents that provide stimulatory and costimulatory signals are localized on the surface of a cell. This can be accomplished by transfecting or transducing a cell with a nucleic acid encoding the binding agent in a form suitable for its expression on the cell surface or alternatively by coupling a binding agent to the cell surface.

In another embodiment, the molecule providing the primary stimulation signal, for example a molecule which provides stimulation through the TCR/CD3 complex or CD2, and the costimulatory molecule are displayed on antigen presenting cells.

In one embodiment, the molecule providing the primary stimulation signal, for example a molecule which provides stimulation through the TCR/CD3 complex or CD2, and the costimulatory molecule are provided on separate surfaces.

In a certain embodiment, one of the binding agents that provide stimulatory and costimulatory signals is soluble (provided in solution) and the other agent(s) is provided on one or more surfaces.

In a particular embodiment, the binding agents that provide stimulatory and costimulatory signals are both provided in a soluble form (provided in solution).

In various embodiments, the methods for manufacturing T cells contemplated herein comprise activating T cells with anti-CD3 and anti-CD28 antibodies.

T cell compositions manufactured by the methods contemplated in particular embodiments comprise T cells activated and/or expanded in the presence of one or more agents that inhibit a PI3K cell signaling pathway. T cells modified to express an anti-CD79A CAR can be activated and expanded before and/or after the T cells are modified. In particular embodiments, a population of T cells is activated, modified to express an anti-CD79A CAR, and then cultured for expansion.

In one embodiment, T cells manufactured by the methods contemplated herein comprise an increased number of T cells expressing markers indicative of high proliferative potential and the ability to self-renew but that do not express or express substantially undetectable markers of T cell differentiation. These T cells may be repeatedly activated and expanded in a robust fashion and thereby provide an improved therapeutic T cell composition.

In one embodiment, a population of T cells activated and expanded in the presence of one or more agents that inhibit a PI3K cell signaling pathway is expanded at least 1.5 fold, at least 2 fold, at least 3 fold, at least 4 fold, at least 5 fold, at least 6 fold, at least 7 fold, at least 8 fold, at least 9 fold, at least 10 fold, at least 25 fold, at least 50 fold, at least 100 fold, at least 250 fold, at least 500 fold, at least 1000 fold, or more compared to a population of T cells activated and expanded without a PI3K inhibitor.

In one embodiment, a population of T cells characterized by the expression of markers young T cells are activated and expanded in the presence of one or more agents that inhibit a PI3K cell signaling pathway is expanded at least 1.5 fold, at least 2 fold, at least 3 fold, at least 4 fold, at least 5 fold, at least 6 fold, at least 7 fold, at least 8 fold, at least 9 fold, at least 10 fold, at least 25 fold, at least 50 fold, at least 100 fold, at least 250 fold, at least 500 fold, at least 1000 fold, or more compared the population of T cells activated and expanded without a PI3K inhibitor.

In one embodiment, expanding T cells activated by the methods contemplated herein further comprises culturing a population of cells comprising T cells for several hours (about 3 hours) to about 7 days to about 28 days or any hourly integer value in between. In another embodiment, the T cell composition may be cultured for 14 days. In a particular embodiment, T cells are cultured for about 21 days. In another embodiment, the T cell compositions are cultured for about 2-3 days. Several cycles of stimulation/activation/expansion may also be desired such that culture time of T cells can be 60 days or more.

In particular embodiments, conditions appropriate for T cell culture include an appropriate media (*e.g.,* Minimal Essential Media or RPMI Media 1640 or, X-vivo 15, (Lonza)) and one or more factors necessary for proliferation and viability including, but not limited to serum (*e.g.,* fetal bovine or human serum), interleukin-2 (IL-2), insulin, IFN-γ, IL-4, IL-7, IL-21, GM-CSF, IL- 10, IL- 12, IL-15, TGFβ, and TNF-α or any other additives suitable for the growth of cells known to the skilled artisan.

Further illustrative examples of cell culture media include, but are not limited to RPMI 1640, Clicks, AIM-V, DMEM, MEM, a-MEM, F-12, X-Vivo 1 5, and X-Vivo 20, Optimizer, with added amino acids, sodium pyruvate, and vitamins, either serum-free or supplemented with an appropriate amount of serum (or plasma) or a defined set of hormones, and/or an amount of cytokine(s) sufficient for the growth and expansion of T cells.

Illustrative examples of other additives for T cell expansion include, but are not limited to, surfactant, piasmanate, pH buffers such as HEPES, and reducing agents such as N-acetyl-cysteine and 2-mercaptoethanol

Antibiotics, *e.g.,* penicillin and streptomycin, are included only in experimental cultures, not in cultures of cells that are to be infused into a subject. The target cells are maintained under conditions necessary to support growth, for example, an appropriate temperature (*e.g.,* 37° C) and atmosphere (*e.g.,* air plus 5% C02).

3. AGENTS

In various embodiments, a method for manufacturing T cells is provided that expands undifferentiated or developmentally potent T cells comprising contacting T cells with an agent that modulates a PI3K pathway in the cells. In various embodiments, a method for manufacturing T cells is provided that expands undifferentiated or developmentally potent T cells comprising contacting T cells with an agent that modulates a PI3K/AKT/mTOR pathway in the cells. The cells may be contacted prior to, during, and/or after activation and expansion. The T cell compositions retain sufficient T cell potency such that they may undergo multiple rounds of expansion without a substantial increase in differentiation.

As used herein, the terms "modulate," "modulator," or "modulatory agent" or comparable term refer to an agent's ability to elicit a change in a cell signaling pathway. A modulator may increase or decrease an amount, activity of a pathway component or increase or decrease a desired effect or output of a cell signaling pathway. In one embodiment, the modulator is an inhibitor. In another embodiment, the modulator is an activator.

An "agent" refers to a compound, small molecule, *e.g.,* small organic molecule, nucleic acid, polypeptide, or a fragment, isoform, variant, analog, or derivative thereof used in the modulation of a PI3K/AKT/mTOR pathway.

A "small molecule" refers to a composition that has a molecular weight of less than about 5 kD, less than about 4 kD, less than about 3 kD, less than about 2 kD, less than about 1 kD, or less than about .5kD. Small molecules may comprise nucleic acids, peptides, polypeptides, peptidomimetics, peptoids, carbohydrates, lipids, components thereof or other organic or inorganic molecules. Libraries of chemical and/or biological mixtures, such as fungal, bacterial, or algal extracts, are known in the art and can be screened with any of the assays. Examples of methods for the synthesis of molecular libraries can be found in: (Carell *et al.*, 1994a; Carell *et al.*, 1994b; Cho *et al.*, 1993; DeWitt *et al.*, 1993; Gallop *et al.*, 1994; Zuckermann *et al.*, 1994).

An "analog" refers to a small organic compound, a nucleotide, a protein, or a polypeptide that possesses similar or identical activity or function(s) as the compound, nucleotide, protein or polypeptide or compound having the desired activity, but need not necessarily comprise a sequence or structure that is similar or identical to the sequence or structure of the preferred embodiment.

A "derivative" refers to either a compound, a protein or polypeptide that comprises an amino acid sequence of a parent protein or polypeptide that has been altered by the introduction of amino acid residue substitutions, deletions or additions, or a nucleic acid or nucleotide that has been modified by either introduction of nucleotide substitutions or deletions, additions or mutations. The derivative nucleic acid, nucleotide, protein or polypeptide possesses a similar or identical function as the parent polypeptide.

In various embodiments, the agent that modulates a PI3K pathway activates a component of the pathway. An "activator," or "agonist" refers to an agent that promotes, increases, or induces one or more activities of a molecule in a PI3K/AKT/mTOR pathway including, without limitation, a molecule that activates one or more activities of a PI3K.

In various embodiments, the agent that modulates a PI3K pathway inhibits a component of the pathway. An "inhibitor" or "antagonist" refers to an agent that inhibits, decreases, or reduces one or more activities of a molecule in a PI3K/AKT/mTOR pathway including, without limitation, a molecule than inhibits one or more activities of a PI3K. In one embodiment, the inhibitor is a dual molecule inhibitor. In particular embodiment, the inhibitor may inhibit a class of molecules have the same or substantially similar activities (a pan-inhibitor) or may specifically inhibit a molecule's activity (a selective or specific inhibitor). Inhibition may also be irreversible or reversible.

In one embodiment, the inhibitor has an IC50 of at least 1nM, at least 2nM, at least 5nM, at least 10nM, at least 50nM, at least 100nM, at least 200nM, at least 500nM, at least 1μM, at least 10μM, at least 50μM, or at least 100μM. IC50 determinations can be accomplished using any conventional techniques known in the art. For example, an IC50 can be determined by measuring the activity of a given enzyme in the presence of a range of concentrations of the inhibitor under study. The experimentally obtained values of enzyme activity then are plotted against the inhibitor concentrations used. The concentration of the inhibitor that shows 50% enzyme activity (as compared to the activity in the absence of any inhibitor) is taken as the "IC50" value. Analogously, other inhibitory concentrations can be defined through appropriate determinations of activity.

In various embodiments, T cells are contacted or treated or cultured with one or more modulators of a PI3K/AKT/mTOR pathway at a concentration of at least1nM, at least 2nM, at least 5nM, at least 10nM, at least 50nM, at least 100nM, at least 200nM, at least 500nM, at least 1μM, at least 10μM, at least 50μM, at least 100μM, or at least 1 M.

In particular embodiments, T cells may be contacted or treated or cultured with one or more modulators of a PI3K/AKT/mTOR pathway for at least 12 hours, 18 hours, at least 1, 2, 3, 4, 5, 6, or 7 days, at least 2 weeks, at least 1, 2, 3, 4, 5, or 6 months or more with 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 or more rounds of expansion.

The phosphatidyl-inositol-3 kinase/Akt/mammalian target of rapamycin pathway serves as a conduit to integrate growth factor signaling with cellular proliferation, differentiation, metabolism, and survival. PI3Ks are a family of highly conserved intracellular lipid kinases. Class IA PI3Ks are activated by growth factor receptor tyrosine kinases (RTKs), either directly or through interaction with the insulin receptor substrate family of adaptor molecules. This activity results in the production of phosphatidyl-inositol-3,4,5-trisphospate (PIP3) a regulator of the serine/threonine kinase Akt. mTOR acts through the canonical PI3K pathway via 2 distinct complexes, each characterized by different binding partners that confer distinct activities. mTORC1 (mTOR in complex with PRAS40, raptor, and mLST8/GbL) acts as a downstream effector of PI3K/Akt signaling, linking growth factor signals with protein translation, cell growth, proliferation, and survival. mTORC2 (mTOR in complex with rictor, mSIN1, protor, and mLST8) acts as an upstream activator of Akt.

Upon growth factor receptor-mediated activation of PI3K, Akt is recruited to the membrane through the interaction of its pleckstrin homology domain with PIP3, thus exposing its activation loop and enabling phosphorylation at threonine 308 (Thr308) by the constitutively active phosphoinositide-dependent protein kinase 1 (PDK1). For maximal activation, Akt is also phosphorylated by mTORC2, at serine 473 (Ser473) of its C-terminal hydrophobic motif. DNA-PK and HSP have also been shown to be important in the regulation of Akt activity. Akt activates mTORC1 through inhibitory phosphorylation of TSC2, which along with TSC1, negatively regulates mTORC1 by inhibiting the Rheb GTPase, a positive regulator of mTORC1. mTORC1 has 2 well-defined substrates, p70S6K (referred to hereafter as S6K1) and 4E-BP1, both of which critically regulate protein synthesis. Thus, mTORC1 is an important downstream effector of PI3K, linking growth factor signaling with protein translation and cellular proliferation.

a. PI3K Inhibitors

As used herein, the term "PI3K inhibitor" refers to a nucleic acid, peptide, compound, or small organic molecule that binds to and inhibits at least one activity of PI3K. The PI3K proteins can be divided into three classes, class 1 PI3Ks, class 2 PI3Ks, and class 3 PI3Ks. Class 1 PI3Ks exist as heterodimers consisting of one of four p110 catalytic subunits (p110α, p110β, p110δ, and p110γ) and one of two families of regulatory subunits. A PI3K inhibitor preferably targets the class 1 PI3K inhibitors. In one embodiment, a PI3K inhibitor will display selectivity for one or more isoforms of the class 1 PI3K inhibitors (*i.e.,* selectivity for p110α, p110β, p110δ, and p110γ or one or more of p110α, p110β, p110δ, and p110γ). In another aspect, a PI3K inhibitor will not display isoform selectivity and be considered a "pan-PI3K inhibitor." In one embodiment, a PI3K inhibitor will compete for binding with ATP to the PI3K catalytic domain.

In certain embodiments, a PI3K inhibitor can, for example, target PI3K as well as additional proteins in the PI3K-AKT-mTOR pathway. In particular embodiments, a PI3K inhibitor that targets both mTOR and PI3K can be referred to as either an mTOR inhibitor or a PI3K inhibitor. A PI3K inhibitor that only targets PI3K can be referred to as a selective PI3K inhibitor. In one embodiment, a selective PI3K inhibitor can be understood to refer to an agent that exhibits a 50% inhibitory concentration with respect to PI3K that is at least 10-fold, at least 20-fold, at least 30-fold, at least 50-fold, at least 100-fold, at least 1000-fold, or more, lower than the inhibitor's IC50 with respect to mTOR and/or other proteins in the pathway.

In a particular embodiment, exemplary PI3K inhibitors inhibit PI3K with an IC50 (concentration that inhibits 50% of the activity) of about 200 nM or less, preferably about 100 nm or less, even more preferably about 60 nM or less, about 25 nM, about 10 nM, about 5 nM, about 1 nM, 100 μM, 50 μM, 25 μM, 10 μM, 1 μM, or less. In one embodiment, a PI3K inhibitor inhibits PI3K with an IC50 from about 2 nM to about 100 nm, more preferably from about 2 nM to about 50 nM, even more preferably from about 2 nM to about 15 nM.

Illustrative examples of PI3K inhibitors suitable for use in the T cell manufacturing methods contemplated in particular embodiments include, but are not limited to, BKM120 (class 1 PI3K inhibitor, Novartis), XL147 (class 1 PI3K inhibitor, Exelixis), (pan-PI3K inhibitor, GlaxoSmithKline), and PX-866 (class 1 PI3K inhibitor; p110α, p110β, and p110γ isoforms, Oncothyreon).

Other illustrative examples of selective PI3K inhibitors include, but are not limited to BYL719, GSK2636771, TGX-221, AS25242, CAL-101, ZSTK474, and IPI-145.

Further illustrative examples of pan-PI3K inhibitors include, but are not limited to BEZ235, LY294002, GSK1059615, TG100713, and GDC-0941.

In a preferred embodiment, the PI3K inhibitor is ZSTK474.

b. AKT Inhibitors

As used herein, the term "AKT inhibitor" refers to a nucleic acid, peptide, compound, or small organic molecule that inhibits at least one activity of AKT. AKT inhibitors can be grouped into several classes, including lipid-based inhibitors (*e.g.,* inhibitors that target the pleckstrin homology domain of AKT which prevents AKT from localizing to plasma membranes), ATP-competitive inhibitors, and allosteric inhibitors. In one embodiment, AKT inhibitors act by binding to the AKT catalytic site. In a particular embodiment, Akt inhibitors act by inhibiting phosphorylation of downstream AKT targets such as mTOR. In another embodiment, AKT activity is inhibited by inhibiting the input signals to activate Akt by inhibiting, for example, DNA-PK activation of AKT, PDK-1 activation of AKT, and/or mTORC2 activation of Akt.

AKT inhibitors can target all three AKT isoforms, AKT1, AKT2, AKT3 or may be isoform selective and target only one or two of the AKT isoforms. In one embodiment, an AKT inhibitor can target AKT as well as additional proteins in the PI3K-AKT-mTOR pathway. An AKT inhibitor that only targets AKT can be referred to as a selective AKT inhibitor. In one embodiment, a selective AKT inhibitor can be understood to refer to an agent that exhibits a 50% inhibitory concentration with respect to AKT that is at least 10-fold, at least 20-fold, at least 30-fold, at least 50-fold, at least 100-fold, at least 1000-fold, or more lower than the inhibitor's IC50 with respect to other proteins in the pathway.

In a particular embodiment, exemplary AKT inhibitors inhibit AKT with an IC50 (concentration that inhibits 50% of the activity) of about 200 nM or less, preferably about 100 nm or less, even more preferably about 60 nM or less, about 25 nM, about 10 nM, about 5 nM, about 1 nM, 100 μM, 50 μM, 25 μM, 10 μM, 1 μM, or less. In one embodiment, an AKT inhibits AKT with an IC50 from about 2 nM to about 100 nm, more preferably from about 2 nM to about 50 nM, even more preferably from about 2 nM to about 15 nM.

Illustrative examples of AKT inhibitors for use in combination with auristatin based antibody-drug conjugates include, for example, perifosine (Keryx), MK2206 (Merck), VQD-002 (VioQuest), XL418 (Exelixis), GSK690693, GDC-0068, and PX316 (PROLX Pharmaceuticals).

An illustrative, non-limiting example of a selective Akt1 inhibitor is A-674563.

An illustrative, non-limiting example of a selective Akt2 inhibitor is CCT128930.

In particular embodiments, the Akt inhibitor DNA-PK activation of Akt, PDK-1 activation of Akt, mTORC2 activation of Akt, or HSP activation of Akt.

Illustrative examples of DNA-PK inhibitors include, but are not limited to, NU7441, PI-103, NU7026, PIK-75, and PP-121.

c. mTOR Inhibitors

The terms "mTOR inhibitor" or "agent that inhibits mTOR" refers to a nucleic acid, peptide, compound, or small organic molecule that inhibits at least one activity of an mTOR protein, such as, for example, the serine/threonine protein kinase activity on at least one of its substrates (*e.g.,* p70S6 kinase 1, 4E-BP1, AKT/PKB and eEF2). mTOR inhibitors are able to bind directly to and inhibit mTORC1, mTORC2 or both mTORC1 and mTORC2.

Inhibition of mTORC1 and/or mTORC2 activity can be determined by a reduction in signal transduction of the PI3K/Akt/mTOR pathway. A wide variety of readouts can be utilized to establish a reduction of the output of such signaling pathway. Some non-limiting exemplary readouts include (1) a decrease in phosphorylation of Akt at residues, including but not limited to 5473 and T308; (2) a decrease in activation of Akt as evidenced, for example, by a reduction of phosphorylation of Akt substrates including but not limited to Fox01/O3a T24/32, GSK3a/β; S21/9, and TSC2 T1462; (3) a decrease in phosphorylation of signaling molecules downstream of mTOR, including but not limited to ribosomal S6 S240/244, 70S6K T389, and 4EBP1 T37/46; and (4) inhibition of proliferation of cancerous cells.

In one embodiment, the mTOR inhibitors are active site inhibitors. These are mTOR inhibitors that bind to the ATP binding site (also referred to as ATP binding pocket) of mTOR and inhibit the catalytic activity of both mTORC1 and mTORC2. One class of active site inhibitors suitable for use in the T cell manufacturing methods contemplated in particular embodiments are dual specificity inhibitors that target and directly inhibit both PI3K and mTOR. Dual specificity inhibitors bind to both the ATP binding site of mTOR and PI3K. Illustrative examples of such inhibitors include, but are not limited to: imidazoquinazolines, wortmannin, LY294002, PI-103 (Cayman Chemical), SF1126 (Semafore), BGT226 (Novartis), XL765 (Exelixis) and NVP-BEZ235 (Novartis).

Another class of mTOR active site inhibitors suitable for use in the methods contemplated in particular embodiments selectively inhibit mTORC1 and mTORC2 activity relative to one or more type I phophatidylinositol 3-kinases, *e.g.,* PI3 kinase α, β, γ, or δ. These active site inhibitors bind to the active site of mTOR but not PI3K. Illustrative examples of such inhibitors

include, but are not limited to: pyrazolopyrimidines, Torin1 (Guertin and Sabatini), PP242 (2-(4-Amino-1-isopropyl-1H-pyrazolo[3,4-d]pyrimidin-3-yl)-1H-indol-5-ol), PP30, Ku-0063794, WAY-600 (Wyeth), WAY-687 (Wyeth), WAY-354 (Wyeth), and AZD8055 (Liu *et al.*, Nature Review, 8, 627-644, 2009). I

In one embodiment, a selective mTOR inhibitor refers to an agent that exhibits a 50% inhibitory concentration (IC50) with respect to mTORC1 and/or mTORC2, that is at least 10-fold, at least 20-fold, at least 50-fold, at least 100-fold, at least 1000-fold, or more, lower than the inhibitor's IC50 with respect to one, two, three, or more type I PI3-kinases or to all of the type I PI3-kinases.

Another class of mTOR inhibitors are referred to herein as "rapalogs". As used herein the term "rapalogs" refers to compounds that specifically bind to the mTOR FRB domain (FKBP rapamycin binding domain), are structurally related to rapamycin, and retain the mTOR inhibiting properties. The term rapalogs excludes rapamycin. Rapalogs include esters, ethers, oximes, hydrazones, and hydroxylamines of rapamycin, as well as compounds in which functional groups on the rapamycin core structure have been modified, for example, by reduction or oxidation. Pharmaceutically acceptable salts of such compounds are also considered to be rapamycin derivatives. Illustrative examples of rapalogs suitable for use in the methods contemplated in particular embodiments include, without limitation, temsirolimus (CC1779), everolimus (RAD001), deforolimus (AP23573), AZD8055 (AstraZeneca), and OSI-027 (OSI).

In one embodiment, the agent is the mTOR inhibitor rapamycin (sirolimus).

In a particular embodiment, exemplary mTOR inhibitors inhibit either mTORC1, mTORC2 or both mTORC1 and mTORC2 with an IC50 (concentration that inhibits 50% of the activity) of about 200 nM or less, preferably about 100 nm or less, even more preferably about 60 nM or less, about 25 nM, about 10 nM, about 5 nM, about 1 nM, 100 μM, 50 μM, 25 μM, 10 μM, 1 μM, or less. In one aspect, a mTOR inhibitor inhibits either mTORC1, mTORC2 or both mTORC1 and mTORC2 with an IC50 from about 2 nM to about 100 nm, more preferably from about 2 nM to about 50 nM, even more preferably from about 2 nM to about 15 nM.

In one embodiment, exemplary mTOR inhibitors inhibit either PI3K and mTORC1 or mTORC2 or both mTORC1 and mTORC2 and PI3K with an IC50 (concentration that inhibits 50% of the activity) of about 200 nM or less, preferably about 100 nm or less, even more preferably about 60 nM or less, about 25 nM, about 10 nM, about 5 nM, about 1 nM, 100 μM, 50 μM, 25 μM, 10 μM, 1 μM, or less. In one aspect, a mTOR inhibitor inhibits PI3K and mTORC1 or mTORC2 or both mTORC1 and mTORC2 and PI3K with an IC50 from about 2 nM to about

100 nm, more preferably from about 2 nM to about 50 nM, even more preferably from about 2 nM to about 15 nM.

Further illustrative examples of mTOR inhibitors suitable for use in particular embodiments include, but are not limited to AZD8055, INK128, rapamycin, PF-04691502, and everolimus.

mTOR has been shown to demonstrate a robust and specific catalytic activity toward the physiological substrate proteins, p70 S6 ribosomal protein kinase I (p70S6K1) and eIF4E binding protein 1 (4EBP1) as measured by phosphor-specific antibodies in Western blotting.

In one embodiment, the inhibitor of the PI3K/AKT/mTOR pathway is a s6 kinase inhibitor selected from the group consisting of: BI-D1870, H89, PF-4708671, FMK, and AT7867.

H. COMPOSITIONS AND FORMULATIONS

The compositions contemplated herein may comprise one or more CAR polypeptides, polynucleotides, vectors comprising same, genetically modified immune effector cells, *etc.*, as contemplated herein. Compositions include, but are not limited to pharmaceutical compositions. A "pharmaceutical composition" refers to a composition formulated in pharmaceutically-acceptable or physiologically-acceptable solutions for administration to a cell or an animal, either alone, or in combination with one or more other modalities of therapy. It will also be understood that, if desired, the compositions may be administered in combination with other agents as well, such as, *e.g.,* cytokines, growth factors, hormones, small molecules, chemotherapeutics, pro-drugs, drugs, antibodies, or other various pharmaceutically-active agents. There is virtually no limit to other components that may also be included in the compositions, provided that the additional agents do not adversely affect the ability of the composition to deliver the intended therapy.

The phrase "pharmaceutically acceptable" is employed herein to refer to those compounds, materials, compositions, and/or dosage forms which are, within the scope of sound medical judgment, suitable for use in contact with the tissues of human beings and animals without excessive toxicity, irritation, allergic response, or other problem or complication, commensurate with a reasonable benefit/risk ratio.

As used herein "pharmaceutically acceptable carrier, diluent or excipient" includes without limitation any adjuvant, carrier, excipient, glidant, sweetening agent, diluent, preservative, dye/colorant, flavor enhancer, surfactant, wetting agent, dispersing agent,

suspending agent, stabilizer, isotonic agent, solvent, surfactant, or emulsifier which has been approved by the United States Food and Drug Administration as being acceptable for use in humans or domestic animals. Exemplary pharmaceutically acceptable carriers include, but are not limited to, to sugars, such as lactose, glucose and sucrose; starches, such as corn starch and potato starch; cellulose, and its derivatives, such as sodium carboxymethyl cellulose, ethyl cellulose and cellulose acetate; tragacanth; malt; gelatin; talc; cocoa butter, waxes, animal and vegetable fats, paraffins, silicones, bentonites, silicic acid, zinc oxide; oils, such as peanut oil, cottonseed oil, safflower oil, sesame oil, olive oil, corn oil and soybean oil; glycols, such as propylene glycol; polyols, such as glycerin, sorbitol, mannitol and polyethylene glycol; esters, such as ethyl oleate and ethyl laurate; agar; buffering agents, such as magnesium hydroxide and aluminum hydroxide; alginic acid; pyrogen-free water; isotonic saline; Ringer's solution; ethyl alcohol; phosphate buffer solutions; and any other compatible substances employed in pharmaceutical formulations.

In particular embodiments, compositions comprise an amount of CAR-expressing immune effector cells contemplated herein. As used herein, the term "amount" refers to "an amount effective" or "an effective amount" of a genetically modified therapeutic cell, *e.g.,* T cell, to achieve a beneficial or desired prophylactic or therapeutic result, including clinical results.

A "prophylactically effective amount" refers to an amount of a genetically modified therapeutic cell effective to achieve the desired prophylactic result. Typically but not necessarily, since a prophylactic dose is used in subjects prior to or at an earlier stage of disease, the prophylactically effective amount is less than the therapeutically effective amount.

A "therapeutically effective amount" of a genetically modified therapeutic cell may vary according to factors such as the disease state, age, sex, and weight of the individual, and the ability of the stem and progenitor cells to elicit a desired response in the individual. A therapeutically effective amount is also one in which any toxic or detrimental effects of the virus or transduced therapeutic cells are outweighed by the therapeutically beneficial effects. The term "therapeutically effective amount" includes an amount that is effective to "treat" a subject (*e.g.,* a patient). When a therapeutic amount is indicated, the precise amount of the compositions to be administered can be determined by a physician with consideration of individual differences in age, weight, tumor size, extent of infection or metastasis, and condition of the patient (subject). It can generally be stated that a pharmaceutical

composition comprising the T cells described herein may be administered at a dosage of 10^2 to 10^{10} cells/kg body weight, preferably 10^5 to 10^6 cells/kg body weight, including all integer values within those ranges. The number of cells will depend upon the ultimate use for which the composition is intended as will the type of cells included therein. For uses provided herein, the cells are generally in a volume of a liter or less, can be 500 mLs or less, even 250 mLs or 100 mLs or less. Hence the density of the desired cells is typically greater than 10^6 cells/ml and generally is greater than 10^7 cells/ml, generally 10^8 cells/ml or greater. The clinically relevant number of immune cells can be apportioned into multiple infusions that cumulatively equal or exceed 10^5, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, or 10^{12} cells. In some aspects, particularly since all the infused cells will be redirected to a particular target antigen, lower numbers of cells, in the range of 10^6/kilogram (10^6-10^{11} per patient) may be administered. CAR expressing cell compositions may be administered multiple times at dosages within these ranges. The cells may be allogeneic, syngeneic, xenogeneic, or autologous to the patient undergoing therapy. If desired, the treatment may also include administration of mitogens (*e.g.,* PHA) or lymphokines, cytokines, and/or chemokines (*e.g.,* IFN-γ, IL-2, IL-12, TNF-alpha, IL-18, and TNF-beta, GM-CSF, IL-4, IL-13, Flt3-L, RANTES, MIP1α, *etc.*) as described herein to enhance induction of the immune response.

Generally, compositions comprising the cells activated and expanded as described herein may be utilized in the treatment and prevention of diseases that arise in individuals who are immunocompromised. In particular embodiments, compositions comprising the CAR-modified T cells contemplated herein are used in the treatment of cancer. The CAR-modified T cells may be administered either alone, or as a pharmaceutical composition in combination with carriers, diluents, excipients, and/or with other components such as IL-2 or other cytokines or cell populations. In particular embodiments, pharmaceutical compositions comprise an amount of genetically modified T cells, in combination with one or more pharmaceutically or physiologically acceptable carriers, diluents or excipients.

Pharmaceutical compositions comprising a CAR-expressing immune effector cell population, such as T cells, may comprise buffers such as neutral buffered saline, phosphate buffered saline and the like; carbohydrates such as glucose, mannose, sucrose or dextrans, mannitol; proteins; polypeptides or amino acids such as glycine; antioxidants; chelating agents such as EDTA or glutathione; adjuvants (*e.g.,* aluminum hydroxide); and preservatives. Compositions are preferably formulated for parenteral administration, *e.g.,* intravascular (intravenous or intraarterial), intraperitoneal or intramuscular administration.

The liquid pharmaceutical compositions, whether they be solutions, suspensions or other like form, may include one or more of the following: sterile diluents such as water for injection, saline solution, preferably physiological saline, Ringer's solution, isotonic sodium chloride, fixed oils such as synthetic mono or diglycerides which may serve as the solvent or suspending medium, polyethylene glycols, glycerin, propylene glycol or other solvents; antibacterial agents such as benzyl alcohol or methyl paraben; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates and agents for the adjustment of tonicity such as sodium chloride or dextrose. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic. An injectable pharmaceutical composition is preferably sterile.

In one embodiment, the T cell compositions contemplated herein are formulated in a pharmaceutically acceptable cell culture medium. Such compositions are suitable for administration to human subjects. In particular embodiments, the pharmaceutically acceptable cell culture medium is a serum free medium.

Serum-free medium has several advantages over serum containing medium, including a simplified and better defined composition, a reduced degree of contaminants, elimination of a potential source of infectious agents, and lower cost. In various embodiments, the serum-free medium is animal-free, and may optionally be protein-free. Optionally, the medium may contain biopharmaceutically acceptable recombinant proteins. "Animal-free" medium refers to medium wherein the components are derived from non-animal sources. Recombinant proteins replace native animal proteins in animal-free medium and the nutrients are obtained from synthetic, plant or microbial sources. "Protein-free" medium, in contrast, is defined as substantially free of protein.

Illustrative examples of serum-free media used in particular compositions includes, but is not limited to QBSF-60 (Quality Biological, Inc.), StemPro-34 (Life Technologies), and X-VIVO 10.

In one preferred embodiment, compositions comprising immune effector cells contemplated herein are formulated in a solution comprising PlasmaLyte A.

In another preferred embodiment, compositions comprising immune effector cells contemplated herein are formulated in a solution comprising a cryopreservation medium. For example, cryopreservation media with cryopreservation agents may be used to maintain a high cell viability outcome post-thaw. Illustrative examples of cryopreservation media used in

particular compositions includes, but is not limited to, CryoStor CS10, CryoStor CS5, and CryoStor CS2.

In a more preferred embodiment, compositions comprising immune effector cells contemplated herein are formulated in a solution comprising 50:50 PlasmaLyte A to CryoStor CS10.

In a particular embodiment, compositions comprise an effective amount of CAR-expressing immune effector cells, alone or in combination with one or more therapeutic agents. Thus, the CAR-expressing immune effector cell compositions may be administered alone or in combination with other known cancer treatments, such as radiation therapy, chemotherapy, transplantation, immunotherapy, hormone therapy, photodynamic therapy, *etc.* The compositions may also be administered in combination with antibiotics. Such therapeutic agents may be accepted in the art as a standard treatment for a particular disease state as described herein, such as a particular cancer. Exemplary therapeutic agents contemplated in particular embodiments include cytokines, growth factors, steroids, NSAIDs, DMARDs, anti-inflammatories, chemotherapeutics, radiotherapeutics, therapeutic antibodies, or other active and ancillary agents.

In certain embodiments, compositions comprising CAR-expressing immune effector cells disclosed herein may be administered in conjunction with any number of chemotherapeutic agents. Illustrative examples of chemotherapeutic agents include alkylating agents such as thiotepa and cyclophosphamide (CYTOXAN™); alkyl sulfonates such as busulfan, improsulfan and piposulfan; aziridines such as benzodopa, carboquone, meturedopa, and uredopa; ethylenimines and methylamelamines including altretamine, triethylenemelamine, trietylenephosphoramide, triethylenethiophosphaoramide and trimethylolomelamine resume; nitrogen mustards such as chlorambucil, chlornaphazine, cholophosphamide, estramustine, ifosfamide, mechlorethamine, mechlorethamine oxide hydrochloride, melphalan, novembichin, phenesterine, prednimustine, trofosfamide, uracil mustard; nitrosureas such as carmustine, chlorozotocin, fotemustine, lomustine, nimustine, ranimustine; antibiotics such as aclacinomysins, actinomycin, authramycin, azaserine, bleomycins, cactinomycin, calicheamicin, carabicin, carminomycin, carzinophilin, chromomycins, dactinomycin, daunorubicin, detorubicin, 6-diazo-5-oxo-L-norleucine, doxorubicin, epirubicin, esorubicin, idarubicin, marcellomycin, mitomycins, mycophenolic acid, nogalamycin, olivomycins, peplomycin, potfiromycin, puromycin, quelamycin, rodorubicin, streptonigrin, streptozocin, tubercidin, ubenimex, zinostatin, zorubicin; anti-

metabolites such as methotrexate and 5-fluorouracil (5-FU); folic acid analogues such as denopterin, methotrexate, pteropterin, trimetrexate; purine analogs such as fludarabine, 6-mercaptopurine, thiamiprine, thioguanine; pyrimidine analogs such as ancitabine, azacitidine, 6-azauridine, carmofur, cytarabine, dideoxyuridine, doxifluridine, enocitabine, floxuridine, 5-FU; androgens such as calusterone, dromostanolone propionate, epitiostanol, mepitiostane, testolactone; anti-adrenals such as aminoglutethimide, mitotane, trilostane; folic acid replenisher such as frolinic acid; aceglatone; aldophosphamide glycoside; aminolevulinic acid; amsacrine; bestrabucil; bisantrene; edatraxate; defofamine; demecolcine; diaziquone; elformithine; elliptinium acetate; etoglucid; gallium nitrate; hydroxyurea; lentinan; lonidamine; mitoguazone; mitoxantrone; mopidamol; nitracrine; pentostatin; phenamet; pirarubicin; podophyllinic acid; 2-ethylhydrazide; procarbazine; PSK®; razoxane; sizofiran; spirogermanium; tenuazonic acid; triaziquone; 2, 2',2”-trichlorotriethylamine; urethan; vindesine; dacarbazine; mannomustine; mitobronitol; mitolactol; pipobroman; gacytosine; arabinoside (“Ara-C”); cyclophosphamide; thiotepa; taxoids, e.g. paclitaxel (TAXOL®, Bristol-Myers Squibb Oncology, Princeton, N.J.) and doxetaxel (TAXOTERE®., Rhne-Poulenc Rorer, Antony, France); chlorambucil; gemcitabine; 6-thioguanine; mercaptopurine; methotrexate; platinum analogs such as cisplatin and carboplatin; vinblastine; platinum; etoposide (VP-16); ifosfamide; mitomycin C; mitoxantrone; vincristine; vinorelbine; navelbine; novantrone; teniposide; daunomycin; aminopterin; xeloda; ibandronate; CPT-11; topoisomerase inhibitor RFS 2000; difluoromethylomithine (DMFO); retinoic acid derivatives such as Targretin™ (bexarotene), Panretin™ (alitretinoin) ; ONTAK™ (denileukin diftitox) ; esperamicins; capecitabine; and pharmaceutically acceptable salts, acids or derivatives of any of the above. Also included in this definition are anti-hormonal agents that act to regulate or inhibit hormone action on cancers such as anti-estrogens including for example tamoxifen, raloxifene, aromatase inhibiting 4(5)-imidazoles, 4-hydroxytamoxifen, trioxifene, keoxifene, LY117018, onapristone, and toremifene (Fareston); and anti-androgens such as flutamide, nilutamide, bicalutamide, leuprolide, and goserelin; and pharmaceutically acceptable salts, acids or derivatives of any of the above.

A variety of other therapeutic agents may be used in conjunction with the compositions described herein. In one embodiment, the composition comprising CAR-expressing immune effector cells is administered with an anti-inflammatory agent. Anti-inflammatory agents or drugs include, but are not limited to, steroids and glucocorticoids (including betamethasone, budesonide, dexamethasone, hydrocortisone acetate,

hydrocortisone, hydrocortisone, methylprednisolone, prednisolone, prednisone, triamcinolone), nonsteroidal anti-inflammatory drugs (NSAIDS) including aspirin, ibuprofen, naproxen, methotrexate, sulfasalazine, leflunomide, anti-TNF medications, cyclophosphamide and mycophenolate.

Other exemplary NSAIDs are chosen from the group consisting of ibuprofen, naproxen, naproxen sodium, Cox-2 inhibitors such as VIOXX® (rofecoxib) and CELEBREX® (celecoxib), and sialylates. Exemplary analgesics are chosen from the group consisting of acetaminophen, oxycodone, tramadol of proporxyphene hydrochloride. Exemplary glucocorticoids are chosen from the group consisting of cortisone, dexamethasone, hydrocortisone, methylprednisolone, prednisolone, or prednisone. Exemplary biological response modifiers include molecules directed against cell surface markers (*e.g.,* CD4, CD5, *etc.*), cytokine inhibitors, such as the TNF antagonists (*e.g.,* etanercept (ENBREL®), adalimumab (HUMIRA®) and infliximab (REMICADE®), chemokine inhibitors and adhesion molecule inhibitors. The biological response modifiers include monoclonal antibodies as well as recombinant forms of molecules. Exemplary DMARDs include azathioprine, cyclophosphamide, cyclosporine, methotrexate, penicillamine, leflunomide, sulfasalazine, hydroxychloroquine, Gold (oral (auranofin) and intramuscular) and minocycline.

Illustrative examples of therapeutic antibodies suitable for combination with the CAR modified T cells contemplated in particular embodiments, include but are not limited to, atezolizumab, avelumab, bavituximab, bevacizumab (avastin), bivatuzumab, blinatumomab, conatumumab, crizotinib, daratumumab, duligotumab, dacetuzumab, dalotuzumab, durvalumab, elotuzumab (HuLuc63), gemtuzumab, ibritumomab, indatuximab, inotuzumab, ipilimumab, lorvotuzumab, lucatumumab, milatuzumab, moxetumomab, nivolumab, ocaratuzumab, ofatumumab, pembrolizumab, rituximab, siltuximab, teprotumumab, and ublituximab.

In certain embodiments, the compositions described herein are administered in conjunction with a cytokine. By "cytokine" as used herein is meant a generic term for proteins released by one cell population that act on another cell as intercellular mediators. Examples of such cytokines are lymphokines, monokines, and traditional polypeptide hormones. Included among the cytokines are growth hormones such as human growth hormone, N-methionyl human growth hormone, and bovine growth hormone; parathyroid hormone; thyroxine; insulin; proinsulin; relaxin; prorelaxin; glycoprotein hormones such as

follicle stimulating hormone (FSH), thyroid stimulating hormone (TSH), and luteinizing hormone (LH); hepatic growth factor; fibroblast growth factor; prolactin; placental lactogen; tumor necrosis factor-alpha and -beta; mullerian-inhibiting substance; mouse gonadotropin-associated peptide; inhibin; activin; vascular endothelial growth factor; integrin; thrombopoietin (TPO); nerve growth factors such as NGF-beta; platelet-growth factor; transforming growth factors (TGFs) such as TGF-alpha and TGF-beta; insulin-like growth factor-I and -II; erythropoietin (EPO); osteoinductive factors; interferons such as interferon-alpha, beta, and -gamma; colony stimulating factors (CSFs) such as macrophage-CSF (M-CSF); granulocyte-macrophage-CSF (GM-CSF); and granulocyte-CSF (G-CSF); interleukins (ILs) such as IL-1, IL-1alpha, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12; IL-15, a tumor necrosis factor such as TNF-alpha or TNF-beta; and other polypeptide factors including LIF and kit ligand (KL). As used herein, the term cytokine includes proteins from natural sources or from recombinant cell culture, and biologically active equivalents of the native sequence cytokines.

In particular embodiments, a composition comprises CAR T cells contemplated herein that are cultured in the presence of a PI3K inhibitor as contemplated herein and express one or more of the following markers: CD3, CD4, CD8, CD27, CD28, CD45RA, CD45RO, CD62L, CD127, and HLA-DR can be further isolated by positive or negative selection techniques. In one embodiment, a composition comprises a specific subpopulation of T cells, expressing one or more of the markers selected from the group consisting of i) CD62L, CCR7, CD28, CD27, CD122, CD127, CD197; ii) CD62L, CD127, CD197, CD38; and iii) CD62L, CD27, CD127, and CD8, is further isolated by positive or negative selection techniques. In various embodiments, compositions do not express or do not substantially express one or more of the following markers: CD57, CD244, CD160, PD-1, CTLA4, TIM3, and LAG3.

In one embodiment, expression of one or more of the markers selected from the group consisting of CD62L, CD127, CD197, and CD38 is increased at least 1.5 fold, at least 2 fold, at least 3 fold, at least 4 fold, at least 5 fold, at least 6 fold, at least 7 fold, at least 8 fold, at least 9 fold, at least 10 fold, at least 25 fold, or more compared to a population of T cells activated and expanded without a PI3K inhibitor.

In one embodiment, expression of one or more of the markers selected from the group consisting of CD62L, CD127, CD27, and CD8 is increased at least 1.5 fold, at least 2 fold, at least 3 fold, at least 4 fold, at least 5 fold, at least 6 fold, at least 7 fold, at least 8 fold, at least 9

fold, at least 10 fold, at least 25 fold, or more compared to a population of T cells activated and expanded without a PI3K inhibitor.

In one embodiment, expression of one or more of the markers selected from the group consisting of CD57, CD244, CD160, PD-1, CTLA4, TIM3, and LAG3 is decreased at least 1.5 fold, at least 2 fold, at least 3 fold, at least 4 fold, at least 5 fold, at least 6 fold, at least 7 fold, at least 8 fold, at least 9 fold, at least 10 fold, at least 25 fold, or more compared to a population of T cells activated and expanded with a PI3K inhibitor.

I. TARGETS CELLS AND ANTIGENS

Genetically modified immune effector cells redirected to a target cell, *e.g.,* cancer cell, and that comprise CARs having a binding domain that binds to CD79A on the target cells are provided in particular embodiments. As used herein, the term "cancer" relates generally to a class of diseases or conditions in which abnormal cells divide without control and can invade nearby tissues

As used herein, the term "malignant" refers to a cancer in which a group of tumor cells display one or more of uncontrolled growth (*i.e.,* division beyond normal limits), invasion (*i.e.,* intrusion on and destruction of adjacent tissues), and metastasis (*i.e.,* spread to other locations in the body via lymph or blood). As used herein, the term "metastasize" refers to the spread of cancer from one part of the body to another. A tumor formed by cells that have spread is called a "metastatic tumor" or a "metastasis." The metastatic tumor contains cells that are like those in the original (primary) tumor.

As used herein, the term "benign" or "non-malignant" refers to tumors that may grow larger but do not spread to other parts of the body. Benign tumors are self-limited and typically do not invade or metastasize.

A "cancer cell" refers to an individual cell of a cancerous growth or tissue. Cancer cells include both solid cancers and liquid cancers. A "tumor" or "tumor cell" refers generally to a swelling or lesion formed by an abnormal growth of cells, which may be benign, pre-malignant, or malignant. Most cancers form tumors, but liquid cancers, *e.g.,* leukemia, do not necessarily form tumors. For those cancers that form tumors, the terms cancer (cell) and tumor (cell) are used interchangeably. The amount of a tumor in an individual is the "tumor burden" which can be measured as the number, volume, or weight of the tumor.

The term "relapse" refers to the diagnosis of return, or signs and symptoms of return, of a cancer after a period of improvement or remission.

"Remission," is also referred to as "clinical remission," and includes both partial and complete remission. In partial remission, some, but not all, signs and symptoms of cancer have disappeared. In complete remission, all signs and symptoms of cancer have disappeared, although cancer still may be in the body.

"Refractory" refers to a cancer that is resistant to, or non-responsive to, therapy with a particular therapeutic agent. A cancer can be refractory from the onset of treatment (*i.e.*, non-responsive to initial exposure to the therapeutic agent), or as a result of developing resistance to the therapeutic agent, either over the course of a first treatment period or during a subsequent treatment period.

In one embodiment, the target cell expresses an antigen, *e.g.*, a target antigen that is not substantially found on the surface of other normal (desired) cells.

In one embodiment, the target cell is a hematopoietic cell, a lymphoid cell, or a myeloid cell.

In certain embodiments, the target cell is part of the blood, a lymphoid tissue, or a myeloid tissue.

In a particular embodiment, the target cell is a cancer cell or cancer stem cell that expresses CD79A.

In a particular embodiment, the target cell is a liquid cancer cell or hematological cancer cell that expresses CD79A.

Illustrative examples of liquid cancers or hematological cancers that may be prevented, treated, or ameliorated with the compositions contemplated in particular embodiments include, but are not limited to: leukemias, lymphomas, and multiple myeloma.

Illustrative examples of cells that can be targeted by anti-CD79A CARs contemplated in particular embodiments include, but are not limited to those of the following leukemias: acute lymphocytic leukemia (ALL), acute myeloid leukemia (AML), myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, hairy cell leukemia (HCL), chronic lymphocytic leukemia (CLL), and chronic myeloid leukemia (CML), chronic myelomonocytic leukemia (CMML) and polycythemia vera.

Illustrative examples of cells that can be targeted by the compositions and methods contemplated in particular embodiments include, but are not limited to those of the following lymphomas: Hodgkin lymphoma, nodular lymphocyte-predominant Hodgkin lymphoma and

Non-Hodgkin lymphoma, including but not limited to B-cell non-Hodgkin lymphomas: Burkitt lymphoma, small lymphocytic lymphoma (SLL), diffuse large B-cell lymphoma (DLBCL), follicular lymphoma, immunoblastic large cell lymphoma, precursor B-lymphoblastic lymphoma, and mantle cell lymphoma; and T-cell non-Hodgkin lymphomas: mycosis fungoides, anaplastic large cell lymphoma, Sézary syndrome, and precursor T-lymphoblastic lymphoma.

Illustrative examples of cells that can be targeted by the compositions and methods contemplated in particular embodiments include, but are not limited to those of the following multiple myelomas: overt multiple myeloma, smoldering multiple myeloma (MGUS), plasma cell leukemia, non-secretory myeloma, IgD myeloma, osteosclerotic myeloma, solitary plasmacytoma of bone, and extramedullary plasmacytoma.

In preferred embodiments, the CD79A expressing target cell is a DLBCL cancer cell.

J. THERAPEUTIC METHODS

The genetically modified immune effector cells contemplated herein provide improved methods of adoptive immunotherapy for use in the prevention, treatment, and amelioration cancers that express CD79A or for preventing, treating, or ameliorating at least one symptom associated with an CD79A expressing cancer.

In various embodiments, the genetically modified immune effector cells contemplated herein provide improved methods of adoptive immunotherapy for use in increasing the cytotoxicity in cancer cells that express CD79A in a subject or for use in decreasing the number of cancer cells expressing CD79A in a subject.

In particular embodiments, the specificity of a primary immune effector cell is redirected to cells expressing CD79A, *e.g.,* cancer cells, by genetically modifying the primary immune effector cell with a CAR contemplated herein. In various embodiments, a viral vector is used to genetically modify an immune effector cell with a particular polynucleotide encoding a CAR comprising an anti-CD79A antigen binding domain that binds an CD79A polypeptide; a hinge domain; a transmembrane (TM) domain, a short oligo- or polypeptide linker, that links the TM domain to the intracellular signaling domain of the CAR; and one or more intracellular co-stimulatory signaling domains; and a primary signaling domain.

In one embodiment, a type of cellular therapy where T cells are genetically modified to express an anti-CD79A CAR that targets CD79A expressing cancer cells, and the CAR T cell is infused to a recipient in need thereof is provided. The infused cell is able to kill

disease causing cells in the recipient. Unlike antibody therapies, CAR T cells are able to replicate *in vivo* resulting in long-term persistence that can lead to sustained cancer therapy.

In one embodiment, anti-CD79A CAR T cells can undergo robust *in vivo* T cell expansion and can persist for an extended amount of time. In another embodiment, anti-CD79A CAR T cells evolve into specific memory T cells or stem cell memory T cells that can be reactivated to inhibit any additional tumor formation or growth.

In particular embodiments, compositions comprising immune effector cells comprising the CARs contemplated herein are used in the treatment of conditions associated with CD79A expressing cancer cells or cancer stem cells.

Illustrative examples of conditions that can be treated, prevented or ameliorated using the immune effector cells comprising the CARs contemplated in particular embodiments

In a particular embodiment, compositions comprising CAR-modified T cells contemplated herein are used in the treatment of liquid or hematological cancers.

In certain embodiments, the liquid or hematological cancer is selected from the group consisting of: leukemias, lymphomas, and multiple myelomas.

In certain embodiments, the liquid or hematological cancer is selected from the group consisting of: acute lymphocytic leukemia (ALL), acute myeloid leukemia (AML), myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, hairy cell leukemia (HCL), chronic lymphocytic leukemia (CLL), and chronic myeloid leukemia (CML), chronic myelomonocytic leukemia (CMML) and polycythemia vera, Hodgkin lymphoma, nodular lymphocyte-predominant Hodgkin lymphoma, Burkitt lymphoma, small lymphocytic lymphoma (SLL), diffuse large B-cell lymphoma, follicular lymphoma, immunoblastic large cell lymphoma, precursor B-lymphoblastic lymphoma, mantle cell lymphoma, marginal zone lymphoma, mycosis fungoides, anaplastic large cell lymphoma, Sézary syndrome, precursor T-lymphoblastic lymphoma, multiple myeloma, overt multiple myeloma, smoldering multiple myeloma, plasma cell leukemia, non-secretory myeloma, IgD myeloma, osteosclerotic myeloma, solitary plasmacytoma of bone, and extramedullary plasmacytoma.

In certain embodiments, the liquid or hematological cancer is selected from the group consisting of: acute lymphocytic leukemia (ALL), chronic lymphocytic leukemia (CLL), hairy cell leukemia (HCL), multiple myeloma (MM), acute myeloid leukemia (AML), or chronic myeloid leukemia (CML).

In preferred embodiments, the liquid or hematological cancer is DLBCL.

In preferred embodiments, the liquid or hematological cancer is relapsed/refractory DLBCL.

In particular embodiments, methods comprising administering a therapeutically effective amount of anti-CD79A CAR-expressing immune effector cells contemplated herein or a composition comprising the same, to a patient in need thereof, alone or in combination with one or more therapeutic agents, are provided. In certain embodiments, the cells are used in the treatment of patients at risk for developing a condition associated with cancer cells that express CD79A. Thus, in particular embodiments, methods for the treatment or prevention or amelioration of at least one symptom of cancer comprising administering to a subject in need thereof, a therapeutically effective amount of the CAR-modified cells contemplated herein.

As used herein, the terms "individual" and "subject" are often used interchangeably and refer to any animal that exhibits a symptom of a disease, disorder, or condition that can be treated with the gene therapy vectors, cell-based therapeutics, and methods contemplated elsewhere herein. In preferred embodiments, a subject includes any animal that exhibits symptoms of a disease, disorder, or condition related to cancer that can be treated with the gene therapy vectors, cell-based therapeutics, and methods contemplated elsewhere herein. Suitable subjects (*e.g.,* patients) include laboratory animals (such as mouse, rat, rabbit, or guinea pig), farm animals, and domestic animals or pets (such as a cat or dog). Non-human primates and, preferably, human patients, are included. Typical subjects include human patients that have an CD79A expressing cancer, have been diagnosed with an CD79A expressing cancer, or are at risk or having an CD79A expressing cancer, *e.g.,* DLBCL.

As used herein, the term "patient" refers to a subject that has been diagnosed with a particular disease, disorder, or condition that can be treated with the gene therapy vectors, cell-based therapeutics, and methods disclosed elsewhere herein.

As used herein "treatment" or "treating," includes any beneficial or desirable effect on the symptoms or pathology of a disease or pathological condition, and may include even minimal reductions in one or more measurable markers of the disease or condition being treated. Treatment can involve optionally either the reduction the disease or condition, or the delaying of the progression of the disease or condition. "Treatment" does not necessarily indicate complete eradication or cure of the disease or condition, or associated symptoms thereof.

As used herein, "prevent," and similar words such as "prevented," "preventing" *etc.*, indicate an approach for preventing, inhibiting, or reducing the likelihood of the occurrence

or recurrence of, a disease or condition. It also refers to delaying the onset or recurrence of a disease or condition or delaying the occurrence or recurrence of the symptoms of a disease or condition. As used herein, "prevention" and similar words also includes reducing the intensity, effect, symptoms and/or burden of a disease or condition prior to onset or recurrence of the disease or condition.

As used herein, the phrase "ameliorating at least one symptom of" refers to decreasing one or more symptoms of the disease or condition for which the subject is being treated. In particular embodiments, the disease or condition being treated is a cancer, wherein the one or more symptoms ameliorated include, but are not limited to, weakness, fatigue, shortness of breath, easy bruising and bleeding, frequent infections, enlarged lymph nodes, distended or painful abdomen (due to enlarged abdominal organs), bone or joint pain, fractures, unplanned weight loss, poor appetite, night sweats, persistent mild fever, and decreased urination (due to impaired kidney function).

By "enhance" or "promote," or "increase" or "expand" refers generally to the ability of a composition contemplated herein, *e.g.,* a genetically modified T cell or vector encoding a CAR, to produce, elicit, or cause a greater physiological response (*i.e.,* downstream effects) compared to the response caused by either vehicle or a control molecule/composition. A measurable physiological response may include an increase in T cell expansion, activation, persistence, and/or an increase in cancer cell killing ability, among others apparent from the understanding in the art and the description herein. An "increased" or "enhanced" amount is typically a "statistically significant" amount, and may include an increase that is 1.1, 1.2, 1.5, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 30 or more times (*e.g.,* 500, 1000 times) (including all integers and decimal points in between and above 1, *e.g.,* 1.5, 1.6, 1.7. 1.8, *etc.*) the response produced by vehicle or a control composition.

By "decrease" or "lower," or "lessen," or "reduce," or "abate" refers generally to the ability of composition contemplated herein to produce, elicit, or cause a lesser physiological response (*i.e.,* downstream effects) compared to the response caused by either vehicle or a control molecule/composition. A "decrease" or "reduced" amount is typically a "statistically significant" amount, and may include an decrease that is 1.1, 1.2, 1.5, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 30 or more times (*e.g.,* 500, 1000 times) (including all integers and decimal points in between and above 1, *e.g.,* 1.5, 1.6, 1.7. 1.8, *etc.*) the response (reference response) produced by vehicle, a control composition, or the response in a particular cell lineage.

By “maintain,” or “preserve,” or “maintenance,” or “no change,” or “no substantial change,” or “no substantial decrease” refers generally to the ability of a composition contemplated herein to produce, elicit, or cause a similar physiological response (*i.e.,* downstream effects) in a cell, as compared to the response caused by either vehicle, a control molecule/composition, or the response in a particular cell lineage. A comparable response is one that is not significantly different or measurable different from the reference response.

In one embodiment, a method of treating cancer in a subject in need thereof comprises administering an effective amount, *e.g.,* therapeutically effective amount of a composition comprising genetically modified immune effector cells contemplated herein. The quantity and frequency of administration will be determined by such factors as the condition of the patient, and the type and severity of the patient's disease, although appropriate dosages may be determined by clinical trials.

In one embodiment, the amount of immune effector cells, *e.g.,* T cells, in the composition administered to a subject is at least 0.1 x 10^5 cells, at least 0.5 x 10^5 cells, at least 1 x 10^5 cells, at least 5 x 10^5 cells, at least 1 x 10^6 cells, at least 0.5 x 10^7 cells, at least 1 x 10^7 cells, at least 0.5 x 10^8 cells, at least 1 x 10^8 cells, at least 0.5 x 10^9 cells, at least 1 x 10^9 cells, at least 2 x 10^9 cells, at least 3 x 10^9 cells, at least 4 x 10^9 cells, at least 5 x 10^9 cells, or at least 1 x 10^{10} cells.

In particular embodiments, about 1 x 10^7 T cells to about 1 x 10^9 T cells, about 2 x 10^7 T cells to about 0.9 x 10^9 T cells, about 3 x 10^7 T cells to about 0.8 x 10^9 T cells, about 4 x 10^7 T cells to about 0.7 x 10^9 T cells, about 5 x 10^7 T cells to about 0.6 x 10^9 T cells, or about 5 x 10^7 T cells to about 0.5 x 10^9 T cells are administered to a subject.

In one embodiment, the amount of immune effector cells, *e.g.,* T cells, in the composition administered to a subject is at least 0.1 x 10^4 cells/kg of bodyweight, at least 0.5 x 10^4 cells/kg of bodyweight, at least 1 x 10^4 cells/kg of bodyweight, at least 5 x 10^4 cells/kg of bodyweight, at least 1 x 10^5 cells/kg of bodyweight, at least 0.5 x 10^6 cells/kg of bodyweight, at least 1 x 10^6 cells/kg of bodyweight, at least 0.5 x 10^7 cells/kg of bodyweight, at least 1 x 10^7 cells/kg of bodyweight, at least 0.5 x 10^8 cells/kg of bodyweight, at least 1 x 10^8 cells/kg of bodyweight, at least 2 x 10^8 cells/kg of bodyweight, at least 3 x 10^8 cells/kg of bodyweight, at least 4 x 10^8 cells/kg of bodyweight, at least 5 x 10^8 cells/kg of bodyweight, or at least 1 x 10^9 cells/kg of bodyweight.

In particular embodiments, about 1 x 10^6 T cells/kg of bodyweight to about 1 x 10^8 T cells/kg of bodyweight, about 2 x 10^6 T cells/kg of bodyweight to about 0.9 x 10^8 T cells/kg of

bodyweight, about 3 x 10^6 T cells/kg of bodyweight to about 0.8 x 10^8 T cells/kg of bodyweight, about 4 x 10^6 T cells/kg of bodyweight to about 0.7 x 10^8 T cells/kg of bodyweight, about 5 x 10^6 T cells/kg of bodyweight to about 0.6 x 10^8 T cells/kg of bodyweight, or about 5 x 10^6 T cells/kg of bodyweight to about 0.5 x 10^8 T cells/kg of bodyweight are administered to a subject.

One of ordinary skill in the art would recognize that multiple administrations of the compositions contemplated herein may be required to effect the desired therapy. For example a composition may be administered 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 or more times over a span of 1 week, 2 weeks, 3 weeks, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 1 year, 2 years, 5, years, 10 years, or more.

In certain embodiments, it may be desirable to administer activated immune effector cells to a subject and then subsequently redraw blood (or have an apheresis performed), activate immune effector cells therefrom, and reinfuse the patient with these activated and expanded immune effector cells. This process can be carried out multiple times every few weeks. In certain embodiments, immune effector cells can be activated from blood draws of from 10cc to 400cc. In certain embodiments, immune effector cells are activated from blood draws of 20cc, 30cc, 40cc, 50cc, 60cc, 70cc, 80cc, 90cc, 100cc, 150cc, 200cc, 250cc, 300cc, 350cc, or 400cc or more. Not to be bound by theory, using this multiple blood draw/multiple reinfusion protocol may serve to select out certain populations of immune effector cells.

The administration of the compositions contemplated herein may be carried out in any convenient manner, including by aerosol inhalation, injection, ingestion, transfusion, implantation or transplantation. In a preferred embodiment, compositions are administered parenterally. The phrases “parenteral administration” and “administered parenterally” as used herein refers to modes of administration other than enteral and topical administration, usually by injection, and includes, without limitation, intravascular, intravenous, intramuscular, intraarterial, intrathecal, intracapsular, intraorbital, intratumoral, intracardiac, intradermal, intraperitoneal, transtracheal, subcutaneous, subcuticular, intraarticular, subcapsular, subarachnoid, intraspinal and intrasternal injection and infusion. In one embodiment, the compositions contemplated herein are administered to a subject by direct injection into a tumor, lymph node, or site of infection.

In one embodiment, a subject in need thereof is administered an effective amount of a composition to increase a cellular immune response to a B cell related condition in the subject. The immune response may include cellular immune responses mediated by cytotoxic T cells capable of killing infected cells, regulatory T cells, and helper T cell

responses. Humoral immune responses, mediated primarily by helper T cells capable of activating B cells thus leading to antibody production, may also be induced. A variety of techniques may be used for analyzing the type of immune responses induced by the compositions, which are well described in the art; *e.g.,* 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, N.Y.

In the case of T cell-mediated killing, CAR-ligand binding initiates CAR signaling to the T cell, resulting in activation of a variety of T cell signaling pathways that induce the T cell to produce or release proteins capable of inducing target cell apoptosis by various mechanisms. These T cell-mediated mechanisms include (but are not limited to) the transfer of intracellular cytotoxic granules from the T cell into the target cell, T cell secretion of pro-inflammatory cytokines that can induce target cell killing directly (or indirectly via recruitment of other killer effector cells), and up regulation of death receptor ligands (e.g. FasL) on the T cell surface that induce target cell apoptosis following binding to their cognate death receptor (*e.g*. Fas) on the target cell.

In one embodiment, a method of treating a subject diagnosed with an CD79A expressing cancer is provided comprising removing immune effector cells from a subject diagnosed with an CD79A expressing cancer, genetically modifying said immune effector cells with a vector comprising a nucleic acid encoding a CAR contemplated herein, thereby producing a population of modified immune effector cells, and administering the population of modified immune effector cells to the same subject. In a preferred embodiment, the immune effector cells comprise T cells.

In certain embodiments, methods for stimulating an immune effector cell mediated immune modulator response to a target cell population in a subject are provided comprising the steps of administering to the subject an immune effector cell population expressing a nucleic acid construct encoding a CAR molecule.

The methods for administering the cell compositions contemplated in particular embodiments includes any method which is effective to result in reintroduction of *ex vivo* genetically modified immune effector cells that either directly express a CAR in the subject or on reintroduction of the genetically modified progenitors of immune effector cells that on introduction into a subject differentiate into mature immune effector cells that express the CAR. One method comprises transducing peripheral blood T cells *ex vivo* with a nucleic acid construct contemplated herein and returning the transduced cells into the subject.

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.

EXAMPLES

EXAMPLE 1

CONSTRUCTION OF ANTI-CD79A CARS

CARs containing humanized anti-CD79A scFv antibodies were designed to contain an MND promoter operably linked to anti-CD79A scFv, a hinge and transmembrane domain from CD8α and a CD137 co-stimulatory domains followed by the intracellular signaling domain of the CD3ζ chain. The anti-CD79A CARs comprise a CD8α signal peptide (SP) sequence for the surface expression on immune effector cells. Table 3 shows the Identity, Genbank Reference, Source Name and Citation for the various nucleotide segments of an exemplary anti-CD79A CAR lentiviral vector. Exemplary CD79A CAR polypeptide sequences are set forth in SEQ ID NOs: 25-30 and exemplary CD79A CAR polynucleotide sequences are set forth in SEQ ID NOs: 31-36.

Table 3.

Nucleotides	Identity	GenBank Reference	Source Name	Citation
1-185	pUC19 plasmid backbone	Accession #L09137.2 nt 1 – 185	pUC19	New England Biolabs
185-222	Linker	Not applicable	Synthetic	Not applicable
223-800	CMV	Not Applicable	pHCMV	(1994) PNAS 91: 9564-68
801-1136	R, U5, PBS, and packaging sequences	Accession #M19921.2 nt 454-789	pNL4-3	Maldarelli, et.al. (1991) J Virol: 65(11):5732-43
1137-1139	Gag start codon (ATG) changed to stop codon (TAG)	Not Applicable	Synthetic	Not applicable
1140-1240	HIV-1 gag sequence	Accession #M19921.2 nt 793-893	pNL4-3	Maldarelli, et.al. (1991) J Virol: 65(11):5732-43
1241-1243	HIV-1 gag sequence changed to a second stop codon	Not Applicable	Synthetic	Not applicable
1244-1595	HIV-1 gag sequence	Accession #M19921.2 nt 897-1248	pNL4-3	Maldarelli, et.al. (1991) J Virol: 65(11):5732-43

Nucleotides	Identity	GenBank Reference	Source Name	Citation
1596-1992	HIV-1 pol cPPT/CTS	Accession #M19921.2 nt 4745-5125	pNL4-3	Maldarelli, et.al. (1991) J Virol: 65(11):5732-43
1993-2517	HIV-1, isolate HXB3 env region (RRE)	Accession #M14100.1 nt 1875-2399	PgTAT-CMV	Malim, M. H. Nature (1988) 335:181-183
2518-2693	HIV-1 env sequences S/A	Accession #M19921.2 nt 8290-8470	pNL4-3	Maldarelli, et.al. (1991) J Virol: 65(11):5732-43
2694-2708	Linker	Not applicable	Synthetic	Not applicable
2709-3096	MNDU3	Not applicable	rSPA.mPro.MND	Haas et al. Journal of Virology. 2003;77(17): 9439-9450
3097-3125	Linker	Not applicable	Synthetic	Not applicable
3126-3188	Signal peptide		Synthetic	Not applicable
variable	Anti-CD79A scFv	Not applicable	Synthetic	Not applicable
3927-3935	Linker	Not applicable	Synthetic	Not applicable
3936-4142	CD8a hinge and TM	Accession # NM_001768	Synthetic	Milone et al (2009) Mol Ther 17(8):1453-64
4143-4268	CD137 (4-1BB) signaling domain	Accession # NM_001561	Synthetic	Milone et al (2009) Mol Ther 17(8):1453-64
4269-4607	CD3-ζ signaling domain	Accession # NM_000734	Synthetic	Milone et al (2009) Mol Ther 17(8):1453-64
4608-4718	HIV-1 ppt and part of U3	Accession #M19921.2 nt 9005-9110	pNL4-3	Maldarelli, et.al. (1991) J Virol: 65(11):5732-43
4719-4835	HIV-1 part of U3 (399bp deletion) and R	Accession #M19921.2 nt 9511-9627	pNL4-3	Maldarelli, et.al. (1991) J Virol: 65(11):5732-43

Nucleotides	Identity	GenBank Reference	Source Name	Citation
4836-4859	Synthetic polyA	Not applicable	Synthetic	Levitt, N. Genes & Dev (1989) 3:1019-1025
4860-4878	Linker	Not applicable	Synthetic	Not Applicable[1]
4879-7351	pUC19 backbone	Accession #L09137.2 nt 2636-2686	pUC19	New England Biolabs (Attached)

EXAMPLE 2

EVALUATION OF HUMAN ANTI-CD79A CAR T CELLS

Chimeric antigen receptors (CARs) specific to CD79A (*e.g.,* SEQ ID NOs: 25, 27, 29, and 30) were evaluated for CAR expression and biological activity against CD79A expressing cells.

Target Antigen Expression

In one experiment, K562 cells, Pfeiffer cells, and Daudi target cells were interrogated for CD79A expression using anti-CD79A antibodies. The cells were incubated with CD79A antibody and expression was assessed by flow cytometry. CD79A expression was not detectable on K562 cells, was moderately expressed on Pfeiffer cells, and was highly expressed on Daudi cells. Figure 1A.

In another experiment, CD79A expression was measured on Daudi, NU-DUL-1, SU-DHL-2, and Pfeiffer target cells using anti-CD79A antibodies. The cells were incubated with CD79A antibody and expression was assessed by flow cytometer. CD79A expression was again highest on Daudi cells, then progressively less on NU-DUL-1, SU-DHL-2, and Pfeiffer cells. Figure 2A.

Anti-CD79A CAR Expression

CAR T cells were produced using a system directly scalable to large clinical manufacturing processes. Briefly, peripheral blood mononuclear cells (PBMC) were cultured in media containing IL-2 (CellGenix) and antibodies specific for CD3 and CD28 (Miltenyi Biotec). Lentiviruses encoding anti-CD79A CARs were added one day after culture initiation. The anti-CD79A CAR T cells were maintained in log-phase by adding fresh media containing IL-2 for a total of ten days of culture. At the end of culture, the anti-CD79A CAR T cells were interrogated for expression using flow cytometry. In one experiment, primary human T cells engineered with

lentiviruses expressing anti-CD79A CARs were stained with Goat-anti-Mouse (GaM) conjugated to biotin and detected with PE-conjugated streptavidin. Figure 1B. In another experiment, anti-CD79A CAR expression on T cells was evaluated by Goat-anti-Mouse (GaM) staining and binding of soluble CD79A antigen to anti-CD79A CAR-T cells was evaluated by staining with a CD79a extracellular domain -Fc fusion protein labeled with phycoerythrin (PE). Figure 2B. These reagents specifically identified T cells expressing anti-CD79A CARs.

Antigen Dependent Anti-CD79A CAR T Cell Activity

In one experiment, the biological activity of anti-CD79A CAR T cells to CD79A-positive (Pfeiffer and Daudi) and CD79A-negative (K562) cell lines was assessed using an interferon-gamma (IFNγ) release assay. Anti-CD79A CAR T cells were co cultured in the absence of target cells or with K562 (CD79A-), Pfeiffer cells (CD79A-low), and Daudi cells (CD79A-high) for 24 hours. Anti-CD79A CAR T cells released IFNγ only in the presence of CD79A positive cell lines. Figure 1C.

In another experiment, the biological activity of anti-CD79A CAR T cells to CD79A-positive (Huh7.CD79A, Daudi, NU-DUL-1, SU-DHL-2, and Pfeiffer) and CD79A-negative (Huh7) cell lines was assessed using an interferon-gamma (IFNγ) release assay. Anti-CD79A CAR T cells were co cultured in the absence of target cells (T cells alone) or with Huh7 cells (CD79A-), Huh7.CD79a cells (CD79A+), Daudi cells (CD79A+), NU-DUL-1 (CD79A+), SU-DHL-2 (CD79A+) or Pfeiffer cells (CD79A+). Figure 2C.

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. A chimeric antigen receptor (CAR) comprising:

a) an extracellular domain that comprises an anti-CD79A antibody or antigen binding fragment thereof that binds one or more epitopes of a human CD79A polypeptide, wherein the anti-CD79A antibody or antigen binding fragment thereof comprises a variable light chain sequence comprising CDRL1-CDRL3 sequences set forth in SEQ ID NOs: 1-3 and a variable heavy chain sequence comprising CDRH1-CDRH3 sequences set forth in SEQ ID NOs: 4-6;

b) a transmembrane domain;

c) one or more intracellular co-stimulatory signaling domains; and

d) a primary signaling domain.

2. The CAR of claim 1, wherein the anti-CD79A antibody or antigen binding fragment thereof comprises a variable light chain sequence as set forth in SEQ ID NO: 7 and/or a variable heavy chain sequence as set forth in SEQ ID NO: 8.

3. The CAR of claim 1 or claim 2, comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 25 or 26.

4. The CAR of any one of claims 1 to 3, comprising an amino acid sequence as set forth in SEQ ID NO: 26.

5. A chimeric antigen receptor (CAR) comprising:

a) an extracellular domain that comprises an anti-CD79A antibody or antigen binding fragment thereof that binds one or more epitopes of a human CD79A polypeptide, wherein the anti-CD79A antibody or antigen binding fragment thereof comprises a variable light chain sequence comprising CDRL1-CDRL3 sequences set forth in SEQ ID NOs: 9-11 and a variable heavy chain sequence comprising CDRH1-CDRH3 sequences set forth in SEQ ID NOs: 12-14;

b) a transmembrane domain;

c) one or more intracellular co-stimulatory signaling domains; and

d) a primary signaling domain.

6. The CAR of claim 5, wherein the anti-CD79A antibody or antigen binding fragment thereof comprises a variable light chain sequence as set forth in SEQ ID NO: 15 and/or a variable heavy chain sequence as set forth in SEQ ID NO: 16.

7. The CAR of claim 5 or claim 6, comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 27 or 28.

8. A chimeric antigen receptor (CAR) comprising:

a) an extracellular domain that comprises an anti-CD79A antibody or antigen binding fragment thereof that binds one or more epitopes of a human CD79A polypeptide, wherein the anti-CD79A antibody or antigen binding fragment thereof comprises a variable light chain sequence comprising CDRL1-CDRL3 sequences set forth in SEQ ID NOs: 17-19 and a variable heavy chain sequence comprising CDRH1-CDRH3 sequences set forth in SEQ ID NOs: 20-22;

b) a transmembrane domain;

c) one or more intracellular co-stimulatory signaling domains; and

d) a primary signaling domain.

9. The CAR of claim 8, wherein the anti-CD79A antibody or antigen binding fragment thereof comprises a variable light chain sequence as set forth in SEQ ID NO: 23 and/or a variable heavy chain sequence as set forth in SEQ ID NO: 24.

10. The CAR of claim 8 or claim 9, comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 29 or 30.

11. The CAR of any one of claims 1 to 10, wherein the anti-CD79A antibody or antigen binding fragment thereof that binds the human CD79A polypeptide is selected from the group consisting of: a Fab' fragment, a F(ab')2 fragment, a bispecific Fab dimer (Fab2), a trispecific Fab trimer (Fab3), an Fv, an single chain Fv protein ("scFv"), a bis-scFv, (scFv)2, a minibody, a diabody, a triabody, a tetrabody, and a disulfide stabilized Fv protein ("dsFv").

12. The CAR of any one of claims 1 to 11, wherein the anti-CD79A antibody or antigen binding fragment that binds the human CD79A polypeptide is an scFv.

13. The CAR of any one of claims 1 to 12, wherein the transmembrane domain is:

a) isolated from a polypeptide selected from the group consisting of: alpha or beta 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, and PD1;

b) isolated from a polypeptide selected from the group consisting of: CD8α, CD28, CD4, CD45, PD1, and CD152; or

c) isolated from CD8α.

14. The CAR of any one of claims 1 to 13, wherein the one or more intracellular co-stimulatory signaling domains:

a) are isolated from a co-stimulatory molecule selected from the group consisting of: TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9, TLR10, CARD11, CD2, CD7, CD27, CD28, CD30, CD40, CD54 (ICAM), CD83, CD134 (OX40), CD137 (4-1BB), CD278 (ICOS), DAP10, LAT, NKD2C, SLP76, TRIM, and ZAP70;

b) are isolated from a co-stimulatory molecule selected from the group consisting of: CD28, CD134, and CD137; or

c) is isolated from CD137.

15. The CAR of any one of claims 1 to 14, wherein the primary signaling domain is:

a) isolated from a polypeptide selected from the group consisting of: FcRγ, FcRβ, CD3γ, CD3δ, CD3ε, CD3ζ, CD22, CD79a, CD79b, and CD66d; or

b) isolated from a CD3ζ.

16. The CAR of any one of claims 1 to 15, further comprising a hinge region polypeptide.

17. The CAR of claim 16, wherein the hinge region polypeptide comprises a hinge region of CD8α.

18. The CAR of any one of claims 1 to 17, wherein the CAR comprises:

a) an anti-CD79A scFv;

b) a CD8α hinge region;

c) a CD8α transmembrane domain;

d) a CD137 intracellular co-stimulatory signaling domain; and

e) a CD3ζ primary signaling domain.

19. A polypeptide comprising the CAR of any one of claims 1 to 18, wherein the polypeptide further comprises a signal peptide.

20. A polynucleotide encoding a CAR of any one of claims 1 to 19, or the sequence set forth in any one of SEQ ID NOs: 31-36.

21. A vector comprising the polynucleotide of claim 20.

22. An immune effector cell comprising the vector of claim 21.

23. A composition comprising the immune effector cell of claim 22 and a physiologically acceptable excipient.

24. The composition of claim 23 for use in treating a cancer in a subject in need thereof.

25. The composition for use according to claim 24, wherein the cancer is a hematological malignancy.

26. The composition for use according to claim 24 or claim 25, wherein the cancer is non-Hodgkin's lymphoma, acute lymphocytic leukemia (ALL), chronic lymphocytic leukemia (CLL), hairy cell leukemia (HCL), multiple myeloma (MM), acute myeloid leukemia (AML), or chronic myeloid leukemia (CML).

27. The composition for use according to claim 26, wherein the non-Hodgkin's lymphoma is:

a) Burkitt's lymphoma, small lymphocytic lymphoma (SLL), diffuse large B cell lymphoma (DLBCL), follicular lymphoma (FL), mantle cell lymphoma (MCL), or marginal zone lymphoma (MZL); or

b) diffuse large B cell lymphoma (DLBCL).

28. Use of the composition of claim 23 in the manufacture of a medicament for treating cancer.

29. The use according to claim 28, wherein the cancer is a hematological malignancy.

30. The use according to claim 28 or claim 29, wherein the cancer is non-Hodgkin's lymphoma, acute lymphocytic leukemia (ALL), chronic lymphocytic leukemia (CLL), hairy cell leukemia (HCL), multiple myeloma (MM), acute myeloid leukemia (AML), or chronic myeloid leukemia (CML).

31. The use according to claim 30, wherein the non-Hodgkin's lymphoma is:

a) Burkitt's lymphoma, small lymphocytic lymphoma (SLL), diffuse large B cell lymphoma (DLBCL), follicular lymphoma (FL), mantle cell lymphoma (MCL), or marginal zone lymphoma (MZL); or

b) diffuse large B cell lymphoma (DLBCL).