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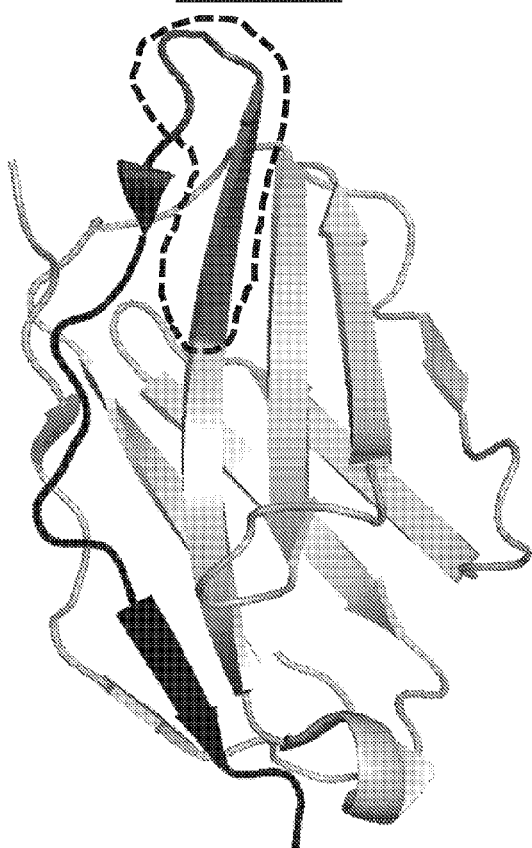


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(54) Title: CHIMERIC ANTIGEN AND T CELL RECEPTORS AND METHODS OF USE

FIG. 1B



(57) Abstract: The invention provides a chimeric antigen receptor (CAR) or a T cell receptor (TCR) comprising extracellular domain disclosed herein. Some aspects of the invention relate to a polynucleotide encoding a chimeric antigen receptor (CAR) or a T cell receptor (TCR) comprising the extracellular domain disclosed herein. Other aspects of the invention relate to cells comprising the CAR or the TCR and their use in a T cell therapy.



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CHIMERIC ANTIGEN AND T CELL RECEPTORS AND METHODS OF USE

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. Provisional Patent Application No. 62/317,258, filed April 1, 2016, which is hereby incorporated by reference in its entirety.

SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on February 28, 2019, is named K-1031_02US_SL.txt and is 450,469 bytes in size.

BACKGROUND OF THE INVENTION

[0003] Human cancers are by their nature comprised of normal cells that have undergone a genetic or epigenetic conversion to become abnormal cancer cells. In doing so, cancer cells begin to express proteins and other antigens that are distinct from those expressed by normal cells. These aberrant tumor antigens can be used by the body's innate immune system to specifically target and kill cancer cells. However, cancer cells employ various mechanisms to prevent immune cells, such as T and B lymphocytes, from successfully targeting cancer cells.

[0004] Current therapies T cell therapies rely on enriched or modified human T cells to target and kill cancer cells in a patient. To increase the ability of T cells to target and kill a particular cancer cell, methods have been developed to engineer T cells to express constructs which direct T cells to a particular target cancer cell. Chimeric antigen receptors (CARs) and engineered T cell receptors (TCRs), which comprise binding domains capable of interacting with a particular tumor antigen, allow T cells to target and kill cancer cells that express the particular tumor antigen.

[0005] A need exists for improved CARs and TCRs for targeting and killing cancer cells.

SUMMARY OF THE INVENTION

[0006] The present invention addresses this need by providing compositions and methods comprising genetically engineered immune cells that express antigen receptors (CARs) or T cell receptors (TCRs) which specifically target and kill cancer cells.

5 **[0007]** A CAR may comprise, for example, (i) an antigen-specific component (“antigen binding molecule”), (ii) one or more costimulatory domains (which includes a hinge domain), and (iii) one or more activating domains. Each domain may be heterogeneous, that is, comprised of sequences derived from different protein chains. CAR-expressing immune cells (such as T cells) may be used in various therapies, including cancer therapies.

10 **[0008]** As described in more detail below, including the Examples section, CARs comprising a costimulatory domain which includes a truncated hinge domain (“THD”) provides unexpectedly superior properties when compared to a CAR comprising a costimulatory domain which includes a complete hinge domain (“CHD”). Polynucleotides encoding such CARs can be transduced into T cells and the CARs are expressed in T cells, *e.g.*,
15 a patient’s own T cells. When the transduced T cells are transplanted back to a patient, the CARs direct the T cells to recognize and bind an epitope present on the surface of cancer cells, thus, allowing binding of cancer cells rather than non-cancerous cells. This binding leads to activation of cytolytic mechanisms in the T cell that specifically kill the bound cancer cells. Prior to the present invention, it was unknown that a CARs comprising a THD is superior to a
20 CAR comprising a CHD. Thus, the present invention satisfies an unmet need that exists for novel and improved therapies for treating cancer.

[0009] An aspect of the present invention is an isolated polynucleotide encoding a chimeric antigen receptor (CAR) or a T cell receptor (TCR), which comprises (i) an antigen binding molecule, (ii) a costimulatory domain, and (iii) an activating domain. The
25 costimulatory domain may comprise an extracellular domain, a transmembrane domain, and an intracellular domain, wherein the extracellular domain comprises a truncated hinge domain consisting essentially of or consisting of (i) an amino acid sequence at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to amino acids 123 to 152 of SEQ
30 ID NO: 1 and, optionally, (ii) one to six amino acids.

[0010] In some embodiments, the one to six amino acids are heterologous amino acids.

[0011] In some embodiments, the truncated hinge domain consists essentially of or consists of an amino acid sequence at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to amino acids 123 to 152 of SEQ ID NO: 1.

5 **[0012]** In some embodiments, the amino acid sequence is encoded by a nucleotide sequence at least about 60%, at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to SEQ ID NO: 2.

[0013] In some embodiments, the transmembrane domain is a transmembrane domain
10 of 4-1BB/CD137, an alpha chain of a T cell receptor, a beta chain of a T cell receptor, CD3 epsilon, CD4, CD5, CD8 alpha, CD9, CD16, CD19, CD22, CD33, CD37, CD45, CD64, CD80, CD86, CD134, CD137, CD154, or a zeta chain of a T cell receptor, or any combination thereof.

[0014] In some embodiments, the transmembrane domain comprises an amino acid
15 sequence at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to SEQ ID NO: 5.

[0015] In some embodiments, the transmembrane domain is encoded by a nucleotide
20 sequence at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to SEQ ID NO: 4.

[0016] In some embodiments, the intracellular domain comprises a signaling region of
4-1BB/CD137, activating NK cell receptors, B7-H3, BAFFR, BLAME (SLAMF8), BTLA, CD100 (SEMA4D), CD103, CD160 (BY55), CD18, CD19, CD19a, CD2, CD247, CD27, CD276 (B7-H3), CD29, CD3 delta, CD3 epsilon, CD3 gamma, CD30, CD4, CD40, CD49a, CD49D, CD49f, CD69, CD7, CD84, CD8alpha, CD8beta, CD96 (Tactile), CD11a, CD11b, CD11c, CD11d, CDS, CEACAM1, CRT AM, cytokine receptors, DAP-10, DNAM1 (CD226), Fc gamma receptor, GADS, GITR, HVEM (LIGHTR), IA4, ICAM-1, ICAM-1, Ig alpha (CD79a), IL2R beta, IL2R gamma, IL7R alpha, Immunoglobulin-like proteins, inducible T cell costimulator (ICOS), integrins, ITGA4, ITGA4, ITGA6, ITGAD, ITGAE, ITGAL, ITGAM, ITGAX, ITGB2, ITGB7, ITGB1, KIRDS2, LAT, LFA-1, LFA-1, a ligand that specifically
30 binds with CD83, LIGHT, LIGHT (tumor necrosis factor superfamily member 14; TNFSF14), LTBR, Ly9 (CD229), lymphocyte function-associated antigen-1 (LFA-1 (CD11a/CD18), MHC class I molecule, NKG2C, NKG2D, NKp30, NKp44, NKp46, NKp80 (KLRF1), OX-40,

PAG/Cbp, programmed death-1 (PD-1), PSGL1, SELPLG (CD162), signaling lymphocytic activation molecules (SLAM proteins), SLAM (SLAMF1; CD150; IPO-3), SLAMF4 (CD244; 2B4), SLAMF6 (NTB-A; Lyl08), SLAMF7, SLP-76, TNF receptor proteins, TNFR2, a Toll ligand receptor, TRANCE/RANKL, VLA1, or VLA-6, or a combination thereof.

5 [0017] In some embodiments, the intracellular domain comprises a 4-1BB/CD137 signaling region.

[0018] In some embodiments, the intracellular domain comprises an amino acid sequence at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical
10 to SEQ ID NO: 7.

[0019] In some embodiments, the intracellular domain comprises an amino acid sequence encoded by a nucleotide sequence at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to SEQ ID NO: 6.

15 [0020] In some embodiments, the antigen binding molecule comprises a heavy chain variable region (VH) and a light chain variable region (VL), wherein the VH comprises 3 complementarity determining regions (CDRs) and the VL comprises 3 CDRs.

[0021] In some embodiments, the antigen binding molecule specifically binds an antigen selected from the group consisting of 5T4, alphafetoprotein, B cell maturation antigen
20 (BCMA), CA-125, carcinoembryonic antigen, CD19, CD20, CD22, CD23, CD30, CD33, CD56, CD123, CD138, c-Met, CSPG4, C-type lectin-like molecule 1 (CLL-1), EGFRvIII, epithelial tumor antigen, ERBB2, FLT3, folate binding protein, GD2, GD3, HER1-HER2 in combination, HER2-HER3 in combination, HER2/Neu, HERV-K, HIV-1 envelope glycoprotein gp41, HIV-1 envelope glycoprotein gp120, IL-11Ralpha, kappa chain, lambda
25 chain, melanoma-associated antigen, mesothelin, MUC-1, mutated p53, mutated ras, prostate-specific antigen, ROR1, or VEGFR2, or a combination thereof.

[0022] In some embodiments, the antigen binding molecule specifically binds BCMA, CLL-1, or FLT3.

[0023] In some embodiments, the activation domain comprises an amino acid sequence
30 at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to SEQ ID NO: 9 or SEQ ID NO: 251.

[0024] In some embodiments, the activation domain is encoded by a nucleotide sequence at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to SEQ ID NO: 8.

5 [0025] In some embodiments, the CAR or TCR further comprises a leader peptide.

[0026] In some embodiments, the leader peptide comprises an amino acid sequence at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to SEQ ID NO: 11.

10 [0027] In some embodiments, the leader peptide is encoded by a nucleotide sequence at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to SEQ ID NO: 10.

[0028] Another aspect of the present invention is a vector comprising the
15 polynucleotide of an above aspect or embodiment.

[0029] In some embodiments, the vector is an adenoviral vector, an adenovirus-associated vector, a DNA vector, a lentiviral vector, a plasmid, a retroviral vector, or an RNA vector, or any combination thereof.

[0030] Yet another aspect of the present invention is a polypeptide encoded by the
20 polynucleotide of an above aspect or embodiment or the vector of an above aspect or embodiment.

[0031] In another aspect, the present invention is a cell comprising the polynucleotide of an above aspect or embodiment, the vector of an above aspect or embodiment, or the polypeptide of an above aspect or embodiment, or any combination thereof.

25 [0032] In some embodiments, the cell is a T cell.

[0033] In some embodiments, the T cell is an allogeneic T cell, an autologous T cell, an engineered autologous T cell (eACT™), or a tumor-infiltrating lymphocyte (TIL).

[0034] In some embodiments, the T cell is a CD4⁺ T cell.

[0035] In some embodiments, the T cell is a CD8⁺ T cell.

30 [0036] In some embodiments, the T cell is an *in vitro* cell.

[0037] In some embodiments, the T cell is an autologous T cell.

[0038] An aspect of the present invention is a composition comprising the polynucleotide of an above aspect or embodiment, comprising the vector of an above aspect or

embodiment, comprising the polypeptide of an above aspect or embodiment, or comprising the cell of an above aspect or embodiment.

[0039] In some embodiments, the composition is formulated to be delivered to a subject, optionally, comprising at least one pharmaceutically-acceptable excipient.

5 **[0040]** Another aspect of the present invention is a method of making a cell expressing a CAR or TCR comprising transducing a cell with the polynucleotide of an above aspect or embodiment under suitable conditions.

[0041] In some embodiments, the method further comprises isolating the cell.

[0042] Yet another aspect of the present invention is a method of inducing an immunity
10 against a tumor comprising administering to a subject an effective amount of a cell comprising the polynucleotide of an above aspect or embodiment, comprising the vector of an above aspect or embodiment, or the polypeptide of an above aspect or embodiment, or any combination thereof.

[0043] In another aspect, the present invention is a method of treating a cancer in a
15 subject in need thereof comprising administering to the subject the polynucleotide of an above aspect or embodiment, the vector of an above aspect or embodiment, the polypeptide of an above aspect or embodiment, the cell of an above aspect or embodiment, or the composition of an above aspect or embodiment.

[0044] In some embodiments, the cancer is a hematologic cancer.

20 **[0045]** In some embodiments, the cancer is of the white blood cells.

[0046] In some embodiments, the cancer is of the plasma cells.

[0047] In some embodiments, the cancer is leukemia, lymphoma, or myeloma.

[0048] In some embodiments, the cancer is acute lymphoblastic leukemia (ALL)
(including non T cell ALL), acute myeloid leukemia, B cell prolymphocytic leukemia, B-cell
25 acute lymphoid leukemia ("BALL"), blastic plasmacytoid dendritic cell neoplasm, Burkitt's lymphoma, chronic lymphocytic leukemia (CLL), chronic myelogenous leukemia (CML), chronic myeloid leukemia, chronic or acute leukemia, diffuse large B cell lymphoma (DLBCL), follicular lymphoma (FL), hairy cell leukemia, Hodgkin's Disease, malignant lymphoproliferative conditions, MALT lymphoma, mantle cell lymphoma, Marginal zone
30 lymphoma, monoclonal gammopathy of undetermined significance (MGUS), multiple myeloma, myelodysplasia and myelodysplastic syndrome, non-Hodgkin's lymphoma (NHL), plasma cell proliferative disorder (including asymptomatic myeloma (smoldering multiple myeloma or indolent myeloma), plasmablastic lymphoma, plasmacytoid dendritic cell

neoplasm, plasmacytomas (including plasma cell dyscrasia; solitary myeloma; solitary plasmacytoma; extramedullary plasmacytoma; and multiple plasmacytoma), POEMS syndrome (also known as Crow-Fukase syndrome; Takatsuki disease; and PEP syndrome), primary mediastinal large B cell lymphoma (PMBC), small cell- or a large cell-follicular lymphoma, splenic marginal zone lymphoma (SMZL), systemic amyloid light chain amyloidosis, T-cell acute lymphoid leukemia ("TALL"), T-cell lymphoma, transformed follicular lymphoma, or Waldenstrom macroglobulinemia, or a combination thereof.

[0049] Generally, the present invention relates to Engineered Autologous Cell Therapy, abbreviated as "eACT™," also known as adoptive cell transfer. eACT™, is a process by which a patient's own T cells are collected and subsequently genetically engineered to recognize and target one or more antigens expressed on the cell surface of one or more specific cancer cells. T cells may be engineered to express, for example, a CAR or TCR. CAR positive (CAR+) T cells are engineered to express a CAR. CARs may comprise, *e.g.*, an extracellular single chain variable fragment (scFv) with specificity for a particular tumor antigen, which is directly or indirectly linked to an intracellular signaling part comprising at least one costimulatory domain, which is directly or indirectly linked to at least one activating domain; the components may be arranged in any order. The costimulatory domain may be derived from a costimulatory protein known in the art, *e.g.*, SEQ ID NO: 1, and the activating domain may be derived from, *e.g.*, any form of CD3-zeta. In some embodiments, the CAR is designed to have two, three, four, or more costimulatory domains. In some embodiments, a CAR is engineered such that the costimulatory domain is expressed as a separate polypeptide chain. Examples of CAR T cell therapies and constructs are described in U.S. Patent Publication Nos. 2013/0287748, 2014/0227237, 2014/0099309, and 2014/0050708; International Patent Publications Nos. WO2012033885, WO2012079000, WO2014127261, WO2014186469, WO2015080981, WO2015142675, WO2016044745, and WO2016090369; and Sadelain *et al*, *Cancer Discovery*, 3: 388-398 (2013), each of which is incorporated by reference in its entirety.

[0050] Any aspect or embodiment described herein may be combined with any other aspect or embodiment as disclosed herein. While the present invention has been described in conjunction with the detailed description thereof, the foregoing description is intended to illustrate and not limit the scope of the present invention, which is defined by the scope of the appended claims. Other aspects, advantages, and modifications are within the scope of the following claims.

[0051] The patent and scientific literature referred to herein establishes the knowledge that is available to those with skill in the art. All United States patents and published or unpublished United States patent applications cited herein are incorporated by reference. All published foreign patents and patent applications cited herein are hereby incorporated by reference. All other published references, dictionaries, documents, manuscripts and scientific literature cited herein are hereby incorporated by reference.

[0052] Other features and advantages of the invention will be apparent from the Drawings and the following Detailed Description, including the Examples, and the claims.

BRIEF DESCRIPTION OF THE FIGURES

[0053] The above and further features will be more clearly appreciated from the following detailed description when taken in conjunction with the accompanying drawings. The drawings however are for illustration purposes only; not for limitation.

[0054] FIG. 1A shows a costimulatory protein having the amino acid sequence of SEQ ID NO: 1. The costimulatory protein's hinge domain (solid underline), transmembrane domain (dotted underline), and signaling domain (dashed underline) are labeled. A novel truncated hinge domain ("THD") is bolded. FIGs. 1B and 1C provide ribbon diagrams of the extracellular domain of the costimulatory protein having the amino acid sequence of SEQ ID NO: 1. FIG. 1B shows an example of a region within the amino acid sequence of SEQ ID NO: 1 used to derive one embodiment of a hinge region in the context of CAR, i.e., a region containing amino acids 114 to 152 of SEQ ID NO: 1 (herein referred to as a complete hinge domain or "CHD"; it is marked in black and dark grey). FIG. 1C shows the THD which contain amino acids 123 to 152 of SEQ ID NO: 1 (marked in black). In FIG. 1B, the portion of the hinge region that is excluded from FIG. 1C is marked dark grey and circled.

[0055] FIGs. 2A-2H show CLUTSTAL W (2.83) multiple sequence alignments of eight example binding molecules disclosed herein. FIG. 2A shows a sequence alignment of example anti-CLL-1 binding molecules comprising a VH domain. CDRs and framework regions FRs are shown, as determined by Chothia numbering (FIG. 2A). FIG. 2B is a table providing the SEQ ID NO for each VH and CDR illustrated in FIG. 2A. FIG. 2C shows a sequence alignment of example anti-CLL-1 binding molecules comprising a VL domain. CDRs and FRs are shown, as determined by Chothia numbering (FIG. 2C). FIG. 2D is a

table providing the SEQ ID NO for each VL and CDR sequence illustrated in FIG. 2C. FIG. 2E shows a sequence alignment of example anti-BCMA binding molecules comprising a VH domain. Complementarity determining regions (CDRs) and framework regions (FRs) are shown, as determined by Chothia numbering (FIG. 2E). SEQ ID NOS 253-260, CDR1 in order from top to bottom; SEQ ID NOS 261-268, CDR2 from top to bottom, SEQ ID NOS 269-276, CDR3 from top to bottom. FIG. 2F is a table providing the SEQ ID NO for each VH and CDR numbered by an alternative method. FIG. 2G shows a sequence alignment of example anti-BCMA binding molecules comprising a VL domain. CDRs and FRs are shown, as determined by Chothia numbering (FIG. 2G). SEQ ID NOS 37-44, CDR1 in order from top to bottom; SEQ ID NOS 45-52, CDR2 from top to bottom, SEQ ID NOS 277-284, CDR3 from top to bottom. FIG. 2H is a table providing the SEQ ID NO for each VL and CDR sequence numbered by an alternative method..

[0056] FIG. 3 depicts CAR expression in primary human T cells electroporated with mRNA encoding for various CARs. Data obtained from CAR having a complete hinge domain (“CHD”) is shown and data obtained from CAR having a truncated hinge domain (“THD”) is shown.

[0057] FIGs. 4A-4X show IFN γ , IL-2, and TNF α production by electroporated anti-FLT3 CAR T cells following 16 hours of co-culture with the indicated target cell lines. FIGs. 4A-4B, 4G-4H, 4M-4N, and 4S-4T show IFN γ production following co-culture with Namalwa, EoL-1, HL60, and MV4;11 target cells, respectively. FIGs. 4C-4D, 4I-4J, 4O-4P, and 4U-4V show IL-2 production following co-culture with Namalwa, EoL-1, HL60, and MV4;11 target cells, respectively. FIGs. 4E-4F, 4K-4L, 4Q-4R, and 4W-4X show TNF α production following co-culture with Namalwa, EoL-1, HL60, and MV4;11 target cells, respectively.

[0058] FIGs. 5A-5H show cytolytic activity of electroporated anti-FLT3 CAR T cells against Namalwa (FIGs. 5A-5B), EoL1 (FIGs. 5C-5D), HL60 (FIGs. 5E-5F), and MV4;11 (FIGs. 5G-5H) target cell lines following 16 hours of co-culture.

[0059] FIGs. 6A-6B depict CAR expression in lentivirus transduced primary human T cells from two healthy donors.

[0060] FIGs. 7A-7F show IFN γ (FIGs. 7A-7B), TNF α (FIGs. 7C-7D), and IL-2 (FIGs. 7E-7F) production by lentivirus transduced CAR T cells from two healthy donors following 16 hours of co-culture with the indicated target cell lines.

[0061] FIGs. 8A-8D show the average cytolytic activity over time from two healthy donors expressing the anti-FLT3 CAR constructs co-cultured with Namalwa (FIG. 8A), EoL1 (FIG. 8B), MV4;11 (FIG. 8C), and HL60 (FIG. 8D) target cell lines for 16, 40, 64, 88, or 112 hours.

[0062] FIGs. 9A-9B depict proliferation of CFSE-labeled lentivirus transduced CAR T cells from two healthy donors following 5 days of co-culture with CD3-CD28 beads or the indicated target cell lines.

[0063] FIGs. 10A-10D depict CAR expression in lentivirus transduced primary human T cells used for *in vivo* studies. FIGs. 10E-10F show graphical representations of measured bioluminescence imaging of labeled acute myeloid leukemia (AML) cells following intravenous injection of either control (mock) or anti-FLT3 CAR T cells (10E3-CHD, 10E3-THD, or 8B5-THD) in a xenogeneic model, performed in duplicate. FIG. 10G provides the p-values for the respective data points in FIG. 10E. FIGs. 10H-10K show survival curves of mice injected with mock or 10E3-CHD (FIG. 10H), mock or 10E3-THD (FIG. 10I), mock or 8B5-THD (FIG. 10J), or 10E3-THD or 8B5-THD (FIG. 10K) CAR T cells.

[0064] FIGs. 11A-11B shows CLL-1 CAR expression determined by protein L 6 hours post mRNA electroporation.

[0065] FIGs. 12A-12C show the results from a cytokine release assay from different CLL-1 CAR-T cell constructs 24 hours after mRNA electroporation. IL-2 (FIG. 12A), IFN γ (FIG. 12B), and TNF α (FIG. 12C) production levels are shown for controls (target alone, mock, GFP, and CD19 CAR T cells) and anti-CLL-1 CAR T cells (24C1_HL-THD, 24C1_HL_CHD, 24C8_HL-CHD, and 24C8_HL_THD) co-cultured with Namalwa, MV4;11, U937, HL60, and EoL-1 cells, as indicated.

[0066] FIGs. 13A-13E show cytolytic activity of different CLL-1 CAR-T cell constructs 24 hours after mRNA electroporation. T cells electroporated with control constructs (mock, GFP, and CD19 CAR) or anti-CLL-1 CAR constructs (24C8_HL-CHD and 24C8_HL_THD) were co-cultured with Namalwa (FIG. 13A), MV;411 (FIG. 13B), EoL-1 (FIG. 13C), HL-60 (FIG. 13D), and U937 target cells, and the percent of specific lysis of each target cell line was determined.

[0067] FIGs. 14A-14C show the results from a cytokine release assay from different transduced anti-CLL-1 CAR T cells 16 hours after co-culture with different cell lines. IFN γ (FIG. 14A), IL-2 (FIG. 14B), and TNF α (FIG. 14C) production levels are shown for controls (target alone and mock) and transduced anti-CLL-1 CAR T cells (10E3_THD and 24C1_LH_THD) co-cultured with Namalwa, HL-60, or MV4;11 target cells, as indicated.

[0068] FIGs. 15A-15C show cytolytic activity from anti-CLL-1 CAR T cells (C1_24C1_LH_THD) 16 hours and 40 hours after co-culture with Namalwa (FIG. 15A), MV4;11 (FIG. 15B), or HL-60 (FIG. 15C) target cells.

5 [0069] FIGs 16A-16F shows IFN γ , TNF α , and IL-2 production by lentivirus transduced CAR T cells from two healthy donors following 16 hours of co-cultured with EoL-1 (Black), NCI-H929 (light grey), or MM1S (grey) target cell lines. FIGs. 16A and 16B show the IFN γ (pg/ml; y-axis) production in lentivirus transduced CAR T cells from a first donor (FIG. 6A) and a second donor (FIG. 16B). FIGs. 16C and 16D show the TNF α (pg/ml; y-axis) production in lentivirus transduced CAR T cells from a first donor (FIG. 16C) and a second donor (FIG. 16D). FIGs. 16E and 16F show the IL-2 production (pg/ml; y-axis) in lentivirus transduced CAR T cells from a first donor (FIG. 16E) and a second donor (FIG. 16F).

10 [0070] FIGs. 17A-17F show the average cytolytic activity (as a percentage of viable target cells remaining; y-axis) over time from two healthy donors expressing the indicated CARs co-cultured with EoL1 (FIGs. 17A and 17B), NCI-H929 (FIGs. 17C and 17D), or MM1S (FIGs. 17E and 17F) target cells for 16 hours, 40 hours, 64 hours, 88 hours, or 112 hours. FIGs. 17A and 17B show the average cytolytic activity of transduced CAR T cells from a first donor (FIG. 17A) and a second donor (FIG. 17B) co-cultured with EoL1 target cells for 16 hours, 40 hours, 64 hours, 88 hours, or 112 hours. FIGs. 17C and 17D show the average cytolytic activity of transduced CAR T cells from a first donor (FIG. 17C) and a second donor (FIG. 17D) co-cultured with NCI-H929 target cells for 16 hours, 40 hours, 64 hours, 88 hours, or 112 hours. FIGs. 17E and 17F show the average cytolytic activity of transduced CAR T cells from a first donor (FIG. 17E) and a second donor (FIG. 17F) co-cultured with MM1S target cells for 16 hours, 40 hours, 64 hours, 88 hours, or 112 hours.

20 [0071] FIGs. 18A and 18B show proliferation of CFSE-labeled lentivirus transduced CAR T cells from a first healthy donor (FIG. 18A) and a second healthy donor (FIG. 18B) following 6 days of co-culture with CD3-CD28 beads (top row), EoL-1 (second row), NCI-H929 (third row), or MM1S (bottom row) target cell lines.

25 [0072] FIG 19A and FIG. 19B are graphs showing thermostability of chimeric antigen receptors (CARs) of the present invention. FIG. 19A: In a phosphate-buffered saline (PBS) solution, a CAR comprising an extracellular domain with a truncated hinge domain (“THD”) has a higher melting temperature relative to a CAR comprising an extracellular domain with a complete hinge domain (“CHD”). FIG. 19B: In the presence of 50 mM NaCl, a CAR comprising an extracellular domain with a THD has a higher melting temperature relative to a CAR comprising an extracellular domain with a CHD.

30 FIG. 20 is a schematic representation of the pGAR vector.

DETAILED DESCRIPTION OF THE INVENTION

[0073] The present invention relates to novel polypeptides comprising a novel truncated hinge domain (“THD”) and polynucleotides encoding the same. Some aspects of the invention relate to a polynucleotide encoding a chimeric antigen receptor (CAR) or a T cell receptor (TCR) comprising the THD disclosed herein. The present invention also provides vectors (*e.g.*, viral vectors) comprising such polynucleotides and compositions comprising such vectors. The present invention further provides polynucleotides encoding such CARs or TCRs and compositions comprising such polynucleotides. The present invention additionally provides engineered cells (*e.g.*, T cells) comprising such polynucleotides and/or transduced with such viral vectors and compositions comprising such engineered cells. The present invention provides compositions (*e.g.*, pharmaceutical compositions) including a plurality of engineered T cells. The present invention provides methods for manufacturing such engineered T cells and compositions and uses (*e.g.*, in treating a melanoma) of such engineered T cells and compositions. And, the present invention provides a method of inducing an immunity against a tumor comprising administering to a subject an effective amount of a cell comprising a polynucleotide, a vector, or a polypeptide of the present invention. Other aspects of the invention relate to cells comprising the CAR or the TCR and their use in a T cell therapy, *e.g.*, an autologous cell therapy (eACT™), for the treatment of a patient suffering from a cancer.

DEFINITIONS

[0074] In order for the present invention to be more readily understood, certain terms are first defined below. Additional definitions for the following terms and other terms are set forth throughout the Specification.

[0075] As used in this Specification and the appended claims, the singular forms “a,” “an” and “the” include plural referents unless the context clearly dictates otherwise.

[0076] Unless specifically stated or obvious from context, as used herein, the term “or” is understood to be inclusive and covers both “or” and “and”.

[0077] The term “and/or” where used herein is to be taken as specific disclosure of each of the two specified features or components with or without the other. Thus, the term “and/or” as used in a phrase such as “A and/or B” herein is intended to include A and B; A or B; A (alone); and B (alone). Likewise, the term “and/or” as used in a phrase such as “A, B, and/or

C” is intended to encompass each of the following aspects: A, B, and C; A, B, or C; A or C; A or B; B or C; A and C; A and B; B and C; A (alone); B (alone); and C (alone).

[0078] The terms “*e.g.*,” and “*i.e.*” as used herein, are used merely by way of example, without limitation intended, and should not be construed as referring only those items explicitly enumerated in the specification.

[0079] The terms “or more”, “at least”, “more than”, and the like, *e.g.*, “at least one” are understood to include but not be limited to at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 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, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149 or 150, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 2000, 3000, 4000, 5000 or more than the stated value. Also included is any greater number or fraction in between.

[0080] Conversely, the term “no more than” includes each value less than the stated value. For example, “no more than 100 nucleotides” includes 100, 99, 98, 97, 96, 95, 94, 93, 92, 91, 90, 89, 88, 87, 86, 85, 84, 83, 82, 81, 80, 79, 78, 77, 76, 75, 74, 73, 72, 71, 70, 69, 68, 67, 66, 65, 64, 63, 62, 61, 60, 59, 58, 57, 56, 55, 54, 53, 52, 51, 50, 49, 48, 47, 46, 45, 44, 43, 42, 41, 40, 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1, and 0 nucleotides. Also included is any lesser number or fraction in between.

[0081] The terms “plurality”, “at least two”, “two or more”, “at least second”, and the like, are understood to include but not limited to at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 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, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149 or 150, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 2000, 3000, 4000, 5000 or more. Also included is any greater number or fraction in between.

[0082] Throughout the specification the word “comprising,” or variations such as “comprises” or “comprising,” will be understood to imply the inclusion of a stated element, integer or step, or group of elements, integers or steps, but not the exclusion of any other element, integer or step, or group of elements, integers or steps. It is understood that wherever aspects are described herein with the language “comprising,” otherwise analogous aspects described in terms of “consisting of” and/or “consisting essentially of” are also provided.

[0083] Unless specifically stated or evident from context, as used herein, the term “about” refers to a value or composition that is within an acceptable error range for the particular value or composition as determined by one of ordinary skill in the art, which will depend in part on how the value or composition is measured or determined, *i.e.*, the limitations of the measurement system. For example, “about” or “comprising essentially of” can mean within one or more than one standard deviation per the practice in the art. “About” or “comprising essentially of” can mean a range of up to 10% (*i.e.*, $\pm 10\%$). Thus, “about” can be understood to be within 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1%, 0.5%, 0.1%, 0.05%, 0.01%, or 0.001% greater or less than the stated value. For example, about 5 mg can include any amount between 4.5 mg and 5.5 mg. Furthermore, particularly with respect to biological systems or processes, the terms can mean up to an order of magnitude or up to 5-fold of a value. When particular values or compositions are provided in the instant disclosure, unless otherwise stated, the meaning of “about” or “comprising essentially of” should be assumed to be within an acceptable error range for that particular value or composition.

[0084] As described herein, any concentration range, percentage range, ratio range or integer range is to be understood to be inclusive of the value of any integer within the recited range and, when appropriate, fractions thereof (such as one-tenth and one-hundredth of an integer), unless otherwise indicated.

[0085] Units, prefixes, and symbols used herein are provided using their Système International de Unites (SI) accepted form. Numeric ranges are inclusive of the numbers defining the range.

[0086] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this disclosure is related. For example, Juo, “The Concise Dictionary of Biomedicine and Molecular Biology”, 2nd ed., (2001), CRC Press; “The Dictionary of Cell & Molecular Biology”, 5th ed., (2013), Academic Press; and “The Oxford Dictionary Of Biochemistry And

Molecular Biology”, Cammack *et al.* eds., 2nd ed, (2006), Oxford University Press, provide those of skill in the art with a general dictionary for many of the terms used in this disclosure.

[0087] “Administering” refers to the physical introduction of an agent to a subject, using any of the various methods and delivery systems known to those skilled in the art.

5 Exemplary routes of administration for the formulations disclosed herein include intravenous, intramuscular, subcutaneous, intraperitoneal, spinal or other parenteral routes of administration, for example by injection or infusion. The phrase “parenteral administration” as used herein means modes of administration other than enteral and topical administration, usually by injection, and includes, without limitation, intravenous, intramuscular, intraarterial, 10 intrathecal, intralymphatic, intralesional, intracapsular, intraorbital, intracardiac, intradermal, intraperitoneal, transtracheal, subcutaneous, subcuticular, intraarticular, subcapsular, subarachnoid, intraspinal, epidural and intrasternal injection and infusion, as well as *in vivo* electroporation. In some embodiments, the formulation is administered via a non-parenteral route, *e.g.*, orally. Other non-parenteral routes include a topical, epidermal or mucosal route of 15 administration, for example, intranasally, vaginally, rectally, sublingually or topically. Administering can also be performed, for example, once, a plurality of times, and/or over one or more extended periods.

[0088] The term “antibody” (Ab) includes, without limitation, a glycoprotein immunoglobulin which binds specifically to an antigen. In general, an antibody can comprise 20 at least two heavy (H) chains and two light (L) chains interconnected by disulfide bonds, or an antigen-binding molecule thereof. Each H chain comprises a heavy chain variable region (abbreviated herein as VH) and a heavy chain constant region. The heavy chain constant region comprises three constant domains, CH1, CH2 and CH3. Each light chain comprises a light chain variable region (abbreviated herein as VL) and a light chain constant region. The light 25 chain constant region comprises one constant domain, CL. The VH and VL regions can be further subdivided into regions of hypervariability, termed complementarity determining regions (CDRs), interspersed with regions that are more conserved, termed framework regions (FR). Each VH and VL comprises three CDRs and four FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, and FR4. The 30 variable regions of the heavy and light chains contain a binding domain that interacts with an antigen. The constant regions of the Abs may mediate the binding of the immunoglobulin to

host tissues or factors, including various cells of the immune system (*e.g.*, effector cells) and the first component (C1q) of the classical complement system.

[0089] Antibodies can include, for example, monoclonal antibodies, recombinantly produced antibodies, monospecific antibodies, multispecific antibodies (including bispecific antibodies), human antibodies, engineered antibodies, humanized antibodies, chimeric antibodies, immunoglobulins, synthetic antibodies, tetrameric antibodies comprising two heavy chain and two light chain molecules, an antibody light chain monomer, an antibody heavy chain monomer, an antibody light chain dimer, an antibody heavy chain dimer, an antibody light chain- antibody heavy chain pair, intrabodies, antibody fusions (sometimes referred to herein as “antibody conjugates”), heteroconjugate antibodies, single domain antibodies, monovalent antibodies, single chain antibodies or single-chain Fvs (scFv), camelized antibodies, affibodies, Fab fragments, F(ab')₂ fragments, disulfide-linked Fvs (sdFv), anti-idiotypic (anti-Id) antibodies (including, *e.g.*, anti-anti-Id antibodies), minibodies, domain antibodies, synthetic antibodies (sometimes referred to herein as “antibody mimetics”), and antigen-binding fragments of any of the above. In certain embodiments, antibodies described herein refer to polyclonal antibody populations.

[0090] An immunoglobulin may derive from any of the commonly known isotypes, including but not limited to IgA, secretory IgA, IgG, IgE and IgM. IgG subclasses are also well known to those in the art and include but are not limited to human IgG1, IgG2, IgG3 and IgG4. “Isotype” refers to the Ab class or subclass (*e.g.*, IgM or IgG1) that is encoded by the heavy chain constant region genes. The term “antibody” includes, by way of example, both naturally occurring and non-naturally occurring Abs; monoclonal and polyclonal Abs; chimeric and humanized Abs; human or nonhuman Abs; wholly synthetic Abs; and single chain Abs. A nonhuman Ab may be humanized by recombinant methods to reduce its immunogenicity in man. Where not expressly stated, and unless the context indicates otherwise, the term “antibody” also includes an antigen-binding fragment or an antigen-binding portion of any of the aforementioned immunoglobulins, and includes a monovalent and a divalent fragment or portion, and a single chain Ab.

[0091] An “antigen binding molecule,” “antigen binding portion,” or “antibody fragment” refers to any molecule that comprises the antigen binding parts (*e.g.*, CDRs) of the antibody from which the molecule is derived. An antigen binding molecule can include the antigenic complementarity determining regions (CDRs). Examples of antibody fragments include, but are not limited to, Fab, Fab', F(ab')₂, and Fv fragments, dAb, linear antibodies,

scFv antibodies, and multispecific antibodies formed from antigen binding molecules. Peptibodies (i.e., Fc fusion molecules comprising peptide binding domains) are another example of suitable antigen binding molecules. In some embodiments, the antigen binding molecule binds to an antigen on a tumor cell. In some embodiments, the antigen binding molecule binds to an antigen on a cell involved in a hyperproliferative disease or to a viral or bacterial antigen. In certain embodiments, the antigen binding molecule binds to BCMA, CLL-1, or FLT3. In further embodiments, the antigen binding molecule is an antibody fragment that specifically binds to the antigen, including one or more of the complementarity determining regions (CDRs) thereof. In further embodiments, the antigen binding molecule is a single chain variable fragment (scFv). In some embodiments, the antigen binding molecule comprises or consists of avimers.

[0092] As used herein, the term “variable region” or “variable domain” is used interchangeably and are common in the art. The variable region typically refers to a portion of an antibody, generally, a portion of a light or heavy chain, typically about the amino-terminal 110 to 120 amino acids in the mature heavy chain and about 90 to 115 amino acids in the mature light chain, which differ extensively in sequence among antibodies and are used in the binding and specificity of a particular antibody for its particular antigen. The variability in sequence is concentrated in those regions called complementarity determining regions (CDRs) while the more highly conserved regions in the variable domain are called framework regions (FR). Without wishing to be bound by any particular mechanism or theory, it is believed that the CDRs of the light and heavy chains are primarily responsible for the interaction and specificity of the antibody with antigen. In certain embodiments, the variable region is a human variable region. In certain embodiments, the variable region comprises rodent or murine CDRs and human framework regions (FRs). In particular embodiments, the variable region is a primate (*e.g.*, non-human primate) variable region. In certain embodiments, the variable region comprises rodent or murine CDRs and primate (*e.g.*, non-human primate) framework regions (FRs).

[0093] The terms “VL” and “VL domain” are used interchangeably to refer to the light chain variable region of an antibody or an antigen-binding molecule thereof.

[0094] The terms “VH” and “VH domain” are used interchangeably to refer to the heavy chain variable region of an antibody or an antigen-binding molecule thereof.

[0095] A number of definitions of the CDRs are commonly in use: Kabat numbering, Chothia numbering, AbM numbering, or contact numbering. The AbM definition is a

compromise between the two used by Oxford Molecular's AbM antibody modelling software. The contact definition is based on an analysis of the available complex crystal structures.

[0096] Table 1. CDR Numbering

Loop	Kabat	AbM	Chothia	Contact
L1	L24--L34	L24--L34	L24--L34	L30--L36
L2	L50--L56	L50--L56	L50--L56	L46--L55
L3	L89--L97	L89--L97	L89--L97	L89--L96
H1	H31--H35B (Kabat Numbering)	H26--H35B	H26--H32..34	H30--H35B
H1	H31--H35 (Chothia Numbering)	H26--H35	H26--H32	H30--H35
H2	H50--H65	H50--H58	H52--H56	H47--H58
H3	H95--H102	H95--H102	H95--H102	H93--H101

[0097] The term "Kabat numbering" and like terms are recognized in the art and refer to a system of numbering amino acid residues in the heavy and light chain variable regions of an antibody, or an antigen-binding molecule thereof. In certain aspects, the CDRs of an antibody can be determined according to the Kabat numbering system (*see, e.g.,* Kabat EA & Wu TT (1971) Ann NY Acad Sci 190: 382-391 and Kabat EA *et al.*, (1991) Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242). Using the Kabat numbering system, CDRs within an antibody heavy chain molecule are typically present at amino acid positions 31 to 35, which optionally can include one or two additional amino acids, following 35 (referred to in the Kabat numbering scheme as 35A and 35B) (CDR1), amino acid positions 50 to 65 (CDR2), and amino acid positions 95 to 102 (CDR3). Using the Kabat numbering system, CDRs within an antibody light chain molecule are typically present at amino acid positions 24 to 34 (CDR1), amino acid positions 50 to 56 (CDR2), and amino acid positions 89 to 97 (CDR3). In a specific

embodiment, the CDRs of the antibodies described herein have been determined according to the Kabat numbering scheme.

[0098] In certain aspects, the CDRs of an antibody can be determined according to the Chothia numbering scheme, which refers to the location of immunoglobulin structural loops (see, e.g., Chothia C & Lesk AM, (1987), J Mol Biol 196: 901-917; Al-Lazikani B *et al.*, (1997) J Mol Biol 273: 927-948; Chothia C *et al.*, (1992) J Mol Biol 227: 799-817; Tramontano A *et al.*, (1990) J Mol Biol 215(1): 175-82; and U.S. Patent No. 7,709,226). Typically, when using the Kabat numbering convention, the Chothia CDR-H1 loop is present at heavy chain amino acids 26 to 32, 33, or 34, the Chothia CDR-H2 loop is present at heavy chain amino acids 52 to 56, and the Chothia CDR-H3 loop is present at heavy chain amino acids 95 to 102, while the Chothia CDR-L1 loop is present at light chain amino acids 24 to 34, the Chothia CDR-L2 loop is present at light chain amino acids 50 to 56, and the Chothia CDR-L3 loop is present at light chain amino acids 89 to 97. The end of the Chothia CDR-H1 loop when numbered using the Kabat numbering convention varies between H32 and H34 depending on the length of the loop (this is because the Kabat numbering scheme places the insertions at H35A and H35B; if neither 35A nor 35B is present, the loop ends at 32; if only 35A is present, the loop ends at 33; if both 35A and 35B are present, the loop ends at 34). In a specific embodiment, the CDRs of the antibodies described herein have been determined according to the Chothia numbering scheme.

[0099] As used herein, the terms “constant region” and “constant domain” are interchangeable and have a meaning common in the art. The constant region is an antibody portion, e.g., a carboxyl terminal portion of a light and/or heavy chain which is not directly involved in binding of an antibody to antigen but which can exhibit various effector functions, such as interaction with the Fc receptor. The constant region of an immunoglobulin molecule generally has a more conserved amino acid sequence relative to an immunoglobulin variable domain.

[0100] As used herein, the term “heavy chain” when used in reference to an antibody can refer to any distinct type, e.g., alpha (α), delta (δ), epsilon (ϵ), gamma (γ) and mu (μ), based on the amino acid sequence of the constant domain, which give rise to IgA, IgD, IgE, IgG and IgM classes of antibodies, respectively, including subclasses of IgG, e.g., IgG₁, IgG₂, IgG₃ and IgG₄.

[0101] As used herein, the term “light chain” when used in reference to an antibody can refer to any distinct type, e.g., kappa (κ) or lambda (λ) based on the amino acid sequence

of the constant domains. Light chain amino acid sequences are well known in the art. In specific embodiments, the light chain is a human light chain.

[0102] “Binding affinity” generally refers to the strength of the sum total of non-covalent interactions between a single binding site of a molecule (*e.g.*, an antibody) and its binding partner (*e.g.*, an antigen). Unless indicated otherwise, as used herein, “binding affinity” refers to intrinsic binding affinity which reflects a 1:1 interaction between members of a binding pair (*e.g.*, antibody and antigen). The affinity of a molecule X for its partner Y can generally be represented by the dissociation constant (K_D). Affinity can be measured and/or expressed in a number of ways known in the art, including, but not limited to, equilibrium dissociation constant (K_D), and equilibrium association constant (K_A). The K_D is calculated from the quotient of k_{off}/k_{on} , whereas K_A is calculated from the quotient of k_{on}/k_{off} . k_{on} refers to the association rate constant of, *e.g.*, an antibody to an antigen, and k_{off} refers to the dissociation of, *e.g.*, an antibody to an antigen. The k_{on} and k_{off} can be determined by techniques known to one of ordinary skill in the art, such as BIACORE® or KinExA.

[0103] As used herein, a “conservative amino acid substitution” is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine, tryptophan), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). In certain embodiments, one or more amino acid residues within a CDR(s) or within a framework region(s) of an antibody or antigen-binding molecule thereof can be replaced with an amino acid residue with a similar side chain.

[0104] As, used herein, the term “heterologous” means from any source other than naturally occurring sequences. For example, a heterologous sequence included as a part of a costimulatory protein having the amino acid sequence of SEQ ID NO: 1, *e.g.*, the corresponding human costimulatory protein, is amino acids that do not naturally occur as, *i.e.*, do not align with, the wild type human costimulatory protein. For example, a heterologous nucleotide sequence refers to a nucleotide sequence other than that of the wild type human costimulatory protein-encoding sequence.

[0105] As used herein, an “epitope” is a term in the art and refers to a localized region of an antigen to which an antibody can specifically bind. An epitope can be, for example, contiguous amino acids of a polypeptide (linear or contiguous epitope) or an epitope can, for example, come together from two or more non-contiguous regions of a polypeptide or polypeptides (conformational, non-linear, discontinuous, or non-contiguous epitope). In certain embodiments, the epitope to which an antibody binds can be determined by, *e.g.*, NMR spectroscopy, X-ray diffraction crystallography studies, ELISA assays, hydrogen/deuterium exchange coupled with mass spectrometry (*e.g.*, liquid chromatography electrospray mass spectrometry), array-based oligo-peptide scanning assays, and/or mutagenesis mapping (*e.g.*, site-directed mutagenesis mapping). For X-ray crystallography, crystallization may be accomplished using any of the known methods in the art (*e.g.*, Giegé R *et al.*, (1994) *Acta Crystallogr D Biol Crystallogr* 50(Pt 4): 339-350; McPherson A (1990) *Eur J Biochem* 189: 1-23; Chayen NE (1997) *Structure* 5: 1269-1274; McPherson A (1976) *J Biol Chem* 251: 6300-6303). Antibody:antigen crystals may be studied using well known X-ray diffraction techniques and may be refined using computer software such as X-PLOR (Yale University, 1992, distributed by Molecular Simulations, Inc.; see *e.g.* *Meth Enzymol* (1985) volumes 114 & 115, eds Wyckoff HW *et al.*,; U.S. 2004/0014194), and BUSTER (Bricogne G (1993) *Acta Crystallogr D Biol Crystallogr* 49(Pt 1): 37-60; Bricogne G (1997) *Meth Enzymol* 276A: 361-423, ed Carter CW; Roversi P *et al.*, (2000) *Acta Crystallogr D Biol Crystallogr* 56(Pt 10): 1316-1323). Mutagenesis mapping studies may be accomplished using any method known to one of skill in the art. *See, e.g.*, Champe M *et al.*, (1995) *J Biol Chem* 270: 1388-1394 and Cunningham BC & Wells JA (1989) *Science* 244: 1081-1085 for a description of mutagenesis techniques, including alanine scanning mutagenesis techniques.

[0106] As used herein, an antigen binding molecule, an antibody, or an antigen binding molecule thereof “cross-competes” with a reference antibody or an antigen binding molecule thereof if the interaction between an antigen and the first binding molecule, an antibody, or an antigen binding molecule thereof blocks, limits, inhibits, or otherwise reduces the ability of the reference binding molecule, reference antibody, or an antigen binding molecule thereof to interact with the antigen. Cross competition can be complete, *e.g.*, binding of the binding molecule to the antigen completely blocks the ability of the reference binding molecule to bind the antigen, or it can be partial, *e.g.*, binding of the binding molecule to the antigen reduces the ability of the reference binding molecule to bind the antigen. In certain embodiments, an antigen binding molecule that cross-competes with a reference antigen binding molecule binds

the same or an overlapping epitope as the reference antigen binding molecule. In other embodiments, the antigen binding molecule that cross-competes with a reference antigen binding molecule binds a different epitope as the reference antigen binding molecule. Numerous types of competitive binding assays can be used to determine if one antigen binding molecule competes with another, for example: solid phase direct or indirect radioimmunoassay (RIA); solid phase direct or indirect enzyme immunoassay (EIA); sandwich competition assay (Stahli et al., 1983, Methods in Enzymology 9:242-253); solid phase direct biotin-avidin EIA (Kirkland et al., 1986, J. Immunol. 137:3614-3619); solid phase direct labeled assay, solid phase direct labeled sandwich assay (Harlow and Lane, 1988, Antibodies, A Laboratory Manual, Cold Spring Harbor Press); solid phase direct label RIA using 1-125 label (Morel et al., 1988, Molec. Immunol. 25:7-15); solid phase direct biotin-avidin EIA (Cheung, et al., 1990, Virology 176:546-552); and direct labeled RIA (Moldenhauer et al., 1990, Scand. J. Immunol. 32:77-82).

[0107] As used herein, the terms “immunospecifically binds,” “immunospecifically recognizes,” “specifically binds,” and “specifically recognizes” are analogous terms in the context of antibodies and refer to molecules that bind to an antigen (*e.g.*, epitope or immune complex) as such binding is understood by one skilled in the art. For example, a molecule that specifically binds to an antigen may bind to other peptides or polypeptides, generally with lower affinity as determined by, *e.g.*, immunoassays, BIACORE[®], KinExA 3000 instrument (Sapidyne Instruments, Boise, ID), or other assays known in the art. In a specific embodiment, molecules that specifically bind to an antigen bind to the antigen with a K_A that is at least 2 logs, 2.5 logs, 3 logs, 4 logs or greater than the K_A when the molecules bind to another antigen.

[0108] In another embodiment, molecules that specifically bind to an antigen bind with a dissociation constant (K_d) of about 1×10^{-7} M. In some embodiments, the antigen binding molecule specifically binds an antigen with “high affinity” when the K_d is about 1×10^{-9} M to about 5×10^{-9} M. In some embodiments, the antigen binding molecule specifically binds an antigen with “very high affinity” when the K_d is 1×10^{-10} M to about 5×10^{-10} M. In one embodiment, the antigen binding molecule has a K_d of 10^{-9} M. In one embodiment, the off-rate is less than about 1×10^{-5} . In other embodiments, the antigen binding molecule binds human BCMA with a K_d of between about 1×10^{-7} M and about 1×10^{-13} M. In yet another embodiment, the antigen binding molecule binds human BCMA with a K_d of about 1×10^{-10} M to about 5×10^{-10} M.

[0109] In a specific embodiment, provided herein is an antibody or an antigen binding molecule thereof that binds to a target human antigen, *e.g.*, human BCMA or human CLL-1, with higher affinity than to another species of the target antigen, *e.g.*, a non-human BCMA or a non-human CLL-1. In certain embodiments, provided herein is an antibody or an antigen binding molecule t thereof that binds to the target human antigen, *e.g.*, human BCMA or human CLL-1, with a 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70% or higher affinity than to another species of the target antigen as measured by, *e.g.*, a radioimmunoassay, surface plasmon resonance, or kinetic exclusion assay. In a specific embodiment, an antibody or an antigen binding molecule thereof described herein, which binds to a target human antigen, will bind to another species of the target antigen with less than 10%, 15%, or 20% of the binding of the antibody or an antigen binding molecule thereof to the human antigen as measured by, *e.g.*, a radioimmunoassay, surface plasmon resonance, or kinetic exclusion assay.

[0110] An “antigen” refers to any molecule that provokes an immune response or is capable of being bound by an antibody or an antigen binding molecule. The immune response may involve either antibody production, or the activation of specific immunologically-competent cells, or both. A person of skill in the art would readily understand that any macromolecule, including virtually all proteins or peptides, can serve as an antigen. An antigen can be endogenously expressed, *i.e.* expressed by genomic DNA, or can be recombinantly expressed. An antigen can be specific to a certain tissue, such as a cancer cell, or it can be broadly expressed. In addition, fragments of larger molecules can act as antigens. In one embodiment, antigens are tumor antigens. In one particular embodiment, the antigen is all or a fragment of BCMA, FLT3, or CLL-1.

[0111] The term “neutralizing” refers to an antigen binding molecule, scFv, antibody, or a fragment thereof, that binds to a ligand and prevents or reduces the biological effect of that ligand. In some embodiments, the antigen binding molecule, scFv, antibody, or a fragment thereof, directly blocking a binding site on the ligand or otherwise alters the ligand's ability to bind through indirect means (such as structural or energetic alterations in the ligand). In some embodiments, the antigen binding molecule, scFv, antibody, or a fragment thereof prevents the protein to which it is bound from performing a biological function.

[0112] As used herein, the term “BCMA” refers to B cell maturation antigen, which can include, but is not limited to, native BCMA, an isoform of BCMA, or an interspecies BCMA homolog of BCMA. BCMA (also known as TNFRSF17, CD269, and TNFRSF13A) is

a member of the tumor necrosis factor (TNF)-receptor superfamily. BCMA is expressed on the surface of multiple myeloma cells, while highly restricted to plasma cells and a subset of mature B cells in healthy tissue. The amino acid sequence of human BCMA (hBCMA) is provided in NCBI Accession Q02223.2 (GI:313104029). As used herein, BCMA includes human BCMA and non-human BCMA homologs, as well as variants, fragments, or post-transnationally modified forms thereof, including, but not limited to, N- and O-linked glycosylated forms of BCMA. BCMA proteins may further include fragments comprising all or a portion of the extracellular domain of BCMA (*e.g.*, all or a portion of amino acids 1-54 of hBCMA).

[0113] As used herein, the term “CLL-1” refers to C-type lectin-like molecule-1, which can include, but is not limited to native CLL-1, an isoform of CLL-1, or an interspecies CLL-1 homolog of CLL-1. CLL-1 (also known as C-type lectin domain family 12 member A, CLEC12A, dendritic cell-associated lectin 2, DCAL-2, myeloid inhibitory C-type lectin-like receptor, and MICL) is a cell surface receptor that modulates signaling cascades and mediates tyrosine phosphorylation of target MAP kinases. CLL-1 expression is observed, *e.g.*, in acute myeloid leukemia (AML) cells. The amino acid sequence of human CLL-1 (hCLL-1) is provided in UniProtKB/Swiss-Prot Accession No. Q5QGZ9.3 (GI:308153619). As used herein, CLL-1 includes human CLL-1 and non-human CLL-1 homologs, as well as variants, fragments, or post-transnationally modified forms thereof, including, but not limited to, N- and O-linked glycosylated forms of CLL-1.

[0114] As used herein the term “FLT3” refers to Fms-like tyrosine kinase 3 (FLT-3), which can include, but is not limited to native FLT3, an isoform of FLT3, or an interspecies FLT3 homolog of FLT3. FLT3 (also known as Cluster of differentiation antigen 135 (CD135), receptor-type tyrosine-protein kinase FLT3, FMS-related tyrosine kinase 3, stem cell tyrosine kinase 1, FL cytokine receptor, growth factor receptor tyrosine kinase type III, STK1, or fetal liver kinase-2 (Flk2)) is a cytokine receptor which belongs to the receptor tyrosine kinase class III. CD135 is the receptor for the cytokine Flt3 ligand (FLT3L). FLT3 is expressed on the surface of various hematopoietic progenitor cells and on the surface of acute myeloid leukemia (AML) cells. The amino acid sequence of human FLT3 (hFLT3) is provided in UniProtKB/Swiss-Prot Accession No. P36888 (GI:156630887). As used herein, FLT3 includes human FLT3 and non-human FLT3 homologs, as well as variants, fragments, or post-transnationally modified forms thereof, including, but not limited to, N- and O-linked glycosylated forms of FLT3.

[0115] The term “autologous” refers to any material derived from the same individual to which it is later to be re-introduced. For example, the engineered autologous cell therapy (eACT™) method described herein involves collection of lymphocytes from a patient, which are then engineered to express, *e.g.*, a CAR construct, and then administered back to the same patient.

[0116] The term “allogeneic” refers to any material derived from one individual which is then introduced to another individual of the same species, *e.g.*, allogeneic T cell transplantation.

[0117] The terms “transduction” and “transduced” refer to the process whereby foreign DNA is introduced into a cell via viral vector (*see* Jones et al., “Genetics: principles and analysis,” Boston: Jones & Bartlett Publ. (1998)). In some embodiments, the vector is a retroviral vector, a DNA vector, a RNA vector, an adenoviral vector, a baculoviral vector, an Epstein Barr viral vector, a papovaviral vector, a vaccinia viral vector, a herpes simplex viral vector, an adenovirus associated vector, a lentiviral vector, or any combination thereof.

[0118] As used herein, the term “truncated” refers to anything less than the whole. For example, a truncated hinge domain (alternatively referred to herein as “THD”) amino acid sequence can include any amino acid sequence shorter than the full length or complete hinge domain (“CHD”). In some embodiments, a THD consists essentially of or consists of amino acids 118-152, 119-152, 120-152, 121-152, 122-152, 123-152, 124-152, 125-152, 126-152, 127-152, 128-152, 129-152, or 130-152, of SEQ ID NO: 1. In one embodiment, the THD consists essentially of or consists of the amino acid sequence of SEQ ID NO: 3, which consists of amino acids 123 to 152 of SEQ ID NO: 1.

[0119] A “cancer” refers to a broad group of various diseases characterized by the uncontrolled growth of abnormal cells in the body. Unregulated cell division and growth results in the formation of malignant tumors that invade neighboring tissues and may also metastasize to distant parts of the body through the lymphatic system or bloodstream. A “cancer” or “cancer tissue” can include a tumor. Examples of cancers that can be treated by the methods of the present invention include, but are not limited to, cancers of the immune system including lymphoma, leukemia, myeloma, and other leukocyte malignancies. In some embodiments, the methods of the present invention can be used to reduce the tumor size of a tumor derived from, for example, bone cancer, pancreatic cancer, skin cancer, cancer of the head or neck, cutaneous or intraocular malignant melanoma, uterine cancer, ovarian cancer, rectal cancer, cancer of the anal region, stomach cancer, testicular cancer, uterine cancer, carcinoma of the fallopian tubes,

carcinoma of the endometrium, carcinoma of the cervix, carcinoma of the vagina, carcinoma of the vulva, multiple myeloma, Hodgkin's Disease, non-Hodgkin's lymphoma (NHL), primary mediastinal large B cell lymphoma (PMBC), diffuse large B cell lymphoma (DLBCL), follicular lymphoma (FL), transformed follicular lymphoma, splenic marginal zone lymphoma (SMZL), cancer of the esophagus, cancer of the small intestine, cancer of the endocrine system, cancer of the thyroid gland, cancer of the parathyroid gland, cancer of the adrenal gland, sarcoma of soft tissue, cancer of the urethra, cancer of the penis, chronic or acute leukemia, acute myeloid leukemia, chronic myeloid leukemia, acute lymphoblastic leukemia (ALL) (including non T cell ALL), chronic lymphocytic leukemia (CLL), solid tumors of childhood, lymphocytic lymphoma, cancer of the bladder, cancer of the kidney or ureter, carcinoma of the renal pelvis, neoplasm of the central nervous system (CNS), primary CNS lymphoma, tumor angiogenesis, spinal axis tumor, brain stem glioma, pituitary adenoma, Kaposi's sarcoma, epidermoid cancer, squamous cell cancer, T-cell lymphoma, environmentally induced cancers including those induced by asbestos, other B cell malignancies, and combinations of said cancers. In one particular embodiment, the cancer is multiple myeloma. The particular cancer can be responsive to chemo- or radiation therapy or the cancer can be refractory. A refractory cancer refers to a cancer that is not amendable to surgical intervention and the cancer is either initially unresponsive to chemo- or radiation therapy or the cancer becomes unresponsive over time.

[0120] An “anti-tumor effect” as used herein, refers to a biological effect that can present as a decrease in tumor volume, a decrease in the number of tumor cells, a decrease in tumor cell proliferation, a decrease in the number of metastases, an increase in overall or progression-free survival, an increase in life expectancy, or amelioration of various physiological symptoms associated with the tumor. An anti-tumor effect can also refer to the prevention of the occurrence of a tumor, *e.g.*, a vaccine.

[0121] A “cytokine,” as used herein, refers to a non-antibody protein that is released by one cell in response to contact with a specific antigen, wherein the cytokine interacts with a second cell to mediate a response in the second cell. A cytokine can be endogenously expressed by a cell or administered to a subject. Cytokines may be released by immune cells, including macrophages, B cells, T cells, and mast cells to propagate an immune response. Cytokines can induce various responses in the recipient cell. Cytokines can include homeostatic cytokines, chemokines, pro-inflammatory cytokines, effectors, and acute-phase proteins. For example, homeostatic cytokines, including interleukin (IL) 7 and IL-15, promote immune cell survival

and proliferation, and pro-inflammatory cytokines can promote an inflammatory response. Examples of homeostatic cytokines include, but are not limited to, IL-2, IL-4, IL-5, IL-7, IL-10, IL-12p40, IL-12p70, IL-15, and interferon (IFN) gamma. Examples of pro-inflammatory cytokines include, but are not limited to, IL-1a, IL-1b, IL-6, IL-13, IL-17a, tumor necrosis factor (TNF)-alpha, TNF-beta, fibroblast growth factor (FGF) 2, granulocyte macrophage colony-stimulating factor (GM-CSF), soluble intercellular adhesion molecule 1 (sICAM-1), soluble vascular adhesion molecule 1 (sVCAM-1), vascular endothelial growth factor (VEGF), VEGF-C, VEGF-D, and placental growth factor (PLGF). Examples of effectors include, but are not limited to, granzyme A, granzyme B, soluble Fas ligand (sFasL), and perforin. Examples of acute phase-proteins include, but are not limited to, C-reactive protein (CRP) and serum amyloid A (SAA).

[0122] “Chemokines” are a type of cytokine that mediates cell chemotaxis, or directional movement. Examples of chemokines include, but are not limited to, IL-8, IL-16, eotaxin, eotaxin-3, macrophage-derived chemokine (MDC or CCL22), monocyte chemotactic protein 1 (MCP-1 or CCL2), MCP-4, macrophage inflammatory protein 1 α (MIP-1 α , MIP-1a), MIP-1 β (MIP-1b), gamma-induced protein 10 (IP-10), and thymus and activation regulated chemokine (TARC or CCL17).

[0123] A “therapeutically effective amount,” “effective dose,” “effective amount,” or “therapeutically effective dosage” of a therapeutic agent, *e.g.*, engineered CAR T cells, is any amount that, when used alone or in combination with another therapeutic agent, protects a subject against the onset of a disease or promotes disease regression evidenced by a decrease in severity of disease symptoms, an increase in frequency and duration of disease symptom-free periods, or a prevention of impairment or disability due to the disease affliction. The ability of a therapeutic agent to promote disease regression can be evaluated using a variety of methods known to the skilled practitioner, such as in human subjects during clinical trials, in animal model systems predictive of efficacy in humans, or by assaying the activity of the agent in *in vitro* assays.

[0124] The term “lymphocyte” as used herein includes natural killer (NK) cells, T cells, or B cells. NK cells are a type of cytotoxic (cell toxic) lymphocyte that represent a major component of the inherent immune system. NK cells reject tumors and cells infected by viruses. It works through the process of apoptosis or programmed cell death. They were termed “natural killers” because they do not require activation in order to kill cells. T-cells play a major role in cell-mediated-immunity (no antibody involvement). Its T-cell receptors (TCR) differentiate

themselves from other lymphocyte types. The thymus, a specialized organ of the immune system, is primarily responsible for the T cell's maturation. There are six types of T-cells, namely: Helper T-cells (*e.g.*, CD4⁺ cells), Cytotoxic T-cells (also known as TC, cytotoxic T lymphocyte, CTL, T-killer cell, cytolytic T cell, CD8⁺ T-cells or killer T cell), Memory T-cells

5 ((i) stem memory T_{SCM} cells, like naive cells, are CD45RO⁻, CCR7⁺, CD45RA⁺, CD62L⁺ (L-selectin), CD27⁺, CD28⁺ and IL-7Rα⁺, but they also express large amounts of CD95, IL-2Rβ, CXCR3, and LFA-1, and show numerous functional attributes distinctive of memory cells); (ii) central memory T_{CM} cells express L-selectin and the CCR7, they secrete IL-2, but not IFNγ or IL-4, and (iii) effector memory T_{EM} cells, however, do not express L-selectin or

10 CCR7 but produce effector cytokines like IFNγ and IL-4), Regulatory T-cells (Tregs, suppressor T cells, or CD4⁺CD25⁺ regulatory T cells), Natural Killer T-cells (NKT) and Gamma Delta T-cells. B-cells, on the other hand, play a principal role in humoral immunity (with antibody involvement). It makes antibodies and antigens and performs the role of antigen-presenting cells (APCs) and turns into memory B-cells after activation by antigen

15 interaction. In mammals, immature B-cells are formed in the bone marrow, where its name is derived from.

[0125] The term “genetically engineered” or “engineered” refers to a method of modifying the genome of a cell, including, but not limited to, deleting a coding or non-coding region or a portion thereof or inserting a coding region or a portion thereof. In some

20 embodiments, the cell that is modified is a lymphocyte, *e.g.*, a T cell, which can either be obtained from a patient or a donor. The cell can be modified to express an exogenous construct, such as, *e.g.*, a chimeric antigen receptor (CAR) or a T cell receptor (TCR), which is incorporated into the cell's genome.

[0126] An “immune response” refers to the action of a cell of the immune system (for

25 example, T lymphocytes, B lymphocytes, natural killer (NK) cells, macrophages, eosinophils, mast cells, dendritic cells and neutrophils) and soluble macromolecules produced by any of these cells or the liver (including Abs, cytokines, and complement) that results in selective targeting, binding to, damage to, destruction of, and/or elimination from a vertebrate's body of invading pathogens, cells or tissues infected with pathogens, cancerous or other abnormal cells,

30 or, in cases of autoimmunity or pathological inflammation, normal human cells or tissues.

[0127] The term “immunotherapy” refers to the treatment of a subject afflicted with, or at risk of contracting or suffering a recurrence of, a disease by a method comprising inducing, enhancing, suppressing or otherwise modifying an immune response. Examples of

immunotherapy include, but are not limited to, T cell therapies. T cell therapy can include adoptive T cell therapy, tumor-infiltrating lymphocyte (TIL) immunotherapy, autologous cell therapy, engineered autologous cell therapy (eACT™), and allogeneic T cell transplantation. However, one of skill in the art would recognize that the conditioning methods disclosed herein would enhance the effectiveness of any transplanted T cell therapy. Examples of T cell therapies are described in U.S. Patent Publication Nos. 2014/0154228 and 2002/0006409, U.S. Patent No. 5,728,388, and International Publication No. WO 2008/081035.

[0128] The T cells of the immunotherapy can come from any source known in the art. For example, T cells can be differentiated *in vitro* from a hematopoietic stem cell population, or T cells can be obtained from a subject. T cells can be obtained from, *e.g.*, peripheral blood mononuclear cells (PBMCs), bone marrow, lymph node tissue, cord blood, thymus tissue, tissue from a site of infection, ascites, pleural effusion, spleen tissue, and tumors. In addition, the T cells can be derived from one or more T cell lines available in the art. T cells can also be obtained from a unit of blood collected from a subject using any number of techniques known to the skilled artisan, such as FICOLL™ separation and/or apheresis. Additional methods of isolating T cells for a T cell therapy are disclosed in U.S. Patent Publication No. 2013/0287748, which is herein incorporated by references in its entirety.

[0129] The term “engineered Autologous Cell Therapy,” which can be abbreviated as “eACT™,” also known as adoptive cell transfer, is a process by which a patient's own T cells are collected and subsequently genetically altered to recognize and target one or more antigens expressed on the cell surface of one or more specific tumor cells or malignancies. T cells can be engineered to express, for example, chimeric antigen receptors (CAR) or T cell receptor (TCR). CAR positive (+) T cells are engineered to express an extracellular single chain variable fragment (scFv) with specificity for a particular tumor antigen linked to an intracellular signaling part comprising at least one costimulatory domain and at least one activating domain. The costimulatory domain can be derived from a naturally-occurring costimulatory domain, *e.g.*, having the amino acid sequence of SEQ ID NO: 1, or a variant thereof, *e.g.*, a variant having a truncated hinge domain (“THD”), and the activating domain can be derived from, *e.g.*, CD3-zeta. In certain embodiments, the CAR is designed to have two, three, four, or more costimulatory domains. The CAR scFv can be designed to target, for example, CD19, which is a transmembrane protein expressed by cells in the B cell lineage, including all normal B cells and B cell malignancies, including but not limited to NHL, CLL, and non-T cell ALL. In some embodiments, the CAR is engineered such that the costimulatory domain is expressed as a

separate polypeptide chain. Example CAR T cell therapies and constructs are described in U.S. Patent Publication Nos. 2013/0287748, 2014/0227237, 2014/0099309, and 2014/0050708, and these references are incorporated by reference in their entirety.

[0130] A “patient” as used herein includes any human who is afflicted with a cancer (e.g., a lymphoma or a leukemia). The terms “subject” and “patient” are used interchangeably herein.

[0131] As used herein, the term “*in vitro* cell” refers to any cell which is cultured *ex vivo*. In particular, an *in vitro* cell can include a T cell.

[0132] The terms “peptide,” “polypeptide,” and “protein” are used interchangeably, and refer to a compound comprised of amino acid residues covalently linked by peptide bonds. A protein or peptide contains at least two amino acids, and no limitation is placed on the maximum number of amino acids that can comprise a protein's or peptide's sequence. Polypeptides include any peptide or protein comprising two or more amino acids joined to each other by peptide bonds. As used herein, the term refers to both short chains, which also commonly are referred to in the art as peptides, oligopeptides and oligomers, for example, and to longer chains, which generally are referred to in the art as proteins, of which there are many types. “Polypeptides” include, for example, biologically active fragments, substantially homologous polypeptides, oligopeptides, homodimers, heterodimers, variants of polypeptides, modified polypeptides, derivatives, analogs, fusion proteins, among others. The polypeptides include natural peptides, recombinant peptides, synthetic peptides, or a combination thereof.

[0133] “Stimulation,” as used herein, refers to a primary response induced by binding of a stimulatory molecule with its cognate ligand, wherein the binding mediates a signal transduction event. A “stimulatory molecule” is a molecule on a T cell, e.g., the T cell receptor (TCR)/CD3 complex, that specifically binds with a cognate stimulatory ligand present on an antigen presenting cell. A “stimulatory ligand” is a ligand that when present on an antigen presenting cell (e.g., an APC, a dendritic cell, a B-cell, and the like) can specifically bind with a stimulatory molecule on a T cell, thereby mediating a primary response by the T cell, including, but not limited to, activation, initiation of an immune response, proliferation, and the like. Stimulatory ligands include, but are not limited to, an anti-CD3 antibody (such as OKT3), an MHC Class I molecule loaded with a peptide, a superagonist anti-CD2 antibody, and a superagonist anti-CD28 antibody.

[0134] A “costimulatory signal,” as used herein, refers to a signal, which in combination with a primary signal, such as TCR/CD3 ligation, leads to a T cell response, such as, but not limited to, proliferation and/or upregulation or down regulation of key molecules.

[0135] A “costimulatory ligand” as used herein, includes a molecule on an antigen

5 presenting cell that specifically binds a cognate co-stimulatory molecule on a T cell. Binding of the costimulatory ligand provides a signal that mediates a T cell response, including, but not limited to, proliferation, activation, differentiation, and the like. A costimulatory ligand induces a signal that is in addition to the primary signal provided by a stimulatory molecule, for instance, by binding of a T cell receptor (TCR)/CD3 complex with a major histocompatibility

10 complex (MHC) molecule loaded with peptide. A co-stimulatory ligand can include, but is not limited to, 3/TR6, 4-1BB ligand, agonist or antibody that binds Toll ligand receptor, B7-1 (CD80), B7-2 (CD86), CD30 ligand, CD40, CD7, CD70, CD83, herpes virus entry mediator (HVEM), human leukocyte antigen G (HLA-G), ILT4, immunoglobulin-like transcript (ILT)

15 3, inducible costimulatory ligand (ICOS-L), intercellular adhesion molecule (ICAM), ligand that specifically binds with B7-H3., lymphotoxin beta receptor, MHC class I chain-related protein A (MICA), MHC class I chain-related protein B (MICB), OX40 ligand, PD-L2, or programmed death (PD) L1. A co-stimulatory ligand includes, without limitation, an antibody that specifically binds with a co-stimulatory molecule present on a T cell, such as, but not limited to, 4-1BB, B7-H3, CD2, CD27, CD28, CD30, CD40, CD7, ICOS, ligand that

20 specifically binds with CD83, lymphocyte function-associated antigen-1 (LFA-1), natural killer cell receptor C (NKG2C), OX40, PD-1, or tumor necrosis factor superfamily member 14 (TNFSF14 or LIGHT).

[0136] A “costimulatory molecule” is a cognate binding partner on a T cell that specifically binds with a costimulatory ligand, thereby mediating a costimulatory response by

25 the T cell, such as, but not limited to, proliferation. Costimulatory molecules include, but are not limited to, A “costimulatory molecule” is a cognate binding partner on a T cell that specifically binds with a costimulatory ligand, thereby mediating a costimulatory response by the T cell, such as, but not limited to, proliferation. Costimulatory molecules include, but are not limited to, 4-1BB/CD137, B7-H3, BAFFR, BLAME (SLAMF8), BTLA, CD 33, CD 45,

30 CD100 (SEMA4D), CD103, CD134, CD137, CD154, CD16, CD160 (BY55), CD18, CD19, CD19a, CD2, CD22, CD247, CD27, CD276 (B7-H3), CD28, CD29, CD3 (alpha; beta; delta; epsilon; gamma; zeta), CD30, CD37, CD4, CD4, CD40, CD49a, CD49D, CD49f, CD5, CD64, CD69, CD7, CD80, CD83 ligand, CD84, CD86, CD8alpha, CD8beta, CD9, CD96 (Tactile),

CD1-la, CD1-lb, CD1-lc, CD1-lf, CDS, CEACAM1, CRT AM, DAP-10, DNAM1 (CD226), Fc gamma receptor, GADS, GITR, HVEM (LIGHTR), IA4, ICAM-1, ICAM-1, ICOS, Ig alpha (CD79a), IL2R beta, IL2R gamma, IL7R alpha, integrin, ITGA4, ITGA4, ITGA6, ITGAD, ITGAE, ITGAL, ITGAM, ITGAX, ITGB2, ITGB7, ITGB1, KIRDS2, LAT, LFA-1, LFA-1, LIGHT, LIGHT (tumor necrosis factor superfamily member 14; TNFSF14), LTBR, Ly9 (CD229), lymphocyte function-associated antigen-1 (LFA-1 (CD1 la/CD18), MHC class I molecule, NKG2C, NKG2D, NKp30, NKp44, NKp46, NKp80 (KLRF1), OX40, PAG/Cbp, PD-1, PSGL1, SELPLG (CD162), signaling lymphocytic activation molecule, SLAM (SLAMF1; CD150; IPO-3), SLAMF4 (CD244; 2B4), SLAMF6 (NTB-A; Lyl08), SLAMF7, SLP-76, TNF, TNFr, TNFR2, Toll ligand receptor, TRANCE/RANKL, VLA1, or VLA-6, or fragments, truncations, or combinations thereof.

[0137] The terms “reducing” and “decreasing” are used interchangeably herein and indicate any change that is less than the original. “Reducing” and “decreasing” are relative terms, requiring a comparison between pre- and post- measurements. “Reducing” and “decreasing” include complete depletions.

[0138] “Treatment” or “treating” of a subject refers to any type of intervention or process performed on, or the administration of an active agent to, the subject with the objective of reversing, alleviating, ameliorating, inhibiting, slowing down or preventing the onset, progression, development, severity or recurrence of a symptom, complication or condition, or biochemical indicia associated with a disease. In one embodiment, “treatment” or “treating” includes a partial remission. In another embodiment, “treatment” or “treating” includes a complete remission.

[0139] To calculate percent identity, the sequences being compared are typically aligned in a way that gives the largest match between the sequences. One example of a computer program that can be used to determine percent identity is the GCG program package, which includes GAP (Devereux et al., 1984, Nucl. Acid Res. 12:387; Genetics Computer Group, University of Wisconsin, Madison, Wis.). The computer algorithm GAP is used to align the two polypeptides or polynucleotides for which the percent sequence identity is to be determined. The sequences are aligned for optimal matching of their respective amino acid or nucleotide (the “matched span,” as determined by the algorithm). In certain embodiments, a standard comparison matrix (*see*, Dayhoff et al., 1978, Atlas of Protein Sequence and Structure 5:345-352 for the PAM 250 comparison matrix; Henikoff et al., 1992, Proc. Natl. Acad. Sci. U.S.A. 89:10915-10919 for the BLOSUM 62 comparison matrix) is also used by the algorithm.

[0140] Various aspects of the invention are described in further detail in the following subsections.

I. Chimeric Antigen Receptors and T Cell Receptors

[0141] Chimeric antigen receptors (CARs or CAR-Ts) and T cell receptors (TCRs) are genetically engineered receptors. These engineered receptors can be readily inserted into and expressed by immune cells, including T cells in accordance with techniques known in the art. With a CAR, a single receptor can be programmed to both recognize a specific antigen and, when bound to that antigen, activate the immune cell to attack and destroy the cell bearing that antigen. When these antigens exist on tumor cells, an immune cell that expresses the CAR can target and kill the tumor cell.

[0142] One aspect of the present invention is directed to polynucleotides encoding chimeric antigen receptors (CARs) or T cell receptors (TCRs) comprising a costimulatory domain comprising a novel extracellular domain comprising a truncated hinge domain ("THD"), and engineered T cells comprising a costimulatory domain comprising the THD. The costimulatory domain can further comprise a transmembrane domain and/or an intracellular domain. In some embodiments, a CAR or TCR encoded by the polynucleotide of the present invention further comprises an antigen binding molecule that specifically binds to a target antigen. In some embodiments, the CAR or TCR encoded by the polynucleotide further comprises an activating domain. In one particular embodiment, the CAR or TCR encoded by the polynucleotide comprises (i) an antigen binding molecule that specifically binds to a target antigen, (ii) a costimulatory domain comprising an extracellular domain, a transmembrane domain, and an intracellular domain, and (iii) an activating domain, wherein the extracellular domain comprises, consists essentially of, or consists of a THD described herein, e.g., SEQ ID NO: 3.

[0143] In some embodiments, an orientation of the CARs in accordance with the invention comprises an antigen binding domain (such as scFv) in tandem with a costimulatory domain and an activating domain. The costimulatory domain can comprise one or more of an extracellular portion, a transmembrane portion, and an intracellular portion. In other embodiments, multiple costimulatory domains can be utilized in tandem.

I.A. Costimulatory Domain.

[0144] Chimeric antigen receptors incorporates costimulatory (signaling) domains to increase their potency. See U.S. Patent Nos. 7,741,465, and 6,319,494, as well as Krause *et al.* and Finney *et al.* (supra), Song *et al.*, Blood 119:696-706 (2012); Kalos *et al.*, Sci Transl. Med. 3:95 (2011); Porter *et al.*, N. Engl. J. Med. 365:725-33 (2011), and Gross *et al.*, Annu. Rev. Pharmacol. Toxicol. 56:59-83 (2016). The costimulatory protein having the amino acid sequence of SEQ ID NO: 1 is a costimulatory protein found naturally on T-cells. The complete native amino acid sequence of this costimulatory protein is described in NCBI Reference Sequence: NP_006130.1. See Figure 1A. The complete native nucleic acid sequence of this costimulatory protein is described in NCBI Reference Sequence: NM_006139.1.

[0145] **Novel Extracellular Domain:** The present disclosure shows that a novel extracellular domain of a costimulatory protein and comprising a truncated hinge domain ("THD") can improve one or more properties of a CAR or a TCR. In some embodiments, the THD domain is a truncated version of a complete hinge domain ("CHD"). In certain embodiments, the isolated polynucleotide encoding a THD comprises (i) an amino acid sequence at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to amino acids 123 to 152 of SEQ ID NO: 1, wherein the THD domain does not contain amino acids 1 to 122 of SEQ ID NO: 1.

[0146] In other embodiments, the THD consists essentially of or consists of an amino acid sequence at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to amino acids 123 to 152 of SEQ ID NO: 1. In other embodiments, the THD consists essentially of or consists of an amino acid sequence encoded by a nucleotide sequence at least about 60%, at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to SEQ ID NO: 3.

[0147] In some embodiments, the isolated polynucleotide encoding a THD consists essentially of or consists of (i) an amino acid sequence at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to amino acids 123 to 152 of SEQ ID NO: 1 and (ii) optionally $\pm$ one amino acid, $\pm$ two amino acids, $\pm$ three amino acids, $\pm$ four amino acids, $\pm$ five amino acids, or $\pm$ six amino acids. In some embodiments, the isolated

polynucleotide encoding a THD consists essentially of or consists of (i) an amino acid sequence at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to amino acids 123 to 152 of SEQ ID NO: 1 and (ii) optionally one or two amino acids, one to three amino acids, one to four amino acids, one to five amino acids, or one to six amino acids. The one to six amino acids that can be added or deleted from the amino acid sequence in the THD can be at either the N-terminus, at the C-terminus, or both the N-terminus and the C-terminus.

[0148] In some embodiments, the isolated polynucleotide encoding a THD consists essentially of or consists of (i) an amino acid sequence at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to amino acids 123 to 152 of SEQ ID NO: 1 and (ii) one additional N-terminal amino acid, two additional N-terminal amino acids, three additional N-terminal amino acids, four additional N-terminal amino acids, five additional N-terminal amino acids, or six additional N-terminal amino acids.

[0149] In some embodiments, the additional amino acids can be N-terminal amino acids. In some embodiments, the additional amino acids can be heterologous. In other embodiments, the additional amino acids are part of the naturally occurring costimulatory protein sequence.

[0150] In some embodiments, the THD consists essentially of or consists of an amino acid sequence at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to amino acids 123 to 152 of SEQ ID NO: 1, amino acids 122 to 152 of SEQ ID NO: 1, amino acids 121 to 152 of SEQ ID NO: 1, amino acids 120 to 152 of SEQ ID NO: 1, amino acids 119 to 152 of SEQ ID NO: 1, amino acids 118 to 152 of SEQ ID NO: 1, or amino acids 117 to 152 of SEQ ID NO: 1.

[0151] In other embodiments, the THD consists essentially of or consists of an amino acid sequence at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to amino acids 124 to 152 of SEQ ID NO: 1, amino acids 125 to 152 of SEQ ID NO: 1, amino acids 126 to 152 of SEQ ID NO: 1, amino acids 127 to 152 of SEQ ID NO: 1, amino acids 128 to 152 of SEQ ID NO: 1, amino acids 129 to 152 of SEQ ID NO: 1, or amino acids 130 to 152 of SEQ ID NO: 1.

[0152] In some embodiments, the THD does not comprise amino acids 1-116 of SEQ ID NO: 1. In some embodiments, the THD does not comprise amino acids 1-117 of SEQ ID NO: 1. In some embodiments, the THD does not comprise amino acids 1-118 of SEQ ID NO: 1. In some embodiments, the THD does not comprise amino acids 1-119 of SEQ ID NO: 1. In some embodiments, the THD does not comprise amino acids 1-120 of SEQ ID NO: 1. In some embodiments, the THD does not comprise amino acids 1-121 of SEQ ID NO: 1. In some embodiments, the THD does not comprise amino acids 1-122 of SEQ ID NO: 1. In some embodiments, the THD does not comprise amino acids 1-123 of SEQ ID NO: 1. In some embodiments, the THD does not comprise amino acids 1-124 of SEQ ID NO: 1. In some embodiments, the THD does not comprise amino acids 1-125 of SEQ ID NO: 1. In some embodiments, the THD does not comprise amino acids 1-126 of SEQ ID NO: 1. In some embodiments, the THD does not comprise amino acids 1-127 of SEQ ID NO: 1. In some embodiments, the THD does not comprise amino acids 1-128 of SEQ ID NO: 1. In some embodiments, the THD does not comprise amino acids 1-129 of SEQ ID NO: 1.

[0153] The corresponding amino acid sequence of the THD is set forth in SEQ ID NO. 3 LDNEKSNGTI IHVKGKHLCP SPLFPGPSKP. A nucleotide sequence encoding the extracellular portion of THD is set forth in SEQ ID NO. 2 CTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTC TGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCA.

[0154] In certain embodiments, the polynucleotide encoding a costimulatory domain in a CAR or TCR comprises a nucleotide sequence at least about 60%, at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to SEQ ID NO: 3, wherein the nucleotide sequence encodes a THD and wherein the CAR or TCR does not comprise amino acids 1 to 122 of SEQ ID NO: 1.

[0155] In one particular embodiment, the THD consists essentially of or consists of an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to the amino acid sequence of SEQ ID NO: 3. In a specific embodiment, the polynucleotide encoding THD consists essentially of or consists of a nucleotide sequence at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%,

at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to the nucleotide sequence of SEQ ID NO: 2.

[0156] In some embodiments, the THD further comprises some or all of a member of the immunoglobulin family such as IgG1, IgG2, IgG3, IgG4, IgA, IgD, IgE, IgM, or fragment thereof.

[0157] In some embodiments, the THD is derived from a human complete hinge domain ("CHD"), e.g., from the costimulatory protein having the amino acid sequence of SEQ ID NO: 1. In other embodiments, the THD is derived from a rodent, murine, or primate (e.g., non-human primate) CHD of a costimulatory protein. In some embodiments, the THD is derived from a chimeric CHD of a costimulatory protein.

[0158] **Transmembrane Domain:** The costimulatory domain for the CAR or TCR of the invention can further comprise a transmembrane domain and/or an intracellular signaling domain. The transmembrane domain can be designed to be fused to the extracellular domain of the CAR. It can similarly be fused to the intracellular domain of the CAR. In one embodiment, the transmembrane domain that naturally is associated with one of the domains in a CAR is used. In some instances, the transmembrane domain can be selected or modified by amino acid substitution to avoid binding of such domains to the transmembrane domains of the same or different surface membrane proteins to minimize interactions with other members of the receptor complex. The transmembrane domain can be derived either from a natural or from a synthetic source. Where the source is natural, the domain can be derived from any membrane-bound or transmembrane protein. Transmembrane regions of particular use in this invention can be derived from (i.e., comprise) 4-1BB/CD137, activating NK cell receptors, an Immunoglobulin protein, B7-H3, BAFR, BLAME (SLAMF8), BTLA, CD100 (SEMA4D), CD103, CD160 (BY55), CD18, CD19, CD19a, CD2, CD247, CD27, CD276 (B7-H3), CD28, CD29, CD3 delta, CD3 epsilon, CD3 gamma, CD30, CD4, CD40, CD49a, CD49D, CD49f, CD69, CD7, CD84, CD8alpha, CD8beta, CD96 (Tactile), CD11a, CD11b, CD11c, CD11d, CDS, CEACAM1, CRT AM, cytokine receptor, DAP-10, DNAM1 (CD226), Fc gamma receptor, GADS, GITR, HVEM (LIGHTR), IA4, ICAM-1, ICAM-1, Ig alpha (CD79a), IL-2R beta, IL-2R gamma, IL-7R alpha, inducible T cell costimulator (ICOS), integrins, ITGA4, ITGA4, ITGA6, ITGAD, ITGAE, ITGAL, ITGAM, ITGAX, ITGB2, ITGB7, ITGB1, KIRDS2, LAT, LFA-1, LFA-1, a ligand that specifically binds with CD83,, LIGHT, LIGHT, LTBR, Ly9 (CD229), lymphocyte function-associated antigen-1 (LFA-1; CD11a/CD18), MHC class 1 molecule, NKG2C, NKG2D, NKp30, NKp44, NKp46, NKp80 (KLRF1), OX-40, PAG/Cbp,

programmed death-1 (PD-1), PSGL1, SELPLG (CD162), Signaling Lymphocytic Activation Molecules (SLAM proteins), SLAM (SLAMF1; CD150; IPO-3), SLAMF4 (CD244; 2B4), SLAMF6 (NTB-A; Lyl08), SLAMF7, SLP-76, TNF receptor proteins, TNFR2, TNFSF14, a Toll ligand receptor, TRANCE/RANKL, VLA1, or VLA-6, or a fragment, truncation, or a combination thereof.

[0159] Optionally, short linkers can form linkages between any or some of the extracellular, transmembrane, and intracellular domains of the CAR.

[0160] In one specific embodiment, the nucleotide sequence of the costimulatory protein's transmembrane domain is set forth in SEQ ID NO. 4:

TTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCAC
CGTGGCTTTTATAATCTTCTGGGTT

[0161] In one embodiment, the polynucleotide encoding a transmembrane domain within a costimulatory domain comprises a nucleotide sequence at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to the nucleotide sequence of SEQ ID NO: 4.

[0162] The amino acid sequence of the costimulatory protein's transmembrane domain is set forth in SEQ ID NO. 5: FWVLVVVGGV LACYSLLVTV AFIIFWV.

[0163] In one particular embodiment, the transmembrane domain within a costimulatory domain comprises an amino acid sequence at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to the amino acid sequence of SEQ ID NO: 5.

[0164] In another embodiment, the transmembrane domain is derived from (i.e., comprises) CD8. In one embodiment, the nucleotide sequence of the CD8 extracellular domain and transmembrane domain is set forth in SEQ ID NO: 238

GCTGCAGCATTGAGCAACTCAATAATGTATTTTAGTCACTTTGTACCAGTGTCTT
GCCGGCTAAGCCTACTACCACACCCGCTCCACGGCCACCTACCCCAGCTCCTACC
ATCGCTTCACAGCCTCTGTCCCTGCGCCCAGAGGCTTGCCGACCGGCCGAGGGG
GCGCTGTTTCATACCAGAGGACTGGATTTTCGCCTGCGATATCTATATCTGGGCACC
CCTGGCCGGAACCTGCGGCGTACTCCTGCTGTCCCTGGTCATCACGCTCTATTGT
AATCACAGGAAC.

[0165] In some embodiments, the polynucleotide encoding a transmembrane domain within a costimulatory domain comprises a nucleotide sequence at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%,
 5 at least about 99%, or about 100% identical to the nucleotide sequence of the CD8 transmembrane domain.

[0166] The amino acid sequence of the CD8 extracellular domain and transmembrane domain is set forth in SEQ ID NO. 239
 AAALSNSIMYFSHFVPVFLPAKPTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVH
 10 TRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCNHRN.

[0167] In one particular embodiment, the transmembrane domain within a costimulatory domain comprises an amino acid sequence at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to the amino acid sequence of the CD8
 15 transmembrane domain.

[0168] ***Intracellular (signaling) Domain:*** The intracellular (signaling) domain of the engineered T cells of the invention can provide signaling to an activating domain, which then activates at least one of the normal effector functions of the immune cell. Effector function of a T cell, for example, can be cytolytic activity or helper activity including the secretion of
 20 cytokines.

[0169] In certain embodiments, suitable intracellular signaling domain include (*i.e.*, comprise), but are not limited to 4-1BB/CD137, activating NK cell receptors, an Immunoglobulin protein, B7-H3, BAFFR, BLAME (SLAMF8), BTLA, CD100 (SEMA4D), CD103, CD160 (BY55), CD18, CD19, CD19a, CD2, CD247, CD27, CD276 (B7-H3), CD28,
 25 CD29, CD3 delta, CD3 epsilon, CD3 gamma, CD30, CD4, CD40, CD49a, CD49D, CD49f, CD69, CD7, CD84, CD8alpha, CD8beta, CD96 (Tactile), CD11a, CD11b, CD11c, CD11d, CDS, CEACAM1, CRT AM, cytokine receptor, DAP-10, DNAM1 (CD226), Fc gamma receptor, GADS, GITR, HVEM (LIGHTR), IA4, ICAM-1, ICAM-1, Ig alpha (CD79a), IL-2R beta, IL-2R gamma, IL-7R alpha, inducible T cell costimulator (ICOS), integrins, ITGA4, ITGA4,
 30 ITGA6, ITGAD, ITGAE, ITGAL, ITGAM, ITGAX, ITGB2, ITGB7, ITGB1, KIRDS2, LAT, LFA-1, LFA-1, ligand that specifically binds with CD83,, LIGHT, LIGHT, LTBR, Ly9 (CD229), Lyl08), lymphocyte function-associated antigen-1 (LFA-1; CD11a/CD18), MHC class 1 molecule, NKG2C, NKG2D, NKp30, NKp44, NKp46, NKp80 (KLRF1), OX-40,

PAG/Cbp, programmed death-1 (PD-1), PSGL1, SELPLG (CD162), Signaling Lymphocytic Activation Molecules (SLAM proteins), SLAM (SLAMF1; CD150; IPO-3), SLAMF4 (CD244; 2B4), SLAMF6 (NTB-A, SLAMF7, SLP-76, TNF receptor proteins, TNFR2, TNFSF14, a Toll ligand receptor, TRANCE/RANKL, VLA1, or VLA-6, or a fragment, truncation, or a combination thereof.

[0170] An example of a nucleotide sequence encoding the intracellular signaling domain is set forth in SEQ ID NO. 6:
 AGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACGC
 CGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCG
 CTGCCTATCGGAGC

[0171] In one embodiment, the polynucleotide encoding an intracellular signaling domain within a costimulatory domain comprises a nucleotide sequence at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to the nucleotide sequence of SEQ ID NO: 6.

[0172] An example of an intracellular signaling domain is set forth in SEQ ID NO. 7:
 RSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRS.

[0173] In one particular embodiment, the intracellular signaling domain within a costimulatory domain comprises an amino acid sequence at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to the amino acid sequence of SEQ ID NO: 7.

[0174] In some embodiments, the costimulatory domain comprises, consists essentially of, or consists of the extracellular THD, and the costimulatory proteins' s transmembrane and intracellular domains. For example, a nucleotide sequence encoding a costimulatory domain is set forth in SEQ ID NO. 240:
 CTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTC
 TGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGT
 GGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCT
 GGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCC

ACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGA
TTTCGCTGCCTATCGGAGC

[0175] In some embodiments, the polynucleotide encoding a costimulatory domain comprises, consists essentially of, or consists of a nucleotide sequence at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to the nucleotide sequence of SEQ ID NO: 240, wherein the costimulatory domain does not comprises amino acids 1 to 122 of SEQ ID NO: 1, amino acids 1 to 121 of SEQ ID NO: 1, amino acids 1 to 120 of SEQ ID NO: 1, amino acids 1 to 119 of SEQ ID NO: 1, amino acids 1 to 118 of SEQ ID NO: 1, or amino acids 1 to 118 of SEQ ID NO: 1.

[0176] The corresponding amino acid sequence of the costimulatory domain is set forth in

SEQ	ID	NO.	241:
LDNEKSNGTIIHVKGKHLCPSPFPGPSKPFVVLVVVGGVLACYSLLVTVAFIIFWVR			
SKRSRLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRS			

[0177] In some embodiments, the costimulatory domain comprises, consists essentially of, or consists of a nucleotide sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to the amino acid sequence of SEQ ID NO: 241, wherein the costimulatory domain does not comprises amino acids 1 to 122 of SEQ ID NO: 1, amino acids 1 to 121 of SEQ ID NO: 1, amino acids 1 to 120 of SEQ ID NO: 1, amino acids 1 to 119 of SEQ ID NO: 1, amino acids 1 to 118 of SEQ ID NO: 1, or amino acids 1 to 118 of SEQ ID NO: 1.

1.B. Activating Domain.

[0178] CD3 is an element of the T cell receptor on native T cells, and has been shown to be an important intracellular activating element in CARs. In one embodiment, the CD3 is CD3 zeta, the nucleotide sequence of which is set forth in SEQ ID NO. 8:

AGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCCAGAAC
CAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGAC
AAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCC
CCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTC
TGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGT

ACCAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAG
CCCTGCCACCTAGG

[0179] In some embodiments, the polynucleotide encoding an activating domain comprises a nucleotide sequence at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to the nucleotide sequence of SEQ ID NO: 8.

[0180] The corresponding amino acid of intracellular CD3 zeta is set forth in SEQ ID NO. 9:

RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ
EGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALP
PR

[0181] In some embodiments, the activating domain comprises a nucleotide sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to the amino acid sequence of SEQ ID NO: 9.

[0182] In some embodiments, the activating domain comprises an amino acid sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to the amino acid sequence of:

RVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQ
EGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALP
PR (SEQ ID NO: 251).

I.C. Antigen Binding Molecules

[0183] CARs can be engineered to bind to an antigen (such as a cell-surface antigen) by incorporating an antigen binding molecule that interacts with that targeted antigen. In some embodiments, the antigen binding molecule is an antibody fragment thereof, e.g., one or more single chain antibody fragment ("scFv"). An scFv is a single chain antibody fragment having the variable regions of the heavy and light chains of an antibody linked together. See U.S. Patent Nos. 7,741,465, and 6,319,494 as well as Eshhar *et al.*, Cancer Immunol Immunotherapy (1997) 45: 131-136. An scFv retains the parent antibody's ability to specifically interact with target antigen. scFvs are useful in chimeric antigen receptors because they can be engineered

to be expressed as part of a single chain along with the other CAR components. *Id.* See also Krause *et al.*, J. Exp. Med., Volume 188, No. 4, 1998 (619–626); Finney *et al.*, *Journal of Immunology*, 1998, 161: 2791–2797. It will be appreciated that the antigen binding molecule is typically contained within the extracellular portion of the CAR such that it is capable of recognizing and binding to the antigen of interest. Bispecific and multispecific CARs are contemplated within the scope of the invention, with specificity to more than one target of interest.

[0184] In some embodiments, the polynucleotide encodes a CAR or a TCR comprising a THD of the present invention and an antigen binding molecule that specifically binds to a target antigen. In some embodiments, the target antigen is a tumor antigen. In some embodiments, the antigen is selected from a tumor-associated surface antigen, such as 5T4, alphafetoprotein (AFP), B7-1 (CD80), B7-2 (CD86), BCMA, B-human chorionic gonadotropin, CA-125, carcinoembryonic antigen (CEA), carcinoembryonic antigen (CEA), CD123, CD133, CD138, CD19, CD20, CD22, CD23, CD24, CD25, CD30, CD33, CD34, CD4, CD40, CD44, CD56, CD8, CLL-1, c-Met, CMV-specific antigen, CSPG4, CTLA-4, disialoganglioside GD2, ductal-epithelial mucine, EBV-specific antigen, EGFR variant III (EGFRvIII), ELF2M, endoglin, ephrin B2, epidermal growth factor receptor (EGFR), epithelial cell adhesion molecule (EpCAM), epithelial tumor antigen, ErbB2 (HER2/neu), fibroblast associated protein (fap), FLT3, folate binding protein, GD2, GD3, glioma-associated antigen, glycosphingolipids, gp36, HBV-specific antigen, HCV-specific antigen, HER1-HER2, HER2-HER3 in combination, HERV-K, high molecular weight-melanoma associated antigen (HMW-MAA), HIV-1 envelope glycoprotein gp41, HPV-specific antigen, human telomerase reverse transcriptase, IGF1 receptor, IGF-II, IL-11R α , IL-13R α 2, Influenza Virus-specific antigen; CD38, insulin growth factor (IGF1)-1, intestinal carboxyl esterase, kappa chain, LAGA-1a, lambda chain, Lassa Virus-specific antigen, lectin-reactive AFP, lineage-specific or tissue specific antigen such as CD3, MAGE, MAGE-A1, major histocompatibility complex (MHC) molecule, major histocompatibility complex (MHC) molecule presenting a tumor-specific peptide epitope, M-CSF, melanoma-associated antigen, mesothelin, mesothelin, MN-CA IX, MUC-1, mut hsp70-2, mutated p53, mutated p53, mutated ras, neutrophil elastase, NKG2D, Nkp30, NY-ESO-1, p53, PAP, prostase, prostase specific antigen (PSA), prostate-carcinoma tumor antigen-1 (PCTA-1), prostate-specific antigen, prostein, PSMA, RAGE-1, ROR1, RU1, RU2 (AS), surface adhesion molecule, surviving and telomerase, TAG-72, the extra domain A (EDA) and extra domain B (EDB) of fibronectin and the A1 domain of tenascin-

C (TnC A1) , thyroglobulin, tumor stromal antigens, vascular endothelial growth factor receptor-2 (VEGFR2), virus-specific surface antigen such as an HIV-specific antigen (such as HIV gpl20), as well as any derivate or variant of these surface markers. In certain embodiments, the antigen binding molecule specifically binds to BCMA. In other
5 embodiments, the antigen binding molecule specifically binds to CLL-1. In other
embodiments, the antigen binding molecule specifically binds to FLT3.

[0185] In some embodiments, the antigen binding molecule specifically binds BCMA. In certain embodiments, the antigen binding molecule comprises (a) a VH CDR1 comprising an amino acid sequence selected from SEQ ID NOs: 13-20; (b) a VH CDR2 comprising an
10 amino acid sequence selected from SEQ ID NOs: 21-28; (c) a VH CDR3 comprising an amino acid sequence selected from SEQ ID NOs: 29-36; (d) a VL CDR1 comprising an amino acid sequence selected from SEQ ID NOs: 37-44; (e) a VL CDR2 comprising an amino acid sequence selected from SEQ ID NOs: 45-52; and/or (f) a VL CDR3 comprising an amino acid sequence selected from SEQ ID NOs: 53-60.

[0186] In one embodiment, the antigen binding molecule comprises (a) a VH CDR1 comprising an amino acid of SEQ ID NO: 13; (b) a VH CDR2 comprising an amino acid sequence of SEQ ID NO: 21; (c) a VH CDR3 comprising an amino acid sequence of SEQ ID
15 NO: 29; (d) a VL CDR1 comprising an amino acid sequence of SEQ ID NO: 37; (e) a VL CDR2 comprising an amino acid sequence of SEQ ID NO: 45; and/or (f) a VL CDR3
20 comprising an amino acid sequence of SEQ ID NO: 53.

[0187] In another embodiment, the antigen binding molecule comprises (a) a VH CDR1 comprising an amino acid of SEQ ID NO: 14; (b) a VH CDR2 comprising an amino acid sequence of SEQ ID NO: 22; (c) a VH CDR3 comprising an amino acid sequence of SEQ
25 ID NO: 30; (d) a VL CDR1 comprising an amino acid sequence of SEQ ID NO: 38; (e) a VL CDR2 comprising an amino acid sequence of SEQ ID NO: 46; and/or (f) a VL CDR3 comprising an amino acid sequence of SEQ ID NO: 54.

[0188] In another embodiment, the antigen binding molecule comprises (a) a VH CDR1 comprising an amino acid of SEQ ID NO: 15; (b) a VH CDR2 comprising an amino acid sequence of SEQ ID NO: 23; (c) a VH CDR3 comprising an amino acid sequence of SEQ
30 ID NO: 31; (d) a VL CDR1 comprising an amino acid sequence of SEQ ID NO: 39; (e) a VL CDR2 comprising an amino acid sequence of SEQ ID NO: 47; and/or (f) a VL CDR3 comprising an amino acid sequence of SEQ ID NO: 55.

[0189] In another embodiment, the antigen binding molecule comprises (a) a VH CDR1 comprising an amino acid of SEQ ID NO: 16; (b) a VH CDR2 comprising an amino acid sequence of SEQ ID NO: 24; (c) a VH CDR3 comprising an amino acid sequence of SEQ ID NO: 32; (d) a VL CDR1 comprising an amino acid sequence of SEQ ID NO: 40; (e) a VL CDR2 comprising an amino acid sequence of SEQ ID NO: 48; and/or (f) a VL CDR3 comprising an amino acid sequence of SEQ ID NO: 56.

[0190] In another embodiment, the antigen binding molecule comprises (a) a VH CDR1 comprising an amino acid of SEQ ID NO: 17; (b) a VH CDR2 comprising an amino acid sequence of SEQ ID NO: 25; (c) a VH CDR3 comprising an amino acid sequence of SEQ ID NO: 33; (d) a VL CDR1 comprising an amino acid sequence of SEQ ID NO: 41; (e) a VL CDR2 comprising an amino acid sequence of SEQ ID NO: 49; and/or (f) a VL CDR3 comprising an amino acid sequence of SEQ ID NO: 57.

[0191] In another embodiment, the antigen binding molecule comprises (a) a VH CDR1 comprising an amino acid of SEQ ID NO: 18; (b) a VH CDR2 comprising an amino acid sequence of SEQ ID NO: 26; (c) a VH CDR3 comprising an amino acid sequence of SEQ ID NO: 34; (d) a VL CDR1 comprising an amino acid sequence of SEQ ID NO: 42; (e) a VL CDR2 comprising an amino acid sequence of SEQ ID NO: 50; and/or (f) a VL CDR3 comprising an amino acid sequence of SEQ ID NO: 58.

[0192] In another embodiment, the antigen binding molecule comprises (a) a VH CDR1 comprising an amino acid of SEQ ID NO: 19; (b) a VH CDR2 comprising an amino acid sequence of SEQ ID NO: 27; (c) a VH CDR3 comprising an amino acid sequence of SEQ ID NO: 35; (d) a VL CDR1 comprising an amino acid sequence of SEQ ID NO: 43; (e) a VL CDR2 comprising an amino acid sequence of SEQ ID NO: 51; and/or (f) a VL CDR3 comprising an amino acid sequence of SEQ ID NO: 59.

[0193] In another embodiment, the antigen binding molecule comprises (a) a VH CDR1 comprising an amino acid of SEQ ID NO: 20; (b) a VH CDR2 comprising an amino acid sequence of SEQ ID NO: 28; (c) a VH CDR3 comprising an amino acid sequence of SEQ ID NO: 36; (d) a VL CDR1 comprising an amino acid sequence of SEQ ID NO: 44; (e) a VL CDR2 comprising an amino acid sequence of SEQ ID NO: 52; and/or (f) a VL CDR3 comprising an amino acid sequence of SEQ ID NO: 60.

[0194] In certain embodiments, the antigen binding molecule comprises a VH comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 77-84 and a VL comprising an amino acid sequence selected from the group consisting of SEQ ID

NOs: 85-92. In one embodiment, the antigen binding molecule comprises a VH comprising an amino acid sequence of SEQ ID NO: 77 and a VL comprising an amino acid sequence of SEQ ID NO: 85. In another embodiment, the antigen binding molecule comprises a VH comprising an amino acid sequence of SEQ ID NO: 78 and a VL comprising an amino acid sequence of SEQ ID NO: 86. In another embodiment, the antigen binding molecule comprises a VH comprising an amino acid sequence of SEQ ID NO: 79 and a VL comprising an amino acid sequence of SEQ ID NO: 87. In another embodiment, the antigen binding molecule comprises a VH comprising an amino acid sequence of SEQ ID NO: 80 and a VL comprising an amino acid sequence of SEQ ID NO: 88. In another embodiment, the antigen binding molecule comprises a VH comprising an amino acid sequence of SEQ ID NO: 81 and a VL comprising an amino acid sequence of SEQ ID NO: 89. In another embodiment, the antigen binding molecule comprises a VH comprising an amino acid sequence of SEQ ID NO: 82 and a VL comprising an amino acid sequence of SEQ ID NO: 90. In another embodiment, the antigen binding molecule comprises a VH comprising an amino acid sequence of SEQ ID NO: 83 and a VL comprising an amino acid sequence of SEQ ID NO: 91. In another embodiment, the antigen binding molecule comprises a VH comprising an amino acid sequence of SEQ ID NO: 84 and a VL comprising an amino acid sequence of SEQ ID NO: 92.

[0195] In one particular embodiment, the polynucleotide of the present invention comprises a nucleotide sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 61-68. In another embodiment, the polynucleotide of the present invention comprises a nucleotide sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 69-76.

[0196] Other known anti-BCMA antibodies or antigen binding molecules thereof can be used as antigen binding molecules of a CAR or TCR comprising a THD of the present invention. Non-limiting examples of such BCMA antibodies or antigen binding molecule thereof include antibodies or antigen binding molecules described in WO2015158671A1, published October 22, 2015 and WO2016014565A2, published January 28, 2016.

[0197] In some embodiments, the antigen binding molecule specifically binds CLL-1. In certain embodiments, the antigen binding molecule comprises (a) a VH CDR1 comprising

an amino acid sequence selected from SEQ ID NOs: 93-96; (b) a VH CDR2 comprising an amino acid sequence selected from SEQ ID NOs: 97-100; (c) a VH CDR3 comprising an amino acid sequence selected from SEQ ID NOs: 101-104; (d) a VL CDR1 comprising an amino acid sequence selected from SEQ ID NOs: 105-108; (e) a VL CDR2 comprising an amino acid sequence selected from SEQ ID NOs: 109-112; and/or (f) a VL CDR3 comprising an amino acid sequence selected from SEQ ID NOs: 113-116.

[0198] In one embodiment, the antigen binding molecule comprises (a) a VH CDR1 comprising an amino acid of SEQ ID NO: 93; (b) a VH CDR2 comprising an amino acid sequence of SEQ ID NO: 97; (c) a VH CDR3 comprising an amino acid sequence of SEQ ID NO: 101; (d) a VL CDR1 comprising an amino acid sequence of SEQ ID NO: 105; (e) a VL CDR2 comprising an amino acid sequence of SEQ ID NO: 109; and/or (f) a VL CDR3 comprising an amino acid sequence of SEQ ID NO: 113.

[0199] In one embodiment, the antigen binding molecule comprises (a) a VH CDR1 comprising an amino acid of SEQ ID NO: 94; (b) a VH CDR2 comprising an amino acid sequence of SEQ ID NO: 98; (c) a VH CDR3 comprising an amino acid sequence of SEQ ID NO: 102; (d) a VL CDR1 comprising an amino acid sequence of SEQ ID NO: 106; (e) a VL CDR2 comprising an amino acid sequence of SEQ ID NO: 110; and/or (f) a VL CDR3 comprising an amino acid sequence of SEQ ID NO: 114.

[0200] In one embodiment, the antigen binding molecule comprises (a) a VH CDR1 comprising an amino acid of SEQ ID NO: 95; (b) a VH CDR2 comprising an amino acid sequence of SEQ ID NO: 99; (c) a VH CDR3 comprising an amino acid sequence of SEQ ID NO: 103; (d) a VL CDR1 comprising an amino acid sequence of SEQ ID NO: 107; (e) a VL CDR2 comprising an amino acid sequence of SEQ ID NO: 111; and/or (f) a VL CDR3 comprising an amino acid sequence of SEQ ID NO: 115.

[0201] In one embodiment, the antigen binding molecule comprises (a) a VH CDR1 comprising an amino acid of SEQ ID NO: 96; (b) a VH CDR2 comprising an amino acid sequence of SEQ ID NO: 100; (c) a VH CDR3 comprising an amino acid sequence of SEQ ID NO: 104; (d) a VL CDR1 comprising an amino acid sequence of SEQ ID NO: 108; (e) a VL CDR2 comprising an amino acid sequence of SEQ ID NO: 112; and/or (f) a VL CDR3 comprising an amino acid sequence of SEQ ID NO: 116.

[0202] In certain embodiments, the antigen binding molecule comprises a VH comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 125-128 and a VL comprising an amino acid sequence selected from the group consisting of SEQ

ID NOs: 129-132. In one embodiment, the antigen binding molecule comprises a VH comprising an amino acid sequence of SEQ ID NO: 125 and a VL comprising an amino acid sequence of SEQ ID NO: 129. In another embodiment, the antigen binding molecule comprises a VH comprising an amino acid sequence of SEQ ID NO: 126 and a VL comprising an amino acid sequence of SEQ ID NO: 130. In another embodiment, the antigen binding molecule comprises a VH comprising an amino acid sequence of SEQ ID NO: 127 and a VL comprising an amino acid sequence of SEQ ID NO: 131. In another embodiment, the antigen binding molecule comprises a VH comprising an amino acid sequence of SEQ ID NO: 128 and a VL comprising an amino acid sequence of SEQ ID NO: 132.

[0203] In one particular embodiment, the polynucleotide of the present invention comprises a nucleotide sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 117-120. In another embodiment, the polynucleotide of the present invention comprises a nucleotide sequence at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 121-124.

[0204] Other examples of anti-CLL-1 antibodies or antigen binding molecules thereof include antibodies or antigen binding molecules described in WO2016014535, published January 28, 2016, and US 2016/0051651 A1, published Feb. 25, 2016.

[0205] The antigen binding molecule encoded by the polynucleotide of the present invention can be single chained or double chained. In some embodiments, the antigen binding molecule is single chained. In certain embodiments, the antigen binding molecule is selected from the group consisting of an scFv, an Fab, an Fab', an Fv, an F(ab')₂, a dAb, and any combination thereof. In one particular embodiment, the antigen binding molecule comprises an scFv.

[0206] In certain embodiments, the antigen binding molecule comprises a single chain, wherein the heavy chain variable region and the light chain variable region are connected by a linker. In some embodiments, the VH is located at the N terminus of the linker and the VL is located at the C terminus of the linker. In other embodiments, the VL is located at the N terminus of the linker and the VH is located at the C terminus of the linker. In some

embodiments, the linker comprises at least about 5, at least about 8, at least about 10, at least about 13, at least about 15, at least about 18, at least about 20, at least about 25, at least about 30, at least about 35, at least about 40, at least about 45, at least about 50, at least about 60, at least about 70, at least about 80, at least about 90, or at least about 100 amino acids. In some
 5 embodiments, the linker comprises at least about 18 amino acids. In certain embodiments, the linker comprises an amino acid sequence that is at least about 75%, at least about 85%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or 100% identical to the amino acid sequence
 10 GSTSGSGKPGSGEGSTKG (SEQ ID NO: 12) or the amino acid sequence GGGGSGGGGSGGGGS (SEQ ID NO: 237). In one embodiment, the linker is a Whitlow linker. In certain embodiments, the binding molecule comprises a single chain, wherein the heavy chain variable region and the light chain variable region are connected by a linker, wherein the linker comprises the amino acid sequence of SEQ ID NO: 12.

[0207] In some embodiments, the antigen binding molecule binds a target antigen (*e.g.*,
 15 human BCMA, human FLT3, or human CLL-1) with a K_D of less than 1×10^{-6} M, less than 1×10^{-7} M, less than 1×10^{-8} M, or less than 1×10^{-9} M. In one particular embodiment, the antigen binding molecule binds a target antigen (*e.g.*, human BCMA, human FLT3, or human CLL-1) with a K_D of less than 1×10^{-7} M. In another embodiment, the antigen binding molecule binds
 20 a target antigen (*e.g.*, human BCMA, human FLT3, or human CLL-1) with a K_D of less than 1×10^{-8} M. In some embodiments, the antigen binding molecule binds a target antigen (*e.g.*, human BCMA, human FLT3, or human CLL-1) with a K_D of about 1×10^{-7} M, about 2×10^{-7} M, about 3×10^{-7} M, about 4×10^{-7} M, about 5×10^{-7} M, about 6×10^{-7} M, about 7×10^{-7} M, about 8×10^{-7} M, about 9×10^{-7} M, about 1×10^{-8} M, about 2×10^{-8} M, about 3×10^{-8} M, about
 25 4×10^{-8} M, about 5×10^{-8} M, about 6×10^{-8} M, about 7×10^{-8} M, about 8×10^{-8} M, about 9×10^{-8} M, about 1×10^{-9} M, about 2×10^{-9} M, about 3×10^{-9} M, about 4×10^{-9} M, about 5×10^{-9} M, about 6×10^{-9} M, about 7×10^{-9} M, about 8×10^{-9} M, about 9×10^{-9} M, about 1×10^{-10} M, or about 5×10^{-10} M. In certain embodiments, the K_D is calculated as the quotient of k_{off}/k_{on} , and the k_{on} and k_{off} are determined using a monovalent antibody, such as a Fab fragment, as measured by, *e.g.*, BIAcore[®] surface plasmon resonance technology. In other embodiments,
 30 the K_D is calculated as the quotient of k_{off}/k_{on} , and the k_{on} and k_{off} are determined using a bivalent antibody, such as a Fab fragment, as measured by, *e.g.*, BIAcore[®] surface plasmon resonance technology.

[0208] In some embodiments, the antigen binding molecule binds a target antigen (*e.g.*, human BCMA, human FLT3, or human CLL-1) with an association rate (k_{on}) of less than $1 \times 10^{-4} \text{ M}^{-1} \text{ s}^{-1}$, less than $2 \times 10^{-4} \text{ M}^{-1} \text{ s}^{-1}$, less than $3 \times 10^{-4} \text{ M}^{-1} \text{ s}^{-1}$, less than $4 \times 10^{-4} \text{ M}^{-1} \text{ s}^{-1}$, less than $5 \times 10^{-4} \text{ M}^{-1} \text{ s}^{-1}$, less than $6 \times 10^{-4} \text{ M}^{-1} \text{ s}^{-1}$, less than $7 \times 10^{-4} \text{ M}^{-1} \text{ s}^{-1}$, less than $8 \times 10^{-4} \text{ M}^{-1} \text{ s}^{-1}$, less than $9 \times 10^{-4} \text{ M}^{-1} \text{ s}^{-1}$, less than $1 \times 10^{-5} \text{ M}^{-1} \text{ s}^{-1}$, less than $2 \times 10^{-5} \text{ M}^{-1} \text{ s}^{-1}$, less than $3 \times 10^{-5} \text{ M}^{-1} \text{ s}^{-1}$, less than $4 \times 10^{-5} \text{ M}^{-1} \text{ s}^{-1}$, less than $5 \times 10^{-5} \text{ M}^{-1} \text{ s}^{-1}$, less than $6 \times 10^{-5} \text{ M}^{-1} \text{ s}^{-1}$, less than $7 \times 10^{-5} \text{ M}^{-1} \text{ s}^{-1}$, less than $8 \times 10^{-5} \text{ M}^{-1} \text{ s}^{-1}$, less than $9 \times 10^{-5} \text{ M}^{-1} \text{ s}^{-1}$, less than $1 \times 10^{-6} \text{ M}^{-1} \text{ s}^{-1}$, less than $2 \times 10^{-6} \text{ M}^{-1} \text{ s}^{-1}$, less than $3 \times 10^{-6} \text{ M}^{-1} \text{ s}^{-1}$, less than $4 \times 10^{-6} \text{ M}^{-1} \text{ s}^{-1}$, less than $5 \times 10^{-6} \text{ M}^{-1} \text{ s}^{-1}$, less than $6 \times 10^{-6} \text{ M}^{-1} \text{ s}^{-1}$, less than $7 \times 10^{-6} \text{ M}^{-1} \text{ s}^{-1}$, less than $8 \times 10^{-6} \text{ M}^{-1} \text{ s}^{-1}$, less than $9 \times 10^{-6} \text{ M}^{-1} \text{ s}^{-1}$, or less than $1 \times 10^{-7} \text{ M}^{-1} \text{ s}^{-1}$. In certain embodiments, the k_{on} is determined using a monovalent antibody, such as a Fab fragment, as measured by, *e.g.*, BIAcore® surface plasmon resonance technology. In other embodiments, the k_{on} is determined using a bivalent antibody as measured by, *e.g.*, BIAcore® surface plasmon resonance technology.

[0209] In some embodiments, the antigen binding molecule binds a target antigen (*e.g.*, human BCMA, human FLT3, or human CLL-1) with an dissociation rate (k_{off}) of less than $1 \times 10^{-2} \text{ s}^{-1}$, less than $2 \times 10^{-2} \text{ s}^{-1}$, less than $3 \times 10^{-2} \text{ s}^{-1}$, less than $4 \times 10^{-2} \text{ s}^{-1}$, less than $5 \times 10^{-2} \text{ s}^{-1}$, less than $6 \times 10^{-2} \text{ s}^{-1}$, less than $7 \times 10^{-2} \text{ s}^{-1}$, less than $8 \times 10^{-2} \text{ s}^{-1}$, less than $9 \times 10^{-2} \text{ s}^{-1}$, less than $1 \times 10^{-3} \text{ s}^{-1}$, less than $2 \times 10^{-3} \text{ s}^{-1}$, less than $3 \times 10^{-3} \text{ s}^{-1}$, less than $4 \times 10^{-3} \text{ s}^{-1}$, less than $5 \times 10^{-3} \text{ s}^{-1}$, less than $6 \times 10^{-3} \text{ s}^{-1}$, less than $7 \times 10^{-3} \text{ s}^{-1}$, less than $8 \times 10^{-3} \text{ s}^{-1}$, less than $9 \times 10^{-3} \text{ s}^{-1}$, less than $1 \times 10^{-4} \text{ s}^{-1}$, less than $2 \times 10^{-4} \text{ s}^{-1}$, less than $3 \times 10^{-4} \text{ s}^{-1}$, less than $4 \times 10^{-4} \text{ s}^{-1}$, less than $5 \times 10^{-4} \text{ s}^{-1}$, less than $6 \times 10^{-4} \text{ s}^{-1}$, less than $7 \times 10^{-4} \text{ s}^{-1}$, less than $8 \times 10^{-4} \text{ s}^{-1}$, less than $9 \times 10^{-4} \text{ s}^{-1}$, less than $1 \times 10^{-4} \text{ s}^{-1}$, or less than $5 \times 10^{-4} \text{ s}^{-1}$. In certain embodiments, the k_{off} is determined using a monovalent antibody, such as a Fab fragment, as measured by, *e.g.*, BIAcore® surface plasmon resonance technology. In other embodiments, the k_{off} is determined using a bivalent antibody as measured by, *e.g.*, BIAcore® surface plasmon resonance technology.

[0210] In some embodiments, the polynucleotide encodes a TCR, wherein the TCR further comprises a fourth complementarity determining region (CDR4). In certain embodiments, the polynucleotide encodes a TCR, wherein the TCR further comprises a constant region. In some embodiments, the constant region is selected from a constant region of IgG1, IgG2, IgG3, IgG4, IgA, IgD, IgE, and IgM.

I.D. Switch Domain

[0211] It will be appreciated that adverse events may be minimized by transducing the immune cells (containing one or more CARs or TCRs) with a suicide gene. It may also be desired to incorporate an inducible “on” or “accelerator” switch into the immune cells. Suitable techniques include use of inducible caspase-9 (U.S. Appl. 2011/0286980) or a thymidine kinase, before, after or at the same time, as the cells are transduced with the CAR construct of the present invention. Additional methods for introducing suicide genes and/or “on” switches include TALENS, zinc fingers, RNAi, siRNA, shRNA, antisense technology, and other techniques known in the art.

[0212] In accordance with the invention, additional on-off or other types of control switch techniques may be incorporated herein. These techniques may employ the use of dimerization domains and optional activators of such domain dimerization. These techniques include, e.g., those described by Wu et al., Science 2014 350 (6258) utilizing FKBP/Rapalog dimerization systems in certain cells, the contents of which are incorporated by reference herein in their entirety. Additional dimerization technology is described in, e.g., Fegan et al. Chem. Rev. 2010, 110, 3315–3336 as well as U.S. Patent Nos. 5,830,462; 5,834,266; 5,869,337; and 6,165,787, the contents of which are also incorporated by reference herein in their entirety. Additional dimerization pairs may include cyclosporine-A/cyclophilin, receptor, estrogen/estrogen receptor (optionally using tamoxifen), glucocorticoids/glucocorticoid receptor, tetracycline/tetracycline receptor, vitamin D/vitamin D receptor. Further examples of dimerization technology can be found in e.g., WO 2014/127261, WO 2015/090229, US 2014/0286987, US 2015/0266973, US 2016/0046700, U.S. Patent No. 8,486,693, US 2014/0171649, and US 2012/0130076, the contents of which are further incorporated by reference herein in their entirety.

I.E. Leader Peptide

[0213] In some embodiments, the polynucleotide of the present invention encodes a CAR or a TCR can further comprises a leader peptide (also referred to herein as a “signal peptide”). In certain embodiments, the leader peptide comprises an amino acid sequence that is at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or 100% identical to the amino acid sequence MALPVTALLLPLALLLHAARP (SEQ ID NO: 11). In some embodiments, the leader peptide comprises the amino acid sequence of SEQ ID NO: 11.

[0214] In some embodiments, the polynucleotide of the present invention encodes a CAR or a TCR, wherein the CAR or the TCR comprises a leader peptide (P), an antigen binding molecule (B), a costimulatory protein's extracellular domain (E), a transmembrane domain (T), a costimulatory region (C), and an activation domain (A), wherein the CAR is configured according to the following: P-B-E-T-C-A. In some embodiments, the antigen binding molecule comprises a VH and a VL, wherein the CAR is configured according to the following: P-VH-VL-E-T-C-A or P-VL-VH-E-T-C-A. In some embodiments, the VH and the VL are connected by a linker (L), wherein the CAR is configured according to the following, from N-terminus to C-terminus: P-VH-L-VL-E-T-C-A or P-VH-L-VL-E-T-C-A.

[0215] In some embodiments, the polynucleotide of the present invention encodes a CAR, wherein the CAR comprises an amino acid sequence at least about 75%, at least about 85%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or 100% identical to an amino acid sequence selected from Table 2. In certain embodiments, the polynucleotide of the present invention encodes a CAR, wherein the CAR comprises an amino acid sequence selected from Table 2.

[0216] Table 2. Example CAR Sequences

CAR Construct	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:
10E3_CHD	ATGGCACTCCCCGTAAGTCTGCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCGCAGGTGACCCTCAAAGAGTCTGGA CCCGTGCTCGTAAACCTACGGAGACCCTGACACTCACCTGCACAGTCTCCGGCTTCA GCCTCATCAATGCCAGGATGGGAGTTTCC TGGATCAGGCAACCGCCGAAAGGCCCT GGAATGGCTCGCACATATTTTCAGTAACG CTGAAAAAGCTATCGGACTTCTCTGAAA AGTCGGCTCACGATTAGTAAGGACACATC CAAGAGCCAAGTGGTGTACGATGACTA ACATGGACCCTGTGGATACTGCAACCTAT TACTGTGCTCGAATCCCTGGTTATGGCGG AAATGGGGACTACCACTACTACGGTATGG ATGTCTGGGGCCAAGGGACCACGGTTACT GTTTCAAGCGGAGGGGAGGGAGTGGGGG TGGCGGATCTGGCGGAGGAGGCAGCGATA TCCAGATGACGCAGTCCCCTAGTTCACTT TCCGCATCCCTGGGGGATCGGGTTACCAT TACATGCCGCGCGTCACAGGTATCCGGA ATGATCTGGGATGGTACCAGCAGAAGCCG GGAAAGGCTCCTAAGCGCTCATCTACGC CAGCTCCACCCTGCAGAGTGGAGTGCCTT CCCGGTTTTTCAGGCAGTGGCTCCGGTACG GAGTTTACTCTTACAATTAGCAGCCTGCA GCCAGAAGATTTTGCAACTTACTACTGTT	242	MALPVTALLLLPLALLL HAARPQVTLKESGPVL VKPTETLTLTCTVSGF SLINARMGVSWIRQPP GKALEWLAHIFSNAEK SYRTSLKSRLTISKDT SKSQVVLMTNMDPVD TATYYCARIPGYGGNG DYHYYGMDVWGQTTV TVSSGGGSGGGSGG GGS DIQMTQSPSSLSA SLGDRVITICRASQGI RNDLGWYQQKPKAPK RLIYASSTLQSGVPSR FSGSGSGTEFTLTIS LQPEDFATYYCLQHNN FPWTFGQTKVEIKRA AAIEVMYPPPYLDNEK SNGTIIHVGKHLCP S PLFPGPSKPFVWL VV GGV LACYSLLVTVAFI IFWVRSKRSRLHSDY MNMTPRRPGPTRKHYQ PYAPPRDFAAYRSRVK FSR SADAPAYQQGQNQ LYNELNLGRREYDVL	243

	TGCAGCATAATAATTTCCCCTGGACCTTT GGTCAGGGCACCAAGGTGGAGATCAAAAG AGCAGCCGCCATCGAAGTAATGTATCCCC CCCCGTACCTTGACAATGAGAAGTCAAAT GGAACCATTATCCATGTTAAGGGCAAACA CCTCTGCCCTTCTCCACTGTTCCCTGGCC CTAGTAAGCCGTTTTGGGTGCTGGTGGTA GTCGGTGGGGTGCTGGCTTGTTACTCTCT TCTCGTGACCGTCGCCTTTATAATCTTTT GGGTGAGATCCAAAAGAAGCCGCCTGCTC CATAGCGATTACATGAATATGACTCCACG CCGCCCTGGCCCCACAAGGAAACACTACC AGCCTTACGCACCACCTAGAGATTTGCT GCCTATCGGAGCCGAGTGAAATTTTCTAG ATCAGCTGATGCTCCCGCTATCAGCAGG GACAGAATCAACTTTACAATGAGCTGAAC CTGGGTGCGCAGAGAAGAGTACGACGTTTT GGACAAACGCCGGGGCCGAGATCCTGAGA TGGGGGGGAAGCCGAGAAGGAAGAATCCT CAAGAAGGCCTGTACAACGAGCTTCAAAA AGACAAAATGGCTGAGGCGTACTCTGAGA TCGGCATGAAGGGCGAGCGGAGACGAGGC AAGGGTCACGATGGCTTGATCAGGGCCT GAGTACAGCCACAAAGGACACCTATGACG CCCTCCACATGCAGGCACTGCCCCACGC TAG		DKRRGRDPEMGGKPRR KNPQEGLYNELQKDKM AEAYSEIGMKGERRRG KGHDGLYQGLSTATKD TYDALHMQALPPR	
10E3_THD	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCCGAAGTTACTTTGAAGGAGTCTGGA CCTGTACTGGTGAAGCCAACCGAGACACT GACACTCACGTGTACAGTGAGTGGTTTTT CCTTGATCAACGCAAGGATGGGCGTCAGC TGGATCAGGCAACCCCTGGCAAGGCTCT GGAATGGCTCGCTCACATATTCAGCAATG CCGAAAAAAGCTACCGGACAAGCCTGAAA TCCCGCCTGACTATTTCCAAGGACACTTC TAAGTCTCAGGTGGTGCTGACCATGACCA ACATGGACCCGGTGGACACCGCCACCTAT TACTGCGCAAGAATCCCTGGGTATGGTGG GAATGGTGACTACCATTATTATGGGATGG ATGTGTGGGGGCAAGGCACAACCGTAACG GTCTCAAGCGGTGGGGGAGGCTCAGGGGG CGGAGGCTCCGGAGGTGGCGGCTCCGACA TTCAGATGACCCAAAGCCCGTCCAGCCTG TCCGCCAGCCTGGGAGATAGAGTGACAAT CACGTGTAGAGCTTCCCAAGGGATAAGAA ATGATCTCGGGTGGTATCAGCAGAAGCCC GGCAAAGCCCCCAAAGGCTTATATATGC TAGTAGTACACTGCAGTCTGGAGTTCCTT CCCGATTTTCAGGTAGCGGCTCCGGTACA GAGTTCACCCTCACGATAAGCTCACTCCA GCCTGAGGATTTTCGAACGTACTACTGCC TCCAGCACACAATTTTCCCTGGACTTTC GGCCAGGGCACCAAGGTGGAGATCAAGAG GGCCGCTGCCCTTGATAATGAAAAGTCAA ACGGAACAATCATTCACGTGAAGGGCAAG CACCTCTGTCCGTCACCTTGTTCCCTGG TCCATCCAAGCCATTCTGGGTGTTGGTCG TAGTGGGTGGAGTCTCGCTTGTTACTCT	244	MALPVTALLLPLALLL HAARPQVTLKESGPVL VKPTETLTLTCTVSGF SLINARMGVSWIRQPP GKALEWLAHIFSNAEK SYRTSLKSRLTISKDT SKSQVVLMTNMDPVD TATYYCARIPGYGGNG DYHYYGMDVWGQGTTV TVSSGGGSGGGGSGG GGSDIQMTQSPSSL SLGDRVITICRASQGI RNDLGWYQQKPGKAPK RLIYASSTLQSGVPSR FSGSGSGTEFTLTIS LQPEDFATYYCLQHN FPWTFGQGTKVEIKRA AALDNEKSNGTIIHVK GKHLCPSPFLFPGPSK FWVLVVVGVLACYSL LVTVAFIIFWVRSKRS RLLHSDYMNMTPRRPG PTRKHYQPYAPPRDFA AYRSRVKFSRSADAPA YQQGQNQLYNELNLGR REEYDVLDRRGRDPE MGGKPRRKNPQEGLYN ELQDKMAEAYSEIGM KGERRRGKGHDGLYQG LSTATKDTYDALHMQA LPPR	245

	CTGCTCGTCACCGTGGCTTTTATAATCTT CTGGGTTAGATCCAAAAGAAGCCGCCTGC TCCATAGCGATTACATGAATATGACTCCA CGCCGCCCTGGCCCCACAAGGAAACACTA CCAGCCTTACGCACCACCTAGAGATTTCTG CTGCCTATCGGAGCCGAGTGAAATTTTCT AGATCAGCTGATGCTCCCGCCTATCAGCA GGGACAGAATCAACTTTACAATGAGCTGA ACCTGGGTCGCAGAGAAGAGTACGACGTT TTGGACAAACGCCGGGGCCGAGATCCTGA GATGGGGGGGAAGCCGAGAAGGAAGAATC CTCAAGAAGGCCTGTACAACGAGCTTCAA AAAGACAAAATGGCTGAGGCGTACTCTGA GATCGGCATGAAGGGCGAGCGGAGACGAG GCAAGGGTCACGATGGCTTGTATCAGGGC CTGAGTACAGCCACAAAGGACACCTATGA CGCCCTCCACATGCAGGCACTGCCCCAC GCTAG			
8B5_CHD	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCCGAGATCCAGTTGGTGGAATCAGGG GGCGGTGTGGTGCAGCCGGGTAGGAGCCT GAGACTGTCATGCGTGGCGTCTGGCTTCA CATTCAAGAACTACGGCATGCACTGGGTG CGACAGGCCCCCGAAAGGGTTTGGAGTG GGTCGCCGTGATCTGGTACGACGGATCTA ATGAGTATTACGGAGATCCTGTGAAGGGA AGGTTACCATTCTCCCGCACAATAGCAA AAATATGCTCTACCTGCAAATGAACTCAC TCAGGGCGGATGATACGGCGGTCTACTAT TGCGCTCGCTCAGGGATTGCTGTGGCCGG CGCATTTCGATTACTGGGGACAGGGTACCC TGGTGACAGTATCAAGCGGAGGCGGCGGC TCTGGCGGCGGCGGATCTGGCGGGGGGG AAGTGAGATTGTGTTGACACAGTCTCCCG ATACCCTGTCACTGTCAACCGGCGAGAAG GCAACGCTGAGTTGCAGAGCAAGCCAGTC AGTCTCCTCTTCTTTTCTGGCCTGGTATC AGCAAAAACCAGGTACGGCACCATTCTCTC CTGATTTACGTTGCCAGCAGACGGGCGGC TGGCATTCCCGACAGGTTCTCTGGAAGCG GATCTGGGACCGATTTTACCCTGACAATT AGCCGCTTGGAGCCCCGAAGACTTTGGTAT GTTTTACTGCCAGCACTACGGAAGGACAC CTTTCACATTTGGCCCCGGGCACGAAAGTC GATATAAAACGCGCAGCCGCCATTGAAGT AATGTACCCACCACCTTATTTGGACAATG AAAAGTCCAATGGTACCATTATTCACGTC AAGGGAAAGCATCTCTGTCCAAGCCCTCT GTTCCCCGGCCCCCTCAAACCATTCTGGG TGCTGGTGGTCTGTCGGCGGAGTTCTGGCC TGCTATTCTCTGCTCGTGACTGTTGCATT CATCATTTTCTGGGTGAGATCCAAAAGAA GCCGCCTGCTCCATAGCGATTACATGAAT ATGACTCCACGCCGCCCTGGCCCCACAAG GAAACACTACCAGCCTTACGCACCACCTA GAGATTTCTGCTGCCTATCGGAGCCGAGTG AAATTTTCTAGATCAGCTGATGCTCCCGC CTATCAGCAGGGACAGAATCAACTTTACA	246	MALPVTALLLPLALLL HAARFQIQLVESGGGV VQPGRSRLRLSCVASGF TFKNYGMHWVRQAPGK GLEWVAWIWYDGSNEY YGDVVKGRFTISRDNS KNMLYLQMNSLRADDT AVYYCARSGIAVAGAF DYWGQGLVTVSSGGG GSGGGSGGGGSEIVL TQSPDTLSLSPGEKAT LSCRASQSVSSSFLAW YQQKPGQAPSLLIYVA SRRAAGIPDRFSGSGS GTDFTLTISRLEPEDF GMFYCQHYGRTPFTFG PGTKVDIKRAAAIEVM YPPPYLDNEKSNGTII HVKGKHLCPSPFPGP SKPFWVLVVGGVLAC YSLLVTVAFIIFWVRS KRSRLHSDYMNMTPR RPGPTRKHYPYAPPR DFAAYRSRVKFSRSAD APAYQQGQNQLYNELN LGRREEYDVLDRRRGR DPEMGGKPRRKNPQEG LYNELQKDKMAEAYSE IGMKGERRRGKHDGL YQGLSTATKDYDALH MQALPPR	247

	ATGAGCTGAACCTGGGTGCGAGAGAAGAG TACGACGTTTTGGACAAACGCCGGGGCCG AGATCCTGAGATGGGGGGGAAGCCGAGAA GGAAGAATCCTCAAGAAGGCCTGTACAAC GAGCTTCAAAAAGACAAAATGGCTGAGGC GTACTCTGAGATCGGCATGAAGGGCGAGC GGAGACGAGGCAAGGGTCACGATGGCTTG TATCAGGGCCTGAGTACAGCCACAAAGGA CACCTATGACGCCCTCCACATGCAGGCAC TGCCCCCAGCTAG			
8B5_THD	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCCGAGATTCAGCTCGTGGAGTCAGGT GGTGGCGTGGTTCAGCCCGACGGTCCCT GCGACTCTCTTGTGTGGCAAGCGGATTTA CCTTTAAGAAGTATGGCATGCACTGGGTG AGGCAGGCCCCCTGGAAAAGGACTGGAGTG GGTTGCTGTGATCTGGTACGACGGGTCCA ACGAATATTATGGCGATCCTGTGAAGGGA CGGTTTACAATCTCACGCGATAACTCAA GAACATGCTGTACCTGCAAATGAAGTCTC TGCGCGCTGATGACACTGCCGTGTATTAT TGCGCTCGGAGTGGTATCGCCGTGCGAGG AGCATTGATTATTGGGGGCAAGGGACCC TCGTGACAGTGAGTTCGGGAGGGGGAGGT TCTGGTGGAGGCGGCTCTGGTGGGGGAGG CAGCGAGATCGTTCTGACCCAGTCTCCTG ACACACTGTCACTGTCCCCTGGTGAAGAAG GCCACACTGTCTTGTAGAGCGTCCAGAG CGTTTCCAGTTCCTTCCTTGCATGGTATC AACAAAAACCCGGGCAGGCTCCAAGCTTG CTGATCTACGTGGCCAGCCGCCGGGCCGC AGGCATCCCTGATAGGTTTTAGCGGTTCTG GGAGCGGGACGGACTTCACCTTGACAATA TCACGGCTGGAACCCGAAGACTTCGGAAT GTTTTATTGCCAGCACTACGGAAGAACTC CATTCACCTTTGGCCCGGGAACGAAGGTA GACATCAAGAGAGCAGCAGCCCTCGACAA CGAGAAATCCAATGGAACCATATCCATG TGAAGGGGAAACATCTCTGCCCTTACCA TTGTTCCCTGGACCCAGCAAGCCTTTTTG GGTTCTGGTCTGGTGGGGGGCGTCTGG CTTGTTACTCCCTCCTCGTTACAGTCGCC TTCATAATCTTTTGGGTTAGATCCAAAAG AAGCCGCCTGCTCCATAGCGATTACATGA ATATGACTCCACGCCGCCCTGGCCCCACA AGGAAACACTACCAGCCTTACGCACCACC TAGAGATTTGCTGCCTATCGGAGCCGAG TGAAATTTTCTAGATCAGCTGATGCTCCC GCCTATCAGCAGGGACAGAATCAACTTTA CAATGAGCTGAACCTGGGTGCGAGAGAAG AGTACGACGTTTTGGACAAACGCCGGGGC CGAGATCCTGAGATGGGGGGGAAGCCGAG AAGGAAGAATCCTCAAGAAGGCCTGTACA ACGAGCTTCAAAAAGACAAAATGGCTGAG GCGTACTCTGAGATCGGCATGAAGGGCGA GCGGAGACGAGGCAAGGGTCACGATGGCT TGTATCAGGGCCTGAGTACAGCCACAAAG	248	MALPVTALLLPLALLL HAARPQIQLVESGGGV VQPGRSLRLSCVASGF TFKNYGMHWVRQAPGK GLEWVAWIWYDGSNEY YGDPVKGRFTISRDN KNMLYLQMNSLRADD AVYYCARSGIAVAGAF DYWQGTLLVTVSSGGG GSGGGSGGGGSEIVL TQSPDTLSLSPGEKAT LSCRASQSVSSSFLAW YQQKPGQAPSLLIYVA SRRAAGIPDRFSGSGS GTDFTLTISRLEPEDF GMFYCQHYGRTPFTFG PGTKVDIKRAAALDNE KSGNTIIHVKGKHLCP SPLEFGPSKPFWVLVV VGGVLACYSLLVTVA IIIFWVRSKRSRLHSD YMNMTPRRPGPTRKHY QPYAPPRDFAAYRSRV KFSRSADAPAYQQGQN QLYNELNLGRREEYDV LDKRRGRDPEMGGKPR RKNPQEGLYNELQKDK MAEAYSEIGMKGERRR GKGHDGLYQGLSTATK DTYDALHMQALPPR	249

	GACACCTATGACGCCCTCCACATGCAGGC ACTGCCCCCAGCTAG			
FS- 21495CARHx L	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCCGAGGTGCAGCTGTTGGAGTCTGGG GGAGGCTTGGTACAGCCTGGGGGGTCCCT GAGACTCTCCTGTGCAGCCTCTGGATTCA CCTTTAGCAGCTATGCCATGAGCTGGGTC CGCCAGGCTCCAGGGAAGGGGCTGGAGTG GGTCTCAGCTATTAGTGGTAGTGGTGGTA GCACATACTACGCAGACTCCGTGAAGGGC CGGTTCCACATCTCCAGAGACAATTCCAA GAACACGCTGTATCTGCAAATGAACAGCC TGAGAGCCGAGGACACGGCGGTGTACTAC TGCGCAAGAGCCGAGATGGGAGCCGTATT CGACATATGGGGTCAGGGTACAATGGTCA CCGTCTCCTCAGGGTCTACATCCGGCTCC GGGAAGCCCCGAAGTGGCGAAGGTAGTAC AAAGGGGGAAATTGTGTTGACACAGTCTC CAGCCACCCTGTCTTTGTCTCCAGGGGAA AGAGCCACCCTCTCCTGCAGGGCCAGTCA GAGTGTTAGCAGGTACTTAGCCTGGTACC AACAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGATGCATCCAACAGGGCCAC TGGCATCCCAGCCAGGTTCACTGAGCAGTG GGTCTGGGACAGACTTCACTCTCACCATC AGCAGCCTAGAGCCTGAAGATTTTGCAGT TTATTACTGTGACGAGAGAATCTCCTGGC CTTTCACTTTTGGCGGAGGGACCAAGGTT GAGATCAAACGGGCGCTGCCCTTGATAA TGAAAAGTCAAACGGAACAATCATTCACG TGAAGGGCAAGCACCTCTGTCCGTCACCC TTGTTCCCTGGTCCATCCAAGCCATTCTG GGTGTGGTCTAGTGGGTGGAGTCCTCG CTTGTTACTCTCTGCTCGTCACCGTGGCT TTTATAATCTTCTGGGTTAGATCCAAAAG AAGCCGCCTGCTCCATAGCGATTACATGA ATATGACTCCACGCCGCCCTGGCCCCACA AGGAAACACTACCAGCCTTACGCACCACC TAGAGATTTGCTGCCTATCGGAGCAGGG TGAAGTTTTCAGATCTGCAGATGCACCA GCGTATCAGCAGGGCCAGAACCAACTGTA TAACGAGCTCAACCTGGGACGCAGGGAAG AGTATGACGTTTTGGACAAGCGCAGAGGA CGGGACCCTGAGATGGGTGGCAAACCAAG ACGAAAAAACCCCCAGGAGGGTCTCTATA ATGAGCTGCAGAAGGATAAGATGGCTGAA GCCTATTCTGAAATAGGCATGAAAGGAGA GCGGAGAAGGGGAAAAGGGCACGACGGTT TGTACCAGGGAAGTCACTGCTACGAAG GATACTTATGACGCTCTCCACATGCAAGC CCTGCCACCTAGGTAA	133	MALPVTALLLPLALLL HAARPEVQLLESGGGL VQPGGSLRLSCAASGF TFSSYAMSWVRQAPGK GLEWVSAISGSGGSTY YADSVKGRFTISRDN KNTLYLQMNSLRAEDT AVYYCARAEMGAVFDI WGQGTMTVSSGSTSG SGKPGSGEGSTKGEIV LTQSPATLSLSPGERA TLSCRASQSVSRYLAW YQQKPGQAPRLLIYDA SNRATGIPARFSGSGS GTDFTLTISSELPEDF AVYYCQQRISWPFTEG GGTKVEIKRAAALDNE KSNGTIIHVKGKHLCP SPLFPGSPKPFVWLVV VGGVLACYSLLVTVAF IIFWVRSKRSRLHSD YMNMTPRRPGPTRKHY QPYAPPRDFAAYRSRV KFSRSADAPAYQQGQN QLYNELNLGRREYDV LDKRRGRDPEMGKPR RKNPQEGLYNELQKDK MAEAYSEIGMKGERRR GKGHDGLYQGLSTATK DTYDALHMQALPPR	134
FS- 21495CARLx H	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCCGAAATTGTGTTGACACAGTCTCCA GCCACCCTGTCTTTGTCTCCAGGGGAAAG AGCCACCCTCTCCTGCAGGGCCAGTCAGA GTGTTAGCAGGTACTTAGCCTGGTACCAA CAGAAACCTGGCCAGGCTCCCAGGCTCCT	135	MALPVTALLLPLALLL HAARPEIVLTQSPATL SLSPGERATLSCRASQ SVSRYLAWYQQKPGQA PRLLIYDASNRATGIP ARFSGSGSGTDFTLTI SSLEPEDFAVYYCQQR	136

	CATCTATGATGCATCCAACAGGGCCACTG GCATCCCAGCCAGGTTCACTGGCAGTGGG TCTGGGACAGACTTCACTCTCACCATCAG CAGCCTAGAGCCTGAAGATTTTGCAGTTT ATTACTGTCAGCAGAGAATCTCCTGGCCT TTCACTTTTGGCGGAGGGACCAAGGTTGA GATCAAACGGGGGTCTACATCCGGCTCCG GGAAGCCCGGAAGTGGCGAAGGTAGTACA AAGGGGGAGGTGCAGCTGTTGGAGTCTGG GGGAGGCTTGGTACAGCCTGGGGGGTCCC TGAGACTCTCCTGTGCAGCCTCTGGATTCT ACCTTTAGCAGCTATGCCATGAGCTGGGT CCGCCAGGCTCCAGGGAAGGGGCTGGAGT GGGTCTCAGCTATTAGTGGTAGTGGTGGT AGCACATACTACGCAGACTCCGTGAAGGG CCGGTTCACCATCTCCAGAGACAATTCCA AGAACACGCTGTATCTGCAAATGAACAGC CTGAGAGCCGAGGACACGGCGGTGTACTA CTGCGCAAGAGCCGAGATGGGAGCCGTAT TCGACATATGGGGTCAGGGTACAATGGTC ACCGTCTCCTCAGCCGCTGCCCTTGATAA TGAAAAGTCAAACGGAACAATCATTCACG TGAAGGGCAAGCACCTCTGTCCGTACCCC TTGTTCCCTGGTCCATCCAAGCCATTCTG GGTGTGGTTCGTAGTGGGTGGAGTCTCTCG CTTGTTACTCTCTGCTCGTCACCGTGGCT TTTATAATCTTCTGGGTTAGATCCAAAAG AAGCCGCCTGCTCCATAGCGATTACATGA ATATGACTCCACGCCGCCCTGGCCCCACA AGGAAACACTACCAGCCTTACGCACCACC TAGAGATTTTCGCTGCCTATCGGAGCAGGG TGAAGTTTTCCAGATCTGCAGATGCACCA GCGTATCAGCAGGGCCAGAACCAACTGTA TAACGAGCTCAACCTGGGACGCAGGGAAG AGTATGACGTTTTGGACAAGCGCAGAGGA CGGGACCCTGAGATGGGTGGCAAACCAAG ACGAAAAAACCCCCAGGAGGGTCTCTATA ATGAGCTGCAGAAGGATAAGATGGCTGAA GCCTATTCTGAAATAGGCATGAAAGGAGA GCGGAGAAGGGGAAAAGGGCACGACGGTT TGTACCAGGGACTCAGCACTGCTACGAAG GATACTTATGACGCTCTCCACATGCAAGC CCTGCCACCTAGGTAA		ISWPFTFGGGTKVEIK RGSTSGSGKPGSGEGS TKGEVQLLESGLLVQ PGGSLRLSCAASGFTF SSYAMSWVRQAPGKGL EWVSAISGSGGSTYYA DSVKGRFTISRDN SKN TLYLQMNSLRAEDTAV YYCARAEMGAVFDIWG QGTMTVVSAAALDNE KSNGTIIHVKGKHLCP SPLFPGPSKPFVVLVV VGGVLACYSLLVTVAF IIFWVRSKRSRLHSD YMNMTPRRPGPTRKHY QPYAPPRDFAAYRSRV KFSSRSADAPAYQQGQN QLYNELNLGRREEYDV LDKRRGRDPEMGGKPR RKNPQEGLYNELQKDK MAEAYSEIGMKGERRR GKGHDGLYQGLSTATK DTYDALHMQALPPR	
PC- 21497CARHx L	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCCGAGGTGCAGCTGGTGGAGTCTGGG GGAGGCGTGGTCCAGCCTGGGAGGTCCCT GAGACTCTCCTGTGCAGCGTCTGGATTCA CCTTCAGTAGCTATGGCATGCACTGGGTC CGCCAGGCTCCAGGCAAGGGGCTGGAGTG GGTGGCAGTTATATCGTATGATGGAAGTA ATAAATACTATGCAGACTCCGTGAAGGGC CGATTACCATCTCCAGAGACAATTCCAA GAACACGCTGTATCTGCAAATGAACAGCC TGAGAGCCGAGGACACGGCGGTGTACTAC TGCGCCAGAGACGGTACTTATCTAGGTGG TCTCTGGTACTTTCGACTTATGGGGGAGAG GTACCTTGGTCACCGTCTCCTCAGGGTCT ACATCCGGCTCCGGAAGCCCGGAAGTGG	137	MALPVTALLLPLALLL HAARPQVQLVESGGGV VQPGRSLRLSCAASGF TFSSYGMHWVRQAPGK GLEWVAVISYDGSN KY YADSVKGRFTISRDN S KNTLYLQMNSLRAEDT AVYYCARDGTYLGGLW YFDLWGRGTLVTVSSG STSGSGKPGSGEGSTK GDIVMTQSPLSLPVT GEPASISCRSSQSL LH SNGYNYLDWYLQKPGQ SPQLLIYLGSNRASGV PDRFSGSGSGTDFTL K ISRVEAEDVGVYYCMQ	138

	CGAAGGTAGTACAAAGGGGGATATTGTGA TGACTCAGTCTCCACTCTCCCTGCCCCGTC ACCCCTGGAGAGCCGGCCTCCATCTCCTG CAGGTCTAGTCAGAGCCTCCTGCATAGTA ATGGATACAACCTATTTGGATTGGTACCTG CAGAAGCCAGGGCAGTCTCCACAGCTCCT GATCTATTTGGGTTCTAATCGGGCCTCCG GGGTCCCTGACAGGTTCACTGGCAGTGGA TCAGGCACAGATTTTACACTGAAAATCAG CAGAGTGGAGGCTGAGGATGTTGGGGTTT ATTACTGCATGCAGGGACTCGGCCTCCCT CTCACTTTTGGCGGAGGGACCAAGGTTGA GATCAAACGGGCGCTGCCCTTGATAATG AAAAGTCAAACGGAACAATCATTACGTG AAGGGCAAGCACCTCTGTCCGTCAACCTT GTTCCCTGGTCCATCCAAGCCATTCTGGG TGTTGGTCGTAGTGGGTGGAGTCCTCGCT TGTTACTCTCTGCTCGTCACCGTGGCTTT TATAATCTTCTGGGTTAGATCCAAAAGAA GCCGCCTGCTCCATAGCGATTACATGAAT ATGACTCCACGCCGCCCTGGCCCCACAAG GAAACACTACCAGCCTTACGCACCACCTA GAGATTTTCGCTGCCTATCGGAGCAGGGTG AAGTTTTCCAGATCTGCAGATGCACCAGC GTATCAGCAGGGCCAGAACCAACTGTATA ACGAGCTCAACCTGGGACGCAGGGAAGAG TATGACGTTTTTGGACAAGCGCAGAGGACG GGACCCTGAGATGGGTGGCAAACCAAGAC GAAAAAACCCCCAGGAGGGTCTCTATAAT GAGCTGCAGAAGGATAAGATGGCTGAAGC CTATTCTGAAATAGGCATGAAAGGAGAGC GGAGAAGGGGAAAAGGGCACGACGGTTTG TACCAGGGACTCAGCACTGCTACGAAGGA TACTTATGACGCTCTCCACATGCAAGCCC TGCCACCTAGGTAA		GLGLPLTFGGGTKVEI KRAAALDNEKSNGTII HVKGKHLCPSPLPFGP SKPFWVLVVVGGVLAC YSLLVTVAFIIFWVRS KRSRLHSDYMNMTPR RPGPTRKHYQPYAPPR DFAAYRSRVKFSRSAD APAYQQGQNQLYNELN LGRREEYDVLDKRRGR DPEMGGKPRRKNPQEG LYNELQKDKMAEAYSE IGMKGERRRRGKHDGL YQGLSTATKDTYDALH MQALPPR	
PC- 21497CARHx L	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCCGATATTGTGATGACTCAGTCTCCA CTCTCCCTGCCCCGTCACCCCTGGAGAGCC GGCCTCCATCTCCTGCAGGTCTAGTCAGA GCCTCCTGCATAGTAATGGATACAACCTAT TTGGATTGGTACCTGCAGAAGCCAGGGCA GTCTCCACAGCTCCTGATCTATTTGGGTT CTAATCGGGCCTCCGGGGTCCCTGACAGG TTCAGTGGCAGTGGATCAGGCACAGATTT TACACTGAAAATCAGCAGAGTGGAGGCTG AGGATGTTGGGGTTTATTACTGCATGCAG GGACTCGGCCTCCCTCTCACTTTTGGCGG AGGGACCAAGGTTGAGATCAAACGGGGGT CTACATCCGGCTCCGGGAAGCCCGGAAGT GGCGAAGGTAGTACAAAGGGGCAGGTGCA GCTGGTGGAGTCTGGGGGAGGCGTGGTCC AGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTACCTTCAGTAGCTA TGGCATGCACTGGGTCCGCCAGGCTCCAG GCAAGGGGCTGGAGTGGGTGGCAGTTATA TCGTATGATGGAAGTAATAAATACTATGC AGACTCCGTGAAGGGCCGATTACCATCT CCAGAGACAATTCCAAGAACACGCTGTAT	139	MALPVTALLLPLALLL HAARPDIVMTQSPLSL PVTPGEPASISCRSSQ SLLHSNGYNYLDWYLQ KPGQSPQLLIYLGSNR ASGVDPDRFSGSGSGTD FTLKISRVEAEDVGVY YCMQGLGLPLTFGGGT KVEIKRGSTSGSGKPG SGEGSTKGQVQLVESG GGVVQPGRSLRLSCAA SGFTFSSYGMHWVRQA PGKGLEWVAVISYDGS NKYYADSVKGRFTISR DNSKNTLYLQMNSLRA EDTAVYYCARDGTYLG GLWYFDLWGRGTLTV SSAAALDNEKSNGTII HVKGKHLCPSPLPFGP SKPFWVLVVVGGVLAC YSLLVTVAFIIFWVRS KRSRLHSDYMNMTPR RPGPTRKHYQPYAPPR DFAAYRSRVKFSRSAD	140

	CTGCAAATGAACAGCCTGAGAGCCGAGGA CACGGCGGTGTACTACTGCGCCAGAGACG GTACTTATCTAGGTGGTCTCTGGTACTTC GACTTATGGGGGAGAGGTACCTTGGTCAC CGTCTCCTCAGCCGCTGCCCTTGATAATG AAAAGTCAAACGGAACAATCATTACGTG AAGGGCAAGCACCTCTGTCCGTACCCCTT GTTCCCTGGTCCATCCAAGCCATTCTGGG TGTTGGTCGTAGTGGGTGGAGTCCTCGCT TGTTACTCTCTGCTCGTCACCGTGGCTTT TATAATCTTCTGGGTTAGATCCAAAAGAA GCCGCCTGCTCCATAGCGATTACATGAAT ATGACTCCACGCCGCCCTGGCCCCACAAG GAAACACTACCAGCCTTACGCACCACCTA GAGATTTTCGCTGCCTATCGGAGCAGGGTG AAGTTTTCCAGATCTGCAGATGCACCAGC GTATCAGCAGGGCCAGAACCAACTGTATA ACGAGCTCAACCTGGGACGCAGGGAAGAG TATGACGTTTTGGACAAGCGCAGAGGACG GGACCCTGAGATGGGTGGCAAACCAAGAC GAAAAAACCCCCAGGAGGGTCTCTATAAT GAGCTGCAGAAGGATAAGATGGCTGAAGC CTATTCTGAAATAGGCATGAAAGGAGAGC GGAGAAGGGGAAAAGGGCACGACGGTTTG TACCAGGGACTCAGCACTGCTACGAAGGA TACTTATGACGCTCTCCACATGCAAGCCC TGCCACCTAGGTAA		APAYQQGQNQLYNELN LGRREEYDVLDRRGR DPEMGGKPRRKNPQEG LYNELQKDKMAEAYSE IGMKGERRRGKGDGL YQGLSTATKDTYDALH MQALPPR	
AJ- 21508CARHx L	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCGCAGGTGCAGCTGGTGCAGTCTGGG GCTGAGGTGAAGAAGCCTGGGGCCTCAGT GAAGGTTTCTGCAAGGCATCTGGATACA CCTTCACCAGCTACTATATGCACTGGGTG CGACAGGCCCCCTGGACAAGGGCTTGAGTG GATGGGAATAATCAACCCTGGTGGTGGTA GCACAAGCTACGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACGTCCAC GAGCACAGTCTACATGGAGCTGAGCAGCC TGAGATCTGAGGACACGGCGGTGTACTAC TGCGCCAGAGAGAGTTGGCCAATGGACGT ATGGGGCCAGGGAACAAGTGTACCGTCT CCTCAGGGTCTACATCCGGCTCCGGGAAG CCCGGAAGTGGCGAAGGTAGTACAAAGGG GGAAATAGTGATGACGCAGTCTCCAGCCA CCCTGTCTGTGTCTCCAGGGGAAAGAGCC ACCCTCTCCTGCAGGGCCAGTCAGAGTGT TAGCAGCAACTTAGCCTGGTACCAGCAGA AACCTGGCCAGGCTCCCAGGCTCCTCATC TATGGTGCATCCACCAGGGCCACTGGTAT CCCAGCCAGGTTCAAGTGGCAGTGGGTCTG GGACAGAGTTCACTCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGAGTTTATTA CTGTCAGCAGTACGCCGCTACCCTACTT TTGGCGGAGGGACCAAGGTTGAGATCAA CGGGCCGCTGCCCTTGATAATGAAAAGTC AAACGGAACAATCATTACGTGAAGGGCA AGCACCTCTGTCCGTACCCCTTGTTCCT GGTCCATCCAAGCCATTCTGGGTGTTGGT CGTAGTGGGTGGAGTCCTCGCTTGTACT	141	MALPVTALLLPLALLL HAARFQVQLVQSGAEV KKPGASVKVSKASGY TFTSYMHWVRQAPGQ GLEWMGIINPGGGSTS YAQKFQGRVTMTRDTS TSTVYMESSLRSED AVYYCARESWPMDVWG QGTTVTVSSGSTSGSG KPGSGEGSTKGEIVMT QSPATLSVSPGERATL SCRASQSVSSNLAWYQ QKPGQAPRLLIYGAST RATGIPARFSGSGST EFTLTITISLQSEDFAV YYCQQYAAAYPTFGGT KVEIKRAAALDNEKSN GTIIHVKGKHLCPSP FPGPSKPFWLVVVG VLACYSLLVTVAFIIF WVRSKRSRLHSDYMN MTPRRPGPTRKHYQPY APPRDFAAYRSRVKFS RSADAPAYQQGQNQLY NELNLGRREEYDVLDR RRGRDPEMGGKPRRKN PQEGLYNELQKDKMAE AYSEIGMKGERRRGKG HDGLYQGLSTATKDTY DALHMQALPPR	142

	CTCTGCTCGTCACCGTGGCTTTTATAATC TTCTGGGTTAGATCCAAAAGAAGCCGCCT GCTCCATAGCGATTACATGAATATGACTC CACGCCGCCCTGGCCCCACAAGGAAACAC TACCAGCCTTACGCACCACCTAGAGATTT CGCTGCCTATCGGAGCAGGGTGAAGTTTT CCAGATCTGCAGATGCACCAGCGTATCAG CAGGGCCAGAACCAACTGTATAACGAGCT CAACCTGGGACGCAGGGAAGAGTATGACG TTTTGGACAAGCGCAGAGGACGGGACCCT GAGATGGGTGGCAAACCAAGACGAAAAA CCCCCAGGAGGGTCTCTATAATGAGCTGC AGAAGGATAAGATGGCTGAAGCCTATTCT GAAATAGGCATGAAAGGAGAGCGGAGAAG GGGAAAAGGGCACGACGGTTTGTACCAGG GACTCAGCACTGCTACGAAGGATACTTAT GACGCTCTCCACATGCAAGCCCTGCCACC TAGGTAA			
AJ- 21508CARLx H	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCCGAAATAGTGATGACGCAGTCTCCA GCCACCCTGTCTGTGTCTCCAGGGGAAAG AGCCACCCTCTCCTGCAGGGCCAGTCAGA GTGTTAGCAGCAACTTAGCCTGGTACCAG CAGAAACCTGGCCAGGCTCCCAGGCTCCT CATCTATGGTGCATCCACCAGGGCCACTG GTATCCCAGCCAGGTTCACTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAG CAGCCTGCAGTCTGAAGATTTTGCAGTTT ATTACTGTCAGCAGTACGCCGCCTACCCT ACTTTTGGCGGAGGGACCAAGTTGAGAT CAAACGGGGGTCTACATCCGGCTCCGGGA AGCCCCGAAGTGGCGAAGGTAGTACAAAG GGGCAGGTGCAGCTGGTGCAGTCTGGGGC TGAGGTGAAGAAGCCTGGGGCCTCAGTGA AGGTTTCCCTGCAAGGCATCTGGATACACC TTCACCAGCTACTATATGCACTGGGTGCG ACAGGCCCCCTGGACAAGGGCTTGAGTGGA TGGGAATAATCAACCCTGGTGGTGGTAGC ACAAGCTACGCACAGAAGTTCCAGGGCAG AGTCACCATGACCAGGGACACGTCCACGA GCACAGTCTACATGGAGCTGAGCAGCCTG AGATCTGAGGACACGGCGGTGTACTACTG CGCCAGAGAGAGTTGGCCAATGGACGTAT GGGGCCAGGGAACAACGTGTCACCGTCTCC TCAGCCGCTGCCCTTGATAATGAAAAGTC AAACGGAACAATCATTCACGTGAAGGGCA AGCACCTCTGTCCGTACCCCTTGTTCCT GGTCCATCCAAGCCATTCTGGGTGTTGGT CGTAGTGGGTGGAGTCCCTCGCTTGTTACT CTCTGCTCGTCACCGTGGCTTTTATAATC TTCTGGGTTAGATCCAAAAGAAGCCGCCT GCTCCATAGCGATTACATGAATATGACTC CACGCCGCCCTGGCCCCACAAGGAAACAC TACCAGCCTTACGCACCACCTAGAGATTT CGCTGCCTATCGGAGCAGGGTGAAGTTTT CCAGATCTGCAGATGCACCAGCGTATCAG CAGGGCCAGAACCAACTGTATAACGAGCT CAACCTGGGACGCAGGGAAGAGTATGACG	143	MALPVTALLLPLALLL HAARPEIVMTQSPATL SVSPGERATLSCRASQ SVSSNLAWYQQKPGQA PRLLIYGASTRATGIP ARFSGSGSGTEFTLTI SSLQSEDFAVYYCQQY AAYPTFGGGTKVEIKR GSTSGSGKPGSGEGST KGQVQLVQSGAEVKKP GASVKVSCKASGYTFT SYMHWRVQAPGQGLE WMGIINPGGSTSYAQ KFQGRVTMTRDTSTST VYMELSLSRSEDYAVY YCARESWPMDVWQGT TVTVSSAAALDNEKSN GTIIHVKGKHLCPSP FPGPSKPFWVLLVVG VLACYSLLVTVAFIIF WVRSKRSRLHSDYMN MTPRRPGPTRKHYPY APPRDFAAAYRSRVKFS RSADAPAYQQGQNQLY NELNLGRREEYDVLDK RRGRDPFMGGKPRRKN PQEGLYNELQKDKMAE AYSEIGMKGERRRGKG HDGLYQGLSTATKDTY DALHMQALPPR	144

	TTTTGGACAAGCGCAGAGGACGGGACCCT GAGATGGGTGGCAAACCAAGACGAAAAA CCCCCAGGAGGGTCTCTATAATGAGCTGC AGAAGGATAAGATGGCTGAAGCCTATTCT GAAATAGGCATGAAAGGAGAGCGGAGAAG GGGAAAAGGGCACGACGGTTTGTACCAGG GACTCAGCACTGCTACGAAGGATACTTAT GACGCTCTCCACATGCAAGCCCTGCCACC TAGGTAA			
NM- 21517CARHx L	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCGCAGCTGCAGCTGCAGGAGTCGGGC CCAGGACTGGTGAAGCCTTCGGAGACCCT GTCCCTCACCTGCACTGTCTCTGGTGGCT CCATCAGCAGTAGTAGTTACTACTGGGGC TGGATCCGCCAGCCCCCAGGGAAGGGGCT GGAGTGGATTGGGAGTATCTCCTATAGTG GGAGCACCTACTACAACCCGTCCTCAAG AGTCGAGTCACCATATCCGTAGACACGTC CAAGAACCAGTTCTCCCTGAAGCTGAGTT CTGTGACCGCCGCAGACACGGCGGTGTAC TACTGCGCCAGAGGCAGGGGATATGCAAC CAGCTTAGCCTTCGATATCTGGGGTCAGG GTACAATGGTCACCGTCTCCTCAGGGTCT ACATCCGGCTCCGGGAAGCCCGGAAGTGG CGAAGGTAGTACAAAGGGGGAAATTGTGT TGACACAGTCTCCAGCCACCCTGTCTTTG TCTCCAGGGGAAAGAGCCACCCTCTCCTG CAGGGCCAGTCAGAGTGTTAGCAGCTACT TAGCCTGGTACCAACAGAACTGGCCAG GCTCCCAGGCTCCTCATCTATGATGCATC CAACAGGGCCACTGGCATCCCAGCCAGGT TCAGTGGCAGTGGGTCTGGGACAGACTTC ACTCTCACCATCAGCAGCCTAGAGCCTGA AGATTTTGCAGTTTATTACTGTCAGCAGA GACACGTCTGGCCTCCTACTTTTGGCGGA GGGACCAAGGTTGAGATCAAACGGGCCGC TGCCCTTGATAATGAAAAGTCAAACGGAA CAATCATTCACGTGAAGGGCAAGCACCTC TGTCCTGTCACCTTGTTCCTGGTCCATC CAAGCCATTCTGGGTGTTGGTCGTAGTGG GTGGAGTCTCGCTTGTTACTCTCTGCTC GTCACCGTGGCTTTTATAATCTTCTGGGT TAGATCCAAAAGAAGCCGCCTGCTCCATA GCGATTACATGAATATGACTCCACGCCGC CCTGGCCCCACAAGGAAACACTACCAGCC TTACGCACCACCTAGAGATTTCTGCTGCCT ATCGGAGCAGGGTGAAGTTTTCCAGATCT GCAGATGCACCAGCGTATCAGCAGGGCCA GAACCAACTGTATAACGAGCTCAACCTGG GACGCAGGGAAGAGTATGACGTTTTGGAC AAGCGCAGAGGACGGGACCCTGAGATGGG TGGCAAACCAAGACGAAAAACCCCCAGG AGGGTCTCTATAATGAGCTGCAGAAGGAT AAGATGGCTGAAGCCTATTCTGAAATAGG CATGAAAGGAGAGCGGAGAAGGGGAAAAG GGCACGACGGTTTGTACCAGGGACTCAGC ACTGCTACGAAGGATACTTATGACGCTCT CCACATGCAAGCCCTGCCACCTAGGTAA	145	MALPVTALLLPLALLL HAARFQLQLQESGPGL VKPSETLSLTCTVSGG SISSSSYYWGWIRQPP GKGLEWIGSISYSGST YYNPSLKSRTISVDT SKNQFSLKLSSVTAAD TAVYYCARGRGYATSL AFDIWGQTMVTVSSG STSGSGKPGSGEGSTK GEIVLTQSPATLSLSP GERATLSCRASQSVSS YLAWYQQKPGQAPRL IYDASNRATGIPARFS GSGSGTDFLTISSE PEDFAVYYCQQRHVWP PTFGGGTKVEIKRAAA LDNEKSNGTIIHVKGK HLCPSPLFPGPSKPFW VLVVVGGVLACYLLV TVAFIIFWVRSKRSRL LHSDYMNMTPRRPGPT RKHYQPYAPPRDFAAY RSRVKFSRSADAPAYQ QGQNQLYNELNLGRRE EYDVLDKRRGRDPEMG GKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKG ERRRGKGHDGLYQGLS TATKDTYDALHMQALP PR	146

NM- 21517CARLx H	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCCGAAATTGTGTTGACACAGTCTCCA GCCACCCTGTCTTTGTCTCCAGGGGAAAG AGCCACCCTCTCCTGCAGGGCCAGTCAGA GTGTTAGCAGCTACTTAGCCTGGTACCAA CAGAAACCTGGCCAGGCTCCCAGGCTCCT CATCTATGATGCATCCAACAGGGCCACTG GCATCCCAGCCAGGTTCACTGGCAGTGGG TCTGGGACAGACTTCACTCTCACCATCAG CAGCCTAGAGCCTGAAGATTTTGCAGTTT ATTACTGTCAGCAGAGACACGTCTGGCCT CCTACTTTTGGCGGAGGGACCAAGGTTGA GATCAAACGGGGGTCTACATCCGGCTCCG GGAAGCCCGGAAGTGGCGAAGGTAGTACA AAGGGGCAGCTGCAGCTGCAGGAGTCGGG CCCAGGACTGGTGAAGCCTTCGGAGACCC TGTCCCTCACCTGCAGTGTCTCTGGTGGC TCCATCAGCAGTAGTAGTTACTACTGGGG CTGGATCCGCCAGCCCCCAGGGAAGGGG TGGAGTGGATTGGGAGTATCTCCTATAGT GGGAGCACCTACTACAACCCGTCCCTCAA GAGTCGAGTCACCATATCCGTAGACACGT CCAAGAACCAGTTCTCCCTGAAGCTGAGT TCTGTGACCGCCGACAGACACGGCGGTGTA CTACTGCGCCAGAGGCAGGGGATATGCAA CCAGCTTAGCCTTCGATATCTGGGGTCAG GGTACAATGGTCACCGTCTCCTCAGCCGC TGCCCTTGATAATGAAAAGTCAAACGGAA CAATCATTCACGTGAAGGGCAAGCACCTC TGTCCGTACCCCTTGTTCCCTGGTCCATC CAAGCCATTCTGGGTGTTGGTCGTAGTGG GTGGAGTCTCGCTTGTTACTCTCTGCTC GTCACCGTGGCTTTTATAATCTTCTGGGT TAGATCCAAAAGAAGCCGCCTGCTCCATA GCGATTACATGAATATGACTCCACGCCGC CCTGGCCCCACAAGGAAACACTACCAGCC TTACGCACCACCTAGAGATTTTCGCTGCCT ATCGGAGCAGGGTGAAGTTTTCAGATCT GCAGATGCACCAGCGTATCAGCAGGGCCA GAACCAACTGTATAACGAGCTCAACCTGG GACGCAGGGAAGAGTATGACGTTTTGGAC AAGCGCAGAGGACGGGACCCTGAGATGGG TGGCAAACCAAGACGAAAAACCCCCAGG AGGGTCTCTATAATGAGCTGCAGAAGGAT AAGATGGCTGAAGCCTATTCTGAAATAGG CATGAAAGGAGAGCGGAGAAGGGGAAAAG GGCACGACGGTTTTGTACCAGGGACTCAGC ACTGCTACGAAGGATACTTATGACGCTCT CCACATGCAAGCCCTGCCACCTAGGTAA	147	MALPVTALLLPLALLL HAARPEIVLTQSPATL SLSPGERATLSCRASQ SVSSYLAWYQQKPGQA PRLLIYDASNRATGIP ARFSGSGSGTDFTLTI SSLEPEDFAVYYCQQR HVWPPTFGGGTKVEIK RGSTSGSGKPGSGEGS TKGQLQLQESGPLVK PSETLSLTCTVSGGSI SSSSYYWGWIRQPPGK GLEWIGSISYSGSTYY NPSLKSRTISVDTSK NQFSLKLSSVTAADTA VYYCARGRGYATSLAF DIWGQGTMTVSSAAA LDNEKSNGTIIHVKGK HLCPSPLFPGPSKPFW VLVVVGVLACYSLLV TVAFIIFWVRSKRSRL LHSDYMNMTPRRPGPT RKHYQPYAPPRDFAAY RSRVKFSRSADAPAYQ QGQNQLYNELNLGRRE EYDVLDRRGRDPEMG GKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKG ERRRGKGHDGLYQGLS TATKDTYDALHMQALP PR	148
TS- 21522CARHx L	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCCGAGGTGCAGCTGGTGGAGTCTGGG GGAGGCTTGGTACAGCCTGGGGGGTCCCT GAGACTCTCCTGTGCAGCCTCTGGATTCA CCTTCAGTAGCTATAGCATGAAGTGGGTC CGCCAGGCTCCAGGGAAGGGGCTGGAGTG GGTTTCAACCATTAGTAGTAGTAGTAGTA CCATATACTACGCAGACTCTGTGAAGGGC	149	MALPVTALLLPLALLL HAARPEVQLVESGGGL VQPGGSLRLSCAASGF TFSSYSMNWVRQAPGK GLEWVSTISSSSTIY YADSVKGRFTISRDNA KNSLYLQMNSLRAEDT AVYYCARGSQEHLIFD YWGQGTILTVSSGSTS	150

	CGATTACCATCTCCAGAGACAATGCCAA GAACTCACTGTATCTGCAAATGAACAGCC TGAGAGCTGAGGACACGGCGGTGTACTAC TGCGCCAGAGGTTCTCAGGAGCACCTGAT TTTCGATTATTGGGGACAGGGTACATTGG TCACCGTCTCCTCAGGGTCTACATCCGGC TCCGGGAAGCCCGGAAGTGGCGAAGGTAG TACAAAGGGGGAAATTGTGTTGACACAGT CTCCAGCCACCCTGTCTTTGTCTCCAGGG GAAAGAGCCACCCTCTCCTGCAGGGCCAG TCAGAGTGTTAGCAGGTACTTAGCCTGGT ACCAACAGAAACCTGGCCAGGCTCCCAGG CTCCTCATCTATGATGCATCCAACAGGGC CACTGGCATCCCAGCCAGGTTCACTGGCA GTGGGTCTGGGACAGACTTCACTCTCACC ATCAGCAGCCTAGAGCCTGAAGATTTTGC AGTTTATTACTGTCTCAGCAGAGATTCTACT ACCCCTTGACTTTTGGCGGAGGGACCAAG GTTGAGATCAAACGGGCCGCTGCCCTTGA TAATGAAAAGTCAAACGGAACAATCATTC ACGTGAAGGGCAAGCACCTCTGTCCGTCA CCCTTGTTCCCTGGTCCATCCAAGCCATT CTGGGTGTTGGTCGTAGTGGGTGGAGTCC TCGCTTGTTACTCTCTGCTCGTCACCGTG GCTTTTATAATCTTCTGGGTTAGATCCAA AAGAAGCCCGCTGCTCCATAGCGATTACA TGAATATGACTCCACGCCGCCCTGGCCCC ACAAGGAAACACTACCAGCCTTACGCACC ACCTAGAGATTTTCGCTGCCTATCGGAGCA GGGTGAAGTTTTCCAGATCTGCAGATGCA CCAGCGTATCAGCAGGGCCAGAACCAACT GTATAACGAGCTCAACCTGGGACGCAGGG AAGAGTATGACGTTTTGGACAAGCGCAGA GGACGGGACCCTGAGATGGGTGGCAAACC AAGACGAAAAAACCCCCAGGAGGGTCTCT ATAATGAGCTGCAGAAGGATAAGATGGCT GAAGCCTATTCTGAAATAGGCATGAAAGG AGAGCGGAGAAGGGGAAAAGGGCACGACG GTTTGTACCAGGGACTCAGCACTGCTACG AAGGATACTTATGACGCTCTCCACATGCA AGCCCTGCCACCTAGGTAA		GSGKPGSGEGSTKGEI VLTQSPATLSLSPGER ATLSCRASQSVSRYLA WYQQKPGQAPRLLIYD ASNRATGIPARFSGSG SGTDFTLTISSLEPED FAVYYCQQRFYYPWTF GGGTKVEIKRAAALDN EKSNGTIIHVKGKHL PSPLFPGPSKPFWVLV VVGGLVACYSLLVTVA FIIFWVRSKRSRLHLS DYMNMTPRRPGPTRKH YQPYAPPRDFAAYRSR VKFSRSADAPAYQQGQ NQLYNELNLGRREEYD VLDKRRGRDPEMGGKP RRKNPQEGLYNELQKD KMAEAYSEIGMKGERR RGKGHDGLYQGLSTAT KDTYDALHMQALPPR	
TS- 21522CARLx H	ATGGCACTCCCCGTAAGTCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCCGAAATTGTGTTGACACAGTCTCCA GCCACCCTGTCTTTGTCTCCAGGGGAAAG AGCCACCCTCTCCTGCAGGGCCAGTCAGA GTGTTAGCAGGTACTTAGCCTGGTACCAA CAGAAACCTGGCCAGGCTCCCAGGCTCCT CATCTATGATGCATCCAACAGGGCCACTG GCATCCCAGCCAGGTTCACTGGCAGTGGG TCTGGGACAGACTTCACTCTCACCATCAG CAGCCTAGAGCCTGAAGATTTTGCAGTTT ATTACTGTCAGCAGAGATTCTACTACCCT TGGACTTTTGGCGGAGGGACCAAGGTTGA GATCAAACGGGGGTCTACATCCGGCTCCG GGAAGCCCGGAAGTGGCGAAGGTAGTACA AAGGGGGAGGTGCAGCTGGTGGAGTCTGG GGGAGGCTTGGTACAGCCTGGGGGGTCCC TGAGACTCTCCTGTGCAGCCTCTGGATTTC	151	MALPVTALLLPLALLL HAARPEIVLTQSPATL SLSPGERATLSCRASQ SVSRYLAWYQQKPGQA PRLLIYDASNRATGIP ARFSGSGSGTDFTLT SSLEPEDFAVYYCQQR FYYPWTFGGGTKVEIK RGSTSGSGKPGSGEGS TKGEVQLVESGGGLVQ PGGSLRLSCAASGFTF SSYSMNWVRQAPGKGL EWVSTISSSSSTIYYA DSVKGRFTISRDNALN SLYLQMNSLRADTAV YYCARGSQEHLIFDYW GQGTIVTVSSAAALDN EKSNGTIIHVKGKHL	152

	ACCTTCAGTAGCTATAGCATGAACTGGGT CCGCCAGGCTCCAGGGAAGGGGCTGGAGT GGGTTTCAACCATTAGTAGTAGTAGT ACCATATACTACGCAGACTCTGTGAAGGG CCGATTCAACATCTCCAGAGACAATGCCA AGAACTCACTGTATCTGCAAATGAACAGC CTGAGAGCTGAGGACACGGCGGTGTACTA CTGCGCCAGAGGTTCTCAGGAGCACCTGA TTTTTCGATTATTGGGGACAGGGTACATTG GTCACCGTCTCCTCAGCCGCTGCCCTTGA TAATGAAAAGTCAAACGGAACAATCATTC ACGTGAAGGGCAAGCACCTCTGTCCGTCA CCCTTGTTCCCTGGTCCATCCAAGCCATT CTGGGTGTTGGTCTAGTGGGTGGAGTCC TCGCTTGTTACTCTCTGCTCGTCACCGTG GCTTTTATAATCTTCTGGGTTAGATCCAA AAGAAGCCGCTGCTCCATAGCGATTACA TGAATATGACTCCACGCCGCCCTGGCCCC ACAAGGAAACACTACCAGCCTTACGCACC ACCTAGAGATTTTCGCTGCCTATCGGAGCA GGGTGAAGTTTTCCAGATCTGCAGATGCA CCAGCGTATCAGCAGGGCCAGAACCAACT GTATAACGAGCTCAACCTGGGACGCAGGG AAGAGTATGACGTTTTGGACAAGCGCAGA GGACGGGACCCTGAGATGGGTGGCAAACC AAGACGAAAAAACCCCGAGGAGGTCTCT ATAATGAGCTGCAGAAGGATAAGATGGCT GAAGCCTATTCTGAAATAGGCATGAAAGG AGAGCGGAGAAGGGGAAAAGGGCACGACG GTTTGTACCAGGGACTCAGCACTGCTACG AAGGATACTTATGACGCTCTCCACATGCA AGCCCTGCCACCTAGGTAA		PSPLFPGPSKPFWVLV VVGGLVACYSLLVTVA FIIFWVRSKRSRLHLS DYMNTPRRPGPTRKH YQPYAPPRDFAAYRSR VKFSRSADAPAYQQGQ NQLYNELNLGRREEYD VLDKRRGRDPFMGGKP RRKNPQEGLYNELQKD KMAEAYSEIGMKGERR RGKGHDGLYQGLSTAT KDTYDALHMQALPPR	
RY- 21527CARHx L	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCCGAGGTGCAGCTGGTGGAGTCTGGG GGAGGCGTGGTCCAGCCTGGGAGGTCCCT GAGACTCTCCTGTGCAGCGTCTGGATTCA CCTTCAGTAGCTATGGCATGCACTGGGTC CGCCAGGCTCCAGGCAAGGGGCTGGAGTG GGTGGCAGTTATATCGTATGATGGAAGTA ATAAATACTATGCAGACTCCGTGAAGGGC CGATTCAACATCTCCAGAGACAATTCCAA GAACACGCTGTATCTGCAAATGAACAGCC TGAGAGCCGAGGACACGGCGGTGTACTAC TGCGCCAGAACTGACTTCTGGAGCGGATC CCCTCCAGGCTTAGATTACTGGGGACAGG GTACATTGGTCACCGTCTCCTCAGGGTCT ACATCCGGCTCCGGAAGCCCGGAAGTGG CGAAGGTAGTACAAAGGGGGACATCCAGT TGACCCAGTCTCCATCTTCCGTGTCTGCA TCTGTAGGAGACAGAGTCACCATCACTTG TCGGGCGAGTCAGGGTATTAGCAGCTGGT TAGCCTGGTATCAGCAGAAACCAGGGAAA GCCCCTAAGCTCCTGATCTATGGTGCATC CAGTTTGCAAAGTGGGGTCCCATCAAGGT TCAGCGGCAGTGGATCTGGGACAGATTTT ACTCTCACCATCAGCAGCCTGCAGCCTGA AGATTTTGCAACTTATTACTGTCAGCAGA TATACACCTTCCCTTTCACTTTTGGCGGA	153	MALPVTALLPLALLL HAARPQVQLVESGGGV VQPGRLRLSCAASGF TFSSYGMHWVRQAPGK GLEWVAIVSYDGSNKY YADSVKGRFTISRDN KNTLYLQMNSLRAEDT AVYYCARTDFWSGSP GLDYWGQGLTVTVSS STSGSGKPGSGEGSTK GDIQLTQSPSSVSASV GDRVITITCRASQGISS WLAWYQQKPKAPKLL IYGASSLQSGVPSRFS GSGSGTDFLTITSSLQ PEDFATYYCQQIYTFP FTFGGKTKEIKRAAA LDNEKSNGTIIHVKGK HLCPSPLFPGPSKPFW VLVVVGGLVACYSLLV TVAFIIFWVRSKRSRL LHSDYMNTPRRPGPT RKHYQPYAPPRDFAAY RSRVKFSRSADAPAYQ QQQNQLYNELNLGRRE EYDVLDRRGRDPFMG GKPRRKNPQEGLYNEL	154

	GGGACCAAGGTTGAGATCAAACGGGCCGC TGCCCTTGATAATGAAAAGTCAAACGGAA CAATCATTCACGTGAAGGGCAAGCACCTC TGTCCGTACCCCTTGTTCCCTGGTCCATC CAAGCCATTCTGGGTGTTGGTCGTAGTGG GTGGAGTCCTCGCTTGTTACTCTCTGCTC GTCACCGTGGCTTTTATAATCTTCTGGGT TAGATCCAAAAGAAGCCGCCTGCTCCATA GCGATTACATGAATATGACTCCACGCCGC CCTGGCCCCACAAGGAAACACTACCAGCC TTACGCACCACCTAGAGATTTCTGCTGCCT ATCGGAGCAGGGTGAAGTTTTCCAGATCT GCAGATGCACCAGCGTATCAGCAGGGCCA GAACCAACTGTATAACGAGCTCAACCTGG GACGCAGGGAAGAGTATGACGTTTTGGAC AAGCGCAGAGGACGGGACCCTGAGATGGG TGGCAAACCAAGACGAAAAACCCCCAGG AGGGTCTCTATAATGAGCTGCAGAAGGAT AAGATGGCTGAAGCCTATTCTGAAATAGG CATGAAAGGAGAGCGGAGAAGGGGAAAAG GGCACGACGGTTTTGTACCAGGGACTCAGC ACTGCTACGAAGGATACTTATGACGCTCT CCACATGCAAGCCCTGCCACCTAGGTAA		QKDKMAEAYSEIGMKG ERRRGKGHDGLYQGLS TATKDTYDALHMQALP PR	
RY- 21527CARLx H	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCGCGACATCCAGTTGACCCAGTCTCCA TCTTCCGTGTCTGCATCTGTAGGAGACAG AGTCACCATCACTTGTCTGGGCGAGTCAGG GTATTAGCAGCTGGTTAGCCTGGTATCAG CAGAAACCAGGGAAAGCCCCCTAAGCTCCT GATCTATGGTGCATCCAGTTTGCAAAGTG GGGTCCCATCAAGGTTTCAGCGGCAGTGGA TCTGGGACAGATTTCACTCTCACCATCAG CAGCCTGCAGCCTGAAGATTTTGCAACTT ATTACTGTCAGCAGATATACACCTTCCCT TTCCTTTTGGCGGAGGGACCAAGGTTGA GATCAAACGGGGGTCTACATCCGGCTCCG GGAAGCCCGGAAGTGGCGAAGGTAGTACA AAGGGGCAGGTGCAGCTGGTGGAGTCTGG GGGAGGCGTGGTCCAGCCTGGGAGGTCCC TGAGACTCTCCTGTGCAGCGTCTGGATTCT ACCTTCAGTAGCTATGGCATGCACTGGGT CCGCCAGGCTCCAGGCAAGGGGCTGGAGT GGGTGGCAGTTATATCGTATGATGGAAGT AATAAATACTATGCAGACTCCGTGAAGGG CCGATTACCATCTCCAGAGACAATTCCA AGAACACGCTGTATCTGCAATGAACAGC CTGAGAGCCGAGGACACGGCGGTGTACTA CTGCGCCAGAAGTACTTCTGGAGCGGAT CCCCTCCAGGCTTAGATTACTGGGGACAG GGTACATTGGTCACCGTCTCCTCAGCCGC TGCCCTTGATAATGAAAAGTCAAACGGAA CAATCATTCACGTGAAGGGCAAGCACCTC TGTCCGTACCCCTTGTTCCCTGGTCCATC CAAGCCATTCTGGGTGTTGGTCGTAGTGG GTGGAGTCCTCGCTTGTTACTCTCTGCTC GTCACCGTGGCTTTTATAATCTTCTGGGT TAGATCCAAAAGAAGCCGCCTGCTCCATA GCGATTACATGAATATGACTCCACGCCGC	155	MALPVTALLLPLALLL HAARPDQLTQSPSSV SASVGDRVTITCRASQ GISSWLAWYQQKPGKA PKLLIYGASSLQSGVP SRFSGSGSTDFTLTI SSLQPEDFATYYCQQI YTFPFTFGGGTKVEIK RGSTSGSGKPGSGEGS TKGVQVLVESGGGVVQ PGRSLRLSCAASGFTF SSYGMHWVRQAPGKGL EWVAVISYDGSNKYYA DSVKGRETIISRDNKN TLYLQMNSLRAEDTAV YYCARTDFWGSPPGL DYWGQGLTVTVSSAAA LDNEKSNGTIIHVKGK HLCPSPLFPGPSKPFW VLVVVGVLACYSLLV TVAFIIFWVRSKRSRL LHSYDMNMTPRRPGPT RKHYQPYAPPRDFAAY RSRVKFSRSADAPAYQ QGQNQLYNELNLGRRE EYDVLDKRRGRDPENG GKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKG ERRRGKGHDGLYQGLS TATKDTYDALHMQALP PR	156

	CCTGGCCCCACAAGGAAACACTACCAGCC TTACGCACCACCTAGAGATTTTCGCTGCCT ATCGGAGCAGGGTGAAGTTTTCCAGATCT GCAGATGCACCAGCGTATCAGCAGGGCCA GAACCAACTGTATAACGAGCTCAACCTGG GACGCAGGGAAGAGTATGACGTTTTGGAC AAGCGCAGAGGACGGGACCCTGAGATGGG TGGCAAACCAAGACGAAAAACCCCCAGG AGGGTCTCTATAATGAGCTGCAGAAGGAT AAGATGGCTGAAGCCTATTCTGAAATAGG CATGAAAGGAGAGCGGAGAAGGGGAAAAG GGCAGCAGGTTTTGTACCAGGGACTCAGC ACTGCTACGAAGGATACTTATGACGCTCT CCACATGCAAGCCCTGCCACCTAGGTAA			
PP- 21528CARHx L	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCCGAGGTGCAGCTGGTGCAGTCTGGG GCTGAGGTGAAGAAGCCTGGGTCTCGGT GAAGGTCTCCTGCAAGGCTTCTGGAGGCA CCTTCAGCAGCTATGCTATCAGCTGGGTG CGACAGGCCCCCTGGACAAGGGCTTGAGTG GATGGGAGGGATCATCCCTATCTTTGGTA CAGCAAACCTACGCACAGAAGTTCCAGGGC AGAGTCACGATTACCGCGGACGAATCCAC GAGCACAGCCTACATGGAGCTGAGCAGCC TGAGATCTGAGGACACGGCGGTGTACTAC TGCGCCAGAACTCCTGAATACTCCTCCAG CATATGGCACTATTACTACGGCATGGACG TATGGGGCCAGGGAACAAGTGTACCGTC TCCTCAGGGTCTACATCCGGCTCCGGGAA GCCCCGAAGTGGCGAAGGTAGTACAAAGG GGGACATCGTGATGACCCAGTCTCCAGAC TCCCTGGCTGTGTCTCTGGGCGAGAGGGC CACCATCAACTGCAAGTCCAGCCAGAGTG TTTTTATACAGCTCCAACAATAAGAACTAC TTAGCTTGGTACCAGCAGAAACCAGGACA GCCTCCTAAGCTGCTCATTTACTGGGCAT CTACCCGGGAATCCGGGGTCCCTGACCGA TTCAGTGGCAGCGGGTCTGGGACAGATTT CACTCTCACCATCAGCAGCCTGCAGGCTG AAGATGTGGCAGTTTATTACTGTGACAG TTCGCCCACACTCCTTTCACTTTTGGCGG AGGGACCAAGGTTGAGATCAAACGGGCCG CTGCCCTTGATAATGAAAAGTCAAACGGA ACAATCATTACGTGAAGGGCAAGCACCT CTGTCCGTACCCCTTGTTCCTGGTCCAT CCAAGCCATTCTGGGTGTTGGTCGTAGTG GGTGGAGTCCTCGCTTGTACTCTCTGCT CGTCACCGTGGCTTTTATAATCTTCTGGG TTAGATCCAAAAGAAGCCGCTGCTCCAT AGCGATTACATGAATATGACTCCACGCCG CCCTGGCCCCACAAGGAAACACTACCAGC CTTACGCACCACCTAGAGATTTTCGCTGCC TATCGGAGCAGGGTGAAGTTTTCCAGATC TGCAGATGCACCAGCGTATCAGCAGGGCC AGAACCAACTGTATAACGAGCTCAACCTG GGACGCAGGGAAGAGTATGACGTTTTGGA CAAGCGCAGAGGACGGGACCCTGAGATGG GTGGCAAACCAAGACGAAAAACCCCCAG	157	MALPVTALLLPLALLL HAARPQVQLVQSGAEV KKPGSSVKVSKASGG TFSSYAISWVRQAPGQ GLEWMGGIIPIFGTAN YAQKFQGRVTITADES TSTAYMELSSLRSED AVYYCARTPEYSSSIW HYYYGMDVWGQGT VSSGSTSGSGKPGSGE GSTKGDIVMTQSPDSL AVSLGERATINCKSSQ SVLYSSNNKNYLAWYQ QKPGQPPKLLIYWAST RESGVPDRFSGSGST DFTLTISSLQAEDVAV YYCQQFAHTPFTFGGG TKVEIKRAAALDNEKS NGTIIHVKGKHLCPSP LFPGPSKPFWVLVVG GVLACYSLLVTVAFI FWVRSKRSRLHSDYM NMTPRRPGPTRKHYQP YAPPRDFAAYRSRVKF SRSADAPAYQQGQNQL YNELNLGRREEYDVL KRRGRDPEMGGKPRRK NPQEGLYNELQKDKMA EAYSEIGMKGERRRGK GHDGLYQGLSTATKDT YDALHMQALPPR	158

	GAGGGTCTCTATAATGAGCTGCAGAAGGA TAAGATGGCTGAAGCCTATTCTGAAATAG GCATGAAAGGAGAGCGGAGAAGGGGAAAA GGGCACGACGGTTTGTACCAGGGACTCAG CACTGCTACGAAGGATACTTATGACGCTC TCCACATGCAAGCCCTGCCACCTAGGTAA			
PP- 21528CARLx H	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCCGACATCGTGATGACCCAGTCTCCA GACTCCCTGGCTGTGTCTCTGGGCGAGAG GGCCACCATCAACTGCAAGTCCAGCCAGA GTGTTTTATACAGCTCCAACAATAAGAAC TACTTAGCTTGGTACCAGCAGAAACCAGG ACAGCCTCCTAAGCTGCTCATTTACTGGG CATCTACCCGGGAATCCGGGGTCCCTGAC CGATTCACTGGCAGCGGGTCTGGGACAGA TTTCACTCTCACCATCAGCAGCCTGCAGG CTGAAGATGTGGCAGTTTATTACTGTCAG CAGTTCGCCCACACTCCTTTCACTTTTGG CGGAGGGACCAAGGTTGAGATCAAACGGG GGTCTACATCCGGCTCCGGGAAGCCCGGA AGTGGCGAAGGTAGTACAAAGGGGCAGGT GCAGCTGGTGCAGTCTGGGGCTGAGGTGA AGAAGCCTGGGTCTCGGTGAAGGTCTCC TGCAAGGCTTCTGGAGGCACCTTCAGCAG CTATGCTATCAGCTGGGTGCGACAGGCCC CTGGACAAGGGCTTGAGTGGATGGGAGGG ATCATCCCTATCTTTGGTACAGCAAACCTA CGCACAGAAGTTCCAGGGCAGAGTCACGA TTACCGCGGACGAATCCACGAGCACAGCC TACATGGAGCTGAGCAGCCTGAGATCTGA GGACACGGCGGTGTACTACTGCGCCAGAA CTCCTGAATACTCCTCCAGCATATGGCAC TATTACTACGGCATGGACGTATGGGGCCA GGGAACAAGTGTACCGTCTCCTCAGCCG CTGCCCTTGATAATGAAAAGTCAAACGGA ACAATCATTCACGTGAAGGGCAAGCACCT CTGTCCGTACCCCTTGTTCCCTGGTCCAT CCAAGCCATTCTGGGTGTTGGTCGTAGTG GGTGGAGTCCTCGCTTGTTACTCTCTGCT CGTCACCGTGGCTTTTATAATCTTCTGGG TTAGATCCAAAAGAAGCCGCCTGCTCCAT AGCGATTACATGAATATGACTCCACGCCG CCCTGGCCCCACAAGGAAACACTACCAGC CTTACGCACCACCTAGAGATTTCGCTGCC TATCGGAGCAGGGTGAAGTTTTCCAGATC TGCAGATGCACCAGCGTATCAGCAGGGCC AGAACCAACTGTATAACGAGCTCAACCTG GGACGCAGGGAAGAGTATGACGTTTTGGA CAAGCGCAGAGGACGGGACCCTGAGATGG GTGGCAAACCAAGACGAAAAACCCCCAG GAGGGTCTCTATAATGAGCTGCAGAAGGA TAAGATGGCTGAAGCCTATTCTGAAATAG GCATGAAAGGAGAGCGGAGAAGGGGAAAA GGGCACGACGGTTTGTACCAGGGACTCAG CACTGCTACGAAGGATACTTATGACGCTC TCCACATGCAAGCCCTGCCACCTAGGTAA	159	MALPVTALLLPLALLL HAARPDIVMTQSPDSL AVSLGERATINCKSSQ SVLYSSNNKNYLAWYQ QKPGQPPKLLIYWAST RESGVPDFRSGSGSGT DFTLTISSLQAEDVAV YYCQQFAHTPFTFGGG TKVEIKRGSTSGSGKP GSGEGSTKGQVQLVQS GAEVKKPGSSVKVSK ASGGTFSSYAIWVRQ APGQGLEWMGGIPIF GTANYAQKFQGRVTIT ADESTSTAYMELSSLR SEDNAVYYCARTPEYS SSIWHYYYGMDVWGQG TTVTVSSAAALDNEKS NGTIIHVKGKHLCPSP LFPGPSKPFVWLTVVVG GVLACYSLLVTVAFI FWVRSKRSRLHSDYM NMTFRRPGPTRKHYQP YAPPRDFAAYRSRVKF SRSADAPAYQQGQNQL YNELNLGRREEYDVLD KRRGRDPGEMGGKPRRK NPQEGLYNELQKDKMA EAYSEIGMKGERRRGK GHDGLYQGLSTATKDT YDALHMQALPPR	160

RD- 21530CARHx L	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCCGAGGTGCAGCTGGTGGAGTCTGGG GGAGGCGTGGTCCAGCCTGGGAGGTCCCT GAGACTCTCCTGTGCAGCGTCTGGATTCA CCTTCAGTAGCTATGGCATGCACTGGGTC CGCCAGGCTCCAGGCAAGGGGCTGGAGTG GGTGGCAGTTATATCGTATGATGGAAGTA ATAAATACTATGCAGACTCCGTGAAGGGC CGATTACCATCTCCAGAGACAATTCCAA GAACACGCTGTATCTGCAAATGAACAGCC TGAGAGCCGAGGACACGGCGGTGTACTAC TGCGTCAAGGGGCCGTTGCAGGAGCCGCC ATACGATTATGGAATGGACGTATGGGGCC AGGGAACAAGTGTACCGTCTCCTCAGGG TCTACATCCGGCTCCGGGAAGCCCGGAAG TGGCGAAGGTAGTACAAAGGGGGAAATAG TGATGACGCAGTCTCCAGCCACCCTGTCT GTGTCTCCAGGGGAAAGAGCCACCCTCTC CTGCAGGGCCAGTCAGAGTGTTAGCAGCA ACTTAGCCTGGTACCAGCAGAAACCTGGC CAGGCTCCCAGGCTCCTCATCTATAGCGC ATCCACCAGGGCCACTGGTATCCCAGCCA GGTTCAGTGGCAGTGGGTCTGGGACAGAG TTCACCTCTCACCATCAGCAGCCTGCAGTC TGAAGATTTTGCAGTTTATTACTGTCAGC AGCACACGTCTGGCCTCTCACTTTTGGC GGAGGGACCAAGGTTGAGATCAAACGGGC CGCTGCCCTTGATAATGAAAAGTCAAACG GAACAATCATTCACGTGAAGGGCAAGCAC CTCTGTCCGTACCCCTTGTTCCCTGGTCC ATCCAAGCCATTCTGGGTGTTGGTCGTAG TGGGTGGAGTCCTCGCTTGTTACTCTCTG CTCGTCACCGTGGCTTTTATAATCTTCTG GGTTAGATCCAAAAGAAGCCGCTGCTCC ATAGCGATTACATGAATATGACTCCACGC CGCCCTGGCCCCACAAGGAAACACTACCA GCCTTACGCACCACCTAGAGATTTTCGCTG CCTATCGGAGCAGGGTGAAGTTTTCCAGA TCTGCAGATGCACCAGCGTATCAGCAGGG CCAGAACCAACTGTATAACGAGCTCAACC TGGGACGCAGGGAAGAGTATGACGTTTTG GACAAGCGCAGAGGACGGGACCCTGAGAT GGGTGGCAAACCAAGACGAAAAACCCCC AGGAGGGTCTCTATAATGAGCTGCAGAAG GATAAGATGGCTGAAGCCTATTCTGAAAT AGGCATGAAAGGAGAGCGGAGAAGGGGAA AAGGGCACGACGGTTTGTACCAGGGACTC AGCACTGCTACGAAGGATACTTATGACGC TCTCCACATGCAAGCCCTGCCACCTAGGT AA	161	MALPVTALLLLPLALLL HAARPQVQLVESGGGV VQPGRSLRLSCAASGF TFSSYGMHWVRQAPGK GLEWVAVISYDGSNKY YADSVKGFTISRDN KNTLYLQMNSLRAEDT AVYYCVKGPLQEPPYD YGMDEVWQGTTVTVSS GSTSGSGKPGSGEGST KGEIVMTQSPATLSVS PGERATLSCRASQSVS SNLAWYQQKPGQAPRL LIYSASTRATGIPARF SGSGSGTEFTLTISL QSEDFAVYYCQQHHVW PLTFGGGTKEIKRAA ALDNEKSNGTIIHVKG KHLCPSPFPGPSKPF WVLVVVGGVLACYSLL VTVAFIIFWVRSKRSR LLHSDYMNMTPRRPGP TRKHYQPYAPPRDFAA YRSRVKFSRSADAPAY QQGQNQLYNELNLGRR EEYDVLDRGRDPEM GKPRRKNPQEGLYNE LQDKMAEAYSEIGMK GERRRGKGHDGLYQGL STATKDTYDALHMQAL PPR	162
RD- 21530CARLx H	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCCGAAATAGTGATGACGCAGTCTCCA GCCACCCTGTCTGTGTCTCCAGGGGAAAG AGCCACCCTCTCCTGCAGGGCCAGTCAGA GTGTTAGCAGCAACTTAGCCTGGTACCAG CAGAAACCTGGCCAGGCTCCCAGGCTCCT CATCTATAGCGCATCCACCAGGGCCACTG	163	MALPVTALLLLPLALLL HAARPEIVMTQSPATL SVSPGERATLSCRASQ SVSSNLAWYQQKPGQA PRLLIYSASTRATGIP ARFSGSGSGTEFTLT SSLQSEDFAVYYCQQH HVWPLTFGGGTKEIK	164

	GTATCCCAGCCAGGTTTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAG CAGCCTGCAGTCTGAAGATTTTGCAGTTT ATTACTGTCAGCAGCACCACGTCTGGCCT CTCACTTTTGGCGGAGGGACCAAGGTTGA GATCAAACGGGGGTCTACATCCGGCTCCG GGAAGCCCGGAAGTGGCGAAGGTAGTACA AAGGGGCAGGTGCAGCTGGTGGAGTCTGG GGGAGGCGTGGTCCAGCCTGGGAGGTCCC TGAGACTCTCCTGTGCAGCGTCTGGATT ACCTTCAGTAGCTATGGCATGCACTGGGT CCGCCAGGCTCCAGGCAAGGGGCTGGAGT GGGTGGCAGTTATATCGTATGATGGAAGT AATAAATACTATGCAGACTCCGTGAAGGG CCGATTCACCATCTCCAGAGACAATTCCA AGAACACGCTGTATCTGCAATGAACAGC CTGAGAGCCGAGGACACGGCGGTGTACTA CTGCGTCAAGGGGCCGTTGCAGGAGCCGC CATACGATTATGGAATGGACGTATGGGGC CAGGGAACAACGTGTCACCGTCTCCTCAGC CGCTGCCCTTGATAATGAAAAGTCAAACG GAACAATCATTCACGTGAAGGGCAAGCAC CTCTGTCCGTCAACCTTGTTCCCTGGTCC ATCCAAGCCATTCTGGGTGTTGGTCGTAG TGGGTGGAGTCCTCGCTTGTTACTCTCTG CTCGTCACCGTGGCTTTTATAATCTTCTG GGTTAGATCCAAAAGAAGCCCGCTGCTCC ATAGCGATTACATGAATATGACTCCACGC CGCCCTGGCCCCACAAGGAAACACTACCA GCCTTACGCACCACCTAGAGATTTCTGCTG CCTATCGGAGCAGGGTGAAGTTTTCCAGA TCTGCAGATGCACCAGCGTATCAGCAGGG CCAGAACCAACTGTATAACGAGCTCAACC TGGGACGCAGGGAAGAGTATGACGTTTTG GACAAGCGCAGAGGACGGGACCCTGAGAT GGGTGGCAAACCAAGACGAAAAACCCCC AGGAGGGTCTCTATAATGAGCTGCAGAAG GATAAGATGGCTGAAGCCTATTCTGAAAT AGGCATGAAAGGAGAGCGGAGAAGGGGAA AAGGGCACGACGGTTTGTACCAGGGACTC AGCACTGCTACGAAGGATACTTATGACGC TCTCCACATGCAAGCCCTGCCACCTAGGT AA		RGSTSGSGKPGSGEGS TKGQVQLVESGGGVVQ PGRSLRLSCAASGFTF SSYGMHWVRQAPGKGL EWVAVISYDGSNKYYA DSVKGRFTISRDNKN TLYLQMNSLRAEDTAV YYCVKGPLQEPYDYG MDVWGQGTITVSSAA ALDNEKSNGTIIHVK KHLCPSPFPGPSKPF WVLVVVGGVLACYSL VTVAFIIFWVRSKRSR LLHSDYMNMTPRRPGP TRKHYQPYAPPDFAA YRSRVKFSRSADAPAY QQGQNQLYNELNLGRR EEYDVLDKRRGRDPEM GGKPRRKNPQEGLYNE LQDKMAEAYSEIGMK GERRRGKGDGLYQGL STATKDTYDALHMQAL PPR	
Clone 24C1 THD CAR DNA HxL	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCCGAGGTCCAAGTGAAGAAAGCGGA CCCGGACTGGTGAAGCCTTCTGAGACACT TAGTCTGACGTGCACGGTCACTGGCGGCT CCATCTCCTCCTATTATTGGTCATGGATA CGACAACCCCCAGGTAAGGGCCTGGAATG GATTGGCTATATCTACTATTAGGAAGCA CGAACTACAATCCAGCCTGAAGTCCCGA GTGACAATTTCACTAGATACCAGTAAAAA CCAGTTCAGTCTTAAACTGTCAAGCGTGA CAGCTGCCGACACCGCTGTGTATTACTGC GTCTCACTGGTGTATTGTGGAGGGGATTG TTATAGCGGGTTTCGATTATTGGGGACAGG GAACCCTGGTGAAGTGTATCTTCCGGCGGC GGCGGCTCAGGGGGTGGCGGTAGTGGCGG	165	MALPVTALLLPLALLL HAARPQVQLQESGPG VKPSETLSLTCTVSGG SISSYYWSWIRQPPGK GLEWIGYIYSGSTNY NPSLKSRTISVDTSK NQFSLKLSSVTAADTA VYYCVSLVYCGGDCYS GFDYWGGTTLVTVSSG GGGSGGGSGGGGSDI QLTQSPSSLSASVGDR VSFTCQASQDINNFLN WYQQKPGKAPKLLIYD ASNLETGVPSRFSGSG SGTDFTFTISSLPED IATYYCQQYGNLPFTF	166

	TGGGGGTTCCGATATTCAACTGACACAAT CCCCCAGCTCACTCAGCGCCAGCGTGGGG GACAGGGTTAGCTTTACCTGTCAAGCCTC TCAGGATATAAATAACTTTCTGAAGTGGT ATCAACAGAAGCCTGGGAAGGCGCCAAA CTCCTGATCTATGATGCGTCCAACCTGGA AACTGGCGTGCCTTCACGCTTTAGCGGCT CTGGCAGTGGTACAGACTTCACTTTTACC ATCTCTTCACTTCAGCCGGAGGACATCGC CACATATTACTGTCAACAGTACGGAAACT TGCCCTTTACTTTTGGAGGCGGCACCAAA GTTGAAATCAAAAGGGCCGCTGCCCTGGA TAACGAAAAGAGCAATGGGACTATAATAC ATGTTAAAGGAAAACACCTGTGTCCATCT CCCCTGTTCCCTGGACCGTCAAAGCCATT TTGGGTGCTCGTGGTTGTGCGTGGCGTTC TCGCCTGTTATAGCTTGCTGGTGACAGTA GCCTTCATTATCTTTTGGGTGAGATCCAA AAGAAGCCGCTGCTCCATAGCGATTACA TGAATATGACTCCACGCCGCCCTGGCCCC ACAAGGAAACACTACCAGCCTTACGCACC ACCTAGAGATTTTCGCTGCCTATCGGAGCA GGGTGAAGTTTTCCAGATCTGCAGATGCA CCAGCGTATCAGCAGGGCCAGAACCAACT GTATAACGAGCTCAACCTGGGACGCAGGG AAGAGTATGACGTTTTGGACAAGCGCAGA GGACGGGACCCTGAGATGGGTGGCAAACC AAGACGAAAAAACCCCGAGGAGGGTCTCT ATAATGAGCTGCAGAAGGATAAGATGGCT GAAGCCTATTCTGAAATAGGCATGAAAGG AGAGCGGAGAAGGGGAAAAGGGCACGACG GTTTGTACCAGGGACTCAGCACTGCTACG AAGGATACTTATGACGCTCTCCACATGCA AGCCCTGCCACCTAGGTAA		GGGTKVEIKRAAALDN EKSNGTIIHVKGKHL PSPLFPGPSKPFVVLV VVGVLACYSLLVTV FIIFWVRSKRSRLLS DYMNMTPRRPGPTRKH YQFYAPPRDFAAYRSR VKFSRSADAPAYQQGQ NQLYNELNLGRREEYD VLDKRRGRDPEMGGKP RRKNPQEGLYNELQKD KMAEAYSEIGMKGERR RGKGHDGLYQGLSTAT KDTYDALHMQALPPR	
(CAR1.1) Clone 24C1 THD CAR DNA HxL	CAGGTCCAAGTGAAGAAAGCGGACCCGG ACTGGTGAAGCCTTCTGAGACACTTAGTC TGACGTGCACGGTCAGTGGCGGCTCCATC TCCTCCTATTATTGGTTCATGGATACGACA ACCCCCAGGTAAGGGCCTGGAATGGATTG GCTATATCTACTATTTCAGGAAGCACGAAC TACAATCCCAGCCTGAAGTCCCGAGTGAC AATTTAGTAGATACAGTAAAAACCACT TCAGTCTTAACTGTCAAGCGTGACAGCT GCCGACACCGCTGTGTATTACTGCGTCTC ACTGGTGTATTGTGGAGGGGATTGTTATA GCGGGTTCGATTATTGGGGACAGGGAACC CTGGTGACTGTATCTTCCGGCGGCGGCGG CTCAGGGGGTGGCGGTAGTGGCGGTGGGG GTTCCGATATTCAACTGACACAATCCCCC AGCTCACTCAGCGCCAGCGTGGGGGACAG GGTTAGCTTTACCTGTCAAGCCTCTCAGG ATATAAATAACTTTCTGAAGTGGTATCAA CAGAAGCCTGGGAAGGCGCCAAACTCCT GATCTATGATGCGTCCAACCTGGAACTG GCGTGCCTTCACGCTTTAGCGGCTCTGGC AGTGGTACAGACTTCACTTTTACCATCTC TTCCTTTCAGCCGGAGGACATCGCCACAT ATTACTGTCAACAGTACGGAACTTGCCC TTTACTTTTGGAGGCGGCACCAAAGTTGA	167	QVQLQESGPGLVKPS E TLSLTCTVSGGSISSY YWSWIRQPPGKLEWI GYIYYSGSTNYPNLSK SRVTISVDTSKNQFSL KLSSVTAADTAVYYCV SLVYCGGDCYSGFDYW GQGTLVTVSSGGGGSG GGGSGGGGSDIQLTQS PSSLSASVGDVRSFTC QASQDINNFLNWYQQK PGKAPKLLIYDASNLE TGVPSRFSGSGSGTDF TFTISSLQPEDATYY CQQYGNLPFTFGGGTK VEIKRAAALDNEKSNG TIIHVKGKHLCPSPFL PGPSKPFVVLVVG LACYSLLVTVAFIIFW VRSKRSRLLSHYQFYA TPRRPGPTRKH PRDFAAYRSRVKFSR SADAPAYQQGQNL ELNLGRREEYDVLDKR RRGRDPEMGGKPRRKNP	168

	AATCAAAAGGGCCGCTGCCCTGGATAACG AAAAGAGCAATGGGACTATAATACATGTT AAAGGAAAACACCTGTGTCCATCTCCCCT GTTCCCTGGACCGTCAAAGCCATTTTGGG TGCTCGTGGTTGTCTGGTGGCGTTCTCGCC TGTTATAGCTTGCTGGTGACAGTAGCCTT CATTATCTTTTGGGTGAGATCCAAAAGAA GCCGCTGCTCCATAGCGATTACATGAAT ATGACTCCACGCCGCCCTGGCCCCACAAG GAAACACTACCAGCCTTACGCACCACCTA GAGATTTTCGCTGCCTATCGGAGCAGGGTG AAGTTTTCCAGATCTGCAGATGCACCAGC GTATCAGCAGGGCCAGAACCAACTGTATA ACGAGCTCAACCTGGGACGCAGGGAAGAG TATGACGTTTTTGGACAAGCGCAGAGGACG GGACCCTGAGATGGGTGGCAAACCAAGAC GAAAAAACCCCCAGGAGGGTCTCTATAAT GAGCTGCAGAAGGATAAGATGGCTGAAGC CTATTCTGAAATAGGCATGAAAGGAGAGC GGAGAAGGGGAAAAGGGCACGACGGTTTG TACCAGGGACTCAGCACTGCTACGAAGGA TACTTATGACGCTCTCCACATGCAAGCCC TGCCACCTAGG		QEGLYNELQKDKMAEA YSEIGMKGERRRGKGH DGLYQGLSTATKDTYD ALHMQALPPR	
(CAR1.2) Clone 24C1 CHD CAR DNA HxL	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCCGAGGTGCAGCTGCAGGAATCCGGA CCGGGGCTGGTGAAGCCCAGCGAGACTCT GAGTCTCACGTGTACAGTTTTCTGGAGGTA GCATTAGCTCCTACTATTGGTCTATGGATA AGGCAGCCCCCGGGAAGGGATTGGAATG GATCGGCTATATTTACTACAGTGGGAGCA CCAATTACAACCCCTCACTGAAGTCTAGA GTTACAATCAGCGTTGACACCTCAAAGAA TCAGTTCAGTTTGAAATTGTCTAGCGTCA CAGCAGCTGATACAGCCGTCTATTATTGT GTTTCTCTGGTCTATTGCGGTGGGGATTG TTACAGTGGCTTTGACTATTGGGGGCAGG GTACTCTGGTTACAGTTTCTTCCGGGGGG GGAGGCTCTGGGGGCGGAGGCTCAGGTGG TGGAGGCAGCGACATCCAGTTGACACAGA GCCCCAGTTCCTTGTCGCCCTCCGTCCGG GATAGAGTGTCAATTTACCTGTGAGGCCTC TCAGGATATTAATAACTTTCTGAATTGGT ATCAGCAAAAGCCCGAAAGGCACCCAAG CTGTTGATTTACGACGCCAGTAACCTGGA GACAGGCGTGCCCTCCCGGTTTAGTGGA GCGGAAGCGGTACGGATTTTACCTTTACT ATCAGCTCTCTCCAACCCGAAGACATTGC AACCTACTATTGTCAACAATATGGAAACC TGCCTTTTACATTTGGCGGCGGCACCAAG GTGGAGATTAAGCGGGCGGCAGCTATTGA GGTGATGTATCCACCGCCTTACCTGGATA ACGAAAAGAGTAACGGTACCATCATTAC GTGAAAGGTAAACACCTGTGTCCTTCTCC CCTCTTCCCCGGGCCATCAAAGCCCTTCT GGGTTCTTGTGGTCTGTGGGAGGCGTGCTT GCTTGTTATTCTCTGCTCGTTACCGTGGC GTTTATCATTTTTTGGGTAGATCCAAA GAAGCCGCTGCTCCATAGCGATTACATG	169	MALPVTALLLPLALLL HAARPQVQLQESGPG VKPSETLSLTCTVSG SISSYYWSWIRQPPG GLEWIGYIYYSGSTNY NPSLKSRTISVDTSK NQFSLKLSSVTAADTA VYYCVSLVYCGGDCYS GFDYWQGTTLTVSSG GGSGGGGSGGGGSDI QLTQSPSSLASVGR VSFTCQASQDINNFLN WYQQKPGKAPKLLIYD ASNLETGVPSRFSGS SGTDFTFTISSLQPED IATYYCQQYGNLPFTF GGGTKVEIKRAAAIEV MYPPPYLDNEKSNGTI IHVKGKHLCPSPFLPG PSKPFVWLTVVGGVLA CYSLLVTVAFIIFWVR SKRSRLHSDYMNMT RRPGPTRKHYQPYAPP RDFAAYSRVRKFSRSA DAPAYQQGQNQLYNEL NLGRREEYDVLDRRG RDPGEMGGKPRRKNPQE GLYNELQKDKMAEAYS EIGMKGERRRGKGH LYQGLSTATKDTYDAL HMQALPPR	170

	AATATGACTCCACGCCGCCCTGGCCCCAC AAGGAAACACTACCAGCCTTACGCACCAC CTAGAGATTTTCGCTGCCTATCGGAGCAGG GTGAAGTTTTCCAGATCTGCAGATGCACC AGCGTATCAGCAGGGCCAGAACCAACTGT ATAACGAGCTCAACCTGGGACGCAGGGAA GAGTATGACGTTTTGGACAAGCGCAGAGG ACGGGACCCCTGAGATGGGTGGCAAACCAA GACGAAAAAACCCCCAGGAGGGTCTCTAT AATGAGCTGCAGAAGGATAAGATGGCTGA AGCCTATTCTGAAATAGGCATGAAAGGAG AGCGGAGAAGGGGAAAAGGGCACGACGGT TTGTACCAGGGACTCAGCACTGCTACGAA GGATACTTATGACGCTCTCCACATGCAAG CCCTGCCACCTAGGTAA			
(CAR1.2) Clone 24C1 CHD CAR DNA HxL	CAGGTGCAGCTGCAGGAATCCGGACCGGG GCTGGTGAAGCCCAGCGAGACTCTGAGTC TCACGTGTACAGTTTTCTGGAGGTAGCATT AGCTCCTACTATTGGTTCATGGATAAGGCA GCCCCCGGGAAGGGATTGGAATGGATCG GCTATATTTACTACAGTGGGAGCACCAAT TACAACCCCTCACTGAAGTCTAGAGTTAC AATCAGCGTTGACACCTCAAAGAATCAGT TCAGTTTGAAATTGTCTAGCGTCACAGCA GCTGATACAGCCGTCTATTATTGTGTTTC TCTGGTCTATTGCGGTGGGGATTGTTACA GTGGCTTTGACTATTGGGGGCAGGGTACT CTGGTTACAGTTTTCTTCCGGGGGGGAGG CTCTGGGGGCGGAGGCTCAGGTGGTGGAG GCAGCGACATCCAGTTGACACAGAGCCCG AGTTCCTTGTCCGCCTCCGTCGGGGATAG AGTGTCAATTTACCTGTCAGGCCTCTCAGG ATATTAATAACTTTCTGAATTGGTATCAG CAAAGCCCCGGAAGGCACCCAAGCTGTT GATTTACGACGCCAGTAACCTGGAGACAG GCGTGCCCTCCCGGTTTAGTGGTAGCGGA AGCGGTACGGATTTTACCTTTACTATCAG CTCTCTCCAACCCGAAGACATTGCAACCT ACTATTGTCAACAATATGGAACCTGCCT TTTACATTTGGCGGCGGCACCAAGGTGGA GATTAAGCGGGCGGCAGCTATTGAGGTGA TGTATCCACCGCCTTACCTGGATAACGAA AAGAGTAACGGTACCATCATTACAGTGAA AGGTAAACACCTGTGTCTTCTCCCCTCT TCCCCGGGCCATCAAAGCCCTTCTGGGTT CTTGTGGTTCGTGGGAGGCGTGCTTGCTTG TTATTCTCTGCTCGTTACCGTGGCGTTTA TCATTTTTTTGGGTTAGATCCAAAAGAAGC CGCCTGCTCCATAGCGATTACATGAATAT GACTCCACGCCGCCCTGGCCCCACAAGGA AACACTACCAGCCTTACGCACCACCTAGA GATTTTCGCTGCCTATCGGAGCAGGGTGAA GTTTTCCAGATCTGCAGATGCACCAGCGT ATCAGCAGGGCCAGAACCAACTGTATAAC GAGCTCAACCTGGGACGCAGGGAAGAGTA TGACGTTTTTGACAAGCGCAGAGGACGGG ACCCTGAGATGGGTGGCAAACCAAGACGA AAAAACCCCCAGGAGGGTCTCTATAATGA GCTGCAGAAGGATAAGATGGCTGAAGCCT	171	QVQLQESGPGLVKPSE TSLTCTVSGGSISSY YWSWIRQPPGKLEWI GYIYSGSTNYPNPSLK SRVTISVDTSKNQFSL KLSSVTAADTAVYYCV SLVYCGGDCYSGFDYW GQGTLVTVSSGGGGSG GGSGGGGSDIQLTQS PSSLSASVGDVRSFTC QASQDINNFLNWXQK PGKAPKLLIYDASNLE TGVPSRFSGSGSTDF TFTISSLQPEDIATYY CQQYGNLPFTFGGGTK VEIKRAAAIEVMYPPP YLDNEKSNGTIIHVK KHLCPSPFLFPGPSKPF WVLVVVGGVLACYSLL VTVAFIIFWVRSKRSR LLHSDYMNMTPRRPGP TRKHYQPYAPPRDFAA YRSRVKFSRSADAPAY QQGQNQLYNELNLGRR EEYDVLDRKRRGRDPEM GGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMK GERRRGKHDGLYQGL STATKDYDALHMQAL PPR	172

	ATTCTGAAATAGGCATGAAAGGAGAGCGG AGAAGGGGAAAAGGGCACGACGGTTTGTA CCAGGGACTCAGCACTGCTACGAAGGATA CTTATGACGCTCTCCACATGCAAGCCCTG CCACCTAGG			
(CAR1.3) Clone 24C1 CD8 CAR DNA HxL	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCCGAGGTGCAATTGCAAGAGTCCGGC CCCGGACTCGTTAAACCCAGTGAGACGCT TAGCCTGACCTGTACCGTCTCAGGGGGCA GCATCTCCTCTTATTACTGGAGCTGGATC AGGCAGCCTCCAGGAAAAGGCCTTGAATG GATTGGGTACATCTACTACTCTGGCTCAA CAAATTATAATCCATCCCTGAAGTCCCGC GTGACTATCTCTGTGGACACCAGCAAGAA TCAGTTTTCTACTGAAGTTGTCTAGTGTTA CCGCGGCCGACACCGCCGTATACTACTGT GTGTCTCTTGTGTACTGTGGCGGCGACTG CTATTCGGGGTTCGACTACTGGGGCCAAG GGACTCTGGTAACCGTGTCTCAGGCGGC GGCGGGTCAGGAGGAGGCGGCAGTGGAGG TGGCGGCTCCGACATCCAGCTGACACAAT CACCATCTTCCCTTTCAGCTTCAGTCGGG GACAGAGTGTCTTACATGCCAGGCCAG CCAGGATATCAATAACTTCTGAAGTGGT ACCAACAGAAACCCGGAAAGGCTCCAAAG CTCCTGATCTATGATGCTTCCAACCTGGA GACCGGCGTGCCCTCCAGGTTCAGTGGTT CAGGATCAGGCACTGACTTTACGTTACC ATATCCAGTCTTACGCCCCGAAGACATTGC AACCTATTACTGCCAACAATACGGGAACC TTCCCTTTACATTTCGGAGGCGGCACCAAG GTGGAAATCAAAGGGCTGCAGCATTGAG CAACTCAATAATGTATTTTAGTCACTTTG TACCAAGTGTCTTGCAGGCTAAGCCTACT ACCACACCCGCTCCACGGCCACCTACCCC AGCTCCTACCATCGCTTACAGCCTCTGT CCCTGCGCCCAGAGGCTTGCCGACCGGCC GCAGGGGGCGCTGTTACATACCAGAGGACT GGATTTGCGCTGCGATATCTATATCTGGG CACCCCTGGCCGGAACCTGCGGCGTACTC CTGCTGTCCCTGGTCATCACGCTCTATTG TAATCACAGGAACAGATCCAAAAGAAGCC GCCTGCTCCATAGCGATTACATGAATATG ACTCCACGCGCCCTGGCCCCACAAGGAA ACACTACCAGCCTTACGCACCACCTAGAG ATTTTCGCTGCCTATCGGAGCAGGGTGAAG TTTTCCAGATCTGCAGATGCACCAGCGTA TCAGCAGGGCCAGAACCAACTGTATAACG AGCTCAACCTGGGACGCAGGGAAGAGTAT GACGTTTTGGACAAGCGCAGAGGACGGGA CCCTGAGATGGGTGGCAAACCAAGACGAA AAAACCCCCAGGAGGGTCTCTATAATGAG CTGCAGAAGGATAAGATGGCTGAAGCCTA TTCTGAAATAGGCATGAAAGGAGAGCGGA GAAGGGGAAAAGGGCACGACGGTTTGTA CAGGGACTCAGCACTGCTACGAAGGATAC TTATGACGCTCTCCACATGCAAGCCCTGC CACCTAGGTAA	173	MALPVTALLLPLALLL HAARPQVQLQESGPG VKPSETLSLTCTVSG SISSYYWSWIRQPPG GLEWIGYIYYSGSTNY NPSLKSRVTISVDTSK NQFSLKLSSVTAADTA VYYCVSLVYCGGDCYS GFDYWQGTTLTVSSG GGGSGGGSGGGGSDI QLTQSPSSLSASVGDR VSFTCQASQDINNFLN WYQQKPGKAPKLLIYD ASNLETGVPSRFSGSG SGTDFTFTISSLQPED IATYYCQQYGNLPFTF GGGTKVEIKRAAALSN SIMYFSHFVPVFLPAK PTTTPAPRPPTPAPT ASQPLSLRPEACRPAA GGAVHTRGLDFACDIY IWAPLAGTCGVLLLSL VITLYCNHRNRSKR LLHSDYMNMTPRRPG TRKHYQPYAPPRDFAA YRSRVKFSRSADAPAY QQGQNQLYNELNLGRR EEYDVLDKRRGRDPEM GGKPRRKNPQEGLYNE LQDKMAEAYSEIGMK GERRRGKGHDGLYQGL STATKDTYDALHMQAL PPR	174

(CAR1.3) Clone 24C1 CD8 CAR DNA HxL	CAGGTGCAATTGCAAGAGTCCGGCCCCGG ACTCGTTAAACCCAGTGAGACGCTTAGCC TGACCTGTACCGTCTCAGGGGGCAGCATC TCCTCTTATTACTGGAGCTGGATCAGGCA GCCTCCAGGAAAAGGCCTTGAATGGATTG GGTACATCTACTACTCTGGCTCAACAAAT TATAATCCATCCCTGAAGTCCCGCGTGAC TATCTCTGTGGACACCAGCAAGAATCAGT TTTCACTGAAGTTGTCTAGTGTTACCGCG GCCGACACCGCCGTATACTACTGTGTGTC TCTTGTGTACTGTGGCGGCGACTGCTATT CCGGGTTTCGACTACTGGGGCCAAGGGACT CTGGTAACCGTGTCTCAGGCGGCGGCGG GTCAGGAGGAGGCGGCGAGTGGAGGTGGCG GCTCCGACATCCAGCTGACACAATCACCA TCTTCCCTTTTCACTTTCAGTCTGGGGACAG AGTGTCTCTTACATGCCAGGCCAGCCAGG ATATCAATAACTTCTGAACTGGTACCAA CAGAAACCCGGAAGGCTCCAAAGCTCCT GATCTATGATGCTTCCAACCTGGAGACCG GCGTGCCCTCCAGGTTTCACTGGTTCAGGA TCAGGCACTGACTTTACGTTTACCATATC CAGTCTTCAGCCCGAAGACATTGCAACCT ATTACTGCCAACAATACGGGAACCTTCCC TTTACATTTCGGAGGCGGCACCAAGGTGGA AATCAAAAGGGCTGCAGCATTGAGCAACT CAATAATGTATTTTAGTCACTTTGTACCA GTGTTCTTGCCGGCTAAGCCTACTACCAC ACCCGCTCCACGGCCACCTACCCAGCTC CTACCATCGCTTACAGCCTCTGTCCCTG CGCCCAGAGGCTTGCCGACCGGCCGAGG GGGCGCTGTTTCATACCAGAGGACTGGATT TCGCCTGCGATATCTATATCTGGGCACCC CTGGCCGGAACCTGCGGCGTACTCCTGCT GTCCCTGGTCATCACGCTCTATTGTAATC ACAGGAACAGATCCAAAAGAAGCCGCCTG CTCCATAGCGATTACATGAATATGACTCC ACGCCGCCCTGGCCCCACAAGGAAACACT ACCAGCCTTACGCACCACCTAGAGATTTT GCTGCCTATCGGAGCAGGTTGAAGTTTTC CAGATCTGCAGATGCACCAGCGTATCAGC AGGGCCAGAACCAACTGTATAACGAGCTC AACCTGGGACGCAGGGAAGAGTATGACGT TTTGGACAAGCGCAGAGGACGGGACCCTG AGATGGGTGGCAAACCAAGACGAAAAAAC CCCCAGGAGGGTCTCTATAATGAGCTGCA GAAGGATAAGATGGCTGAAGCCTATTCTG AAATAGGCATGAAAGGAGAGCGGAGAAGG GGAAAAGGGCACGACGGTTTGTACCAGGG ACTCAGCACTGCTACGAAGGATACTTATG ACGCTCTCCACATGCAAGCCCTGCCACCT AGG	175	QVQLQESGPGLVKPSE TSLTCTVSGGSISSY YWSWIRQPPGKGLEWI GYIYSGSTNYPNPSLK SRVTISVDTSKNQFSL KLSSVTAADTAVYYCV SLVYCGGDCYSGFDYW GQGTLVTVSSGGGGSG GGSGGGGSDIQLTQS PSSLASVGDVVSFTC QASQDINNFLNWYQQK PGKAPKLLIYDASNLE TGVPSRFSGSGSGTDF TFTISSLQPEDATYY CQQYGNLPFTFGGGTK VEIKRAAALSNSIMYF SHFVPVFLPAKPTTTP APRPPTPAPTIASQPL SLRPEACRPAAGGAVH TRGLDFACDIYIWAPL AGTCGVLLLSLVITLY CNHRNRSKRSRLHSD YMNMTPRRPGPTRKHY QPYAPPRDFAAYRSRV KFSRSADAPAYQQGQN QLYNELNLGRREEYDV LDKRRGRDPEMGKPR RKNPQEGLYNELQDK MAEAYSEIGMKGERRR GKGHDGLYQGLSTATK DTYDALHMQALPPR	176
(CAR1.4) Clone 24C1 THD CAR DNA LxH	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCGGATATCCAGCTCACGCAATCCCC TCAAGCTTGAGTGCCTCCGTGGGCGACCG GGTGTCTTTCACATGTCAGGCAAGCCAAG ACATAAATAATTTCTGAAATGGTACCAA CAAAAACCCGGAAGGCTCCCAAACCTCCT	177	MALPVTALLLPLALLL HAARPDIQLTQSPSSL SASVGDVVSFTCQASQ DINNFLNWYQQKPKA PKLLIYDASNLETGVP SRFSGSGSGTDFFTI SSLQPEDATYYCQQY	178

	GATTTATGATGCCTCCAATCTGGAGACCG GGGTCCCTTCTAGATTACAGCGGAAGTGGC AGCGGCACAGACTTTTACATTTACTATCTC TTCTCTGCAACCAGAGGACATCGCCACAT ACTATTGCCAGCAATACGGCAATCTGCCC TTCACCTTCGGAGGCGGAACCAAGGTAGA AATTAAAAGGGGCGGTGGAGGCTCCGGAG GGGGGGGCTCTGGCGGAGGGGGCTCCCAA GTACAATTGCAGGAGTCAGGGCCTGGACT CGTGAAGCCTTCAGAACTTTGTCACTGA CATGTACAGTGTCCGGCGGAAGCATTTC AGTTACTATTGGTCTCTGGATTAGACAGCC ACCCGGCAAAGGACTGGAATGGATTGGAT ATATCTACTACTCTGGATCTACAACTAT AATCCCAGCCTCAAATCCAGGGTCACTAT TAGTGTGGATACATCAAAGAATCAGTTCT CCTTGAAGCTGAGCTCAGTCACTGCTGCC GACACCGCAGTGTACTATTGTGTGAGCCT GGTCTACTGCGGCGGAGATTGCTACAGCG GTTTCGATTACTGGGGCCAGGGCACCCCTG GTTACCGTTAGTTCGCGGGCTGCTCTTGA TAACGAGAAGTCCAACGGTACGATTATCC ACGTTAAGGGTAAGCACCTTTGCCCTAGC CCGCTGTTCCCAGGCCCCAGTAAGCCCTT TTGGGTCTCGTTGTGGTAGGTGGGGTAC TCGCCTGCTACTCCCTGCTCGTCACTGTC GCATTCATCATCTTCTGGGTCAAGTCCAA AAGAAGCCGCTGCTCCATAGCGATTACA TGAATATGACTCCACGCCGCCCTGGCCCC ACAAGGAAACACTACCAGCCTTACGCACC ACCTAGAGATTTTCGCTGCCTATCGGAGCA GGGTGAAGTTTTCCAGATCTGCAGATGCA CCAGCGTATCAGCAGGGCCAGAACCAACT GTATAACGAGCTCAACCTGGGACGCAGGG AAGAGTATGACGTTTTGGACAAGCGCAGA GGACGGGACCCTGAGATGGGTGGCAAACC AAGACGAAAAAACCCCCAGGAGGGTCTCT ATAATGAGCTGCAGAAGGATAAGATGGCT GAAGCCTATTCTGAAATAGGCATGAAAGG AGAGCGGAGAAGGGGAAAAGGGCACGACG GTTTGTACCAGGGACTCAGCACTGCTACG AAGGATACTTATGACGCTCTCCACATGCA AGCCCTGCCACCTAGGTAA		GNLPFTFGGGTKVEIK RGGGSGGGGSGGGGS QVQLQESGPGLVKPS TSLTCTVSGGSISSY YWSWIRQPPGKLEWI GYIYSGSTNYPNPSLK SRVTISVDTSKNQFSL KLSSVTAADTAVYYCV SLVYCGGDCYSGFDYW GQGTTLVTVSSAAALDN EKSNGTIHVKGKHL PSPLFPGPSKPFVWL VVGGLVACYSLLVTV FIIFWVRSKRSRLHS DYMNTPRRPGPTRKH YQPYAPPDFAAAYRSR VKFSRSADAPAYQQGQ NQLYNELNLGRREEYD VLDKRRGRDPEMGGKP RRKNPQEGLYNELQKD KMAEAYSEIGMKGER RGKGDGLYQGLSTAT KDTYDALHMQALPPR	
(CAR1.4) Clone 24C1 THD CAR DNA LxH	GATATCCAGCTCACGCAATCCCCCTCAAG CTTGAGTGCCTCCGTGGGCGACCGGGTGT CCTTCACATGTCAGGCAAGCCAAGACATA AATAATTTCTGAATTGGTACCAACAAAA ACCCGGCAAGGCTCCCAAACCTCTGATTT ATGATGCCTCCAATCTGGAGACCGGGGTC CCTTCTAGATTACAGCGGAAGTGGCAGCGG CACAGACTTTACATTTACTATCTCTTCTC TGCAACCAGAGGACATCGCCACATACTAT TGCCAGCAATACGGCAATCTGCCCTTCAC CTTCGGAGGCGGAACCAAGGTAGAAATTA AAAGGGGCGGTGGAGGCTCCGGAGGGGGG GGCTCTGGCGGAGGGGGCTCCCAAGTACA ATTGCAGGAGTCAGGGCCTGGACTCGTGA AGCCTTCAGAACTTTGTCACTGACATGT ACAGTGTCCGGCGGAAGCATTTCCAGTTA	179	DIQLTQSPSSLSASVG DRVSFTCQASQDINNF LNWYQQKPGKAPKLLI YDASNLETGVPSRFSG SGSGTDFTFITISLQP EDIATYYCQQYGNLPF TFGGGTKVEIKRGGGG SGGGSGGGGSQVQLQ ESGPGLVKPSSETLSLT CTVSGGSISSYYWSWI RQPPGKLEWIGYIYY SGSTNYPNPSLKSRVTI SVDTSKNQFSLKLSSV TAADTAVYYCVSLVYC GGDCYSGFDYWQGT VTVSSAAALDNEKSN	180

	CTATTGGTCCTGGATTAGACAGCCACCCG GCAAAGGACTGGAATGGATTGGATATATC TACTACTCTGGATCTACAACTATAATCC CAGCCTCAAATCCAGGGTCACTATTAGTG TGGATACATCAAAGAATCAGTTCTCCTTG AAGCTGAGCTCAGTCACTGCTGCCGACAC CGCAGTGTACTATTGTGTGAGCCTGGTCT ACTGCGGCGGAGATTGCTACAGCGGTTTC GATTACTGGGGCCAGGGCACCTTGTTAC CGTTAGTTCCGCGGCTGCTCTTGATAACG AGAAGTCCAACGGTACGATTATCCACGTT AAGGGTAAGCACCTTTGCCCTAGCCCGCT GTTCCCAGGCCCCAGTAAGCCCTTTTGGG TCCTCGTTGTGGTAGGTGGGGTACTCGCC TGCTACTCCCTGCTCGTCACTGTGCGATT CATCATCTTCTGGGTGAGATCCAAAAGAA GCCGCCTGCTCCATAGCGATTACATGAAT ATGACTCCACGCCGCCCTGGCCCCACAAG GAAACACTACCAGCCTTACGCACCACCTA GAGATTTTCGCTGCCTATCGGAGCAGGGTG AAGTTTTCCAGATCTGCAGATGCACCAGC GTATCAGCAGGGCCAGAACCAACTGTATA ACGAGCTCAACCTGGGACGCAGGGAAGAG TATGACGTTTTTGGACAAGCGCAGAGGACG GGACCCTGAGATGGGTGGCAAACCAAGAC GAAAAAACCCCCAGGAGGGTCTCTATAAT GAGCTGCAGAAGGATAAGATGGCTGAAGC CTATTCTGAAATAGGCATGAAAGGAGAGC GGAGAAGGGGAAAAGGGCACGACGGTTTG TACCAGGGACTCAGCACTGCTACGAAGGA TACTTATGACGCTCTCCACATGCAAGCCC TGCCACCTAGG		TIIHVKGKHLCPSPFLF PGPSKPFWVLVVVGGV LACYSLLVTVAFIIFW VRSKRSRLHSDYMN TPRRPGPTRKHYQPYA PPRDFAAAYRSRVKFSR SADAPAYQQGQNQLYN ELNLGRREEYDVLDR RGRDPGEMGGKPRRKNP QEGLYNELQKDKMAEA YSEIGMKGERRRGKGH DGLYQGLSTATKDTYD ALHMQALPPR	
(CAR1.5) Clone 24C1 CHD CAR DNA LxH	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCGGATATCCAGCTGACCCAGTCTCCA TCCTCTTTGAGTGCCTCCGTGGGTGACCG CGTCTCTTTCACTTGCCAAGCCAGCCAAG ACATCAACAACCTTTCTGAATTGGTACCAG CAGAAACCAGGCAAAGCACCAAGCTCCT CATCTACGACGCCTCCAACCTGGAAACCG GGGTGCCCAGCAGGTTTAGCGGGAGCGGT TCTGGCACGGATTTTACGTTACCATCTC CTCTCTGCAGCCCCAGGATATAGCTACTT ATTACTGTCAGCAGTACGGGAATCTGCCA TTTACTTTTTGGGGTGGAATAAGGTGGA AATCAAAGGGGCGGCGGGGAAGCGGGG GCGGGGGCTCAGGTGGCGGAGGGAGCCAG GTGCAACTCCAGGAAAGTGGCCCAGGATT GGTGAAGCCCAGCGAGACCCTTTCCCTTA CTTGTAAGTGTAGCGGAGGCAGCATAAGC AGCTACTATTGGTCCTGGATCAGACAGCC ACCAGGGAAAGGGCTTGAATGGATTGGCT ACATTTACTATTCCGGGTCCACCAACTAC AACCCTATCCCTCAAGTCCCGCGTGACAAT TTCCGTCGACACAAGCAAGAACCAGTTCT CCCTGAACTTAGTAGCGTCACTGCTGCA GATACAGCAGTGTACTATTGTGTGAGCCT TGTCTACTGTGGCGGCGACTGCTACAGTG GCTTTGATTACTGGGGACAGGGCACGCTC	181	MALPVTALLPLALLL HAARPDIQLTQSPSSL SASVGDVRSFTCQASQ DINNFLNWWYQKPGKA PKLLIYDASNLETGVP SRFSGSGSGTDFFTI SSLQPEDIATYYCQQY GNLPFTFGGGTKVEIK RGGGSGGGGSGGGGS QVQLQESGPGLVKPE TSLTCTVSGGSISSY YWSWIRQPPGKLEWI GYIYSGSTNYPNPSLK SRVTISVDTSKNQFSL KLSSVTAADTAVYYCV SLVYCGGDCYSGFDYW GQGTLLVTSSAAAIEV MYPPPYLDNEKSNGTI IHKVKGKHLCPSPFLFPG PSKPFWVLVVVGGVLA CYSLLVTVAFIIFWVR SKRSRLHSDYMNMT RRPGPTRKHYQPYAPP RDFAAAYRSRVKFSR DAPAYQQGQNQLYNEL NLGRREEYDVLDRRG RDPGEMGGKPRRKNPQE	182

	GTGACAGTGTCCAGCGCTGCGGCTATCGA GGTAATGTATCCGCCACCGTATCTGGACA ACGAGAAGTCTAATGGGACAATCATTAC GTGAAGGGGAAGCACCTGTGTCCATCCCC CCTGTTTCCGGGTCCCAGTAAACCCCTTCT GGGTGCTTGTGTGCTTGGCGGGGTGCTG GCCTGCTATTCCCTGCTGGTGACCGTCGC GTTTATTATTTTCTGGGTTAGATCCAAAA GAAGCCCGCTGCTCCATAGCGATTACATG AATATGACTCCACGCCGCCCTGGCCCCAC AAGGAAACACTACCAGCCTTACGCACCAC CTAGAGATTTTCGCTGCCTATCGGAGCAGG GTGAAGTTTTCCAGATCTGCAGATGCACC AGCGTATCAGCAGGGCCAGAACCAACTGT ATAACGAGCTCAACCTGGGACGCAGGGAA GAGTATGACGTTTTGGACAAGCGCAGAGG ACGGGACCCTGAGATGGGTGGCAAACCAA GACGAAAAAACCCCAAGGAGGGTCTCTAT AATGAGCTGCAGAAGGATAAGATGGCTGA AGCCTATTCTGAAATAGGCATGAAAGGAG AGCGGAGAAGGGGAAAAGGGCACGACGGT TTGTACCAGGGACTCAGCACTGCTACGAA GGATACTTATGACGCTCTCCACATGCAAG CCCTGCCACCTAGGTAA		GLYNELQKDKMAEAYS EIGMKGERRRRGKGDG LYQGLSTATKDTYDAL HMQALPPR	
(CAR1.5) Clone 24C1 CHD CAR DNA LxH	GATATCCAGCTGACCCAGTCTCCATCCTC TTTGAGTGCCTCCGTGGGTGACCGCGTCT CTTTCACTTGCCAAGCCAGCCAAGACATC AACAACTTTCTGAATTGGTACCAGCAGAA ACCAGGCAAAGCACCAAAGCTCCTCATCT ACGACGCCTCCAACCTGGAAACCGGGGTG CCCAGCAGGTTTAGCGGGAGCGGTTCTGG CACGGATTTTACGTTACCATCTCCTCTC TGCAGCCCGAGGATATAGCTACTTATTAC TGTCAGCAGTACGGGAATCTGCCATTTAC TTTTGGGGGTGGAATAAGGTGGAAATCA AAAGGGGCGGCGGGGGAAGCGGGGCGGG GGCTCAGGTGGCGGAGGGAGCCAGGTGCA ACTCCAGGAAAGTGGCCCAGGATTGGTGA AGCCCAGCGAGACCCTTTCCCTTACTTGT ACTGTTAGCGGAGGCAGCATAAGCAGCTA CTATTGGTCTTGGATCAGACAGCCACCAG GGAAAGGGCTTGAATGGATTGGCTACATT TACTATTCCGGGTCCACCAACTACAACCC ATCCCTCAAGTCCCGCGTGACAATTTCCG TCGACACAAGCAAGAACCAGTTCTCCCTG AAACCTAGTAGCGTCACTGCTGCAGATAC AGCAGTGTACTATTGTGTGAGCCTTGTCT ACTGTGGCGGCGACTGCTACAGTGGCTTT GATTACTGGGGACAGGGCACGCTCGTGAC AGTGTCCAGCGCTGCGGCTATCGAGGTAA TGTATCCGCCACCGTATCTGGACAACGAG AAGTCTAATGGGACAATCATTACGTGAA GGGGAAGCACCTGTGTCCATCCCCCTGT TTCCGGGTCCCAGTAAACCCCTTCTGGGTG CTTGTTGTGCTTGGCGGGGTGCTGGCCTG CTATTCCCTGCTGGTGACCGTCGCGTTTA TTATTTTCTGGGTTAGATCCAAAAGAAGC CGCCTGCTCCATAGCGATTACATGAATAT GACTCCACGCCGCCCTGGCCCCACAAGGA	183	DIQLTQSPSSLSASVG DRVSFTCQASQDINNF LNWYQQKPGKAPKLLI YDASNLETGVPSRFSG SGSCTDFTFTISSLQP EDIATYYCQQYGNLFF TFGGGTKVEIKRGGGG SGGGSGGGGSQVQLQ ESGPGLVKPSETLSLT CTVSGGSISSYYWSWI RQPPGKGLEWIGYIYY SGSTNYPNPSLKSRTI SVDTSKNQFSLKLSSV TAADTAVYYCVSLVYC GGDCYSGFYWGQGTLL VTVSSAAAIEVMYPPP YLDNEKSNGTIIHVKG KHLCPSPFLFPGPSKPF WVLVVVGGVLACYSLL VTVAFIIFWVRSKRSR LLHSDYMNMTPRRPGP TRKHYPYAPPRDFAA YRSRVKFSRSADAPAY QQQQNQLYNELNLGRR EEYDVLDKRRGRDP GGGKPRRKNPQEGLYNE LQDKMAEAYSEIGMK GERRRGKGDGLYQGL STATKDTYDALHMQAL PPR	184

	AACACTACCAGCCTTACGCACCACCTAGA GATTTTCGCTGCCTATCGGAGCAGGGTGAA GTTTTCCAGATCTGCAGATGCACCAGCGT ATCAGCAGGGCCAGAACCAACTGTATAAC GAGCTCAACCTGGGACGCAGGGAAGAGTA TGACGTTTTGGACAAGCGCAGAGGACGGG ACCTGAGATGGGTGGCAAACCAAGACGA AAAAACCCCGAGGAGGGTCTCTATAATGA GCTGCAGAAGGATAAGATGGCTGAAGCCT ATTCTGAAATAGGCATGAAAGGAGAGCGG AGAAGGGGAAAAGGGCACGACGGTTTGTA CCAGGGACTCAGCACTGCTACGAAGGATA CTTATGACGCTCTCCACATGCAAGCCCTG CCACCTAGG			
(CAR1.6) Clone 24C1 CD8 CAR DNA LxH	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCCGACATTCAATTGACCCAGTCCCCT AGCAGTCTCTCAGCAAGTGTGGGAGATAG GGTGTCAATTCACCTGTGAGGCTTCACAGG ACATCAACAACCTTCTCAATTGGTATCAG CAGAAGCCAGGGAAGGCACCAAAGCTGCT CATATATGACGCTTCAAACCTTGAAACCG GAGTACCTAGCCGCTTCAGCGGAAGCGGA TCAGGGACTGACTTCACTTTTACCATCTC TTCAGTGCAGCCCGAAGACATCGCCACAT ACTACTGCCAGCAGTACGGAACTTGCCCT TTTACATTTGGGGGCGGCACCAAAGTGGA GATTAAGCGAGGGGGAGGCGGCTCAGGAG GCGGTGGCTCCGGAGGCGGGGTTCCAG GTCCAGCTCCAGGAATCCGGCCCAGGTCT GGTTAAGCCAGTGAACTTTGTCCCTCA CGTGTACTGTGAGCGGTGGTTCAATCTCC TCATACTATTGGTCTTGATACGGCAACC TCCTGGAAAGGGCCTCGAGTGGATCGGCT ATATCTACTATAGTGGCTCCACTAATTAC AACCCTTCCCTCAAGTCCAGAGTCACCAT TTCCGTGGACACATCTAAGAACCAGTTCA GTCTGAAGTTGTCCAGCGTTACAGCCGCA GACACAGCCGTTTATTACTGTGTGTCTCT TGTTTACTGCGGGGAGACTGTTATAGCG GCTTCGATTACTGGGGCCAGGGCACCTTG GTCACAGTCTCTCCGCGGCCGCCCTCTC TAACAGTATTATGTACTTTTCTCATTTTG TACCCGTGTTCTTCCCGCTAAGCCAACT ACTACCCCGGGCCACGGCCGCCTACCCC TGCACCCACAATAGCCAGTCAGCCTTTGA GCCTGAGACCTGAGGCTTGTGCGCCGGCT GCTGGGGGTGAGTGCACACACGAGGTCT TGATTTTGCTTGCGACATATACATCTGGG CCCCTCTGGCCGGGACCTGTGGGGTGCTG CTTCTGAGCTTGGTCATCACGCTCTATTG CAACCATCGCAACAGATCCAAAAGAAGCC GCCTGCTCCATAGCGATTACATGAATATG ACTCCACGCCGCCCTGGCCCCACAAGGAA ACACTACCAGCCTTACGCACCACCTAGAG ATTTTCGCTGCCTATCGGAGCAGGGTGAAG TTTTCCAGATCTGCAGATGCACCAGCGTA TCAGCAGGGCCAGAACCAACTGTATAACG AGCTCAACCTGGGACGCAGGGAAGAGTAT	185	MALPVTALLLPALALL HAARPDQLTQSPSSL SASVGDVRSFTCQASQ DINNFLNWXQKPGKA PKLLIYDASNLETGVP SRFSGSGSGTDFFTI SSLQPEDATYYCQQY GNLPFTFGGGTKVEIK RGGGSGGGSGGGGS QVQLQESGPGLVKPE TSLTCTVSGGSISSY YWSWIRQPPGKLEWI GYIYSGSTNYPNPSLK SRVTISVDTSKNQFSL KLSSVTAADTAVYCV SLVYCGGDCYSGFYD GQGTLVTVSSAAALSN SIMYFHFVFPVFLPAK PTTTPAPRPPTPPTI ASQPLSLRPEACRPAA GGAVHTRGLDFACDIY IWAPLAGTCGVLLLSL VITLYCNHRNRSKRSL LLHSDYMNMTPRRPGP TRKHYQPYAPPRDFAA YRSRVKFSRSADAPAY QQGQNQLYNELNLGRR EEYDVLDRRGRDPPEM GGKPRRKNPQEGLYNE LQDKMAEAYSEIGMK GERRRGKHDGLYQGL STATKDTYDALHMQAL PPR	186

	GACGTTTTGGACAAGCGCAGAGGACGGGA CCCTGAGATGGGTGGCAAACCAAGACGAA AAAACCCCCAGGAGGGTCTCTATAATGAG CTGCAGAAGGATAAGATGGCTGAAGCCTA TTCTGAAATAGGCATGAAAGGAGAGCGGA GAAGGGGAAAAGGGCACGACGGTTTGTAC CAGGGACTCAGCACTGCTACGAAGGATAC TTATGACGCTCTCCACATGCAAGCCCTGC CACCTAGGTAA			
(CAR1.6) Clone 24C1 CD8 CAR DNA LxH	GACATTCAATTGACCCAGTCCCCTAGCAG TCTCTCAGCAAGTGTGGGAGATAGGGTGT CATTACCTGTCAGGCTTCACAGGACATC AACAACTTCCTCAATTGGTATCAGCAGAA GCCAGGGAAGGCACCAAAGCTGCTCATAT ATGACGCTTCAAACCTTGAAACCGGAGTA CCTAGCCGCTTCAGCGGAAGCGGATCAGG GACTGACTTCACTTTTACCATCTCTTCAC TGCAGCCCGAAGACATCGCCACATACTAC TGCCAGCAGTACGGAACTTGCCCTTTTAC ATTTGGGGGCGGCACCAAAGTGGAGATTA AGCGAGGGGGAGGCGGCTCAGGAGGCGGT GGCTCCGGAGGCGGGGGTCCCAGGTCCA GCTCCAGGAATCCGGCCAGGTCTGGTTA AGCCCAGTGAACCTTTGTCCCTCACGTGT ACTGTGAGCGGTGGTTCAATCTCCTCATA CTATTGGTCTTGGATACGGCAACCTCCTG GAAAGGGCCTCGAGTGGATCGGCTATATC TACTATAGTGGCTCCACTAATTACAACCC TTCCCTCAAGTCCAGAGTCACCATTTCG TGGACACATCTAAGAACCAGTTCACTCTG AAGTTGTCCAGCGTTACAGCCGCAGACAC AGCCGTTTATTACTGTGTGTCTCTTGT ACTGCGGGGAGACTGTTATAGCGGCTTC GATTACTGGGGCCAGGGCACCTTGGTCAC AGTCTCTTCCGCGGCCGCCCTCTCTAACA GTATTATGTACTTTTCTCATTTTGTACCC GTGTTCCCTCCCGCTAAGCCAACACTAC CCCGGGCCCCACGGCCGCCTACCCCTGCAC CCACAATAGCCAGTCAGCCTTTGAGCCTG AGACCTGAGGCTTGTCGGCCGGCTGCTGG GGGTGCAGTGCACACACGAGGTCTTGATT TTGCTTGGCAGATATACATCTGGGCCCT CTGGCCGGGACCTGTGGGTGCTGCTTCT GAGCTTGGTCATCACGCTCTATTGCAACC ATCGCAACAGATCCAAAAGAAGCCGCCTG CTCCATAGCGATTACATGAATATGACTCC ACGCCGCCCTGGCCCCACAAGGAAACACT ACCAGCCTTACGCACCACCTAGAGATTTT GCTGCCTATCGGAGCAGGGTGAAGTTTTT CAGATCTGCAGATGCACCAGCGTATCAGC AGGGCCAGAACCAACTGTATAACGAGCTC AACCTGGGACGCAGGGAAGAGTATGACGT TTTGGACAAGCGCAGAGGACGGGACCCTG AGATGGGTGGCAAACCAAGACGAAAAAAC CCCCAGGAGGGTCTCTATAATGAGCTGCA GAAGGATAAGATGGCTGAAGCCTATTCTG AAATAGGCATGAAAGGAGAGCGGAGAAGG GGAAAAGGGCACGACGGTTTGTACCAGGG ACTCAGCACTGCTACGAAGGATACTTATG	187	DIQLTQSPSSLSASVG DRVSFTCQASQDINN LNWYQQKPGKAPKLLI YDASNLETGVPSRFSG SGSGTDFTFTISSLQP EDIATYYCQQYGNLPP TFGGGTKEIKRGGGG SGGGSGGGGSQVQLQ ESGPGLVKPSETLSLT CTVSGGSISSYYWSWI RQPPGKGLEWIGYIYY SGSTNYPNPSLKSRTI SVDTSKNQFSLKLSSV TAADTAVYYCVSLVYC GGDCYSGFDYWGGTTL VTVSSAAALSNSIMYF SHFVPVFLPAKPTTTP APRPPTPAPTIASQPL SLRPEACRPAAGAVH TRGLDFACDIYIWAPL AGTCGVLLLSLVITLY CNHRNRSKRSRLHSD YMNMTPRRPGPTRKHY QPYAPPRDFAAYRSRV KFSRSADAPAYQQGQN QLYNELNLGRREEYDV LDKRRGRDPEMGGKPR RKNPQEGLYNELQKDK MAEAYSEIGMKGERRR GKGHDGLYQGLSTATK DTYDALHMQALPPR	188

	ACGCTCTCCACATGCAAGCCCTGCCACCT AGG			
(CAR2.1) Clone 24C8 THD CAR DNA HxL	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCCGAGGTACAGCTGCAGGAATCTGGG CCCGGACTTGTCAGCAAGCCAAGTCAGACACT TTCTCTTACATGTACCGTGAGCGGCGGAA GTATAAGCAGTGGAGGCTTTTACTGGTCT TGGATACGGCAGCACCCAGGCAAAGGCTT GGAGTGGATTGGATACATTATCATTCAG GATCTACACACTATAATCCATCCCTTAAG TCCCGGGTCACCATTAGCATTGATACGTC TAAGAATCTGTTCACTCTCAGGCTGTCCT CCGTCACCTGCTGCCGACACAGCCGTGTAC TACTGCGCCTCCTTGGTTTACTGCGGAGG CGACTGTTATAGCGGCTTTGATTATTGGG GGCAGGGGACCCTCGTAACCGTGAGCTCT GGAGGGGGTGGGAGCGGGGGAGGAGGTTT AGGGGGGGGCGGCTCCGATATCCAGCTCA CTCAAAGCCCCTCTAGTCTCTCTGCCTCA GTGGGGGATCGGGTCAGTTTTACTTGTCA AGCTTCACAGGATATCAACAACCTTCTTA ATTGGTATCAGCAGAAGCCAGGAAAAGCA CCCAAGCTGCTCATCTATGATGCCTCAAA TTTGGAGACGGGTGTTCCAGTCGATTCT CTGGGTGAGGGTCCGGGACCGACTTTACG TTTACGATCTCCTCTCTGACGCCGAAGA CATCGCCACATACTATTGTCAACAGTACG GCAACTTGCCTTTTACATTTGGGGGCGGG ACTAAGGTTGAAATCAAGAGGGCCGCTGC ACTGGACAATGAGAAGTCCAACGGCACCA TCATCCACGTGAAGGGCAAGCACCTGTGC CCTAGTCCTCTGTTCCCAGGCCCATCCAA ACCTTTTTGGGTTCTTGTGTGGTCGGGG GGGTGCTGGCCTGCTATTCTCTGCTGGTC ACGGTGGCCTTCATAATTTTCTGGGTTAG ATCCAAAAGAAGCCGCTGCTCCATAGCG ATTACATGAATATGACTCCACGCCGCCCT GGCCCCACAAGGAAACACTACCAGCCTTA CGCACCACCTAGAGATTTGCTGCCTATC GGAGCAGGGTGAAGTTTTCCAGATCTGCA GATGCACCAGCGTATCAGCAGGGCCAGAA CCAAGTGTATAACGAGCTCAACCTGGGAC GCAGGGAAGAGTATGACGTTTTGGACAAG CGCAGAGGACGGGACCCCTGAGATGGGTGG CAAACCAAGACGAAAAAACCCCAAGGAGG GTCTCTATAATGAGCTGCAGAAGGATAAG ATGGCTGAAGCCTATTCTGAAATAGGCAT GAAAGGAGAGCGGAGAAGGGGAAAAGGGC ACGACGGTTTGTACCAGGGACTCAGCACT GCTACGAAGGATACTTATGACGCTCTCCA CATGCAAGCCCTGCCACCTAGGTAA	189	MALPVTALLLPLALLL HAARPQVQLQESGPGL VKPSQTLSTCTVSGG SISSGGFYWSWIRQHP GKGLEWIGYIHHSGST HYNPSLKSRTISIDT SKNLFSRLSSVTAAD TAVYYCASLVYCGDC YSGFDYWGQGLVTVS SGGGSGGGSGGGGS DIQLTQSPSSLSASVG DRVSFTCQASQDINNF LNWYQQKPKAPKLLI YDASNLETGVPSRFSG SGSGTDFTFITISLQP EDIATYYCQQYGNLPF TFGGTKVEIKRAAAL DNEKSNGTIIHVKGKH LCPSPLFPGPSKPFV LVVVGVLACYSLLVT VAFIIFWVRSKRSRL HSDYMNMTPRRPGPTR KHYQPYAPPRDFAAYR SRVKFSRSADAPAYQQ GQNQLYNELNLGRREE YDVLDKRRGRDPEMGG KPRRKNPQEGLYNELQ KDKMAEAYSEIGMKGE RRRGKGHDGLYQGLST ATKDTYDALHMQALPP R	190
(CAR2.1) Clone 24C8 THD CAR DNA HxL	CAGGTACAGCTGCAGGAATCTGGGCCCCG ACTTGTCAAGCCAAGTCAGACACTTTCTC TTACATGTACCGTGAGCGGCGGAAGTATA AGCAGTGGAGGCTTTTACTGGTCTTGGAT ACGGCAGCACCCAGGCAAAGGCTTGGAGT GGATTGGATACATTATCATTCAGGATCT ACACACTATAATCCATCCCTTAAGTCCCG	191	QVQLQESGPGLVKPSQ TLSTCTVSGGSISSG GFYWSWIRQHPGKGLE WIGYIHHSGSTHYNPS LKSRTISIDTSKRLF SLRLSSVTAADTAVYY CASLVYCGGDCYSGFD	192

	GGTCACCATTAGCATTGATACGTCTAAGA ATCTGTTTCAGTCTCAGGCTGTCTCCGTC ACTGCTGCCGACACAGCCGTGTACTACTG CGCCTCCTTGGTTTACTGCGGAGGCGACT GTTATAGCGGCTTTGATTATTGGGGGCAG GGGACCCTCGTAACCGTGAGCTCTGGAGG GGGTGGGAGCGGGGAGGAGGTTCAAGGG GGGGCGGCTCCGATATCCAGCTCACTCAA AGCCCCTCTAGTCTCTCTGCCTCAGTGGG GGATCGGGTCAGTTTTACTTGTCAAGCTT CACAGGATATCAACAACCTTCTTAATTGG TATCAGCAGAAGCCAGGAAAAGCACCCAA GCTGCTCATCTATGATGCCTCAAATTTGG AGACGGGTGTTCCAGTCGATTCTCTGGG TCAGGGTCCGGGACCGACTTTACGTTTAC GATCTCCTCTCTGCAGCCCGAAGACATCG CCACATACTATTGTCAACAGTACGGCAAC TTGCCTTTCACATTTGGGGGCGGGACTAA GGTTGAAATCAAGAGGGCGCTGCACTGG ACAATGAGAAGTCCAACGGCACCATCATC CACGTGAAGGGCAAGCACCTGTGCCCTAG TCCTCTGTTCCAGGCCCATCCAAACCTT TTTGGGTCTTGTGTGGTCTGGGGGGGTG CTGGCCTGCTATTCTCTGCTGGTCACGGT GGCCTTCATAATTTTCTGGGTTAGATCCA AAAGAAGCCGCTGCTCCATAGCGATTAC ATGAATATGACTCCACGCCCGCTGGCCC CACAAGGAAACACTACCAGCCTTACGCAC CACCTAGAGATTTCTGCTGCCTATCGGAGC AGGGTGAAGTTTTCCAGATCTGCAGATGC ACCAGCGTATCAGCAGGGCCAGAACCAAC TGTATAACGAGCTCAACCTGGGACGCAGG GAAGAGTATGACGTTTTGGACAAGCGCAG AGGACGGGACCCTGAGATGGGTGGCAAAC CAAGACGAAAAAACCCCGAGGAGGTCTC TATAATGAGCTGCAGAAGGATAAGATGGC TGAAGCCTATTCTGAAATAGGCATGAAAG GAGAGCGGAGAAGGGGAAAAGGGCACGAC GGTTTGTACCAGGGACTCAGCACTGCTAC GAAGGATACTTATGACGCTCTCCACATGC AAGCCCTGCCACCTAGG		YWGQGLTVTVSSGGGG SGGGGSGGGGSDIQLT QSPSSLSASVGDVRSF TCQASQDINNFLNWFQ QKPGKAPKLLIYDASN LETGVPSRFSGSGSGT DFTFTISSLQPEDAT YYCQYGNLPTFTGGG TKVEIKRAAALDNEKS NGTIIHVKGKHLCPSP LFPGPSKPFVVLVVVG GVLACYSLLVTVAFI FWVRSKRSRLHSDYM NMTPRRPGPTRKHYP YAPPRDFAAYRSRVKF SRSADAPAYQQGQNL YNELNLGRREEYDVL KRRGRDPEMGGKPRR NPQEGLYNELQKDKMA EAYSEIGMKGERRRGK GHDGLYQGLSTATKDT YDALHMQALPPR	
(CAR2.2) Clone 24C8 CHD CAR DNA HxL	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCCGAGGTGCAGCTGCAGGAAAGCGGT CCGGGACTTGTCAAGCCGTCCCAACGCT GAGTCTGACGTGTACTGTCTCTGGTGGCT CTATTTCTTCCGGGGGCTTTTATTGGTCT TGGATCAGACAACACCCTGGCAAAGGGCT GGAGTGGATAGGGTATATTCACTACTCTG GGTCCACTCACTACAACCCATCATTGAAA TCCAGAGTGAATATCTCAATCGACACATC CAAGAACCTTTTCAAGCTGAGGTTGTCT CAGTTACCGCCGCTGACACCGCGGTGTAT TATTGCGCCTCTCTCGTGTACTGCGGTGG CGATTGTTATAGTGGCTTTGACTACTGGG GGCAGGGGACATTGGTTACCGTTTCAAGT GGAGGCGGTGGGTCTGGCGGGGGCGGTAG CGGAGGTGGGGGAGCGACATACAGCTTA CGCAGAGCCCCCTCCAGCCTTTTCAAGCTCC	193	MALPVTALLLPLALLL HAARPQVQLQESGPG VKPSQTLSTCTVSGG SISGGFYWSWIRQHP GKGLEWIGYIHHSST HYNPSLKSRTISIDT SKNLFSRLSSVTAAD TAVYYCASLVYCGGDC YSGFDYWGQGLTVTVS SGGGGSGGGGSGGGG DIQLTQSPSSLSASV DRVSFTCQASQDINN LNWFQKPGKAPKLLI YDASNLETGVPSRFS SGSGTDFTFTISSLP EDIATYYCQYGNLPT TFGGGTKVEIKRAAI EVMYPPPYLDNEKSN	194

	GTGGGGGATAGGGTGTCTTTACCTGCCA GGCTTCCCAGGACATAAACAACCTTCCTCA ATTGGTATCAGCAAAAGCCCGGGAAAGCA CCAAAGCTGCTCATCTACGATGCCAGCAA CCTGGAACCGGAGTGCCGTCTCGCTTCT CTGGAAGTGGCAGTGGGACCGATTCTACT TTTACAATCTCAAGTTTGCAGCCAGAAGA CATTGCAACATACTACTGTCAACAGTACG GCAATCTCCCTTTACATTTGGGGGGGA ACTAAAGTGGAGATTAAGCGCGCTGCAGC CATTGAAGTTATGTATCCGCCCCCGTATC TGGATAACGAGAAATCTAATGGTACCATA ATACATGTGAAGGGGAAGCACCTCTGTCC ATCACCGCTGTTCCCGGCCCTTCAAAC CTTTCTGGGTACTCGTTGTCTGGGTGGA GTTCTGGCCTGCTATAGTCTGCTGGTGAC CGTGGCGTTTATCATCTTCTGGGTAAAGAT CCAAAAGAAGCCGCTGCTCCATAGCGAT TACATGAATATGACTCCACGCCGCCCTGG CCCCACAAGGAAACACTACCAGCCTTACG CACCACCTAGAGATTTTCGCTGCCTATCGG AGCAGGGTGAAGTTTTCAGATCTGCAGA TGCACCAGCGTATCAGCAGGGCCAGAACC AACTGTATAACGAGCTCAACCTGGGACGC AGGGAAGAGTATGACGTTTTGGACAAGCG CAGAGGACGGGACCTGAGATGGGTGGCA AACCAAGACGAAAAACCCCGAGGAGGGT CTCTATAATGAGCTGCAGAAGGATAAGAT GGCTGAAGCCTATTCTGAAATAGGCATGA AAGGAGAGCGGAGAAGGGGAAAAGGGCAC GACGGTTTGTACCAGGGACTCAGCACTGC TACGAAGGATACTTATGACGCTCTCCACA TGCAAGCCCTGCCACCTAGGTAA		TIHVKGKHLCPSPFLF PGPSKPFWVLVVGGV LACYSLLVTVAFIIFW VRSKRSRLHSDYMN TPRRPGPTRKHYQPYA PPRDFAAAYRSRVKFSR SADAPAYQQGQNQLYN ELNLGRREEYDVLDR RGRDPGEMGGKPRRKNP QEGLYNELQKDKMAEA YSEIGMKGERRRGKGH DGLYQGLSTATKDTYD ALHMQALPPR	
(CAR2.2) Clone 24C8 CHD CAR DNA HxL	CAGGTGCAGCTGCAGGAAAGCGGTCCGGG ACTTGTCAAGCCGTCCCAAACGCTGAGTC TGACGTGTACTGTCTCTGGTGGCTCTATT TCTTCCGGGGGCTTTTATTGGTCTTGGAT CAGACAACACCCTGGCAAAGGGCTGGAGT GGATAGGGTATATTACCACTCTGGGTCC ACTCACTACAACCCATCATTGAAATCCAG AGTGACTATCTCAATCGACACATCCAAGA ACCTTTTCAGCCTGAGGTTGTCTCATCAGTT ACCGCCGCTGACACCGCGGTGTATTATTG CGCCTCTCTCGTGTACTGCGGTGGCGATT GTTATAGTGGCTTTGACTACTGGGGGCAG GGGACATTGGTTACCGTTTCAAGTGGAGG CGGTGGGTCTGGCGGGGGCGGTAGCGGAG GTGGGGGGAGCGACATACAGCTTACGCAG AGCCCCCTCCAGCCTTTCAGCCTCCGTGGG GGATAGGGTGTCTTTACCTGCCAGGCTT CCCAGGACATAAACAACCTTCTCAATTGG TATCAGCAAAAGCCCGGGAAAGCACCAAA GCTGCTCATCTACGATGCCAGCAACCTGG AAACCGGAGTGCCGTCTCGCTTCTCTGGA AGTGGCAGTGGGACCGATTCTCACTTTTAC AATCTCAAGTTTGCAGCCAGAAGACATTG CAACATACTACTGTCAACAGTACGGCAAT CTCCCCTTTACATTTGGGGGGGGAATAA AGTGGAGATTAAGCGCGCTGCAGCCATTG	195	QVQLQESGPGLVKPSQ TSLTCTVSGGSISSG GFYWSWIRQHPGKGLE WIGYIHHSGSTHYNPS LKSRVTISIDTSKNLF SLRLSSVTAADTAVYY CASLVYCGGDCYSGFD YWGQGTLLTVSSGGGG SGGGSGGGGSDIQLT QSPSSLSASVGDRVSF TCQASQDINNFLNWFQ QKPGKAPKLLIYDASN LETGVPSPRFSGSGSGT DFTFTISSQLQPEDIAT YYCQQYGNLPFTFGGG TKVEIKRAAAIEVMYP PPYLDNEKSNGTIIHV KGKHLCPSPFLFPGPSK PFWVLVVGGLVACYS LLVTVAFIIFWVRSKR SRLHSDYMNMTPRRP GPTKHYQPYAPPDF AAAYRSRVKFSRSADAP AYQQGQNQLYNELNLG RREEYDVLDRGRDP EMGGKPRRKNPQEGLY	196

	AAGTTATGTATCCGCCCCGTATCTGGAT AACGAGAAATCTAATGGTACCATAATACA TGTGAAGGGGAAGCACCTCTGTCCATCAC CGCTGTTCCCCGGCCCTTCAAAACCTTTC TGGGTACTCGTTGTCTGCTGGGTGGAGTTCT GGCCTGCTATAGTCTGCTGGTGACCGTGG CGTTTATCATCTTCTGGGTAAGATCCAAA AGAAGCCGCCTGCTCCATAGCGATTACAT GAATATGACTCCACGCCGCCCTGGCCCCA CAAGGAAACACTACCAGCCTTACGCACCA CCTAGAGATTTTCGCTGCCTATCGGAGCAG GGTGAAGTTTTCCAGATCTGCAGATGCAC CAGCGTATCAGCAGGGCCAGAACCAACTG TATAACGAGCTCAACCTGGGACGCAGGGA AGAGTATGACGTTTTGGACAAGCGCAGAG GACGGGACCCTGAGATGGGTGGCAAACCA AGACGAAAAAACCCCCAGGAGGGTCTCTA TAATGAGCTGCAGAAGGATAAGATGGCTG AAGCCTATTCTGAAATAGGCATGAAAGGA GAGCGGAGAAGGGGAAAAGGGCACGACGG TTTGTACCAGGGACTCAGCACTGCTACGA AGGATACTTATGACGCTCTCCACATGCAA GCCCTGCCACCTAGG		NELQKDKMAEAYSEIG MKGERRRGKGHDGLYQ GLSTATKDTYDALHMQ ALPPR	
(CAR2.3) Clone 24C8 CD8 CAR DNA HxL	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCCGAGGTGCAGTTGCAGGAAAGCGGG CCTGGCCTTGTGAAACCAAGCCAGACACT GAGCCTGACATGCACTGTGTCGGCGGGT CCATATCTTCCGGGGGTTTTTATTGGTCC TGGATACGCCAGCATCCCCGGGAAAGGACT TGAATGGATTGGATATATCCACCATTCCG GAAGCACCCACTACAATCCAAGCCTTAAA TCCCCGGGTGACAATCTCCATCGACACCTC AAAGAATCTTTTTTCCCTGCGGTTGTCTT CAGTAACTGCCGCCGATACCGCTGTGTAC TACTGTGCCAGCCTCGTCTATTGCGGCGG AGATTGTTATTCTGGGTTTCGATTATTGGG GTCAAGGCACACTGGTAACTGTCAGCAGC GGAGGCGGCGGTTCCGGGGGGCGGGGGCAG TGGAGGGGGCGGATCTGACATTACGCTTA CGCAGTCCCCATCTTCACTTAGCGCCAGC GTTGGCGATCGGGTCAGCTTACGTGTCA AGCAAGTCAGGATATCAACAACCTTTCTTA ACTGGTACCAGCAGAAGCCAGGCAAGGCA CCCAAGTTGCTGATTTACGATGCTTCTAA CCTCGAGACGGGAGTGCCTAGCCGCTTCT CCGGGAGCGGCAGCGGCACAGACTTTACC TTTACGATTTCCAGTCTGCAGCCAGAGGA TATAGCAACTTATTACTGTCAGCAGTATG GCAACCTCCCTTTTACCTTCGGTGGTGGC ACAAAGGTGAGATTAAAGAGCCGCAGC GTTGTCCAACCTCCATAATGTATTTTTCTC ATTTTGTGCCCCGTCTTTCTGCCTGCCAAA CCTACCACCACCCCCGCCCCACGACCACC TACTCCAGCCCCCACCATCGCCTCCAGC CCCTCAGCCTGAGGCCAGAGGCTTGTCGC CCTGCTGCGGGGGGCGCTGTCCATACCAG AGGACTCGACTTCGCCTGCGATATTTATA TATGGGCCCCCTCGCCGGCACCTGCGGA	197	MALPVTALLLPLALLL HAARPQVQLQESGPG VKPSQTLSTCTVSGG SISGGFYWSWIRQHP GKLEWIGYIHHSGST HYNPSLKSRTISIDT SKNLFSLRLSSVTAAD TAVYYCASLVYCGGDC YSGFDYWQGTLTVS SGGGSGGGSGGGGS DIQLTQSPSSLSASVG DRVSFTCQASQDINN LNWYQQKPKAPKLLI YDASNLETGVPSRFS SGSGTDFFTTISLQP EDIATYYCQQYGNL TFGGGTKVEIKRAA SNSIMYFSHFVPVFL AKPTTTPAPRPPTP TIASQPLSLRPEAC AAGGAVHTRGLDFAC IYIWAPLAGTCGVLL SLVITLYCNHRNRSK SRLHSDYMNMTPRRP GPTRKHYQPYAPPRD AAYRSRVKFSRSADAP AYQQGQNQLYNELNL RREEYDVLDKRRGRDP EMGGKPRRKNPQEGLY NELQKDKMAEAYSEIG MKGERRRGKGHDGLYQ GLSTATKDTYDALHMQ ALPPR	198

	GTCTTGCTCCTGAGCCTTGTGATCACGCT TTATTGTAACCATCGGAATAGATCCAAAA GAAGCCGCTGCTCCATAGCGATTACATG AATATGACTCCACGCCGCCCTGGCCCCAC AAGGAAACACTACCAGCCTTACGCACCAC CTAGAGATTTTCGCTGCCTATCGGAGCAGG GTGAAGTTTTCCAGATCTGCAGATGCACC AGCGTATCAGCAGGGCCAGAACCAACTGT ATAACGAGCTCAACCTGGGACGCAGGGAA GAGTATGACGTTTTTGACAAGCGCAGAGG ACGGGACCCTGAGATGGGTGGCAAACCAA GACGAAAAAACCCCAAGGAGGGTCTCTAT AATGAGCTGCAGAAGGATAAGATGGCTGA AGCCTATTCTGAAATAGGCATGAAAGGAG AGCGGAGAAGGGGAAAAGGGCACGACGGT TTGTACCAGGGACTCAGCACTGCTACGAA GGATACTTATGACGCTCTCCACATGCAAG CCCTGCCACCTAGGTAA			
(CAR2.3) Clone 24C8 CD8 CAR DNA HxL	CAGGTGCAGTTGCAGGAAAGCGGGCCTGG CCTTGTGAAACCAAGCCAGACACTGAGCC TGACATGCACTGTGTCCGGCGGGTCCATA TCTTCCGGGGGTTTTTATTGGTCCTGGAT ACGCCAGCATCCCGGGAAAGGACTTGAAT GGATTGGATATATCCACCATTCCGGAAGC ACCCACTACAATCCAAGCCTTAAATCCCG GGTGACAATCTCCATCGACACCTCAAAGA ATCTTTTTTCCCTGCGGTTGTCTTCAGTA ACTGCCGCCGATACCGCTGTGTACTACTG TGCCAGCCTCGTCTATTGCGGCGGAGATT GTTATTCTGGGTTTCGATTATTGGGGTCAA GGCACACTGGTAACTGTCAGCAGCGGAGG CGGCGGTTCCGGGGGCGGGGCGAGTGGAG GGGGCGGATCTGACATTACGCTTACGCAG TCCCCATCTTCACTTAGCGCCAGCGTTGG CGATCGGGTCAGCTTACGTTGTCAGCAA GTCAGGATATCAACAACCTTTCTTAAGTGG TACCAGCAGAAGCCAGGCAAGGCACCCAA GTTGCTGATTTACGATGCTTCTAACCTCG AGACGGGAGTGCCTAGCCGCTTCTCCGGG AGCGGCAGCGGCACAGACTTTACCTTTAC GATTTCCAGTCTGCAGCCAGAGGATATAG CAACTTATTACTGTCAGCAGTATGGCAAC CTCCCTTTTACCTTCCGTGGTGGCACAAA GGTCGAGATTAAAAGAGCCGCAGCGTTGT CCAACCTCATAATGTATTTTTTCTCATTTT GTGCCCCTCTTTCTGCCTGCCAACCTAC CACCACCCCGCCCCACGACCACCTACTC CAGCCCCCACCATCGCCTCCCAGCCCCCTC AGCCTGAGGCCAGAGGCTTGTGCGCCCTGC TGCGGGGGGCGCTGTCCATACCAGAGGAC TCGACTTCGCCTGCGATATTTATATATGG GCCCCCTCGCCGGCACCTGCGGAGTCTT GCTCCTGAGCCTTGTGATCACGCTTTATT GTAACCATCGGAATAGATCCAAAAGAAGC CGCCTGCTCCATAGCGATTACATGAATAT GACTCCACGCCGCCCTGGCCCCACAAGGA AACACTACCAGCCTTACGCACCACCTAGA GATTTTCGCTGCCTATCGGAGCAGGGTGAA GTTTTCCAGATCTGCAGATGCACCAGCGT	199	QVQLQESGPGLVKPSQ TSLTCTVSGGSISSG GFYWSWIRQHPGKGLE WIGYIHHSGSTHYNPS LKSRVTISIDTSKNLF SLRLSSVTAADTAVYY CASLVYCGGDCYSGF YWGQGLVTVSSGGGG SGGGSGGGGSDIQLT QSPSSLSASVGDVRSF TCQASQDINNFLNWYQ QKPGKAPKLLIYDASN LETGVPSRFSGSGSGT DFTFTISSLQPEDIA YYCQQYGNLPFTFGG TKVEIKRAAALSNSIM YFSHFVPVFLPAKPTT TPAPRPPTPAPTIA PLSLRPEACRPAAGGA VHTRGLDFACDIYIWA PLAGTCGVLLLSLVIT LYCNHRNRSKRSRLH SDYMNMTPRRPGPTRK HYQPYAPPRDFAAYRS RVKFSRSADAPAYQQG QNQLYNELNLGRREEY DVLDKRRGRDPEMGK PRRKNPQEGLYNELQK DKMAEAYSEIGMKGER RRGKGHDGLYQGLSTA TKDITYDALHMQALPPR	200

	ATCAGCAGGGCCAGAACCAACTGTATAAC GAGCTCAACCTGGGACGCAGGGAAGAGTA TGACGTTTTGGACAAGCGCAGAGGACGGG ACCCTGAGATGGGTGGCAAACCAAGACGA AAAAACCCCCAGGAGGGTCTCTATAATGA GCTGCAGAAGGATAAGATGGCTGAAGCCT ATTCTGAAATAGGCATGAAAGGAGAGCGG AGAAGGGGAAAAGGGCACGACGGTTTGTA CCAGGGACTCAGCACTGCTACGAAGGATA CTTATGACGCTCTCCACATGCAAGCCCTG CCACCTAGG			
(CAR3.1) Clone 20C5.1 THD CAR DNA HxL	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCCGAGGTCCAAGTGGTGCAGTCCGGA GCCGAAGTCAAGAAACAGGTGCCTCCGT TAAAGTGAGTTGCAAAGTCTCTGGATACA CTCTGACCGAGCTCTCTATGCACTGGGTC CGGCAGGCCCCCGGAAGGGATTGGAATG GATGGGCGGGTTCGATCCTGAGGACGGAG AGACTATCTACGCTCAAAAATTCCAGGGA CGAGTGACTGTGACCGAAGACACTAGTAC CGACACTGCCTACATGGAACCTTCTCTC TGCGATCAGAAGATACCGCAGTGTACTAC TGTGCTACTGAATCTAGGGGCATTGGATG GCCCTACTTCGATTACTGGGGTCAGGGAA CTCTGGTGACTGTCTCCAGCGGTGGAGGT GGCAGCGGTGGTGGCGGAAGCGGGGGGG CGGCTCTGATATTGATGACTCAATCTC CTTCTTCTCTGTCCGCTTCCGTGGGCGAT AGAGTGACCATTACTTGTAGGGCGTCCCA GTCAATCTCCAGTTATTTGAATTGGTATC AGCAGAAGCCCCGGGAAAGCACCTAAGCTG TTGATCAGCGGGGCTTCTAGCCTGAAGAG TGGGGTACCTTCACGGTTCAGCGGAAGCG GAAGCGGAACCGATTTACCCCTGACTATC AGCAGCCTGCCACCTGAGGACTTTGCAAC TTACTACTGCCAACAGTCATACAGCACTC CGATCACTTTCCGGCCAGGGCACCCGGCTC GAAATCAAGCGCGCTGCTGCTTTGGACAA TGAGAAGTCAAACGGCACCATCATACATG TTAAAGGTAAACATCTGTGTCCCTCCCCG CTGTTCCCCGGCCCTTCCAAACCGTTCTG GGTTCTGGTGGTGGTGGGAGGCGTACTCG CTTGCTATAGTCTGCTGGTAAGTGTGCGC TTCATCATCTTTTGGGTGAGATCCAAAAG AAGCCGCCTGCTCCATAGCGATTACATGA ATATGACTCCACGCCGCCCTGGCCCCACA AGGAAACACTACCAGCCTTACGCACCACC TAGAGATTTTCGCTGCCTATCGGAGCAGGG TGAAGTTTTCCAGATCTGCAGATGCACCA GCGTATCAGCAGGGCCAGAACCAACTGTA TAACGAGCTCAACCTGGGACGCAGGGAAG AGTATGACGTTTTGGACAAGCGCAGAGGA CGGGACCCTGAGATGGGTGGCAAACCAAG ACGAAAAACCCCCAGGAGGGTCTCTATA ATGAGCTGCAGAAGGATAAGATGGCTGAA GCCTATTCTGAAATAGGCATGAAAGGAGA GCGGAGAAGGGGAAAAGGGCACGACGGTT TGTACCAGGGACTCAGCACTGCTACGAAG	201	MALPVTALLLPALLLL HAARPQVQLVQSGAEV KKPGASVKVSKVSGY TLTELSMHWRQAPGK GLEWMGGFDPEDGETI YAQKFQGRVTVTEDTS TDTAYMELSSLRSED AVYYCATESRGIGWPY FDYWGQGLVTVSSGG GGSGGGSGGGGSDIQ MTQSPSSLSASVGDRV TITCRASQSISSYLNW YQQKPGKAPKLLISGA SSLKSGVPSRFSGSGS GTDFTLTITSSLPEDF ATYYCQQSYSTPITFG QGTRELEIKRAALDNE KSNGTIIHVKGKHLCP SPLFPGPSKPFWLVV VGGVLACYSLVTVAF IIFWVRSKRSRLHSD YMNMTPRRPGPTRKHY QPYAPPRDFAAYRSRV KFSRSADAPAYQQGQN QLYNELNLGRREEYDV LDKRRGRDPEMGGKPR RKNPQEGLYNELQKDK MAEAYSEIGMKGERRR GKGHDGLYQGLSTATK DTYDALHMQALPPR	202

	GATACTTATGACGCTCTCCACATGCAAGC CCTGCCACCTAGGTAA			
(CAR3.1) Clone 20C5.1 THD CAR DNA HxL	CAGGTCCAACCTGGTGCAGTCCGGAGCCGA AGTCAAGAAACCAGGTGCCTCCGTAAAG TGAGTTGCAAAGTCTCTGGATACACTCTG ACCGAGCTCTCTATGCACTGGGTCCGGCA GGCCCCCGGCAAGGGATTGGAATGGATGG GCGGGTTCGATCCTGAGGACGGAGAGACT ATCTACGCTCAAAAATTCCAGGGACGAGT GACTGTGACCGAAGACACTAGTACCGACA CTGCCTACATGGAACCTTCTCTCTGCGA TCAGAAGATAACCGCAGTGTACTACTGTGC TACTGAATCTAGGGGCATTGGATGGCCCT ACTTCGATTACTGGGGTCAGGGAACCTCTG GTGACTGTCTCCAGCGGTGGAGGTGGCAG CGGTGGTGGCGGAAGCGGGGGGGCGGCT CTGATATTGAGATGACTCAATCTCCTTCT TCTCTGTCCGCTTCCGTGGGCGATAGAGT GACCATTACTTGTAGGGCGTCCCAGTCAA TCTCCAGTTATTTGAATTGGTATCAGCAG AAGCCCGGGAAGCACCTAAGCTGTTGAT CAGCGGGGCTTCTAGCCTGAAGAGTGGGG TACCTTCACGGTTCAGCGGAAGCGGAAGC GGAACCGATTTACCCCTGACTATCAGCAG CCTGCCACCTGAGGACTTTGCAACTTACT ACTGCCAACAGTCATACAGCACTCCGATC ACTTTCGGCCAGGGCACCCGGCTCGAAAT CAAGCGCGTCTGCTGCTTTGGACAATGAGA AGTCAAACGGCACCATCATACATGTTAAA GGTAAACATCTGTGTCCCTCCCCGCTGTT CCCCGGCCCTTCCAAACCGTTCTGGGTTC TGGTGGTGGTTCGAGGCGTACTCGCTTGC TATAGTCTGCTGGTAACTGTGCCTTTCAT CATCTTTTGGGTGAGATCCAAAAGAAGCC GCCTGCTCCATAGCGATTACATGAATATG ACTCCACGCCGCCCTGGCCCCACAAGGAA ACACTACCAGCCTTACGCACCACCTAGAG ATTTTCGCTGCCTATCGGAGCAGGGTGAAG TTTTCCAGATCTGCAGATGCACCAGCGTA TCAGCAGGGCCAGAACCAACTGTATAACG AGCTCAACCTGGGACGCAGGGAAGAGTAT GACGTTTTTGACAAGCGCAGAGGACGGGA CCCTGAGATGGGTGGCAAACCAAGACGAA AAAACCCCCAGGAGGGTCTCTATAATGAG CTGCAGAAGGATAAGATGGCTGAAGCCTA TTCTGAAATAGGCATGAAAGGAGAGCGGA GAAGGGGAAAAGGGCACGACGGTTTGTAC CAGGGACTCAGCACTGCTACGAAGGATAC TTATGACGCTCTCCACATGCAAGCCCTGC CACCTAGG	203	QVQLVQSGAEVVKPGA SVKVSCKVSGYTLTEL SMHWVRQAPGKGLEWM GGFDPEDGETIYAQKF QGRVTVTEDTSTDY MELSSLRSEDYAVYYC ATESRGIGWPYFDYWG QGTSLTVSSGGGSSGG GGSGGGSDIQMTQSP SSLSASVGDRTITCR ASQSISSYLNWYQQKP GKAPKLLISGASSLKS GVPSRFSGSGSGTDFT LTISSLPPEDFATYYC QQSYSTPITFGQTRL EIKRAAALDNEKSNGT IIHVKGKHLCPSPFLP GPSKPFWVLVVGVL ACYSLLVTVAFIIFWV RSKRSLHSDYMNMT PRRPGPTRKHYQPYAP PRDFAAYRSRVKFSRS ADAPAYQQGQNQLYNE LNLGRREEYDVLDRR GRDPEMGKPRRKNPQ EGLYNELQKDKMAEAY SEIGMKGERRRGKGDH GLYQGLSTATKDTYDA LHMQUALPPR	204
(CAR3.2) Clone 20C5.1 CHD CAR DNA HxL	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCCGAGGTGCAGCTTGTGCAGAGCGGG GCCGAGGTGAAGAAGCCGGGGCCAGCGT CAAAGTGTCTGTAAAGTCAAGCGTTACA CCCTCACCGAGCTGAGCATGCACTGGGTA CGGCAGGCTCCCGGCAAAGGTCTTGAGTG GATGGGTGGATTTGATCCAGAAGATGGAG AGACTATCTACGCCAGAAAGTTCCAGGGC	205	MALPVTALLLPALALL HAARPQVQLVQSGAEV KKPGASVKVSKVSGY TLTELSMHWVRQAPGK GLEWMGGFDPEDGETI YAQKFQGRVTVTEDTS TDYAMELSSLRSEDY AVYYCATESRGIGWPY FDYWGQGTSLTVSSGG	206

	CGGGTCACCGTAACAGAAGACACCTCAAC TGACACCGCTTACATGGAGCTGAGTTCAC TGCGGTCCGAGGACACGGCCGTGTATTAT TGTGCCACCGAGAGCCGCGGAATCGGATG GCCTTACTTCGACTACTGGGGACAGGGTA CACTTGTTACAGTATCATCCGGGGGTGGC GGCTCTGGTGGGGGCGGCTCCGGAGGGGG TGGATCAGATATCCAAATGACTCAAAGTC CAAGTTCCTGTCTGCCTCAGTCGGAGAT AGAGTCACCATAACCTGCAGGGCAAGTCA GTCCATCTCCTCCTATCTGAACTGGTACC AACAGAAACCTGGAAAGGCGCCTAAGCTC CTGATCTCCGGAGCCTCATCTTTGAAATC CGGTGTCCCATCTCGCTTCAGTGGCTCTG GAAGCGGTACAGATTTTACTTTGACCATT AGCAGCCTCCCACCGGAAGACTTTGCTAC ATATTACTGCCAGCAGTCTTACTCAACCC CAATCACCTTCGGGCAAGGCACCAGACTC GAAATAAAAAGAGCAGCTGCTATCGAGGT TATGTACCCACCGCCGTACTTGGATAACG AAAAAAGCAATGGGACCATCATTCATGTG AAGGGTAAGCACCTTTGCCCTAGCCCACT GTTTCCTGGCCCGAGTAAACCTTTTGGG TACTTGTGGTCGTCCGGCGGCGTGTGGCC TGCTACTCACTCCTGGTTACCGTCGCATT CATCATCTTTTGGGTGAGATCCAAAAGAA GCCGCCTGCTCCATAGCGATTACATGAAT ATGACTCCACGCCGCCCTGGCCCCACAAG GAAACACTACCAGCCTTACGCACCACCTA GAGATTTTCGCTGCCTATCGGAGCAGGGTG AAGTTTTCCAGATCTGCAGATGCACCAGC GTATCAGCAGGGCCAGAACCAACTGTATA ACGAGCTCAACCTGGGACGCAGGGAAGAG TATGACGTTTTTGGACAAGCGCAGAGGACG GGACCCTGAGATGGGTGGCAAACCAAGAC GAAAAAACCCCCAGGAGGGTCTCTATAAT GAGCTGCAGAAGGATAAGATGGCTGAAGC CTATTCTGAAATAGGCATGAAAGGAGAGC GGAGAAGGGGAAAAGGGCACGACGGTTTG TACCAGGGACTCAGCACTGCTACGAAGGA TACTTATGACGCTCTCCACATGCAAGCCC TGCCACCTAGGTAA		GGSGGGSGGGGSDIQ MTQSPSSLSASVGD TITCRASQSISSYL YQQKPGKAPKLLIS SSLKSGVPSRFSGS GTDFTLTISLPPED ATYYCQQSYSTPIT QGTRLEIKRAAAIE YPPPYLDNEKSNGT HVKGKHLCPSPFP SKPFWVLVVVGGV YSLLVTVAFIIFW KRSRLHSDYMNMT RPGPTRKHYPYAP DFAAYRSRVKFSR APAYQQGQNQLYN LGRREEYDVLDRR DPEMGGKPRRKNP LYNELQKDKMAEY IGMKGERRRRGKH YQGLSTATKDTYD MQALPPR	
(CAR3.2) Clone 20C5.1 CHD CAR DNA HxL	CAGGTGCAGCTTGTGCAGAGCGGGGCCGA GGTGAAGAAGCCCGGGGCCAGCGTCAAAG TGTCCGTGTAAGGTCAGCGGTTACACCCTC ACCGAGCTGAGCATGCACTGGGTACGGCA GGCTCCCGGCAAAGGTCTTGAGTGGATGG GTGGATTTGATCCAGAAGATGGAGAGACT ATCTACGCCCAGAAGTTCCAGGGCCGGGT CACCGTAACAGAAGACACCTCAACTGACA CCGCTTACATGGAGCTGAGTTCACTGCGG TCCGAGGACACGGCCGTGTATTATTGTGC CACCGAGAGCCGCGGAATCGGATGGCCTT ACTTCGACTACTGGGGACAGGGTACACTT GTTACAGTATCATCCGGGGGTGGCGGCTC TGGTGGGGGCGGCTCCGGAGGGGGTGGAT CAGATATCCAAATGACTCAAAGTCCAAGT TCCCTGTCTGCCTCAGTCGGAGATAGAGT CACCATAACCTGCAGGGCAAGTCAGTCCA	207	QVQLVQSGAEVKKPGA SVKVSCKVSGYTLTEL SMHWVRQAPGKLEWM GGFDPEDGETIYAQKF QGRVTVTEDTSTDYAY MELSSLRSEDTAVYYC ATESRGIGWPYFDYWG QGTLLTVSSGGGSGG GGSGGGGSDIQMTQSP SSLSASVGDRTITCR ASQSISSYLNWYQQK GKAPKLLISGASSLKS GVPSRFSGSGSGTDF LTISLPPEDFATYYC QQSYSTPITFGQGTRL EIKRAAAIEVMYPPPY LDNEKSNGTIIHVKGK	208

	TCTCCTCCTATCTGAACTGGTACCAACAG AAACCTGGAAAGGCGCCTAAGCTCCTGAT CTCCGGAGCCTCATCTTTGAAATCCGGTG TCCCATCTCGCTTCAGTGGCTCTGGAAGC GGTACAGATTTTACTTTGACCATTAGCAG CCTCCCACCGGAAGACTTTGCTACATATT ACTGCCAGCAGTCTTACTCAACCCCAATC ACCTTCGGGCAAGGCACAGACTCGAAAT AAAAAGAGCAGCTGCTATCGAGGTTATGT ACCCACCGCCGTACTTGGATAACGAAAAA AGCAATGGGACCATCATTCATGTGAAGGG TAAGCACCTTTGCCCTAGCCCACTGTTTC CTGGCCCCGAGTAAACCCTTTTGGGTACTT GTGGTCGTCGGCGGCGTGCTGGCCTGCTA CTCACTCCTGGTTACCGTCGCATTTCATCA TCTTTTGGGTGAGATCCAAAAGAAGCCGC CTGCTCCATAGCGATTACATGAATATGAC TCCACGCCGCCCTGGCCCCACAAGGAAAC ACTACCAGCCTTACGCACCACCTAGAGAT TTCGCTGCCTATCGGAGCAGGGTGAAGTT TTCCAGATCTGCAGATGCACCAGCGTATC AGCAGGGCCAGAACCAACTGTATAACGAG CTCAACCTGGGACGCAGGGAAGAGTATGA CGTTTTGGACAAGCGCAGAGGACGGGACC CTGAGATGGGTGGCAAACCAAGACGAAAA AACCCCCAGGAGGGTCTCTATAATGAGCT GCAGAAGGATAAGATGGCTGAAGCCTATT CTGAAATAGGCATGAAAGGAGAGCGGAGA AGGGGAAAAGGGCACGACGGTTTGTACCA GGGACTCAGCACTGCTACGAAGGATACTT ATGACGCTCTCCACATGCAAGCCCTGCCA CCTAGG		HLCPSPLEFPGPSKPFW VLVVVGGVLACYSLLV TVAFIIFWVRSKRSRL LHSDYMNMTPRRPGPT RKHYQPYAPPRDFAAY RSRVKFSRSADAPAYQ QGQNQLYNELNLGRRE EYDVLDKRRGRDPEMG GKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKG ERRRGKGHDGLYQGLS TATKDTYDALHMQALP PR	
(CAR3.3) Clone 20C5.1 CD8 CAR DNA HxL	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCCGAGGTGCAGTTGGTGCAAAGCGGC GCAGAAGTTAAGAAACCTGGGGCGTCAGT TAAGGTGTCTTGCAAAGTATCTGGCTATA CCCTCACTGAGCTGTCCATGCATTGGGTA AGGCAGGCTCCTGGAAAGGGGCTCGAATG GATGGGAGGATTTGACCCTGAAGACGGAG AGACCATCTACGCCCAGAAATTCCAGGGT AGAGTAACAGTGACTGAGGACACTAGCAC TGACACAGCGTACATGGAGCTGAGTTCTC TGAGAAGTGAGGACACAGCCGTTTACTAC TGCGCTACCGAGTCCAGAGGTATTGGCTG GCCATACTTCGACTATTGGGGTCAGGGCA CCCTGGTTACAGTGAGTTCAGGAGGCGGG GGCTCTGGGGGGGGCGGTTCCGGAGGGGG GGGCTCAGATATACAGATGACGCAGAGTC CATCAAGTCTCTCAGCCAGCGTGGGAGAT CGCGTGACTATTACTTGCCGCGCCAGCCA GAGTATTAGCTCCTATCTGAATTGGTACC AGCAAAAGCCCCGGAAGGCCCTAAGCTT CTGATTTCTGGCGCCTCCTCTTTGAAGTC AGGTGTGCCAAGCAGATTTAGCGGGTCTG GAAGTGGCACTGACTTTACACTTACTATC TCCAGCCTGCCCCAGAGGATTTGCCAC ATATTACTGTCAGCAAAGCTACTCTACTC CAATCACTTTCCGCCAGGGCACAAGATTG	209	MALPVTALLPLALLL HAARPQVQLVQSGAEV KKPGASVKVSKVSGY TLTELSMHVVRQAPGK GLEWMGGFDPEDEGTI YAQKFQGRVTVTEDTS TDTAYMELSSLRSED AVYYCATESRGIGWPY FDYWGQGTLVTVSSGG GGSGGGSGGGGSDIQ MTQSPSSLSASVGDRV TITCRASQSISSYLNW YQQKPKAPKLLISGA SSLKSGVPSRFSGSGS GTDFTLTITSSLPEDF ATYYCQQSYSTPITFG QGTRLEIKRAAALSNS IMYFSHFVPVFLPAKP TTTPAPRPPTPAPTIA SQPLSLRPEACRPAAG GAVHTRGLDFACDIYI WAPLAGTCGVLLLSLV ITLYCNHRNRSKRSRL LHSDYMNMTPRRPGPT RKHYQPYAPPRDFAAY RSRVKFSRSADAPAYQ QGQNQLYNELNLGRRE	210

	GAGATTAAGAGGGCTGCCGCACTTTCAAA TTCCATCATGTATTTTCAGCCATTTTGTGC CTGTTTTTCTTCCGGCCAAACCTACAACC ACTCCCGCCCCACGCCACCTACTCCCGC CCCTACCATTGCCTCCCAGCCTCTGTCTC TTAGACCTGAGGCTTGTAGACCTGCTGCC GGCGGAGCCGTGCACACTCGCGGTCTGGA CTTCGCCTGCGACATCTATATCTGGGCCC CTCTGGCCGGCACCTGCGGCGTTCTCCTT CTCTCACTCGTAATCACACTCTATTGCAA TCACAGGAACAGATCCAAAAGAAGCCGCC TGCTCCATAGCGATTACATGAATATGACT CCACGCCGCCCTGGCCCCACAAGGAAACA CTACCAGCCTTACGCACCACCTAGAGATT TCGCTGCCTATCGGAGCAGGGTGAAGTTT TCCAGATCTGCAGATGCACCAGCGTATCA GCAGGGCCAGAACCAACTGTATAACGAGC TCAACCTGGGACGCAGGGAAGAGTATGAC GTTTTGGACAAGCGCAGAGGACGGGACCC TGAGATGGGTGGCAAACCAAGACGAAAAA ACCCCCAGGAGGGTCTCTATAATGAGCTG CAGAAGGATAAGATGGCTGAAGCCTATTC TGAAATAGGCATGAAAGGAGAGCGGAGAA GGGGAAAAGGGCACGACGGTTTGTACCAG GGACTCAGCACTGCTACGAAGGATACTTA TGACGCTCTCCACATGCAAGCCCTGCCAC CTAGGTAA		EYDVLDKRRGRDPEMG GKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKG ERRRGKGHDGLYQGLS TATKDTYDALHMQALP PR	
(CAR3.3) Clone 20C5.1 CD8 CAR DNA HxL	CAGGTGCAGTTGGTGCAAAGCGGCGCAGA AGTTAAGAAACCTGGGGCGTCAGTTAAGG TGTCTTGCAAAGTATCTGGCTATAACCCTC ACTGAGCTGTCCATGCATTGGGTAAGGCA GGCTCCTGGAAAGGGGCTCGAATGGATGG GAGGATTTGACCCTGAAGACGGAGAGACC ATCTACGCCCAGAAATTCCAGGGTAGAGT AACAGTGA CTGAGGACACTAGCACTGACA CAGCGTACATGGAGCTGAGTTCTCTGAGA AGTGAGGACACAGCCGTTTACTACTGCGC TACCGAGTCCAGAGGTATTGGCTGGCCAT ACTTCGACTATTGGGGTCAGGGCACCCCTG GTTACAGTGA GTTCAGGAGGCGGGGGCTC TGGGGGGGGCGGTTCCGGAGGGGGGGGCT CAGATATACAGATGACGCAGAGTCCATCA AGTCTCTCAGCCAGCGTGGGAGATCGCGT GACTATTACTTGCCGCGCCAGCCAGAGTA TTAGCTCCTATCTGAATTGGTACCAGCAA AAGCCCGGGAAGGCCCTAAGCTTCTGAT TTCTGGCGCCTCCTCTTTGAAGTCAGGTG TGCCAAGCAGATTTAGCGGGTCTGGAAGT GGCACTGACTTTACACTTACTATCTCCAG CCTGCCCCCAGAGGATTTTGCCACATATT ACTGTCAGCAAAGCTACTCTACTCCAATC ACTTTCCGGCCAGGGCACAAGATTGGAGAT TAAGAGGGCTGCCGCACTTTCAAATTCCA TCATGTATTTTCAGCCATTTTGTGCCTGTT TTTCTTCCGGCCAAACCTACAACCACTCC CGCCCCACGCCACCTACTCCCGCCCCTA CCATTGCCTCCCAGCCTCTGTCTCTTAGA CCTGAGGCTTGTAGACCTGCTGCCGGCGG AGCCGTGCACACTCGCGGTCTGGACTTCG	211	QVQLVQSGAEVKKPGA SVKVSCKVS GYTLTEL SMHWVRQAPGKGLEWM GGFDPEDGETIYAQKF QGRVTVTEDTSTDY MELSSLRSED TAVYYC ATESRGIGWPFYDWG QGT LVTVSSGGGSGG GSGGGGSDIQMTQSP SSLSASVGDRTITCR ASQSISSYLNWYQQKP GKAPKLLISGASSLKS GVPSRFSGSGSGTDF LTISSLPPEDFATYYC QQSYSTPITFGQTRL EIKRAAALSNSIMYFS HFVPVFLPAKPTTTPA PRPPTPAPTIASQPLS LRPEACRPAAGGAVHT RGLDFACDIYIWAPLA GTCGVLLLSLVITLYC NHRNRSKRSRLHSDY MNMTPRRPGPTRKHYQ PYAPPRDFAAYRSRVK FSRSADAPAYQQGQNG LYNELNLGRREEDVL DKRRGRDPEMGKPRR KNPQEGLYNELQKDKM AEAYSEIGMKGERRRG KGHDGLYQGLSTATKD TYDALHMQALPPR	212

	CCTGCGACATCTATATCTGGGCCCCCTCTG GCGGGCACCTGCGGCGTTCTCCTTCTCTC ACTCGTAATCACACTCTATTGCAATCACA GGAACAGATCCAAAAGAAGCCGCCTGCTC CATAGCGATTACATGAATATGACTCCACG CCGCCCTGGCCCCACAAGGAAACACTACC AGCCTTACGCACCACCTAGAGATTTTCGCT GCCTATCGGAGCAGGGTGAAGTTTTCCAG ATCTGCAGATGCACCAGCGTATCAGCAGG GCCAGAACCAACTGTATAACGAGCTCAAC CTGGGACGCAGGGAAGAGTATGACGTTTT GGACAAGCGCAGAGGACGGGACCCTGAGA TGGGTGGCAAACCAAGACGAAAAACCCC CAGGAGGGTCTCTATAATGAGCTGCAGAA GGATAAGATGGCTGAAGCCTATTCTGAAA TAGGCATGAAAGGAGAGCGGAGAAGGGGA AAAGGGCACGACGGTTTTGTACCAGGGACT CAGCACTGCTACGAAGGATACTTATGACG CTCTCCACATGCAAGCCCTGCCACCTAGG			
(CAR4.1) Clone 20C5.2 THD CAR DNA HxL	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCCGAGGTCCAGTTGGTCGAAAGTGGC GGTGGTGTAGTGCAGCCGGGCCGAGTTT GAGGCTTTTCTGTGCGGCTTCAGGCTTTA CTTTTTCCAGCTATGGAATGCACTGGGTG CGGCAGGCCCCCGGCAAAGGACTTGAGTG GGTGGCCGTCAATTTCTTATGACGGATCAG ATAAGTACTACGTGGACAGCGTCAAGGGC AGATTCACCATCTCTAGGGACAACAGTAA AAATAGACTCTACCTCCAGATGAATAGCC TCAGAGCTGAAGACACGGCCGTCTACTAT TGTGCTCGGGAGCGGTATAGTGGCAGAGA CTACTGGGGGCAGGGCACACTCGTTACAG TGAGTAGCGGCGGAGGAGGGAGTGGGGGC GGTGGCTCCGGTGGAGGAGTTCTGAGAT TGTTATGACCCAGAGTCTGCGACCCCTCT CAGTCAGCCCCGGGGAGCGCGCAACTTTG TCTTGCAAGCTAGTCACTCGGTGTCCTC TCTTCTGACATGGTACCAGCAAAAGCCCG GGCAGGCTCCGCGCCTTTTGATCTTTGGG GCTTCAACAAGAGCCACTGGGATTCCCGC ACGATTCTCTGGCTCCGGGAGCGGTACTG GTTTCAACCCTGACGATTAGCAGTCTCCAG AGCGAGGACTTCGCCGTATACTACTGCCA GCAGTACGATACGTGGCCATTCACTTTTG GACCAGGGACTAAAGTGGATTTTAAGCGC GCCGCCGCTCTCGATAACGAAAAGTCAAA TGGCACCATAATCCACGTCAAAGGCAAGC ACCTGTGCCCTTCCCCGCTCTTCCCCGGA CCCAGTAAACCATTTTGGGTGCTGGTTGT TGTGGGGGGCGTGCTGGCCTGCTATAGCC TTTTGGTCACTGTAGCCTTCATTATTTTT TGGGTCAAGATCCAAAAGAAGCCGCCTGCT CCATAGCGATTACATGAATATGACTCCAC GCCGCCCTGGCCCCACAAGGAAACACTAC CAGCCTTACGCACCACCTAGAGATTTTCGC TGCCTATCGGAGCAGGGTGAAGTTTTCCA GATCTGCAGATGCACCAGCGTATCAGCAG GGCCAGAACCAACTGTATAACGAGCTCAA	213	MALPVTALLLPLALLL HAARPQVQLVESGGGV VQPGRLRLSCAASGF TFSSYGMHWVRQAPGK GLEWVAVISYDGS DKY YVDSVKGRFTISR DNS KNRLYLQMNSLR AEDT AVYYCARE RYSGRDIW GQGT LVT VSSGGGSG GGSGGGGSEIVMTQS PATLSVSPGERATLSC RASQSVSSLLTWYQQK PGQAPRLLI FGASTRA TGIPARFSGSGSGTGF TLTISSLQSEDFAVYY CQQYDTWPF TFGPGTK VDFKRAAALDNEKSNG TIIHVKGKHLCP SPLF PGPSKPFWLVVVGGV LACYSLLVTVAFIIFW VRSKRSRL LHS DYNM TPRRPGPTRKHYQPYA PPRDFAA YRSRVKFSR SADAPAYQQGQNQLYN ELNLGRREEYDVLDKR RGRDPEMGGKPRRKNP QEGLYNELQKDKMAEA YSEIGMKGERRRGKGH DGLYQGLSTATKDTYD ALHMQALPPR	214

	CCTGGGACGCAGGGAAGAGTATGACGTTT TGGACAAGCGCAGAGGACGGGACCCTGAG ATGGGTGGCAAACCAAGACGAAAAACCC CCAGGAGGGTCTCTATAATGAGCTGCAGA AGGATAAGATGGCTGAAGCCTATTCTGAA ATAGGCATGAAAGGAGAGCGGAGAAGGGG AAAAGGGCACGACGGTTTGTACCAGGGAC TCAGCACTGCTACGAAGGATACTTATGAC GCTCTCCACATGCAAGCCCTGCCACCTAG GTAA			
(CAR4.1) Clone 20C5.2 THD CAR DNA HxL	CAGGTCCAGTTGGTCGAAAGTGGCGGTGG TGTAAGTGCAGCCGGGCGCAGTTTGAGGC TTTCCTGTGCGGCTTCAGGCTTTACTTTT TCCAGCTATGGAATGCACTGGGTGCGGCA GGCCCCCGGCAAAGGACTTGAGTGGGTGG CCGTCATTTCTTATGACGGATCAGATAAG TACTACGTGGACAGCGTCAAGGGCAGATT CACCATCTCTAGGGACAACAGTAAAAATA GACTCTACCTCCAGATGAATAGCCTCAGA GCTGAAGACACGGCCGTCTACTATTGTGC TCGGGAGCGGTATAGTGGCAGAGACTACT GGGGGCAGGGCACACTCGTTACAGTGAGT AGCGGCGGAGGAGGGAGTGGGGGCGGTGG CTCCGGTGGAGGAGGTTCTGAGATTGTTA TGACCCAGAGTCTTGCAGCCCTCTCAGTC AGCCCCGGGAGCGCGCAACTTTGTCTTG CAGAGCTAGTCAGTCCGTGTCTCTCTTC TGACATGGTACCAGCAAAGACCCGGGCAG GCTCCGCGCCTTTTGATCTTTGGGGCTTC AACAAGAGCCACTGGGATTCCCGCACGAT TCTCTGGCTCCGGGAGCGGTACTGGTTTC ACCCTGACGATTAGCAGTCTCCAGAGCGA GGACTTCGCCGTATACTACTGCCAGCAGT ACGATACGTGGCCATTCACTTTTGGACCA GGGACTAAAGTGGATTTTAAGCGCGCCGC CGCTCTCGATAACGAAAAGTCAAATGGCA CCATAATCCACGTCAAAGGCAAGCACCTG TGCCCTTCCCCGCTCTTCCCCGGACCCAG TAAACCATTTTGGGTGCTGGTTGTTGTGG GGGGCGTGCTGGCCTGCTATAGCCTTTTG GTCAGTGTAGCCTTCATTATTTTTTGGGT CAGATCCAAAAGAAGCCGCCTGCTCCATA GCGATTACATGAATATGACTCCACGCCGC CCTGGCCCCACAAGGAAACACTACCAGCC TTACGCACCACCTAGAGATTTTCGCTGCCT ATCGGAGCAGGGTGAAGTTTTCCAGATCT GCAGATGCACCAGCGTATCAGCAGGGCCA GAACCAACTGTATAACGAGCTCAACCTGG GACGCAGGGAAGAGTATGACGTTTTGGAC AAGCGCAGAGGACGGGACCCTGAGATGGG TGGCAAACCAAGACGAAAAACCCCCAGG AGGGTCTCTATAATGAGCTGCAGAAGGAT AAGATGGCTGAAGCCTATTCTGAAATAGG CATGAAAGGAGAGCGGAGAAGGGGAAAAG GGCACGACGGTTTGTACCAGGGACTCAGC ACTGCTACGAAGGATACTTATGACGCTCT CCACATGCAAGCCCTGCCACCTAGG	215	QVQLVESGGGVVQPGR SLRLSCAASGFTFSSY GMHWVRQAPGKGLEWV AVISYDGS DKYYVDSV KGRFTISRDN SKNRLY LQMNSLR AEDTAVYYC ARERYSGRDYWGQGT L VTVSSGGGSGGGGSG GGGSEIVMTQSPATLS VSPGERATLSCRASQS VSSLLTWYQQKPGQAP RLLI FGASTRATGIPA RFGSGSGTGFTLTIS SLQSEDFAVYYCQQYD TWPFTFGPGTKVDFKR AAALDNEKSNGTIIHV KGKHLCPSP LFPGPSK PFWVLVVGVLACYS LLVTVAFIIFWVRSKR SRL LHS DYMNMTPRRP GPTRKHYQPYAPPRDF AAYRSRVKFSRSADAP AYQQGQNQLYNELNLG RREEYDVL DKRRGRDP EMGGKPRRKNPQEGLY NELQKDKMAEAYSEIG MKGERRRGKGHDGLYQ GLSTATKDTYDALHMQ ALPPR	216
(CAR4.2) Clone	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC	217	MALPVTALLLPLALLL HAARPQVQLVESGGGV	218

20C5.2 CHD CAR DNA HxL	GCCCCGAGGTGCAGCTCGTGGAGTCTGGC GGCGGCGTGGTCCAGCCCGCCGGTCCCT GCGCCTGTCCTGCGCCGCCAGCGGGTTTA CTTTTTCCTCCTACGGCATGCACTGGGTG CGCCAGGCTCCCGGCAAGGGCCTCGAGTG GGTCGCGGTGATCTCATACGATGGGTGAG ACAAATACTATGTCGATTCTGTAAAGGG CGGTTTACCATTTCAAGAGATAACTCTAA GAATAGGCTGTATTTGCAGATGAACAGCC TGAGGGCTGAAGATACCGCAGTGTACTAT TGCGCTAGGGAGCGGTATAGTGGCCGCGA TTACTGGGGACAGGGTACACTGGTGACCG TGAGCTCTGGGGGTGGCGGAAGCGGGGGT GGCGGAAGCGGCGGAGGGGGTAGTGAAAT TGTGATGACCCAGTCTCCGGCTACACTTT CAGTCTCCCCTGGGGAGAGAGCTACACTG TCATGCAGAGCGTCCAGTCCGTCTCTTC TCTCCTTACCTGGTATCAGCAGAAGCCCG GCCAGGCTCCTCGACTGCTGATCTTCGGT GCCTCCACAAGGGCGACCGGGATTCCAGC CCGCTTCTCAGGTTCTGGGAGCGGAAGT GTTTCACTTTGACAATCAGTTCAGTGCAG TCAGAGGATTTGCGCGTGTACTACTGCCA GCAATACGACACATGGCCATTCACTTTG GACCCGGTACCAAAGTCGATTTCAAGAGA GCCGCGGCCATCGAGGTTATGTACCCACC ACCATATCTGGACAATGAAAAAGCAATG GAACCATTATCCATGTGAAGGGTAAACAC CTCTGCCCTAGCCCACTTTTCCCTGGCCC ATCAAAGCCCTTCTGGGTCTTGGTGGTCG TGGGGGGTGTGCTGGCCTGTTACAGCCTT CTGGTGACGGTTGCTTTTATTATCTTCTG GGTTAGATCCAAAAGAAGCCGCTGCTCC ATAGCGATTACATGAATATGACTCCACGC CGCCCTGGCCCCACAAGGAAACACTACCA GCCTTACGCACCACCTAGAGATTTTCGCTG CCTATCGGAGCAGGGTGAAGTTTTCCAGA TCTGCAGATGCACCAGCGTATCAGCAGGG CCAGAACCAACTGTATAACGAGCTCAACC TGGGACGCAGGGAAGAGTATGACGTTTTG GACAAGCGCAGAGGACGGGACCCTGAGAT GGGTGGCAAACCAAGACGAAAAACCCCC AGGAGGGTCTCTATAATGAGCTGCAGAAG GATAAGATGGCTGAAGCCTATTCTGAAAT AGGCATGAAAGGAGAGCGGAGAAGGGGAA AAGGGCACGACGGTTTGTACCAGGGACTC AGCACTGCTACGAAGGATACTTATGACGC TCTCCACATGCAAGCCCTGCCACCTAGGT AA		VQPGRSLRLSCAASGF TFSSYGMHWVRQAPGK GLEWVAVISYDGS DKY YVDSVKGRFTISR DNS KNRLYLQMNSLRAEDT AVYYCAREYSGRDY W GQGT LVT VSSGGGSG GGSGGGGSEIVMTQS PATLSVSPGERATLSC RASQSVSSLLTWYQ QK PGQAPRLLI FGASTRA TGIPARFSGSGSGTGF TLTISSLQSEDFAVYY CQQYDTWPFTFGPGTK VDFKRAAAIEVMYPPP YLDNEKSNGTIIHVKG KHLCPSP LFPGPSKPF WVLVVVGGVLACYSLL VTVAFIIFWVRSKRSR LLHSDYMNMTPRRPGP TRKHYQPYAPPRDFAA YRSRVKFSRSADAPAY QQGQNQLYNELNLGRR EEYDVL DKRRGRDP EM GGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMK GERRRGKGHDGLYQGL STATKDTYDALHMQAL PPR	
(CAR4.2) Clone 20C5.2 CHD CAR DNA HxL	CAGGTGCAGCTCGTGGAGTCTGGCGGCGG CGTGGTCCAGCCCGGCGGTCCCTGCGCC TGTCCTGCGCCGCCAGCGGGTTTACTTTT TCCTCCTACGGCATGCACTGGGTGCGCCA GGCTCCCGGCAAGGGCCTCGAGTGGGTG CCGTGATCTCATACGATGGGTGAGACAAA TACTATGTCGATTCTGTAAAGGGCGGTT TACCATTTCAAGAGATAACTCTAAGAATA GGCTGTATTTGCAGATGAACAGCCTGAGG GCTGAAGATACCGCAGTGTACTATTGCGC	219	QVQLVESGGGVVQPGR SLRLSCAASGFTFSSY GMHWVRQAPGKGLEWV AVISYDGS DKYYVDSV KGRFTISR DNSKNRLY LQMNSLRAEDTAVYYC ARERYSGRDYWGQGT L VTVSSGGGSGGGGSG GGGSEIVMTQSPATLS VSPGERATLSCRASQS	220

	TAGGGAGCGGTATAGTGGCCGCGATTACT GGGGACAGGGTACACTGGTGACCGTGAGC TCTGGGGGTGGCGGAAGCGGGGTGGCGG AAGCGGCGGAGGGGGTAGTGAAATTGTGA TGACCCAGTCTCCGGCTACACTTTCAGTC TCCCCTGGGGAGAGAGCTACACTGTCATG CAGAGCGTCCCAGTCCGTCTCTTCTCTCC TTACCTGGTATCAGCAGAAGCCCGGCCAG GCTCCTCGACTGCTGATCTTCGGTGCCCTC CACAAGGGCGACCGGGATTCCAGCCCGCT TCTCAGGTTCTGGGAGCGGAAGTGGTTTC ACTTTGACAATCAGTTCACTGCAGTCAGA GGATTTTCGCCGTGTACTACTGCCAGCAAT ACGACACATGGCCATTCACTTTTCGGACCC GGTACCAAAGTCGATTTCAAGAGAGCCGC GGCCATCGAGGTTATGTACCCACCACCAT ATCTGGACAATGAAAAAGCAATGGAACC ATTATCCATGTGAAGGGTAAACACCTCTG CCCTAGCCCACTTTTCCCTGGCCCATCAA AGCCCTTCTGGGTCTTGGTGGTTCGTGGG GGTGTGCTGGCCTGTTACAGCCTTCTGGT GACGGTTGCTTTCATTATCTTCTGGGTTA GATCCAAAAGAAGCCGCCTGCTCCATAGC GATTACATGAATATGACTCCACGCCGCC TGGCCCCACAAGGAAACACTACCAGCCTT ACGCACCACCTAGAGATTTTCGTGCTAT CGGAGCAGGGTGAAGTTTTCCAGATCTGC AGATGCACCAGCGTATCAGCAGGGCCAGA ACCAACTGTATAACGAGCTCAACCTGGGA CGCAGGGAAGAGTATGACGTTTTGGACAA GCGCAGAGGACGGGACCCTGAGATGGGTG GCAAACCAAGACGAAAAACCCCCAGGAG GGTCTCTATAATGAGCTGCAGAAGGATAA GATGGCTGAAGCCTATTCTGAAATAGGCA TGAAAGGAGAGCGGAGAAGGGGAAAAGGG CACGACGGTTTGTACAGGGACTCAGCAC TGCTACGAAGGATACTTATGACGCTCTCC ACATGCAAGCCCTGCCACCTAGG		VSSLLTWYQQKPGQAP RLLIFGASTRATGIPA RFSGSGSGTGFTLTIS SLQSEDFAVYYCQQYD TWPFTFGPGTKVDFKR AAAIEVMYPPPYLDNE KSNGTIIHVKGKHLCP SPLFPGPSKPFWVLVV VGGVLACYSLLVTVAF IIFWVRSKRSRLHSD YMNMTPRRPGPTRKHY QPYAPPRDFAAYRSRV KFSRSADAPAYQQGQN QLYNELNLGRREEYDV LDKRRGRDPEMGGKPR RKNPQEGLYNELQKDK MAEAYSEIGMKGERRR GKGHDGLYQGLSTATK DTYDALHMQALPPR	
(CAR4.3) Clone 20C5.2 CD8 CAR DNA HxL	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCCGAGGTGCAGTTGGTTGAATCAGGA GGGGGTGTGGTGCAACCCGGTCGGTCACT GCGCCTCAGTTGTGCTGCTTCCGGGTTTA CTTTCAGCTCATATGGGATGCACTGGGTA CGGCAGGCTCCAGGTAAAGGCTTGGAATG GGTGGCGGTGATCAGCTATGACGGCTCTG ACAAATATTATGTGGACTCCGTGAAAGGC AGATTCACCATCAGTCGAGACAACCTCAA GAATAGACTCTACTTGCAGATGAATAGCC TCCGGGCCGAAGATACTGCAGTCTATTAT TGCGCCCCGGGAGCGCTACAGTGGAAGAGA CTATTGGGGGCAAGGAACCTCTTGTCACAG TCTCATCTGGCGGGCGGCGGAGCGGTGGG GGCGGATCTGGCGGGGGCGGCAGCGAAAT CGTTATGACTCAGAGTCCTGCCACACTGA GCGTTAGCCCTGGTGAGAGAGCAACACTT AGCTGCAGAGCTAGTCAGAGTGTTCAG TCTTTTGACATGGTACCAACAGAAGCCG GTCAAGCTCCACGACTGCTCATCTTCGGT	221	MALPVTALLLPLALLL HAARPQVQLVESGGGV VQPGRSRLRLSCAASGF TFSSYGMHWVRQAPGK GLEWVAVISYDGS DKY YVDSVKGRFTISRDN KNRLYLQMNLSRAEDT AVYYCAREYSGRDY GQGTILVTSSGGGSG GGSGGGGSEIVMTQS PATLSVSPGERATLSC RASQSVSSLLTWYQQK PGQAPRLLIFGASTRA TGIPARFSGSGSGTG TLTISSLQSEDFAVYY CQQYDTWPFTFGPGTK VDFKRAAALNSIMYF SHFVPVFLPAKPTTTP APRPPTPAPTIASQPL SLRPEACRPAAGGAVH TRGLDFACDIYIWAPL	222

	GCATCCACCCGCGCAACCGGGATACCCGC CCGGTTTTCCGGTTCTGGAAGTGGCACAG GATTCACGCTCACCATTTCTTCTCTGCAG TCTGAAGACTTTGCCGTGTATTACTGCCA GCAGTACGATACCTGGCCCTTTACCTTTG GCCCAGGTACTAAAGTGGATTTTAAACGA GCTGCTGCACTTTCCAATAGTATTATGTA CTTTTACATTTTGTGCCGTGTTCTCTGC CTGCGAAGCCTACGACAACCCAGCCCT AGGCCGCCCACACCGGCCCAACTATTGC CTCCCAGCCATTGTCTCTGAGACCCGAAG CTTGACAGACCTGCTGCTGGAGGCGCCGTT CACACCCGAGGATTGGATTTTCGCATGTGA CATTTACATCTGGGCCCTTTGGCCGGAA CCTGCGGTGTGCTGCTGCTGCTCACTCGTG ATTACACTTTACTGCAACCACCGAAACAG ATCCAAAAGAAGCCGCTGCTCCATAGCG ATTACATGAATATGACTCCACGCCGCCCT GGCCCCACAAGGAAACACTACCAGCCTTA CGCACCACCTAGAGATTTTCGCTGCCTATC GGAGCAGGGTGAAGTTTTCCAGATCTGCA GATGCACCAGCGTATCAGCAGGGCCAGAA CCAACTGTATAACGAGCTCAACCTGGGAC GCAGGGAAGAGTATGACGTTTTGGACAAG CGCAGAGGACGGGACCCTGAGATGGGTGG CAAACCAAGACGAAAAACCCCGAGGAGG GTCTCTATAATGAGCTGCAGAAGGATAAG ATGGCTGAAGCCTATTCTGAAATAGGCAT GAAAGGAGAGCGGAGAAGGGGAAAAGGGC ACGACGGTTTTGTACCAGGGACTCAGCACT GCTACGAAGGATACTTATGACGCTCTCCA CATGCAAGCCCTGCCACCTAGGTAA		AGTCGVLLLSLVITLY CNHRNRSKRSRLHSD YMNMTPRRPGPTRKHY QPYAPPRDFAAYRSRV KFSRSADAPAYQQGQN QLYNELNLGRREEYDV LDKRRGRDPGEMGGKPR RKNPQEGLYNELQKDK MAEAYSEIGMKGERRR GKGHDGLYQGLSTATK DTYDALHMQALPPR	
(CAR4.3) Clone 20C5.2 CD8 CAR DNA HxL	CAGGTGCAGTTGGTTGAATCAGGAGGGGG TGTGGTGCAACCCGGTCCGTCCTGCGCC TCAGTTGTGCTGCTTCCGGGTTTACTTTC AGCTCATATGGGATGCACTGGGTACGGCA GGCTCCAGGTAAAGGCTTGAATGGGTGG CGGTGATCAGCTATGACGGCTCTGACAAA TATTATGTGGACTCCGTGAAAGGCAGATT CACCATCAGTCGAGACAACCTCAAAGAATA GACTCTACTTGCAAGTGAATAGCCTCCGG GCCGAAGATACTGCAGTCTATTATTGCGC CCGGGAGCGCTACAGTGGAAGAGACTATT GGGGGCAAGGAACCTTGTGTCAGTCTCA TCTGGCGGGCGGCGCAGCGGTGGGGCGG ATCTGGCGGGGGCGGCGAGCGAAATCGTTA TGACTCAGAGTCCTGCCACACTGAGCGTT AGCCCTGGTGAGAGAGCAACACTTAGCTG CAGAGCTAGTCAGAGTGTTCAGTCTTT TGACATGGTACCAACAGAAGCCCGGTCAA GCTCCACGACTGCTCATCTTCGGTGATC CACCCGCGCAACCGGGGATACCCGCCCGGT TTTCCGGTCTGGAAGTGGCACAGGATTC ACGCTCACCATTTCTTCTCTGAGTCTGA AGACTTTGCCGTGTATTACTGCCAGCAGT ACGATACCTGGCCCTTTACCTTTGGCCCA GGTACTAAAGTGGATTTTAAACGAGCTGC TGCACTTTCCAATAGTATTATGACTTTT CACATTTTGTGCCCGTGTTCCTGCCTGCG	223	QVQLVESGGGVVQPGR SLRLSCAASGFTFSSY GMHWVRQAPGKGLEWV AVISYDGSCKYYVDSV KGRFTISRDNKSNRLY LQMNSLRAEDTAVYYC ARERYSGRDYWGQGT VTVSSGGGSGGGGSG GGGSEIVMTQSPATLS VSPGERATLSCRASQS VSSLLTWYQQKPGQAP RLLI FGASTRATGIPA RFSGSGSGTGFTLTIS SLQSEDFAVYYCQQYD TWPFTFGPGTKVDFKR AAALSNSIMYFSHFVP VFLPAKPTTTPAPRPP TPAPTIASQPLSLRPE ACRPAAGGAVHTRGLD FACDIYIWAPLAGTCG VLLLSLVITLYCNHRN RSKRSRLHSDYMNMT PRRPGPTRKHYQPYAP PRDFAAYRSRVKFSRS ADAPAYQQGQNQLYNE LNLGRREEYDVLDRR GRDPGEMGGKPRRKNPQ	224

	AAGCCTACGACAACCCCAGCCCCTAGGCC GCCCACACCGGCCCAACTATTGCCTCCC AGCCATTGTCTCTGAGACCCGAAGCTTGC AGACCTGCTGCTGGAGGCGCCGTTACAC CCGAGGATTGGATTTTCGCATGTGACATTT ACATCTGGGCCCCCTTTGGCCGGAACCTGC GGTGTGCTGCTGCTGTCACTCGTGATTAC ACTTTACTGCAACCACCGAAACAGATCCA AAAGAAGCCGCTGCTCCATAGCGATTAC ATGAATATGACTCCACGCCGCCCTGGCCC CACAAGGAAACACTACCAGCCTTACGCAC CACCTAGAGATTTTCGCTGCCTATCGGAGC AGGGTGAAGTTTTCCAGATCTGCAGATGC ACCAGCGTATCAGCAGGGCCAGAACCAAC TGTATAACGAGCTCAACCTGGGACGCAGG GAAGAGTATGACGTTTTGGACAAGCGCAG AGGACGGGACCCTGAGATGGGTGGCAAAC CAAGACGAAAAACCCCCAGGAGGGTCTC TATAATGAGCTGCAGAAGGATAAGATGGC TGAAGCCTATTCTGAAATAGGCATGAAAG GAGAGCGGAGAAGGGGAAAAGGGCACGAC GGTTTGTACCAGGGACTCAGCACTGCTAC GAAGGATACTTATGACGCTCTCCACATGC AAGCCCTGCCACCTAGG		EGLYNELQKDKMAEAY SEIGMKGERRRGKGDH GLYQGLSTATKDTYDA LHMQUALPPR	
(CAR4.4) Clone 20C5.2 THD CAR DNA LxH	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCGGAGATTGTGATGACCCAGTCCCCT GCTACCCTGTCCGTGCTCGGGCCAGCCAGT AGCCACCTTGTGCTGCTCGGGCCAGCCAGT CCGTCAGCAGTCTCCTGACTTGGTATCAG CAAAAACCAGGGCAGGCACCGCGGCTTTT GATTTTTGGTGCAAGCACACGCGCCACTG GCATTCCAGCTAGGTTTTCTGGAAGTGGA TCTGGGACAGGCTTCACTCTGACAATCAG TAGCCTGCAGAGTGAGGACTTTGCTGTTT ACTACTGTCAACAGTACGACACCTGGCCA TTCACATTCCGGGCCCCGCCACCAAGGTGCA CTTCAAGAGGGGCGGTGGAGGTTCAAGTG GTGGCGGGTCAGGCGGCGGTGGGTCTCAG GTTCAACTGGTGGAATCAGGTGGCGGCGT TGTCACACCGGGGCGATCACTTCACTTTT CCTGTGCTGCCTCAGGCTTTACTTTTTCA TCCTATGGGATGCACTGGGTTCGGCAGGC TCCCGGAAAAGGACTCGAGTGGGTTCAG TGATCTCTTACGATGGCTCAGACAAGTAT TATGTGGACTCAGTCAAGGGGAGATTAC AATAAGCCGAGACAACCTCAAAAACCGGC TTTATCTCCAGATGAACAGCCTTAGAGCG GAAGATACCGCGGTATACTACTGTGCCCCG CGAGAGGTATTCCGGCAGAGACTACTGGG GACAGGGCACACTGGTCACCGTGAGTTCT GCCGCAGCGCTCGATAACGAAAAGAGCAA CGGAACCATTATCCACGTTAAGGGCAAGC ACCTGTGCCCCAGTCCCCTCTTCCAGGA CCATCTAAACCCTTCTGGGTTCTGGTAGT AGTTGGAGGGGTCCTTGCATGTTACTCCC TTTTGGTCACCGTCGCCTTCATTATTTTC TGGGTGAGATCCAAAAGAAGCCGCGCTGCT CCATAGCGATTACATGAATATGACTCCAC	225	MALPVTALLLPLALLL HAARPEIVMTQSPATL SVSPGERATLSCRASQ SVSSLLTWYQQKPGQA PRLLI FGASTRATGIP ARFSGSGSGTGFTLTI SSLQSEDFAVYYCQQY DTWPF TFGPGTKVDFK RGGGSGGGSGGGGS QVQLVESGGGVVQPGR SLRLSCAASGFTFSSY GMHWVRQAPGKLEWV AVISYDGS DKYYVDSV KGRFTISRDN SKNRLY LQMNSLR AEDTAVYYC ARERYSGRDYWGQGTL VTVSSAAALDNEKSNG TIIHVKGKHLCPSPFL PGPSKPFVWL VVVG LACYSLLVTVAFIIFW VRSKRSRL LHSYMN TPRRPGPTRKHYQPYA PFRDFAAYRSRVKFSR SADAPAYQQGQNQLYN ELNLGRREEYDVLDR RGRDP EMGGKPRRKNP QEGLYNELQKDKMAEA YSEIGMKGERRRGKGDH DGLYQGLSTATKDTYD ALHMQUALPPR	226

	GCCGCCCTGGCCCCACAAGGAAACACTAC CAGCCTTACGCACCACCTAGAGATTTTCGC TGCCTATCGGAGCAGGGTGAAGTTTTCCA GATCTGCAGATGCACCAGCGTATCAGCAG GGCCAGAACCAACTGTATAACGAGCTCAA CCTGGGACGCAGGGAAGAGTATGACGTTT TGGACAAGCGCAGAGGACGGGACCCTGAG ATGGGTGGCAAACCAAGACGAAAAAACC CCAGGAGGGTCTCTATAATGAGCTGCAGA AGGATAAGATGGCTGAAGCCTATTCTGAA ATAGGCATGAAAGGAGAGCGGAGAAGGGG AAAAGGGCACGACGGTTTGTACCAGGGAC TCAGCACTGCTACGAAGGATACTTATGAC GCTCTCCACATGCAAGCCCTGCCACCTAG GTAA			
(CAR4.4) Clone 20C5.2 THD CAR DNA LxH	GAGATTGTGATGACCCAGTCCCCTGCTAC CCTGTCCGTCACTCCGGGCGAGAGAGCCA CCTTGTCATGCCGGGCCAGCCAGTCCGTC AGCAGTCTCCTGACTTGGTATCAGCAAAA ACCAGGGCAGGCACCGCGGCTTTTGATTT TTGGTGCAAGCACACGCGCCACTGGCATT CCAGCTAGGTTTTCTGGAAGTGGATCTGG GACAGGCTTCACTCTGACAATCAGTAGCC TGCAGAGTGAGGACTTTGCTGTTTACTAC TGTCAACAGTACGACACCTGGCCATTAC ATTCGGGCCCCGGCACCAAGGTCGACTTCA AGAGGGGCGGTGGAGGTTCAAGTGGTGGC GGGTCAAGGCGCGGTGGGTCTCAGGTTCA ACTGGTGGAATCAGGTGGCGCGTTGTCC AACCAGGGCGATCACTTCGACTTTCCTGT GCTGCCTCAGGCTTTACTTTTTTCATCCTA TGGGATGCACTGGGTTTCGGCAGGCTCCCG GAAAAGGACTCGAGTGGGTTGCAGTGATC TCTTACGATGGCTCAGACAAGTATTATGT GGACTCAGTCAAGGGGAGATTACAATAA GCCGAGACAACCTCAAAAACCGGCTTTAT CTCCAGATGAACAGCCTTAGAGCGGAAGA TACCGCGGTATACTACTGTGCCCGCGAGA GGTATTCGGCAGAGACTACTGGGGACAG GGCACACTGGTCACCGTGAGTTCTGCCGC AGCGCTCGATAACGAAAAGAGCAACGGAA CCATTATCCACGTTAAGGGCAAGCACCTG TGCCCCAGTCCCCTCTTCCCAGGACCATC TAAACCCTTCTGGGTTCTGGTAGTAGTTG GAGGGGTCTTGCATGTTACTCCCTTTTG GTCACCGTCGCCTTCATTATTTTCTGGGT GAGATCCAAAAGAAGCCGCCTGCTCCATA GCGATTACATGAATATGACTCCACGCCGC CCTGGCCCCACAAGGAAACACTACCAGCC TTACGCACCACCTAGAGATTTTCGCTGCCT ATCGGAGCAGGGTGAAGTTTTCCAGATCT GCAGATGCACCAGCGTATCAGCAGGGCCA GAACCAACTGTATAACGAGCTCAACCTGG GACGCAGGGAAGAGTATGACGTTTTGGAC AAGCGCAGAGGACGGGACCCTGAGATGGG TGGCAAACCAAGACGAAAAAACCCTCAGG AGGGTCTCTATAATGAGCTGCAGAAGGAT AAGATGGCTGAAGCCTATTCTGAAATAGG CATGAAAGGAGAGCGGAGAAGGGGAAAAG	227	EIVMTQSPATLSVSPG ERATLSCRASQSVSSL LTWYQQKPGQAPRLLI FGASTRATGIPARFSG SGSGTGFTLTISLQS EDFAVYYCQQYDTPWF TFGPGTKVDFKRGGGG SGGGSGGGGSQVQLV ESGGGVVQPGRSRLRS CAASGFTFSSYGMHVV RQAPGKGLEWVAVISY DGSDDKYVDVSVKGRFT ISRDN SKNRLYLQMN LRAEDTAVYYCARERY SGRDYWGQGTLLVTVSS AAALDNEKSNGTIIHV KGKHLCPSPLEFPGPSK PFWVLVVVGGVLACYS LLVTVAFIIFWVRSKR SRLHSDYMNMTPRRP GPTRKHYQPYAPPRDF AAYRSRVKFSRSADAP AYQQGQNQLYNELNLG RREEYDVLDRRRGRDP EMGGKPRRKNPQEGLY NELQKDKMAEAYSEIG MKGERRRGKGDGLYQ GLSTATKDTYDALHMQ ALPPR	228

	GGCACGACGGTTTGTACCAGGGACTCAGC ACTGCTACGAAGGATACTTATGACGCTCT CCACATGCAAGCCCTGCCACCTAGG			
(CAR4.5) Clone 20C5.2 CHD CAR DNA LxH	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCCGAGATCGTCATGACACAGAGTCCA GCTACCCTGAGCGTGTCCCCTGGAGAGAG AGCCACCCTGTCTGTAGGGCTAGTCAGA GTGTGTCCAGCCTCCTCACCTGGTATCAA CAGAAGCCCTGGTCAAGCTCCCCGGCTGCT TATCTTCGGGGCCAGCACGCGAGCCACAG GCATCCCCGGCCAGATTCTCTGGCTCTGGC AGTGGCACCGGGTTCCTCTCACGATCTC ATCCCTGCAGTCAGAGGATTTCTGCTGTGT ATTACTGTCAGCAGTACGATACATGGCCC TTCACCTTCGGCCCCGGGCACAAAAGTAGA TTTCAAGCGCGGGCGGGGGGTAGTGGGG GCGGGGGATCAGGAGGAGGGGGCTCCCAA GTACAGCTGGTTGAGAGCGGCGGGGGGT GGTTCAGCCCGGGCGCAGCCTCAGGCTGA GTTGCGCAGCATCAGGATTCACATTCAGT TCTTATGGAATGCATTGGGTGAGACAGGC TCCCGGAAGGGCCTTGAATGGGTGGCAG TCATTAGCTACGACGGAAGCGATAAGTAC TATGTGGACTCAGTTAAAGGGAGATTTAC TATCAGCCGCGACAATTCCAAAAACAGAT TGTATTTGCAGATGAACCTCCCTCAGGGCG GAGGACACTGCTGTATATTACTGCGCACG AGAGAGATACTCCGGCCGAGACTATTGGG GCCAAGGAACATTGGTAAGTGTGAGCTCC GCCGCAGCTATTGAGGTCATGTACCCCCC ACCTTATCTCGATAATGAGAAGAGTAATG GGACTATAATTACGTAAAGGGCAAACAC CTGTGCCCTTCCCCGCTGTTTCCAGGTCC AAGTAAGCCGTTCTGGGTCTGTTGTGG TGGGAGGGGTGCTGGCCTGCTATTCTCTG TTGGTTACCGTGGCCTTTATCATTTTCTG GGTGAGATCCAAAAGAAGCCGCTGCTCC ATAGCGATTACATGAATATGACTCCACGC CGCCCTGGCCCCACAAGGAAACACTACCA GCCTTACGCACCACCTAGAGATTTCTGCTG CCTATCGGAGCAGGGTGAAGTTTTCCAGA TCTGCAGATGCACCAGCGTATCAGCAGGG CCAGAACCAACTGTATAACGAGCTCAACC TGGGACGCAGGGAAGAGTATGACGTTTTG GACAAGCGCAGAGGACGGGACCCTGAGAT GGGTGGCAAACCAAGACGAAAAAACCCCC AGGAGGGTCTCTATAATGAGCTGCAGAAG GATAAGATGGCTGAAGCCTATTCTGAAAT AGGCATGAAAGGAGAGCGGAGAAGGGGAA AAGGGCACGACGGTTTGTACCAGGGACTC AGCACTGCTACGAAGGATACTTATGACGC TCTCCACATGCAAGCCCTGCCACCTAGGT AA	229	MALPVTALLLPLALLL HAARPEIVMTQSPATL SVSPGERATLSCRASQ SVSSLLTWYQQKPGQA PRLLIFGASTRATGIP ARFSGSGSGTGFTLT SSLQSEDFAVYYCQQY DTWPFTFGPGTKVDFK RGGGSGGGSGGGGS QVQLVESGGGVVQPGR SLRLSCAASGFTFSSY GMHWVRQAPGKGLEWV AVISYDGS DKYYVDSV KGRFTISRDN SKNRLY LQMNSLR AEDTAVYYC AREYSGRDYWGQGT VTVSSAAAI EVMYPPP YLDNEKSNGTIIHVK KHLCPSP LFPGPSKPF WVLVVGGV LACYSLL VTVAFIIFWVR SKRSR LLHSDYMNMTPRRPGP TRKHYQPYAPPRDFAA YRSRVKFSRSADAPAY QQGQNQLYNELNLGR EEYDVLDRRGRDPEM GGKPRRKNPQEGLYNE LQKDKMAEAYSEIGMK GERRRGKGHDGLYQGL STATKDTYDALHMQAL PPR	230
(CAR4.5) Clone 20C5.2 CHD CAR DNA LxH	GAGATCGTCATGACACAGAGTCCAGCTAC CCTGAGCGTGTCCCCTGGAGAGAGAGCCA CCCTGTCCTGTAGGGCTAGTCAGAGTGTG TCCAGCCTCCTCACCTGGTATCAACAGAA GCCTGGTCAAGCTCCCCGGCTGCTTATCT	231	EIVMTQSPATLSVSPG ERATLSCRASQSVSSL LTWYQQKPGQAPRLLI FGASTRATGIPARFSG SGSGTGFTLTISLQS	232

	TCGGGGCCAGCACGCGAGCCACAGGCATC CCGGCCAGATTCTCTGGCTCTGGCAGTGG CACC GGTTCACTCTCACGATCTCATCCC TGCACTCAGAGGATTTCTGCTGTGTATTAC TGTCAGCAGTACGATACATGGCCCTTCAC CTTCGGCCCCGGGCACAAAAGTAGATTTCA AGCGCGGCGGGGGGGTAGTGGGGGCGGG GGATCAGGAGGAGGGGGCTCCCAAGTACA GCTGGTTGAGAGCGGCGGGGGTGGTTC AGCCCGGGCGCAGCCTCAGGCTGAGTTGC GCAGCATCAGGATTCACATTCAGTTCTTA TGGAATGCATTGGGTGAGACAGGCTCCCG GGAAGGGCCTTGAATGGGTGGCAGTCATT AGCTACGACGGAAGCGATAAGTACTATGT GGACTCAGTTAAAGGGAGATTTACTATCA GCCGCGACAATTCCAAAACAGATTGTAT TTGCAGATGAACTCCCTCAGGGCGGAGGA CACTGCTGTATATTACTGCGCACGAGAGA GATACTCCGGCCGAGACTATTGGGGCCAA GGAACATTGGTAACTGTGAGCTCCGCGCG AGCTATTGAGGTCATGTACCCCCACCTT ATCTCGATAATGAGAAGAGTAATGGGACT ATAATTACGTAAGGGCAAACACCTGTG CCCTTCCCCGCTGTTTCCAGGTCCAAGTA AGCCGTTCTGGGTCTGTTGTGGTGGGA GGGGTGCTGGCCTGCTATTCTCTGTTGGT TACCGTGGCCTTTATCATTCTGTTGGTGA GATCCAAAAGAAGCGCCTGCTCCATAGC GATTACATGAATATGACTCCACGCGCGCC TGGCCCCACAAGGAAACACTACCAGCCTT ACGCACCACCTAGAGATTTCTGCTGCCTAT CGGAGCAGGGTGAAGTTTTCCAGATCTGC AGATGCACCAGCGTATCAGCAGGGCCAGA ACCAACTGTATAACGAGCTCAACCTGGGA CGCAGGGAAGAGTATGACGTTTTGGACAA GCGCAGAGGACGGGACCCTGAGATGGGTG GCAAACCAAGACGAAAAACCCCCAGGAG GGTCTCTATAATGAGCTGCAGAAGGATAA GATGGCTGAAGCCTATTCTGAAATAGGCA TGAAAGGAGAGCGGAGAAGGGGAAAAGGG CACGACGGTTTGTACCAGGGACTCAGCAC TGCTACGAAGGATACTTATGACGCTCTCC ACATGCAAGCCCTGCCACCTAGG		EDFAVYYCQQYDTWPF TFGPGTKVDFKRGGGG SGGGGSGGGGSQVQLV ESGGGVVQPGRSLRLS CAASGFTFSSYGMHWV RQAPGKGLEWVAVISY DGS DKYYVDSVKGRFT ISRDNSKNRLYLQMNS LRAEDTAVYYCARERY SGRDYWGQGTILVTVSS AAAIEVMYPPPYLDNE KSNGTIIHVKGKHLCP SPLFPGPSKPFVVLV VGGVLACYSLLVTVAF IIFWVRSKRSRLHSD YMNMTPRRPGPTRKHY QPYAPPRDFAAYRSRV KFSRSADAPAYQQGQN QLYNELNLGRREEYDV LDKRRGRDPEMGGKPR RKNPQEGLYNELQKDK MAEAYSEIGMKGERRR GKGHDGLYQGLSTATK DTYDALHMQALPPR	
(CAR4.6) Clone 20C5.2 CD8 CAR DNA LxH	ATGGCACTCCCCGTAAGTCTGCTGCTGCT GCCGTTGGCATTGCTCCTGCACGCCGCAC GCCCCGAAATAGTGATGACTCAGTCCCCG GCCACCCTCAGCGTGTCCCCGGGGAGCG AGCGACCCTGTCTGTCAGGGCTTCCAGAG GTGTCAGCTCCCTGCTCACTTGGTATCAG CAAAAGCCGGGGCAGGCTCCCCGCCTCCT CATCTTCGGGGCATCACTAGGGCCACCG GCATTCTGCAAGATTTTCCGGGTCTGGC AGCGGCACCGGCTTACCCTTACCATTAG CTCTCTGCAGTCTGAGGACTTCGCCGTTT ACTATTGTCAGCAGTATGATACTTGGCCC TTTACCTTCGGTCCCGGAACTAAGGTGGA CTTCAAGCGCGGGGGGGGTGGATCTGGAG GTGGTGGCTCCGGGGGCGGTGGAAGCCAG GTCCAGTTGGTTGAGAGCGGCGGGGAGT	233	MALPVTALLLPLALLL HAARPEIVMTQSPATL SVSPGERATLSCRASQ SVSSLLTWYQQKPGQA PRLLI FGASTRATGIP ARFSGSGSGTGFTLTI SSLQSEDFAVYYCQQY DTWPF TFGPGTKVDFK RGGGSGGGSGGGGS QVQLVESGGGVVQPGR SLRLSCAASGFTFSSY GMHWVRQAPGKLEWV AVISYDGS DKYYVDSV KGRFTISRDNSKNRLY LQMNSLRAEDTAVYYC ARERYSGRDYWGQGT	234

	GGTGCAGCCCGGGAGGTCTTGCGGCTGA GCTGTGCAGCCTCCGGTTTTACTTTTTCT AGCTATGGAATGCATTGGGTAAGACAGGC TCCCGGAAAAGGCCTCGAGTGGGTGGCGG TCATTAGCTATGATGGATCTGATAAATAC TATGTGGACTCAGTTAAGGGGCGCTTCAC AATCTCAAGAGACAATAGCAAAAATAGAC TGTACCTGCAGATGAATAGTCTGCGCGCC GAGGACACTGCCGTGTACTACTGCGCCCG CGAGAGATACAGCGGACGGGATTACTGGG GCCAGGGTACCCTCGTAACGGTGTCTCC GCTGCCGCCCTTAGCAACAGCATTATGTA CTTTTCTCATTTCTGCGCAGTCTTTCTCC CAGCAAAGCCCACCACTACCCCGGCCCCC AGGCCGCCTACTCCTGCCCCCACTATCGC GTCTCAGCCTCTCTCCTTGCGGCCCGAGG CCTGCCGGCCAGCCGCAGGGGGCGCCGTA CATACTCGGGGTTTGATTTCGCTTGCGA CATATATATTTGGGCCCCCTCGCCGGCA CATGTGGAGTGCTGCTCCTGAGTCTCGTT ATAACCCTCTATTGCAACCATAGAAACAG ATCCAAAAGAAGCCGCCTGCTCCATAGCG ATTACATGAATATGACTCCACGCCGCCCT GGCCCCACAAGGAAACACTACCAGCCTTA CGCACCACTAGAGATTTGCTGCTATC GGAGCAGGGTGAAGTTTTCCAGATCTGCA GATGCACCAGCGTATCAGCAGGGCCAGAA CCAAGTGTATAACGAGCTCAACCTGGGAC GCAGGGAAGAGTATGACGTTTTGGACAAG CGCAGAGGACGGGACCCTGAGATGGGTGG CAAACCAAGACGAAAAACCCCCAGGAGG GTCTCTATAATGAGCTGCAGAAGGATAAG ATGGCTGAAGCCTATTCTGAAATAGGCAT GAAAGGAGAGCGGAGAAGGGGAAAAGGGC ACGACGGTTTGTACCAGGGACTCAGCACT GCTACGAAGGATACTTATGACGCTCTCCA CATGCAAGCCCTGCCACCTAGGTAA		VTVSSAAALSNSIMYF SHFVPVFLPAKPTTTP APRPPTPAPTIASQPL SLRPEACRPAAGGAVH TRGLDFACDIYIWAPL AGTCGVLLLSLVITLY CNHRNRSKRSRLHSD YMNMTPRRPGPTRKHY QPYAPPRDFAAYRSRV KFSRSADAPAYQQGQN QLYNELNLGRREEYDV LDKRRGRDPEMGGKPR RKNPQEGLYNELQKDK MAEAYSEIGMKGERRR GKGHDGLYQGLSTATK DTYDALHMQALPPR	
(CAR4.6) Clone 20C5.2 CD8 CAR DNA LxH	GAAATAGTGATGACTCAGTCCCCGGCCAC CCTCAGCGTGTCCCCGGGGAGCGAGCGA CCCTGTCATGCAGGGCTTCCCAGAGTGTC AGCTCCCTGCTCACTTGGTATCAGCAAAA GCCGGGGCAGGCTCCCCGCCTCCTCATCT TCGGGGCATCAACTAGGGCCACCGGCATT CCTGCAAGATTTTCCGGGTCTGGCAGCGG CACCGGCTTACCCTTACCATTAGCTCTC TGCAGTCTGAGGACTTCGCCGTTTACTAT TGTCAGCAGTATGATACTTGGCCCTTTAC CTTCGGTCCCGGAACCTAAGGTGGACTTCA AGCGCGGGGGGGTGGATCTGGAGGTGGT GGCTCCGGGGGGCGGTGGAAGCCAGGTCCA GTTGGTTGAGAGCGGCGGCGGAGTGGTGC AGCCCGGGAGGTCTTGGCGCTGAGCTGT GCAGCCTCCGGTTTTACTTTTTCTAGCTA TGGAATGCATTGGGTAAGACAGGCTCCCG GAAAAGGCCTCGAGTGGGTGGCGGTCATT AGCTATGATGGATCTGATAAATACTATGT GGACTCAGTTAAGGGGCGCTTCACAATCT CAAGAGACAATAGCAAAAATAGACTGTAC CTGCAGATGAATAGTCTGCGCGCCGAGGA	235	EIVMTQSPATLSVSPG ERATLSCRASQSVSSL LTWYQQKPGQAPRLLI FGASTRATGIPARFSG SGSGTGFTLTISLSQS EDFAVYYCQQYDTWPF TFPGTKVDFKRGGGG SGGGSGGGGSQVQLV ESGGGVVQPGRLRLS CAASGFTFSSYGMHWV RQAPGKGLEWVAVISY DGSDKYYVDSVKGRFT ISRDN SKNRLYLQMN LRAEDTAVYYCARERY SGRDYWGQGLVTVSS AAALSNSIMYF SHFVP VFLPAKPTTTPAPRPP TPAPTIASQPLSLRPE ACRPAAGGAVHTRGLD FACDIYIWAPLAGTCG VLLLSLVITLYCNHRN RSKRSRLHSDYMNMT	236

CACTGCCGTGTACTACTGCGCCCGCGAGA GATACAGCGGACGGGATTACTGGGGCCAG GGTACCCTCGTAACGGGTGTCTCCGCTGC CGCCCTTAGCAACAGCATTATGTACTTTT CTCATTTTCGTGCCAGTCTTTCTCCCAGCA AAGCCCACCACTACCCCGGCCCCCAGGCC GCCTACTCCTGCCCCCACTATCGCGTCTC AGCCTCTCTCCTTGCGGCCCCGAGGCCTGC CGGCCAGCCGCAGGGGGCGCCGTACATAC TCGGGGTTTGGATTTTCGCTTGCACATAT ATATTTGGGCCCCCTCGCCGGCACATGT GGAGTGCTGCTCCTGAGTCTCGTTATAAC CCTCTATTGCAACCATAGAAACAGATCCA AAAGAAGCCGCCTGCTCCATAGCGATTAC ATGAATATGACTCCACGCCGCCCTGGCCC CACAAGGAAACACTACCAGCCTTACGCAC CACCTAGAGATTTTCGCTGCCTATCGGAGC AGGGTGAAGTTTTCCAGATCTGCAGATGC ACCAGCGTATCAGCAGGGCCAGAACCAAC TGTATAACGAGCTCAACCTGGGACGCAGG GAAGAGTATGACGTTTTGGACAAGCGCAG AGGACGGGACCCTGAGATGGGTGGCAAAC CAAGACGAAAAAACCCCCAGGAGGGTCTC TATAATGAGCTGCAGAAGGATAAGATGGC TGAAGCCTATTCTGAAATAGGCATGAAAG GAGAGCGGAGAAGGGGAAAAGGGCACGAC GGTTTGTACCAGGGACTCAGCACTGCTAC GAAGGATACTTATGACGCTCTCCACATGC AAGCCCTGCCACCTAGG	PRRPGPTRKHYQPYAP PRDFAAYRSRVKFSRS ADAPAYQQGQNQLYNE LNLGRREEYDVLDRR GRDPEMGGKPRRKNPQ EGLYNELQKDKMAEAY SEIGMKGERRRRGKGD GLYQGLSTATKDYDA LHMQUALPPR

[0217] In some embodiments, the polynucleotide of the present invention encodes a CAR, wherein the CAR comprises an amino acid sequence at least about 75%, at least about 85%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 178, 180, 190, 192, 202, 204, 214, 216, 226, and 228. In certain embodiments, the CAR comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 178, 180, 190, 192, 202, 204, 214, 216, 226, and 228.

[0218] In some embodiments, the polynucleotide of the present invention comprises an nucleotide sequence at least about 50%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 85%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 177, 179, 189, 191, 201, 203, 213, 215, 225, and 227. In certain embodiments, the polynucleotide

comprises a nucleotide sequence selected from the group consisting of SEQ ID NOs: 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 177, 179, 189, 191, 201, 203, 213, 215, 225, and 227.

II. *Vectors, Cells, and Pharmaceutical Compositions*

5 [0219] In certain aspects, provided herein are vectors comprising a polynucleotide of the present invention. In some embodiments, the present invention is directed to a vector or a set of vectors comprising a polynucleotide encoding a CAR or a TCR comprising the truncated hinge domain (“THD”) domain, as described above.

[0220] Any vector known in the art can be suitable for the present invention. In some
10 embodiments, the vector is a viral vector. In some embodiments, the vector is a retroviral vector, a DNA vector, a murine leukemia virus vector, an SFG vector, a plasmid, a RNA vector, an adenoviral vector, a baculoviral vector, an Epstein Barr viral vector, a papovaviral vector, a vaccinia viral vector, a herpes simplex viral vector, an adenovirus associated vector (AAV), a lentiviral vector, or any combination thereof.

15 [0221] In an embodiment, a vector that can be employed in the context of the present invention is pGAR and has the coding sequence:

CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCA
GCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTTCGCTTTCTTCCCT
TCCTTTCTCGCCACGTTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCC
20 TTTAGGGTTCCGATTTAGTGCTTTACGGCACCTCGACCCCAAAAACTTGATTAG
GGTGATGGTTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGA
CGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAACTGGAACAACACT
CAACCCTATCTCGGTCTATTCTTTTGATTTATAAGGGATTTTGCCGATTTTCGGCCT
ATTGGTTAAAAAATGAGCTGATTTAACAAAAATTTAACGCGAATTTTAACAAAAAT
25 ATTAACGCTTACAATTTGCCATTTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGG
CGATCGGTGCGGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTG
CAAGGCGATTAAAGTTGGGTAACGCCAGGGTTTTCCAGTCACGACGTTGTAAAAC
GACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGACCCGGGGATGGCGCG
CCAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCGCGGTT
30 ACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCGGCCCAT
TGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTG
ACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTG
TATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCT
GGCATTATGCCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTA
35 CGTATTAGTCATCGCTATTACCATGCTGATGCGGTTTTGGCAGTACATCAATGGG
CGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCA
ATGGGAGTTTGTGTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAA
CTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATAT
AAGCAGAGCTGGTTTAGTGAACCGGGGTCTCTCTGGTTAGACCAGATCTGAGCCT

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10 TGGGACAGCTACAACCATCCCTTCAGACAGGATCAGAAGAAGCTTAGATCATTAT
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20 CCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCC
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30 AACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGCAAGCAGCAGATTACGCG
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CCAACCTGATCTTCAGCATCTTTTACTTTACCAGCGTTTCTGGGTGAGCAAAAAC
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CGCACATTTCCCCGAAAAGTGCCAC (SEQ ID NO: 252)

[0222] The pGAR vector map is set forth in FIG. 20. Suitable additional exemplary
5 vectors include e.g., pBABE-puro, pBABE-neo largeTcDNA, pBABE-hygro-hTERT,
pMKO.1 GFP, MSCV-IRES-GFP, pMSCV PIG (Puro IRES GFP empty plasmid), pMSCV-
loxp-dsRed-loxp-eGFP-Puro-WPRE, MSCV IRES Luciferase, pMIG, MDH1-PGK-GFP_2.0,
TtRMPVIR, pMSCV-IRES-mCherry FP, pRetroX GFP T2A Cre, pRXTN, pLncEXP, and
pLXIN-Luc.

[0223] In other aspects, provided herein are cells comprising a polynucleotide or a
10 vector of the present invention. In some embodiments, the present invention is directed to cells,
e.g., in vitro cells, comprising a polynucleotide encoding a CAR or a TCR comprising a TCD
described herein. In other embodiments, the present invention is directed to cells, e.g., in vitro
cells, comprising a polypeptide encoded by a CAR or a TCR comprising a TCD described
15 herein.

[0224] Any cell may be used as a host cell for the polynucleotides, the vectors, or the
polypeptides of the present invention. In some embodiments, the cell can be a prokaryotic cell,
fungal cell, yeast cell, or higher eukaryotic cells such as a mammalian cell. Suitable prokaryotic
cells include, without limitation, eubacteria, such as Gram-negative or Gram-positive
20 organisms, for example, *Enterobactehaceae* such as *Escherichia*, e.g., *E. coli*; *Enterobacter*;
Erwinia; *Klebsiella*; *Proteus*; *Salmonella*, e.g., *Salmonella typhimurium*; *Serratia*, e.g.,

Serratia marcescans, and *Shigella*; *Bacilli* such as *B. subtilis* and *B. licheniformis*; *Pseudomonas* such as *P. aeruginosa*; and *Streptomyces*. In some embodiments, the cell is a human cell. In some embodiments, the cell is an immune cell. In some embodiments, the immune cell is selected from the group consisting of a T cell, a B cell, a tumor infiltrating lymphocyte (TIL), a TCR expressing cell, a natural killer (NK) cell, a dendritic cell, a granulocyte, an innate lymphoid cell, a megakaryocyte, a monocyte, a macrophage, a platelet, a thymocyte, and a myeloid cell. In one embodiment, the immune cell is a T cell. In another embodiment, the immune cell is an NK cell. In certain embodiments, the T cell is a tumor-infiltrating lymphocyte (TIL), autologous T cell, engineered autologous T cell (eACT™), an allogeneic T cell, a heterologous T cell, or any combination thereof.

[0225] The cell of the present invention may be obtained through any source known in the art. For example, T cells can be differentiated in vitro from a hematopoietic stem cell population, or T cells can be obtained from a subject. T cells can be obtained from, *e.g.*, peripheral blood mononuclear cells, bone marrow, lymph node tissue, cord blood, thymus tissue, tissue from a site of infection, ascites, pleural effusion, spleen tissue, and tumors. In addition, the T cells can be derived from one or more T cell lines available in the art. T cells can also be obtained from a unit of blood collected from a subject using any number of techniques known to the skilled artisan, such as FICOLL™ separation and/or apheresis. In certain embodiments, the cells collected by apheresis are washed to remove the plasma fraction, and placed in an appropriate buffer or media for subsequent processing. In some embodiments, the cells are washed with PBS. As will be appreciated, a washing step can be used, such as by using a semiautomated flowthrough centrifuge, *e.g.*, the Cobe™ 2991 cell processor, the Baxter CytoMate™, or the like. In some embodiments, the washed cells are resuspended in one or more biocompatible buffers, or other saline solution with or without buffer. In certain embodiments, the undesired components of the apheresis sample are removed. Additional methods of isolating T cells for a T cell therapy are disclosed in U.S. Patent Publication No. 2013/0287748, which is herein incorporated by references in its entirety.

[0226] In certain embodiments, T cells are isolated from PBMCs by lysing the red blood cells and depleting the monocytes, *e.g.*, by using centrifugation through a PERCOLL™ gradient. In some embodiments, a specific subpopulation of T cells, such as CD4⁺, CD8⁺, CD28⁺, CD45RA⁺, and CD45RO⁺ T cells is further isolated by positive or negative selection techniques known in the art. For example, enrichment of a T cell population by negative selection can be accomplished with a combination of antibodies directed to surface markers

unique to the negatively selected cells. In some embodiments, cell sorting and/or selection via negative magnetic immunoadherence or flow cytometry that uses a cocktail of monoclonal antibodies directed to cell surface markers present on the cells negatively selected can be used. For example, to enrich for CD4⁺ cells by negative selection, a monoclonal antibody cocktail typically includes antibodies to CD8, CD11b, CD14, CD16, CD20, and HLA-DR. In certain
5 embodiments, flow cytometry and cell sorting are used to isolate cell populations of interest for use in the present invention.

[0227] In some embodiments, PBMCs are used directly for genetic modification with the immune cells (such as CARs or TCRs) using methods as described herein. In certain
10 embodiments, after isolating the PBMCs, T lymphocytes are further isolated, and both cytotoxic and helper T lymphocytes are sorted into naive, memory, and effector T cell subpopulations either before or after genetic modification and/or expansion.

[0228] In some embodiments, CD8⁺ cells are further sorted into naive, central memory, and effector cells by identifying cell surface antigens that are associated with each of these
15 types of CD8⁺ cells. In some embodiments, the expression of phenotypic markers of central memory T cells includes CCR7, CD3, CD28, CD45RO, CD62L, and CD127 and are negative for granzyme B. In some embodiments, central memory T cells are CD8⁺, CD45RO⁺, and CD62L⁺ T cells. In some embodiments, effector T cells are negative for CCR7, CD28, CD62L, and CD127 and positive for granzyme B and perforin. In certain embodiments, CD4⁺ T cells
20 are further sorted into subpopulations. For example, CD4⁺ T helper cells can be sorted into naive, central memory, and effector cells by identifying cell populations that have cell surface antigens.

[0229] In some embodiments, the immune cells, *e.g.*, T cells, are genetically modified following isolation using known methods, or the immune cells are activated and expanded (or
25 differentiated in the case of progenitors) in vitro prior to being genetically modified. In another embodiment, the immune cells, *e.g.*, T cells, are genetically modified with the chimeric antigen receptors described herein (*e.g.*, transduced with a viral vector comprising one or more nucleotide sequences encoding a CAR) and then are activated and/or expanded in vitro. Methods for activating and expanding T cells are known in the art and are described, *e.g.*, in
30 U.S. Patent Nos. 6,905,874; 6,867,041; and 6,797,514; and PCT Publication No. WO 2012/079000, the contents of which are hereby incorporated by reference in their entirety. Generally, such methods include contacting PBMC or isolated T cells 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. Anti-CD3 and anti-CD28 antibodies attached to the same bead serve as a “surrogate” antigen presenting cell (APC). One example is The Dynabeads[®] system, a CD3/CD28 activator/stimulator system for physiological activation of human T cells. In other embodiments, the T cells are activated and stimulated to proliferate with feeder cells and appropriate antibodies and cytokines using methods such as those described in U.S. Patent Nos. 6,040,177 and 5,827,642 and PCT Publication No. WO 2012/129514, the contents of which are hereby incorporated by reference in their entirety.

[0230] In certain embodiments, the T cells are obtained from a donor subject. In some embodiments, the donor subject is human patient afflicted with a cancer or a tumor. In other embodiments, the donor subject is a human patient not afflicted with a cancer or a tumor.

[0231] Other aspects of the present invention are directed to compositions comprising a polynucleotide described herein, a vector described herein, a polypeptide described herein, or an in vitro cell described herein. In some embodiments, the composition comprises a pharmaceutically acceptable carrier, diluent, solubilizer, emulsifier, preservative and/or adjuvant. In some embodiments, the composition comprises an excipient. In one embodiment, the composition comprises a polynucleotide encoding a CAR or a TCR comprising a truncated hinge domain (“THD”) described herein. In another embodiment, the composition comprises a CAR or a TCR comprising a TCD encoded by a polynucleotide of the present invention. In another embodiment, the composition comprises a T cell comprising a CAR or a TCR comprising a TCD described herein.

[0232] In other embodiments, the composition is selected for parenteral delivery, for inhalation, or for delivery through the digestive tract, such as orally. The preparation of such pharmaceutically acceptable compositions is within the ability of one skilled in the art. In certain embodiments, buffers are used to maintain the composition at physiological pH or at a slightly lower pH, typically within a pH range of from about 5 to about 8. In certain embodiments, when parenteral administration is contemplated, the composition is in the form of a pyrogen-free, parenterally acceptable aqueous solution comprising a composition described herein, with or without additional therapeutic agents, in a pharmaceutically acceptable vehicle. In certain embodiments, the vehicle for parenteral injection is sterile distilled water in which composition described herein, with or without at least one additional therapeutic agent, is formulated as a sterile, isotonic solution, properly preserved. In certain embodiments, the preparation involves the formulation of the desired molecule with polymeric

compounds (such as polylactic acid or polyglycolic acid), beads or liposomes, that provide for the controlled or sustained release of the product, which are then be delivered via a depot injection. In certain embodiments, implantable drug delivery devices are used to introduce the desired molecule.

5 **III. Methods of the Invention**

[0233] Another aspect of the invention is directed to a method of making a cell expressing a CAR or a TCR comprising transducing a cell with a polynucleotide disclosed herein under suitable conditions. In some embodiments, the method comprises transducing a cell with a polynucleotide encoding a CAR or a TCR, as disclosed herein. In some
10 embodiments, the method comprises transducing a cell with a vector comprising the polynucleotide encoding a CAR or a TCR.

[0234] Another aspect of the present invention is directed to a method of inducing an immunity against a tumor comprising administering to a subject an effective amount of a cell comprising a polynucleotide described herein, a vector described herein, or a CAR or a TCR
15 described herein. In one embodiment, the method comprises administering to a subject an effective amount of a cell comprising a polynucleotide encoding a CAR or a TCR disclosed herein. In another embodiment, the method comprises administering to a subject an effective amount of a cell comprising a vector comprising a polynucleotide encoding a CAR or a TCR disclosed herein. In another embodiment, the method comprises administering to a subject an
20 effective amount of a cell comprising a CAR or a TCR encoded by a polynucleotide disclosed herein.

[0235] Another aspect of the present invention is directed to a method of inducing an immune response in a subject comprising administering an effective amount of the engineered immune cells of the present application. In some embodiments, the immune response is a T
25 cell-mediated immune response. In some embodiments, the T cell-mediated immune response is directed against one or more target cells. In some embodiments, the engineered immune cell comprises a CAR or a TCR, wherein the CAR or the TCR comprises a THD described in the present disclosure. In some embodiments, the target cell is a tumor cell.

[0236] Another aspect of the present invention is directed to a method for treating or
30 preventing a malignancy, said method comprising administering to a subject in need thereof an effective amount of at least one immune cell, wherein the immune cell comprises at least one CAR or TCR, and wherein the CAR or the TCR comprises a THD described herein.

[0237] Another aspect of the present invention is directed to a method of treating a cancer in a subject in need thereof comprising administering to the subject a polynucleotide, a vector, a CAR or a TCR, a cell, or a composition disclosed herein. In one embodiment, the method comprises administering a polynucleotide encoding a CAR or a TCR. In another embodiment, the method comprises administering a vector comprising a polynucleotide encoding a CAR or a TCR. In another embodiment, the method comprises administering a CAR or a TCR encoded by a polynucleotide disclosed herein. In another embodiment, the method comprises administering a cell comprising the polynucleotide, or a vector comprising the polynucleotide, encoding a CAR or a TCR.

[0238] In some embodiments, the methods of treating a cancer in a subject in need thereof comprise a T cell therapy. In one embodiment, the T cell therapy of the present invention is engineered Autologous Cell Therapy (eACT™). According to this embodiment, the method can include collecting blood cells from the patient. The isolated blood cells (*e.g.*, T cells) can then be engineered to express a CAR or a TCR of the present invention. In a particular embodiment, the CAR T cells or the TCR T cells are administered to the patient. In some embodiments, the CAR T cells or the TCR T cells treat a tumor or a cancer in the patient. In one embodiment the CAR T cells or the TCR T cells reduce the size of a tumor or a cancer.

[0239] In some embodiments, the donor T cells for use in the T cell therapy are obtained from the patient (*e.g.*, for an autologous T cell therapy). In other embodiments, the donor T cells for use in the T cell therapy are obtained from a subject that is not the patient.

[0240] The T cells can be administered at a therapeutically effective amount. For example, a therapeutically effective amount of the T cells can be at least about 10^4 cells, at least about 10^5 cells, at least about 10^6 cells, at least about 10^7 cells, at least about 10^8 cells, at least about 10^9 , or at least about 10^{10} . In another embodiment, the therapeutically effective amount of the T cells is about 10^4 cells, about 10^5 cells, about 10^6 cells, about 10^7 cells, or about 10^8 cells. In one particular embodiment, the therapeutically effective amount of the CAR T cells or the TCR T cells is about 2×10^6 cells/kg, about 3×10^6 cells/kg, about 4×10^6 cells/kg, about 5×10^6 cells/kg, about 6×10^6 cells/kg, about 7×10^6 cells/kg, about 8×10^6 cells/kg, about 9×10^6 cells/kg, about 1×10^7 cells/kg, about 2×10^7 cells/kg, about 3×10^7 cells/kg, about 4×10^7 cells/kg, about 5×10^7 cells/kg, about 6×10^7 cells/kg, about 7×10^7 cells/kg, about 8×10^7 cells/kg, or about 9×10^7 cells/kg.

IV. Cancer Treatment

[0241] The methods of the invention can be used to treat a cancer in a subject, reduce the size of a tumor, kill tumor cells, prevent tumor cell proliferation, prevent growth of a tumor, eliminate a tumor from a patient, prevent relapse of a tumor, prevent tumor metastasis, induce remission in a patient, or any combination thereof. In certain embodiments, the methods induce a complete response. In other embodiments, the methods induce a partial response.

[0242] Cancers that may be treated include tumors that are not vascularized, not yet substantially vascularized, or vascularized. The cancer may also include solid or non-solid tumors. In some embodiments, the cancer is a hematologic cancer. In some embodiments, the cancer is of the white blood cells. In other embodiments, the cancer is of the plasma cells. In some embodiments, the cancer is leukemia, lymphoma, or myeloma. In certain embodiments, the cancer is acute lymphoblastic leukemia (ALL) (including non T cell ALL), acute lymphoid leukemia (ALL), and hemophagocytic lymphohistocytosis (HLH)), B cell prolymphocytic leukemia, B-cell acute lymphoid leukemia ("BALL"), blastic plasmacytoid dendritic cell neoplasm, Burkitt's lymphoma, chronic lymphocytic leukemia (CLL), chronic myelogenous leukemia (CML), chronic myeloid leukemia (CML), chronic or acute granulomatous disease, chronic or acute leukemia, diffuse large B cell lymphoma, diffuse large B cell lymphoma (DLBCL), follicular lymphoma, follicular lymphoma (FL), hairy cell leukemia, hemophagocytic syndrome (Macrophage Activating Syndrome (MAS), Hodgkin's Disease, large cell granuloma, leukocyte adhesion deficiency, malignant lymphoproliferative conditions, MALT lymphoma, mantle cell lymphoma, Marginal zone lymphoma, monoclonal gammopathy of undetermined significance (MGUS), multiple myeloma, myelodysplasia and myelodysplastic syndrome (MDS), myeloid diseases including but not limited to acute myeloid leukemia (AML), non-Hodgkin's lymphoma (NHL), plasma cell proliferative disorders (e.g., asymptomatic myeloma (smoldering multiple myeloma or indolent myeloma), plasmablastic lymphoma, plasmacytoid dendritic cell neoplasm, plasmacytomas (e.g., plasma cell dyscrasia; solitary myeloma; solitary plasmacytoma; extramedullary plasmacytoma; and multiple plasmacytoma), POEMS syndrome (Crow-Fukase syndrome; Takatsuki disease; PEP syndrome), primary mediastinal large B cell lymphoma (PMBC), small cell- or a large cell- follicular lymphoma, splenic marginal zone lymphoma (SMZL), systemic amyloid light chain amyloidosis, T-cell acute lymphoid leukemia ("TALL"), T-cell lymphoma, transformed follicular lymphoma, Waldenstrom macroglobulinemia, or a combination thereof.

[0243] In one embodiment, the cancer is a myeloma. In one particular embodiment, the cancer is multiple myeloma. In another embodiment, the cancer is a leukemia. In one embodiment, the cancer is acute myeloid leukemia.

[0244] In some embodiments, the methods further comprise administering a chemotherapeutic. In certain embodiments, the chemotherapeutic selected is a lymphodepleting (preconditioning) chemotherapeutic. Beneficial preconditioning treatment regimens, along with correlative beneficial biomarkers are described in U.S. Provisional Patent Applications 62/262,143 and 62/167,750 which are hereby incorporated by reference in their entirety herein. These describe, *e.g.*, methods of conditioning a patient in need of a T cell therapy comprising administering to the patient specified beneficial doses of cyclophosphamide (between 200 mg/m²/day and 2000 mg/m²/day) and specified doses of fludarabine (between 20 mg/m²/day and 900 mg/m²/day). One such dose regimen involves treating a patient comprising administering daily to the patient about 500 mg/m²/day of cyclophosphamide and about 60 mg/m²/day of fludarabine for three days prior to administration of a therapeutically effective amount of engineered T cells to the patient.

[0245] In other embodiments, the antigen binding molecule, transduced (or otherwise engineered) cells (such as CARs or TCRs), and the chemotherapeutic agent are administered each in an amount effective to treat the disease or condition in the subject.

[0246] In certain embodiments, compositions comprising CAR- and/or TCR-expressing immune effector cells disclosed herein may be administered in conjunction with any number of chemotherapeutic agents. Examples of chemotherapeutic agents include alkylating agents such as thiotepa and cyclophosphamide (CYTOXANTM); alkyl sulfonates such as busulfan, improsulfan and piposulfan; aziridines such as benzodopa, carboquone, meturedopa, and uredopa; ethylenimines and methylamelamines including altretamine, triethylenemelamine, triethylenephosphoramide, triethylenethiophosphoramide and trimethylolomelamine; 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, carabycin, 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-mercaptapurine, 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, mepitiothane, testolactone; anti-adrenals such as aminogluthethimide, 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) and doxetaxel (TAXOTERE[®], Rhone-Poulenc Rorer); 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 RFS2000; 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. In some embodiments, compositions comprising CAR- and/or TCR-expressing immune effector cells disclosed herein may be administered in conjunction with an anti-hormonal agent that acts to regulate or inhibit hormone action on tumors 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. Combinations of chemotherapeutic agents are also administered where appropriate, including, but not limited to CHOP, i.e.,

Cyclophosphamide (Cytosan[®]), Doxorubicin (hydroxydoxorubicin), Vincristine (Oncovin[®]), and Prednisone.

[0247] In some embodiments, the chemotherapeutic agent is administered at the same time or within one week after the administration of the engineered cell or nucleic acid. In other
 5 embodiments, the chemotherapeutic agent is administered from 1 to 4 weeks or from 1 week to 1 month, 1 week to 2 months, 1 week to 3 months, 1 week to 6 months, 1 week to 9 months, or 1 week to 12 months after the administration of the engineered cell or nucleic acid. In some
 10 embodiments, the chemotherapeutic agent is administered at least 1 month before administering the cell or nucleic acid. In some embodiments, the methods further comprise administering two or more chemotherapeutic agents.

[0248] A variety of additional therapeutic agents may be used in conjunction with the compositions described herein. For example, potentially useful additional therapeutic agents include PD-1 inhibitors such as nivolumab (OPDIVO[®]), pembrolizumab (KEYTRUDA[®]),
 15 pembrolizumab, pidilizumab (CureTech), and atezolizumab (Roche).

[0249] Additional therapeutic agents suitable for use in combination with the invention include, but are not limited to, ibrutinib (IMBRUVICA[®]), ofatumumab (ARZERRA[®]), rituximab (RITUXAN[®]), bevacizumab (AVASTIN[®]), trastuzumab (HERCEPTIN[®]),
 20 trastuzumab emtansine (KADCYLA[®]), imatinib (GLEEVEC[®]), cetuximab (ERBITUX[®]), panitumumab (VECTIBIX[®]), catumaxomab, ibritumomab, ofatumumab, tositumomab, brentuximab, alemtuzumab, gemtuzumab, erlotinib, gefitinib, vandetanib, afatinib, lapatinib, neratinib, axitinib, masitinib, pazopanib, sunitinib, sorafenib, toceranib, lestaurtinib, axitinib, cediranib, lenvatinib, nintedanib, pazopanib, regorafenib, semaxanib, sorafenib, sunitinib, tivozanib, toceranib, vandetanib, entrectinib, cabozantinib, imatinib, dasatinib, nilotinib, ponatinib, radotinib, bosutinib, lestaurtinib, ruxolitinib, pacritinib, cobimetinib, selumetinib,
 25 trametinib, binimetinib, alectinib, ceritinib, crizotinib, aflibercept, adipotide, denileukin diftitox, mTOR inhibitors such as Everolimus and Temsirolimus, hedgehog inhibitors such as sonidegib and vismodegib, CDK inhibitors such as CDK inhibitor (palbociclib).

[0250] In additional embodiments, the composition comprising CAR- and/or TCR-containing immune are administered with an anti-inflammatory agent. Anti-inflammatory
 30 agents or drugs can 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. Exemplary NSAIDs include ibuprofen, naproxen, naproxen sodium, Cox-2 inhibitors, and sialylates. Exemplary analgesics include acetaminophen, oxycodone, tramadol of propoxyphene hydrochloride. Exemplary glucocorticoids include 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.

[0251] In certain embodiments, the compositions described herein are administered in conjunction with a cytokine. “Cytokine” as used herein is meant to refer to proteins released by one cell population that act on another cell as intercellular mediators. Examples of 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 (HGF); fibroblast growth factor (FGF); prolactin; placental lactogen; mullerian-inhibiting substance; mouse gonadotropin-associated peptide; inhibin; activin; vascular endothelial growth factor; integrin; thrombopoietin (TPO); nerve growth factors (NGFs) 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.

[0252] All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be incorporated by reference. However, the citation of a reference herein should not be construed as an
5 acknowledgement that such reference is prior art to the present invention. To the extent that any of the definitions or terms provided in the references incorporated by reference differ from the terms and discussion provided herein, the present terms and definitions control.

[0253] The present invention is further illustrated by the following examples which should not be construed as further limiting. The contents of all references cited throughout this
10 application are expressly incorporated herein by reference.

EXAMPLES

EXAMPLE 1

[0254] Plasmids encoding a T7 promoter, CAR construct and a beta globin stabilizing sequence were linearized by overnight digestion of 10 µg DNA with EcoRI and BamHI (NEB).
15 DNA was then digested for 2 hours at 50°C with proteinase K (Thermo Fisher, 600 U/ml) purified with phenol/chloroform and precipitated by adding sodium acetate and two volumes of ethanol. Pellets were then dried, resuspended in RNase/DNase-free water and quantified using NanoDrop. One µg of the linear DNA was then used for in vitro transcription using the mMESSAGE mMACHINE T7 Ultra (Thermo Fisher) following the manufacturer's
20 instructions. RNA was further purified using the MEGAClear Kit (Thermo Fisher) following the manufacturer's instructions and quantified using NanoDrop. mRNA integrity was assessed using mobility on an agarose gel. PBMCs were isolated from healthy donor leukopaks (Hemacare) using ficoll-paque density centrifugation per manufacturer's instructions. PBMCs were stimulated using OKT3 (50 ng/ml, Miltenyi Biotec) in R10 medium + IL-2 (300 IU/ml,
25 Proleukin®, Prometheus® Therapeutics and Diagnostics). Seven days post-stimulation, T cells were washed twice in Opti-MEM medium (Thermo Fisher Scientific) and resuspended at a final concentration of 2.5×10^7 cells/ml in Opti-MEM medium. Ten µg of mRNA was used per electroporation. Electroporation of cells was performed using a Gemini X2 system (Harvard Apparatus BTX) to deliver a single 400 V pulse for 0.5 ms in 2 mm cuvettes (Harvard
30 Apparatus BTX). Cells were immediately transferred to R10 + IL-2 medium and allowed to recover for 6 hours. To examine CAR expression, T cells were stained with FLT-3-HIS (Sino

Biological Inc.) or biotinylated Protein L (Thermo Scientific) in stain buffer (BD Pharmingen) for 30 minutes at 4°C. Cells were then washed and stained with anti-HIS-PE (Miltenyi Biotec) or PE Streptavidin (BD Pharmingen) in stain buffer for 30 minutes at 4°C. Cells were then washed and resuspended in stain buffer with propidium iodide (BD Pharmingen) prior to data acquisition. Expression of FLT3 CARs in electroporated T cells is shown in FIG. 3.

[0255] T cells were electroporated with plasmids encoding an anti-FLT3 CAR comprising a 10E3, 2E7, 8B5, 4E9, or 11F11 anti-FLT3 binding molecule and a hinge region selected from the full length hinge domain (a complete hinge domain or “CHD”) or a truncated hinge domain (“THD”). The electroporated anti-FLT3 CAR T cells were then co-cultured with Namalwa (FLT3 negative), EoL1 (FLT3 positive), HL60 (FLT3 positive), or MV4;11 (FLT3 positive) target cells at a 1:1 E:T ratio in R10 medium. Sixteen hours post-co-culture, supernatants from Namalwa (FIGs. 4A-4F), EoL1 (FIGs. 4G-4L), HL60 (FIGs. 4M-4R, and MV4;11 (4S-4X) were analyzed by Luminex (EMD Millipore) for production of IFN γ (FIGs. 4A, 4B, 4G, 4H, 4M, 4N, 4S, and 4T), IL-2 (FIGs. 4C, 4D, 4I, 4J, 4O, 4P, 4U, and 4V), and TNF α (FIGs. 4E, 4F, 4K, 4L, 4Q, 4R, 4W, and 4X).

[0256] Target cell viability was assessed by flow cytometric analysis of propidium iodide (PI) uptake by CD3-negative cells. The electroporated anti-FLT3 CAR T cells were co-cultured with Namalwa (FIGs. 5A-5B), EoL1 (FIGs. 5C-5D), HL60 (FIGs. 5E-5F, and MV4;11 (5G-5H) target cells at 16 hours post-co-culture.

EXAMPLE 2

[0257] A third generation lentiviral transfer vector containing the different CAR constructs was used along with the ViraPower Lentiviral Packaging Mix (Life Technologies) to generate the lentiviral supernatants. Briefly, a transfection mix was generated by mixing 15 μ g of DNA and 22.5 μ l of polyethileneimine (Polysciences, 1 mg/ml) in 600 μ l of OptiMEM medium. The mix was incubated for 5 minutes at room temperature. Simultaneously, 293T cells (ATCC) were trypsinized, counted and a total of 10×10^6 total cells were plated in a T75 flask along the transfection mix. Three days after the transfection, supernatants were collected and filtered through a 0.45 μ m filter and stored at -80°C until used. PBMCs were isolated from healthy donor leukopaks (Hemacare) using ficoll-paque density centrifugation per manufacturer's instructions. PBMCs were stimulated using OKT3 (50 ng/ml, Miltenyi Biotec) in R10 medium + IL-2 (300 IU/ml, PROLEUKIN®, PROMETHEUS® Therapeutics and Diagnostics). Forty eight hours post-stimulation, cells were transduced using lentivirus at an

MOI = 10. Cells were maintained at $0.5\text{--}2.0 \times 10^6$ cells/ml prior to use in activity assays. To examine CAR expression, T cells were stained with FLT-3-HIS (Sino Biological Inc.) or biotinylated Protein L (Thermo Scientific) in stain buffer (BD Pharmingen) for 30 minutes at 4°C. Cells were then washed and stained with anti-HIS-PE (Miltenyi Biotec) or PE Streptavidin (BD Pharmingen) in stain buffer for 30 minutes at 4°C. Cells were then washed and resuspended in stain buffer with propidium iodide (BD Pharmingen) prior to data acquisition. Expression of FLT3 CARs in T cells from two healthy donors is shown in FIG. 6A-6B.

[0258] T cells from two healthy donors were transduced with lentiviral vectors encoding anti-FLT3 CAR T cells comprising a 10E3, 8B5, or 11F11 binding molecule and a hinge region selected from the complete hinge domain (“CHD”), a truncated hinge domain (“THD”), and the CD8 hinge region. Transduced T cells were co-cultured with target cells at a 1:1 E:T ratio in R10 medium. Sixteen hours post-co-culture, supernatants were analyzed by Luminex (EMD Millipore) for production of IFN γ (FIGs. 7A-7B), TNF α (FIGs. 7C-7D), and IL-2 (FIGs. 7E-7F).

[0259] Target cell viability was assessed by flow cytometric analysis of propidium iodide (PI) uptake by CD3-negative cells. Average cytolytic activity of lentivirus-transduced CAR T cells (from two healthy donors) co-cultured with Namalwa (FIG. 8A), EoL1 (FIG. 8B), MV4;11 (FIG. 8C), and HL60 (FIG. 8D) target cells was measured.

[0260] To assess CAR T cell proliferation in response to FLT3 expressing target cells, T cells were labeled with CFSE prior to co-culture with target cells at a 1:1 E:T ratio in R10 medium. Five days later, T cell proliferation was assessed by flow cytometric analysis of CFSE dilution. Proliferation of FLT3 CAR T cells is shown in FIGs. 9A-9B.

EXAMPLE 3

[0261] To examine in vivo anti-leukemic activity, FLT3 CAR T cells were generated for use in a xenogeneic model of human AML. CAR expression of the various effector lines used in the xenogeneic model of human AML are shown in FIGs. 10A-10D. Luciferase-labeled MV4;11 cells (2×10^6 cells/animal) were injected intravenously into 5 to 6 week-old female NSG mice. After 6 days, 6×10^6 T cells (~50% CAR+) in 200 μ l PBS were injected intravenously, and the tumor burden of the animals was measured weekly using bioluminescence imaging (FIGs. 10E-10G). Survival analysis was performed by injection of controls (mock) or 10E3-CHD (FIG. 10H), 10E3-THD (FIG. 10I), or 8B5-THD (FIG. 10J) expressing CAR T cells.

EXAMPLE 4

[0262] T cells were electroporated with plasmids encoding the anti-CLL-1 CAR constructs 24C8_HL-CHD CAR (comprising a complete hinge domain of the costimulatory protein) and 24C8_HL-THD CAR (comprising a truncated hinge domain of the costimulatory protein). Anti-CLL-1 expression by electroporated T cells is shown in FIGs. 11A-11D. The anti-CLL-1 CAR T cells were then cultured with the target Namalwa (ATCC; CLL-1 negative), U937 (ATCC; CLL-1 positive), HL-60 (ATCC; CLL-1 positive), EoL-1 (Sigma; CLL-1 positive), KG1a (ATCC; CLL-1 positive) and MV4;11 (ATCC; CLL-1 positive) cells at a 1:1 E:T ratio in R10 media 6 hours after mRNA electroporation. Sixteen hours post-co-culture, supernatants were analyzed by Luminex (EMD Millipore), according to the manufacturer's instructions, for production of IL-2 (FIG. 12A), IFN γ (FIG. 12B), and TNF α (FIG. 12C).

[0263] Target cell viability was assessed by flow cytometric analysis of propidium iodide (PI) uptake. The electroporated anti-CLL-1 CAR T cells were co-cultured with Namalwa (FIG. 13A), MV4;11 (FIG. 13B), EoL-1 (FIG. 13C), HL-60 (FIG. 13D), or U937 (FIG. 13E) target cells for 16 hours. As expected, Namalwa cells co-cultured with the anti-CLL-1 CAR T cells showed little change in target cell viability, relative to controls (FIG. 13A). However, increased cytolytic activity was observed in MV4;11 cells co-cultured with 24C8_HL-CHD and 24C8_HL-THD T cells, relative to controls, with a greater target cell cytolytic activity observed in the 24C8_HL-THD T cell co-culture (FIG. 13B). In addition, increased cytolytic activity was observed in EoL-1 cells co-cultured with 24C8_HL-CHD and 24C8_HL-THD T cells, relative to controls (FIG. 13C). Increased cytolytic activity was observed in HL-60 cells co-cultured with 24C8_HL-CHD and 24C8_HL-THD T cells, relative to controls (FIG. 13D). Increased cytolytic activity was observed in U937 cells co-cultured with 24C8_HL-CHD and 24C8_HL-THD T cells, relative to controls, with a greater target cell cytolytic activity observed in the 24C8_HL-THD T cell co-culture (FIG. 13E).

EXAMPLE 5

[0264] T cells transduced with lentiviral vectors comprising an anti-CLL-1 CAR construct with a truncated hinge domain ("THD") of the costimulatory protein, 10E3_THD or 24C1_LH_THD, were co-cultured with Namalwa, U937, HL-60, EoL-1, KG1a and MV4;11 target cells at a 1:1 E:T ratio in R10 media 12 days after T cell stimulation. Sixteen hours post-co-culture, supernatants were analyzed by Luminex (EMD Millipore), according to the manufacturer's instructions, for production of the cytokines IFN γ (FIG. 14A), IL-2 (FIG. 14B),

and TNF α (FIG. 14C) in co-cultures of effector 10E3_THD CAR T cells and 24C1_LH_THD CAR T cells with target Namalwa, HL-60, or MVA;11 cells, as indicated.

[0265] Target cell viability was assessed by flow cytometric analysis of propidium iodide (PI) uptake. Transduced effector 24C1_LH_THD CAR T cells were co-cultured with Namalwa, U937, HL-60, EoL-1, KG1a, or MV4;11 target cells for 16 hours or 40 hours. Co-culture of Namalwa target cells with transduced C1_24C1_LH_THD CAR T cells had no effect on the percent of viable Namalwa target cells at 16 hours and 40 hours, as compared to mock controls (FIG. 15A). However, C1_24C1_LH_THD CAR T cells co-cultured with either MV4;11 (FIG. 15B) or HL-60 (FIG. 15C) target cells resulted in a lower percent of viable target cells at both 16 hours and 40 hours, as compared to mock controls.

EXAMPLE 6

[0266] CAR T cells transduced with anti-BCMA CAR constructs comprising a truncated hinge domain ("THD") of the costimulatory protein were cultured with target cells at a 1:1 effector cell to target cell (E:T) ratio in R10 media 12 days after T cell stimulation. Cell lines tested included EoL-1 (Sigma; BCMA negative), NCI-H929 (Molecular Imaging; BCMA positive), and MM1S (Molecular Imaging; BCMA positive). Sixteen hours post-co-culture, supernatants were analyzed by Luminex (EMD Millipore), according to the manufacturer's instructions, for production of the cytokines IFN γ (FIGs. 16A-16B), TNF α (FIGs. 16C-16D), and IL-2 (FIGs. 16E-16F). IFN γ (FIGs. 16A-16B), TNF α (FIGs. 16C-16D), and IL-2 (FIGs. 16E-16F) were observed in the supernatant of NCI-H929 and MM1S target cell co-cultures for each anti-BCMA CAR T cell tested in both donors (FIGs. 16A-16B); however, IFN γ (FIGs. 16A-16B), TNF α (FIGs. 16C-16D), and IL-2 (FIGs. 16E-16F) were only observed in the supernatant of EoL-1 target cell co-cultures above background for the IR negative control T cells (FIG. 16A).

[0267] Target cell viability was assessed by flow cytometric analysis of propidium iodide (PI) uptake of CD3 negative cells. The anti-BCMA CAR T cells were co-cultured with EoL1 (FIGs. 17A-17B), NCI-H929 (FIGs. 17C-17D), or MM1S (FIGs. 17E-17F) target cells for 16 hours, 40 hours, 64 hours, 88 hours, or 112 hours. Little cytolytic activity was observed in the EoL-1 co-cultures at any time period for the anti-BCMA CAR T cells (FIG. 17A-17B). However, co-culture of the anti-BCMA CAR T cells and the NCI-H929 or MM1S target cells resulted in a decrease in the percentage of viable target cells at each time point measured for each of the anti-BCMA CAR T cells.

[0268] To examine proliferation, anti-BCMA CAR T cells were labeled with carboxyfluorescein succinimidyl ester (CFSE) prior to co-culture with EoL-1, NCI-H929, or MM1S target cells at a 1:1 E:T ratio in R10 media. Five days later, T cell proliferation was assessed by flow cytometric analysis of CFSE dilution (FIGs. 18A-18B).

5 EXAMPLE 7

[0269] Enhanced stability is a desired property of proteins. This is often assessed by determining the melting temperature of a protein under various conditions. Proteins with a higher melting temperature are generally stable for longer times. When a CAR is more thermostable, it may be functionally active for longer periods of time on the surface of a cell.

10 [0270] Thermal stability of the CAR extracellular domain (ECD) with the longer hinge domain, i.e., the complete hinge domain ("CHD") and the thermal stability of the CAR ECD with a truncated hinge domain ("THD") was measured using a Bio-Rad C1000 thermal cycler, CFX96 Real-Time system. Unfolding of the proteins was monitored using the fluorescent dye SYPRO Orange (Invitrogen) which binds to hydrophobic amino acids that become solvent
15 exposed as the protein unfolds. A temperature gradient was set up from 25 °C to 95 °C with 1 °C / 1 minute increments. Each sample contained 10 µM recombinant CAR ECD protein and 5X SYPRO Orange (Molecular Probes™ SYPRO™ Orange Protein Gel Stain (5,000X Concentrate in DMSO)). The assay was performed in PBS with or without 50 mM NaCl.

[0271] As shown in FIG. 19A and FIG. 19B, a CAR's ECD which has a THD shows
20 enhanced thermostability compared to a CAR's ECD which has a CHD, e.g., including the IEVMYPPPY (SEQ ID NO: 250) motif. These method described in this example is a useful method for testing stability of mRNA encoding a CAR and the CAR itself, because once a T cell has been transduced with the mRNA encoding a CAR, the transduced T cell will express the CAR and the stability of an individual mRNA or protein cannot be readily assessed.

CLAIMS

What is claimed is:

1. An isolated polynucleotide encoding a chimeric antigen receptor (CAR) which comprises (i) an antigen binding molecule, (ii) a costimulatory domain, and (iii) an activating domain, wherein the costimulatory domain comprises an extracellular domain with a hinge, a transmembrane domain, and an intracellular domain, characterized in that the said hinge is a truncated hinge domain consisting of: (a) amino acids 123 to 152 of SEQ ID NO: 1, or (b) an amino acid sequence at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to the amino acid sequence of (a).
2. The polynucleotide of claim 1, wherein truncated hinge domain consists of (a) amino acids 123 to 152 of SEQ ID NO: 1.
3. The polynucleotide of claim 1 or 2, wherein the transmembrane domain is a transmembrane domain of 4-1BB/CD137, an alpha chain of a T cell receptor, a beta chain of a T cell receptor, CD3 epsilon, CD4, CD5, CD8 alpha, CD9, CD16, CD19, CD22, CD33, CD37, CD45, CD64, CD80, CD86, CD134, CD137, CD154, or a zeta chain of a T cell receptor, or any combination thereof, or wherein the transmembrane domain comprises an amino acid sequence at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to SEQ ID NO: 5.
4. The polynucleotide of claim 1 or 2, wherein the intracellular domain comprises a signaling region of 4-1BB/CD137, activating NK cell receptors, B7-H3, BAFFR, BLAME (SLAMF8), BTLA, CD100 (SEMA4D), CD103, CD160 (BY55), CD18, CD19, CD19a, CD2, CD247, CD27, CD276 (B7-H3), CD29, CD3 delta, CD3 epsilon, CD3 gamma, CD30, CD4, CD40, CD49a, CD49D, CD49f, CD69, CD7, CD84, CD8alpha, CD8beta, CD96 (Tactile), CD11a, CD11b, CD11c, CD11d, CDS, CEACAM1, CRT AM, cytokine receptors, DAP-10, DNAM1 (CD226), Fc gamma receptor, GADS, GITR, HVEM (LIGHTR), IA4, ICAM-1, ICAM-1, Ig alpha (CD79a), IL2R beta, IL2R gamma, IL7R alpha, Immunoglobulin-like proteins, inducible T cell costimulator (ICOS), integrins, ITGA4, ITGA4, ITGA6, ITGAD, ITGAE, ITGAL, ITGAM, ITGAX, ITGB2, ITGB7, ITGB1, KIRDS2, LAT, LFA-1, a ligand that specifically

binds with CD83, LIGHT, LIGHT (tumor necrosis factor superfamily member 14; TNFSF14), LTBR, Ly9 (CD229), lymphocyte function-associated antigen-1 (LFA-1 (CD11a/CD18)), MHC class I molecule, NKG2C, NKG2D, NKp30, NKp44, NKp46, NKp80 (KLRF1), OX-40, PAG/Cbp, programmed death-1 (PD-1), PSGL1, SELPLG (CD162), signaling lymphocytic activation molecules (SLAM proteins), SLAM (SLAMF1; CD150; IPO-3), SLAMF4 (CD244; 2B4), SLAMF6 (NTB-A; Lyl08), SLAMF7, SLP-76, TNF receptor proteins, TNFR2, a Toll ligand receptor, TRANCE/RANKL, VLA1, or VLA-6, or a combination thereof, or wherein the intracellular domain comprises an amino acid sequence at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to SEQ ID NO: 7.

5. The polynucleotide of claim 1 or 2, wherein the antigen binding molecule comprises a heavy chain variable region (VH) and a light chain variable region (VL), wherein the VH comprises 3 complementarity determining regions (CDRs) and the VL comprises 3 CDRs.

6. The polynucleotide of claim 1 or 2, wherein the antigen binding molecule specifically binds an antigen selected from the group consisting of 5T4, alphafetoprotein, B cell maturation antigen (BCMA), CA-125, carcinoembryonic antigen, CD19, CD20, CD22, CD23, CD30, CD33, CD56, CD123, CD138, c-Met, CSPG4, C-type lectin-like molecule 1 (CLL-1), EGFRvIII, epithelial tumor antigen, ERBB2, FLT3, folate binding protein, GD2, GD3, HER1-HER2 in combination, HER2-HER3 in combination, HER2/Neu, HERV-K, HIV-1 envelope glycoprotein gp41, HIV-1 envelope glycoprotein gp120, IL-11R α , kappa chain, lambda chain, melanoma-associated antigen, mesothelin, MUC-1, mutated p53, mutated ras, prostate-specific antigen, ROR1, or VEGFR2, or a combination thereof.

7. The polynucleotide of claim 1 or 2, wherein the activation domain comprises an amino acid sequence at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to SEQ ID NO: 9 or SEQ ID NO: 251.

8. The polynucleotide of any one of claims 1 to 7, wherein the CAR further comprises a leader peptide wherein the leader peptide comprises an amino acid sequence at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%,

at least about 97%, at least about 98%, at least about 99%, or about 100% identical to SEQ ID NO: 11.

5 9. A vector comprising the polynucleotide of any one of claims 1 to 8, wherein the vector is an adenoviral vector, an adenovirus-associated vector, a DNA vector, a lentiviral vector, a plasmid, a retroviral vector, or an RNA vector, or any combination thereof.

10. A polypeptide encoded by the polynucleotide of any one of claims 1 to 8 or the vector of claim 9.

11. A cell comprising the polynucleotide of any one of claims 1 to 8, the vector of claim 9, the polypeptide of claim 10, or any combination thereof.

10 12. The cell of claim 11, wherein the cell is a T cell.

13. The cell of claim 12, wherein the T cell is a CD4⁺ T cell or a CD8⁺ T cell.

14. The cell of claim 12, wherein the T cell is an *in vitro* cell.

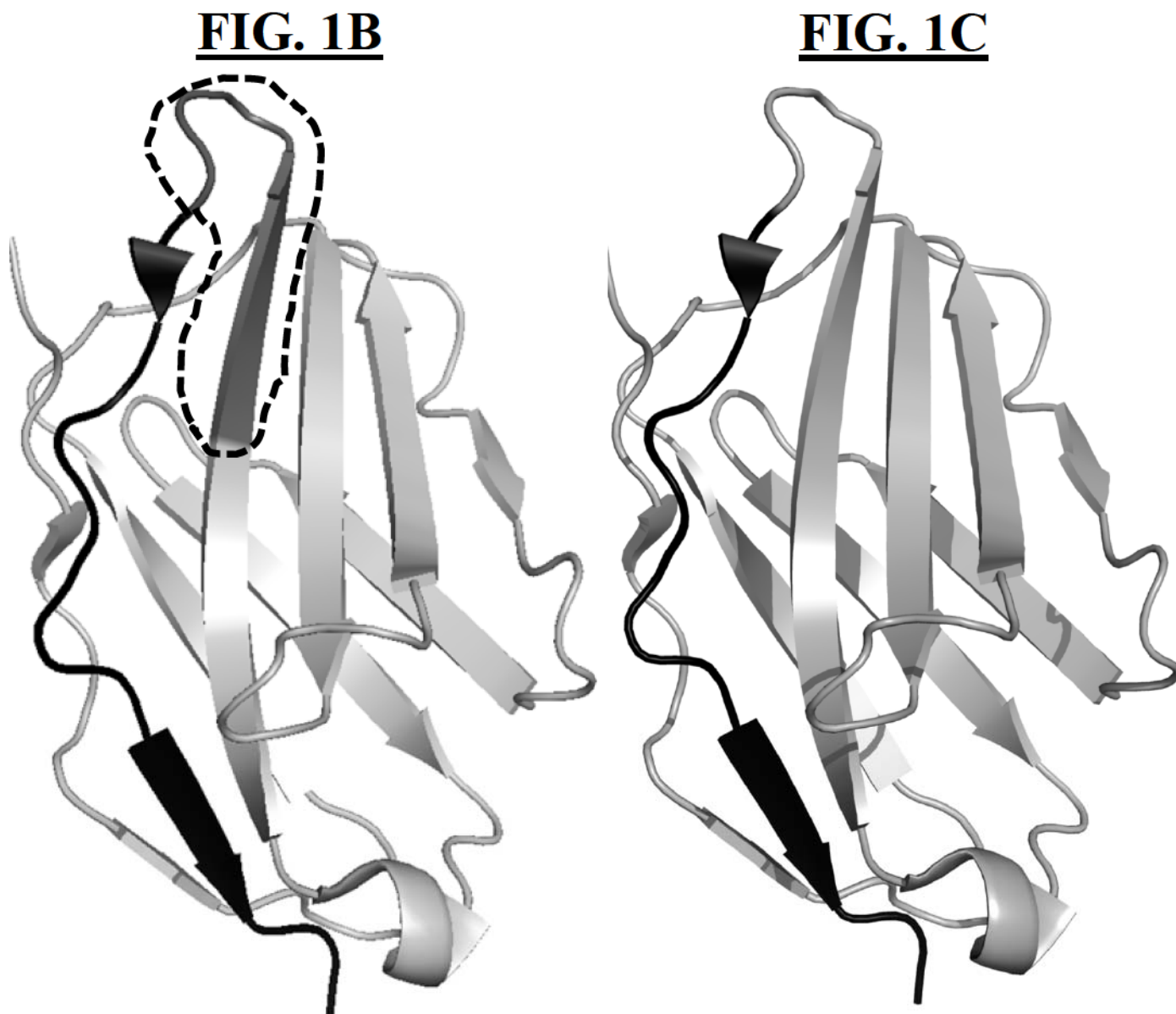
15. The cell of claim 12, wherein the T cell is an autologous T cell.

15 16. A composition comprising the polynucleotide of any one of claims 1 to 8, the vector of claim 9, the polypeptide of claim 10, or the cell of any one of claims 11 to 15.

17. The composition of claim 16, which is formulated to be delivered to a subject.

18. The composition of claims 16 or 17, further comprising at least one pharmaceutically-acceptable excipient.

MLRLLLLALNLFPSIQVTGNKILVKQSPMLVAYDNAVNLSCKYSYNLFSREFRASLH
KGLDSAVEVCVVYGNYSQQQLQVYSKTGFNCDGKLGNESVTFYLQNLVYNQTDIYFC
KIEVMYPPPY**LDNEKSNGTI**IHVKGKHLCPSP**LPGPSKP**FWVLVVVGGVLACYSL
Hinge Domain *Transmembrane*
LVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRS
Domain *Signaling Domain*



2017240667 23 Sep 2019

FIG. 2A – Anti-CLL-1 Binding Molecules

	FR1	CDR1	FR2	CDR2	
24C1_VH	QVQLQESGPGLVKPSSETLSLTCTVS	GGSISS--YY	WSWIRQPPGKGLEWIGYI	YYSGS-T	
24C8_VH	QVQLQESGPGLVKPSQTLSTCTVS	GGSISSGGFY	WSWIRQHPGKGLEWIGYI	HHSGS-T	
20C5.1_VH	QVQLVQSGAEVKKPGASVKVSKVSG	GYTLT--EL	SMHWVRQAPGKGLEWMGGFDP	EDGET	
20C5.2_VH	QVQLVESGGGVVQPGRSLRLSCAAS	GFTFSS--Y	GMHWVRQAPGKGLEWVAVISYD	GSDK	
	**** : * : : * . :: : * . * :::		* : ** ***** : . :		
	FR3		CDR3	FR4	
24C1_VH	NYNPSLKSRTISVDTSKNQFSLKLSS	VTAA	D	AVYYCVSLVYCGGDCYSGFDYWGQ	GTL
24C8_VH	HYNPSLKSRTISIDTSKNLFSLRLSS	VTAA	D	AVYYCASLVYCGGDCYSGFDYWGQ	GTL
20C5.1_VH	IYAQKFQGRVTVTEDTSTD	TAYMELSSLR	SEDTAVYYC	ATESRGIG--WPYFDYWGQ	GTL
20C5.2_VH	YYVDSVKGRFTISRDN	SKNRLYLQMN	SLRAEDTAVYYC	ARERYSG-----RDYWGQ	GTL
	* * , * : : * , * . : : * : : ***** ,				*****
	FR4				
24C1_VH	VTVSS				
24C8_VH	VTVSS				
20C5.1_VH	VTVSS				
20C5.2_VH	VTVSS				

<u>FIG. 2B</u>	SEQ ID NO:			
	VH	CDR1	CDR2	CDR3
24C1 VH	125	93	97	101
24C8 VH	126	94	98	102
20C5.1 VH	127	95	99	103
20C5.2 VH	128	96	100	104

2017240667 23 Sep 2019

FIG. 2C – Anti-CLL-1 Binding Molecules

	FR1	CDR1	FR2	CDR2	FR3
24C1_VL	DIQLTQSPSSLSASVGDRVSFTQ	QASQDINNFLN	WYQQKPGKAPKLLIY	DASNLET	GVPS
24C8_VL	DIQLTQSPSSLSASVGDRVSFTQ	QASQDINNFLN	WYQQKPGKAPKLLIY	DASNLET	GVPS
20C5.1_VL	DIQMTQSPSSLSASVGDRVTITQ	RASQSISSYLN	WYQQKPGKAPKLLIS	GASSLKSG	GVPS
20C5.2_VL	EIVMTQSPATLSVSPGERATLSC	RASQSVSSLLT	WYQQKPGQAPRLLI	FGA	STRATGIPA
	:* :*****:***.* *:*.:::*	:*****:.. *.*****:***:***	.***. :*:::		
	FR3	CDR3	FR4		
24C1_VL	RFSGSGSGTDFTFTISSLQPED	IATYYCQQYGNLP	FTFGGGTKVEIKR		
24C8_VL	RFSGSGSGTDFTFTISSLQPED	IATYYCQQYGNLP	FTFGGGTKVEIKR		
20C5.1_VL	RFSGSGSGTDFTLTISLPPED	FATYYCQQSYSTP	ITFGQGTRLEIKR		
20C5.2_VL	RFSGSGSGTGFTLTISLQSE	DFAVYYCQQYDTW	PFTFGPGTKVDFKR		
	*****.**:***** .**:*.******	.*:***	**:::***		

<u>FIG. 2D</u>	SEQ ID NO:			
	VL	CDR1	CDR2	CDR3
24C1 VL	129	105	109	113
24C8 VL	130	106	110	114
20C5.1 VL	131	107	111	115
20C5.2 VL	132	108	112	116

FIG. 2E – Anti-BCMA Binding Molecules

2017240667 23 Sep 2019

	FR1	CDR1	FR2	CDR2
FS-21495 VH	EVQLLESGGGLVQPGGSLRLSCAASG	--FTFSSY	AMSWVRQAPGKGLEWVS	AIISGSGGST
PC-21497 VH	QVQLVESGGGVVQPGRSLRLSCAASG	--FTFSSY	GMHWVRQAPGKGLEWVA	VISYDGSNK
AJ-21508 VH	QVQLVQSGAEVKKPGASVKVSCKASG	--YTFTSY	YMHWRQAPGQGLEWMGI	INPGGGST
NM-21517 VH	QLQLQESGPGLVKPSSETLSLTCTVSG	SISSSSY	YWGWIROPKGLEWIGS	ISYSG-ST
TS-21522 VH	EVQLVESGGGLVQPGGSLRLSCAASG	--FTFSSY	SMNWVRQAPGKGLEWVS	TISSSSSTI
RY-21527 VH	QVQLVESGGGVVQPGRSLRLSCAASG	--FTFSSY	GMHWVRQAPGKGLEWVA	VISYDGSNK
PP-21528 VH	QVQLVQSGAEVKKPGSSVKVSCKASG	--GTFSSY	AIWVRQAPGQGLEWMGI	PIFGTA
RD-21530 VH	QVQLVESGGGVVQPGRSLRLSCAASG	--FTFSSY	GMHWVRQAPGKGLEWVA	VISYDGSNK
	::** : ** : : * . : : : * . *	: : **	* : ** . ** : ** : . *	.

	CDR2	FR3	CDR3
FS-21495 VH	YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYC	AR-AEM-----	GAVFDIWGQ
PC-21497 VH	YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYC	ARDGTYLGGI---	WY-FDLWGR
AJ-21508 VH	SYAQKFQGRVTMTTRDTSTSTVYMEISSLRSEDTAVYYC	AR-----	ESWPMDVWGQ
NM-21517 VH	YINPSLKSRTVTSVDTSKNQFSLKLSSVTAADTAVYYC	ARGRGYATS----	LAFDIWGQ
TS-21522 VH	YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYC	ARGSQE-----	HLIFDYWGQ
RY-21527 VH	YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYC	CARTDFWSGSP---	PG-LDYWGQ
PP-21528 VH	NYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYC	CARTPEYSSSIWHY	YYYGMDVWGQ
RD-21530 VH	YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYC	VKGPLQEPFY---	DYGMDVWGQ
	* *	* : . . . : * : * : * : *	: * : * : *

	FR4
FS-21495 VH	GTMVTVSS
PC-21497 VH	GTLVTVSS
AJ-21508 VH	GTTVTVSS
NM-21517 VH	GTMVTVSS
TS-21522 VH	GTLVTVSS
RY-21527 VH	GTLVTVSS
PP-21528 VH	GTTVTVSS
RD-21530 VH	GTTVTVSS
	** *****

FIG. 2F	SEQ ID NO:			
	VH	CDR1	CDR2	CDR3
FS-21495 VH	77	13	21	29
PC-21497 VH	78	14	22	30
AJ-21508 VH	79	15	23	31
NM-21517 VH	80	16	24	32
TS-21522 VH	81	17	25	33
RY-21527 VH	82	18	26	34
PP-21528 VH	83	19	27	35
RD-21530 VH	84	20	28	36

FIG. 2G – Anti-BCMA Binding Molecules

	FR1	CDR1	FR2	CDR2
FS-21495_VL	EIVLTQSPATLSLSPGERATLSCRASQSVSR-----YLA	WYQQKPGQAPRLLIYDASNR		
PC-21497_VL	DIVMTQSPISLPVTPGEPASISCRSSQSLHSNG-YNYL	DWYLQKPGQSPQLLIYLG		
AJ-21508_VL	EIVMTQSPATLSVSPGERATLSCRASQSVSS-----NLA	WYQQKPGQAPRLLIYGASTR		
NM-21517_VL	EIVLTQSPATLSLSPGERATLSCRASQSVSS-----YLA	WYQQKPGQAPRLLIYDASNR		
TS-21522_VL	EIVLTQSPATLSLSPGERATLSCRASQSVSR-----YLA	WYQQKPGQAPRLLIYDASNR		
RY-21527_VL	DIQLTQSPSSVSASVGDRVTITCRASQGISS-----WLA	WYQQKPGKAPKLLIYGASSL		
PP-21528_VL	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLA	WYQQKPGQPPKLLIYWASTR		
RD-21530_VL	EIVMTQSPATLSVSPGERATLSCRASQSVSS-----NLA	WYQQKPGQAPRLLIYSASTR		
	:* :**** :. : * : . : . : * : : * : . : *	* ** ***** : . : ***** . *		
	CDR2	FR3	CDR3	FR4
FS-21495_VL	ATGIPARESGSGSGTDFTLTISSLEPEDFAVYYCQQRISW	PFTFGGGTKVEIK		
PC-21497_VL	ASGVPDFRSGSGSGTDFTLKISRVEAEDVGYYCMQGLGL	PLTFGGGTKVEIK		
AJ-21508_VL	ATGIPARESGSGSGTEFTLTISSLQSEDFAVYYCQQYAA	YP-TFGGGTKVEIK		
NM-21517_VL	ATGIPARESGSGSGTDFTLTISSLEPEDFAVYYCQQRHV	WPPTFGGGTKVEIK		
TS-21522_VL	ATGIPARESGSGSGTDFTLTISSLEPEDFAVYYCQQRFY	YPWTFGGGTKVEIK		
RY-21527_VL	QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQIYT	FPFTFGGGTKVEIK		
PP-21528_VL	ESGVPDFRSGSGSGTDFTLTISSLQAEDEVAVYYCQQFA	HTPFTFGGGTKVEIK		
RD-21530_VL	ATGIPARESGSGSGTEFTLTISSLQSEDFAVYYCQQHHV	WPLTFGGGTKVEIK		
	:* :* ***** : * * * * * : . : * * . . . * * *	* * *****		

<u>FIG. 2H</u>	SEQ ID NO:			
	VL	CDR1	CDR2	CDR3
FS-21495_VL	85	37	45	53
PC-21497_VL	86	38	46	54
AJ-21508_VL	87	39	47	55
NM-21517_VL	88	40	48	56
TS-21522_VL	89	41	49	57
RY-21527_VL	90	42	50	58
PP-21528_VL	91	43	51	59
RD-21530_VL	92	44	52	60

FIG. 3

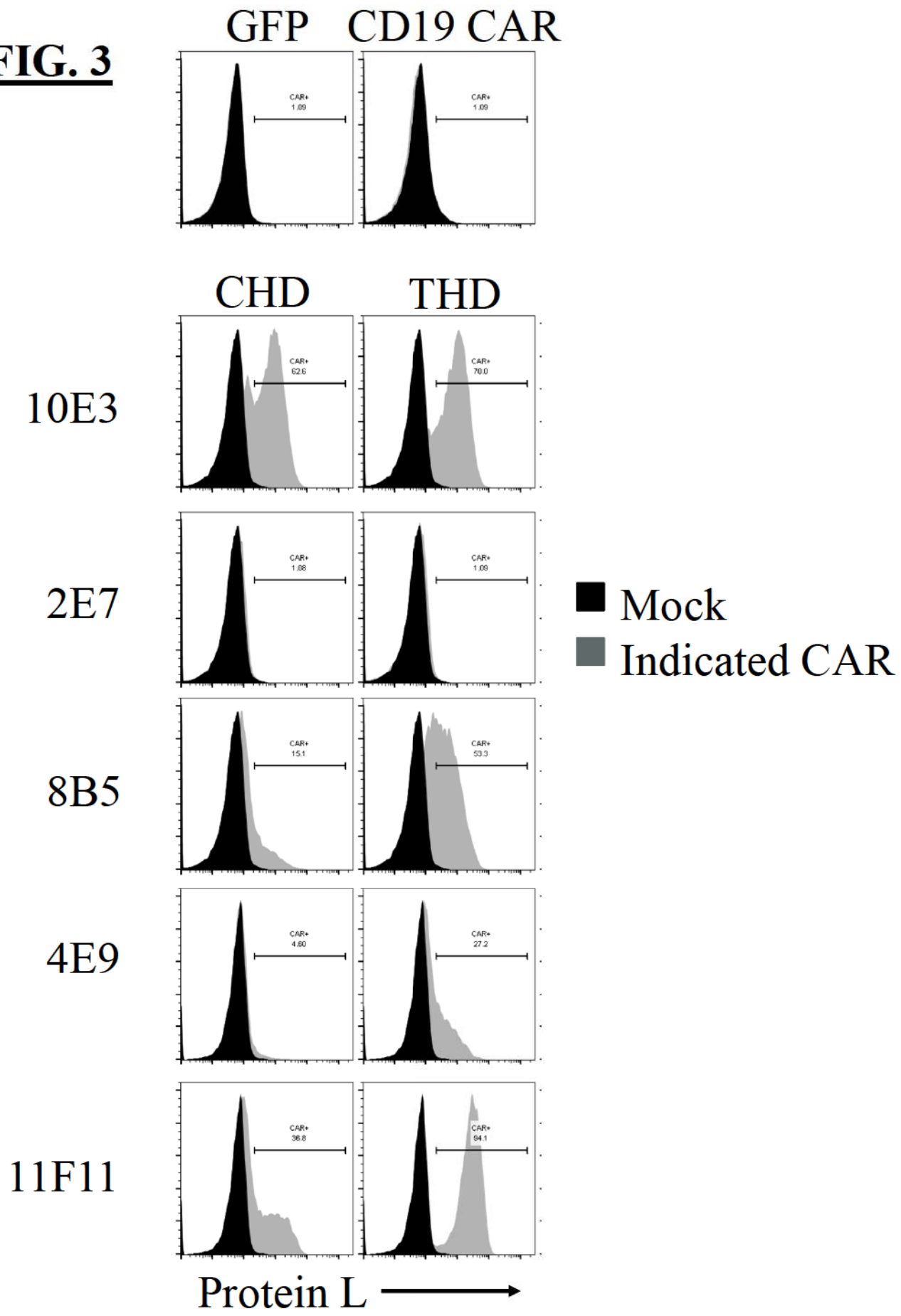


FIG. 4A
Namalwa IFN γ

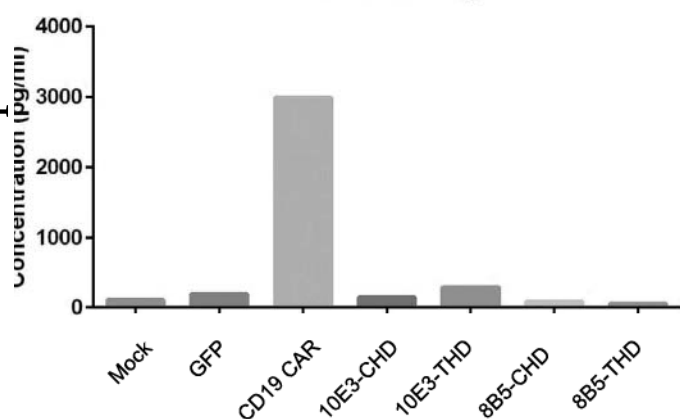


FIG. 4B
Namalwa IFN γ

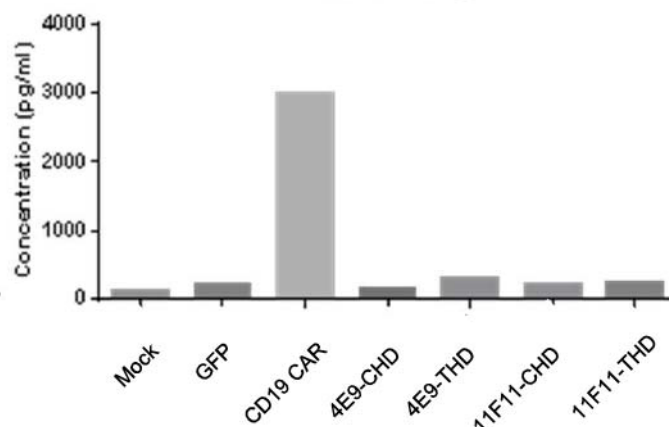


FIG. 4C
Namalwa IL-2

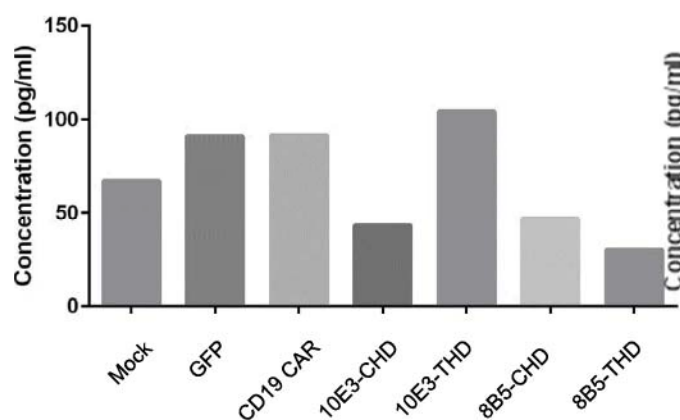


FIG. 4D
Namalwa IL-2

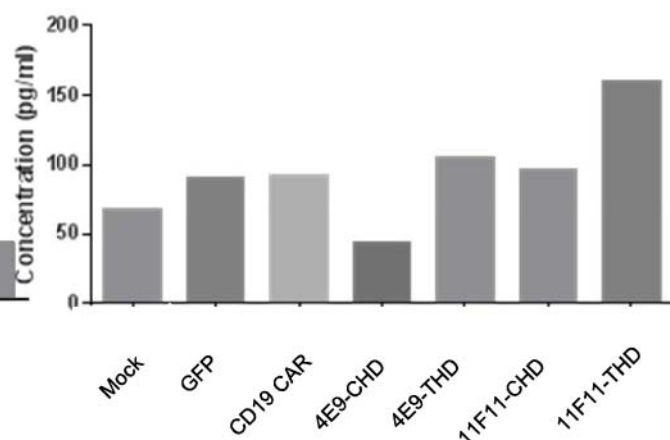


FIG. 4E
Namalwa TNF α

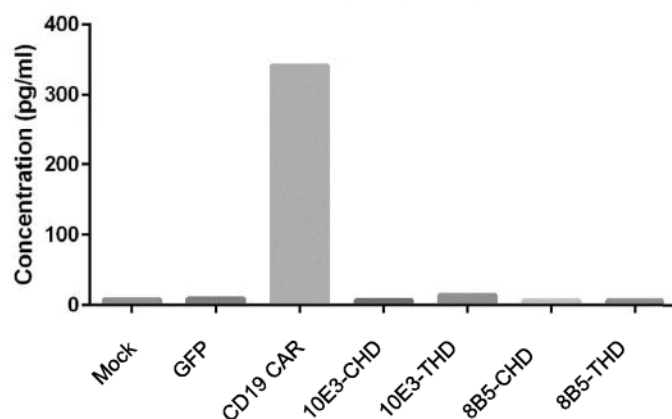


FIG. 4F
Namalwa TNF α

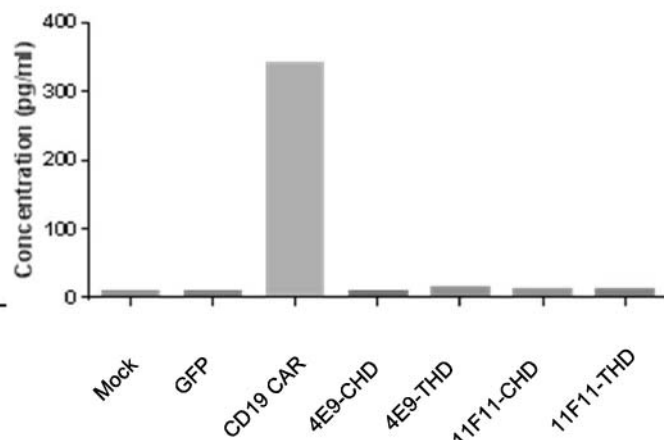


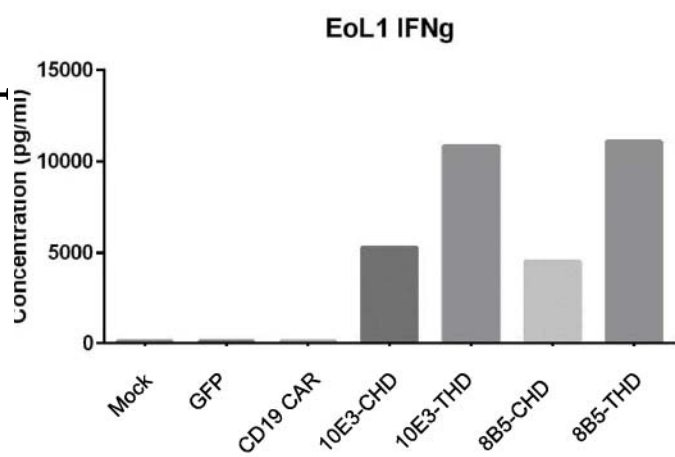
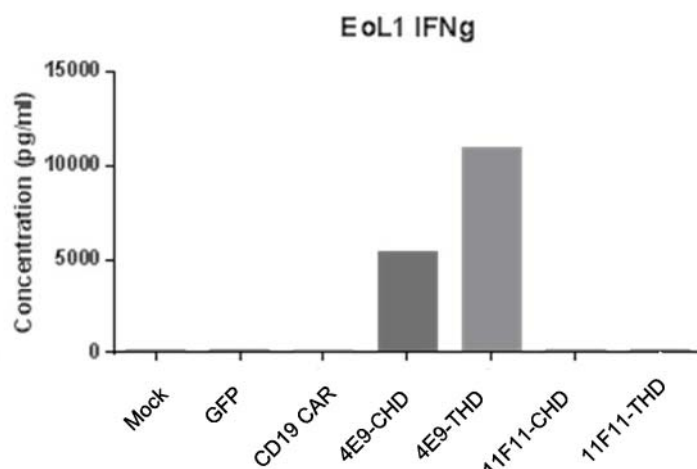
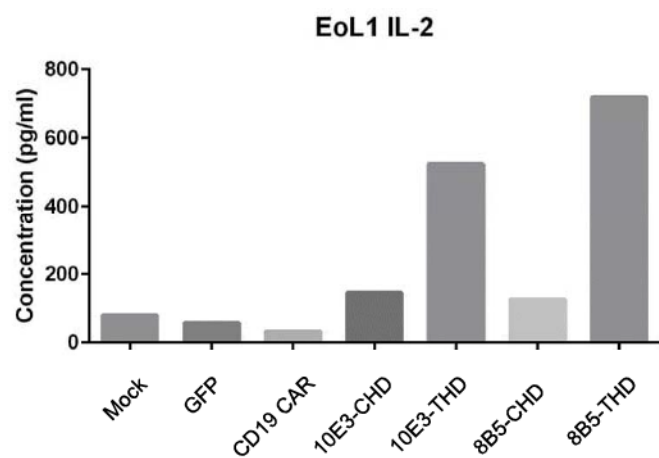
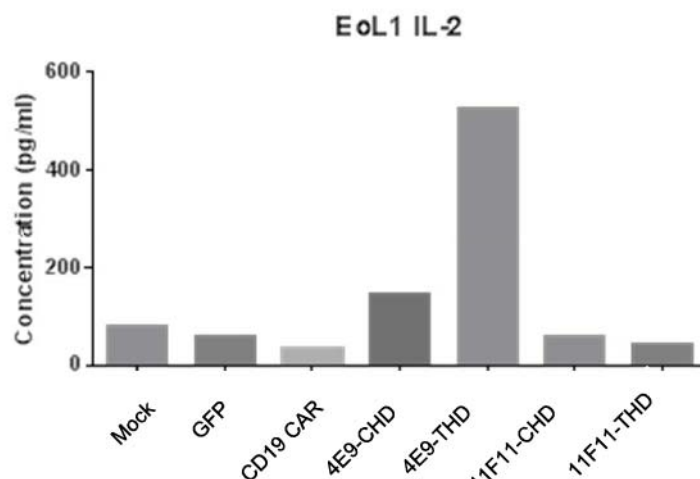
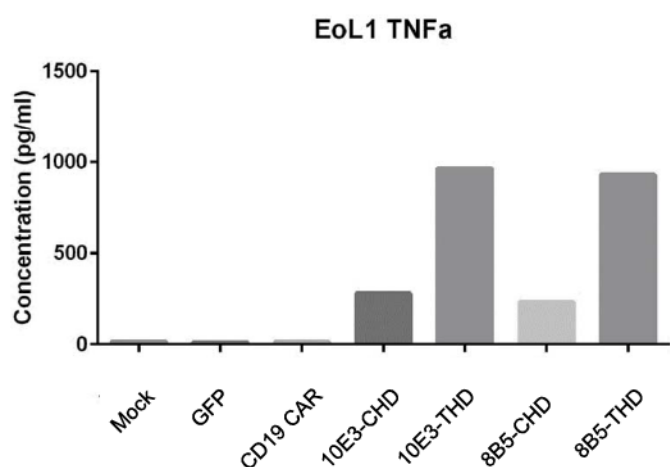
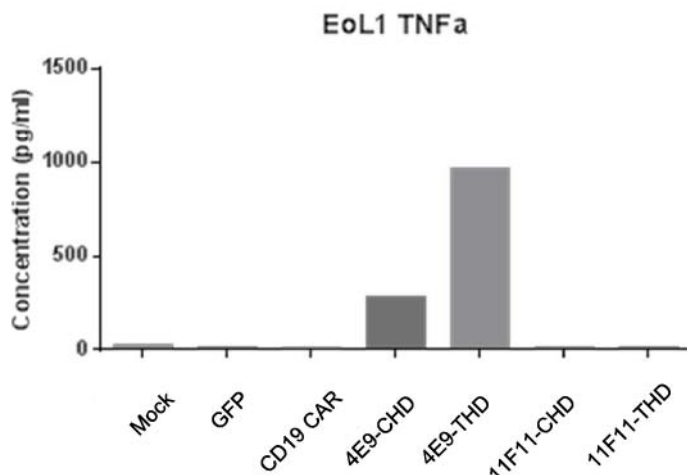
FIG. 4G**FIG. 4H****FIG. 4I****FIG. 4J****FIG. 4K****FIG. 4L**

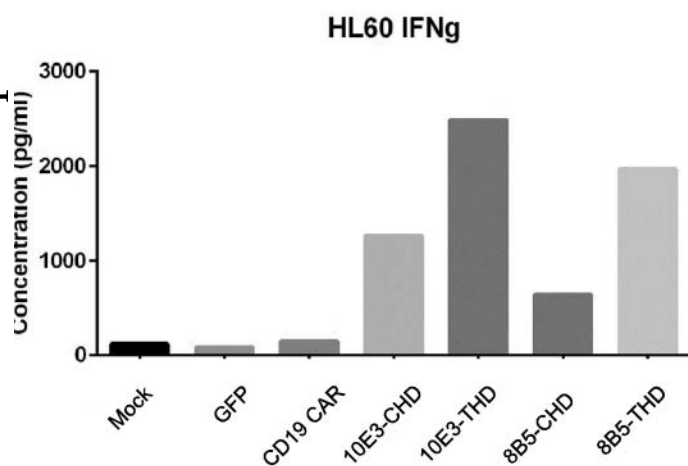
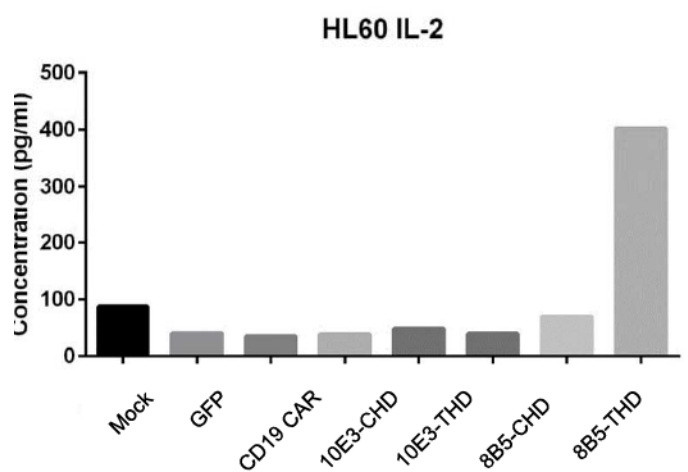
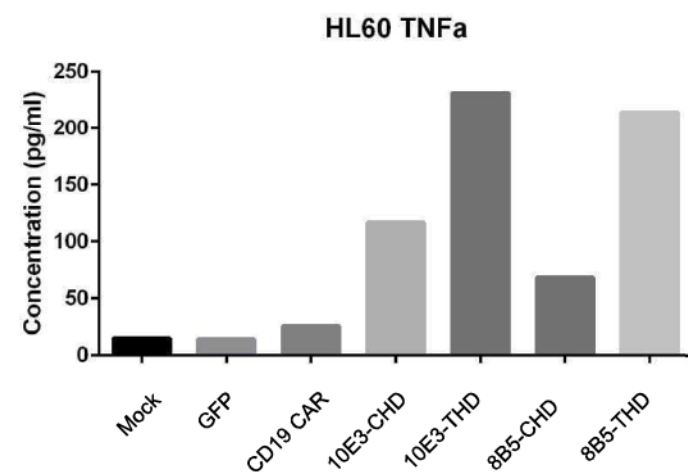
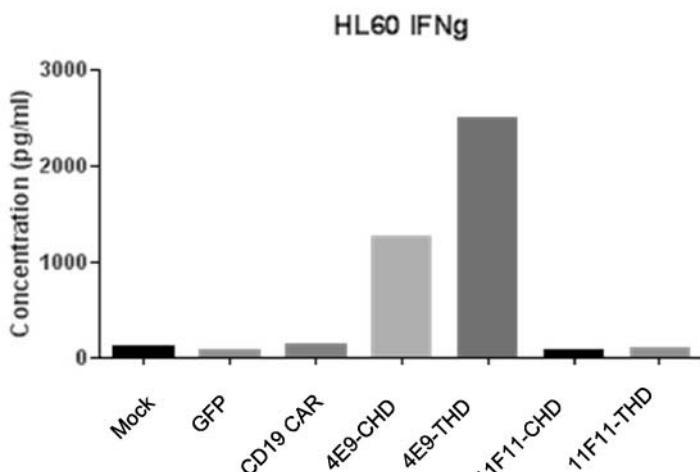
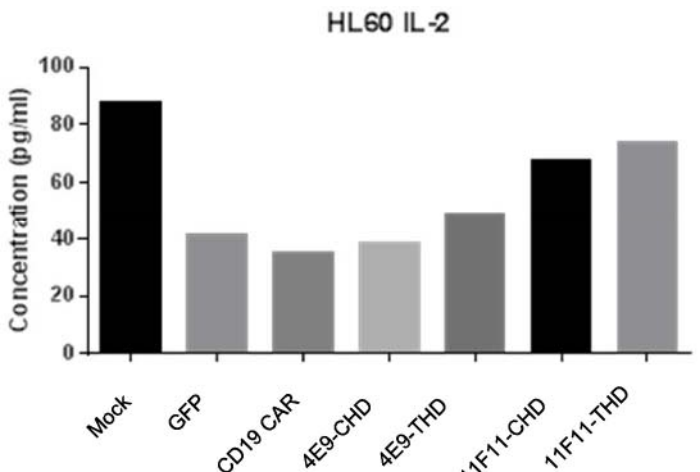
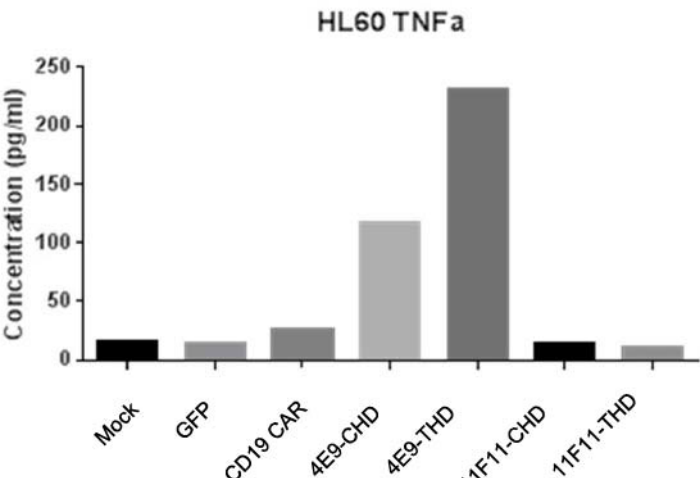
FIG. 4M**FIG. 4O****FIG. 4Q****FIG. 4N****FIG. 4P****FIG. 4R**

FIG. 4S

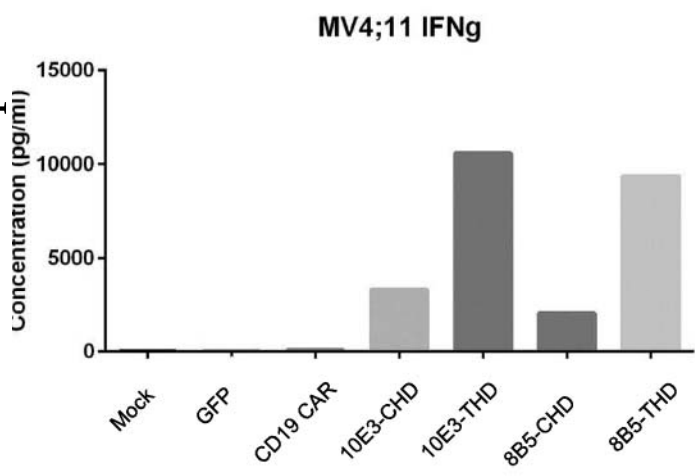


FIG. 4T

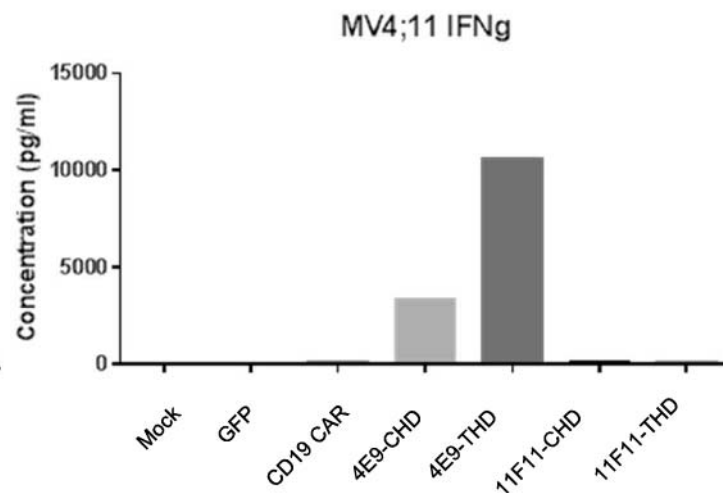


FIG. 4U

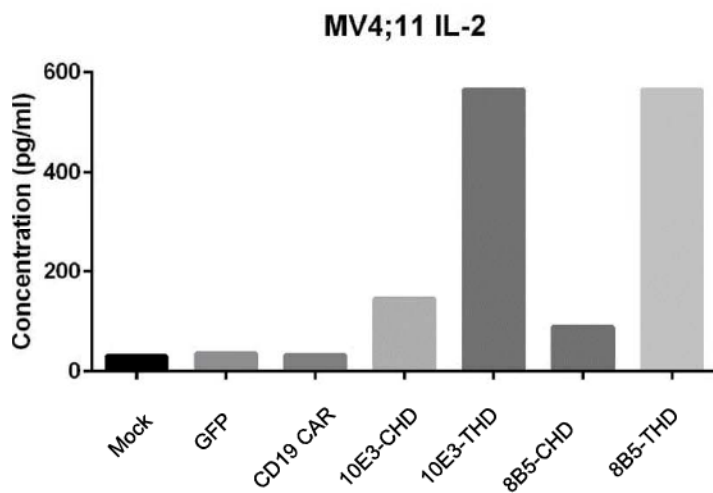


FIG. 4V

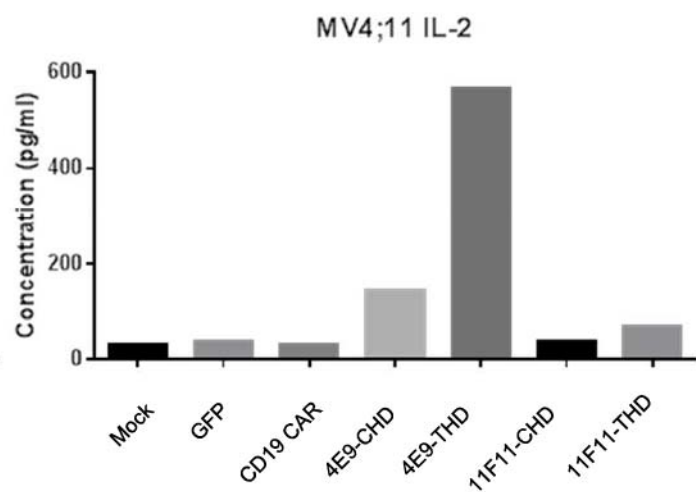


FIG. 4W

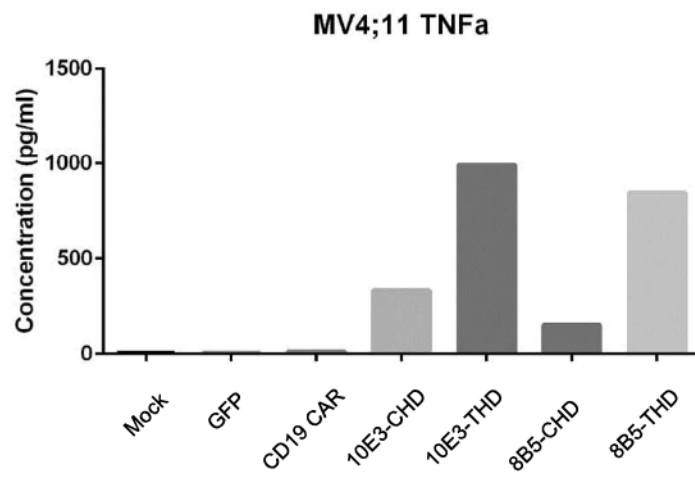
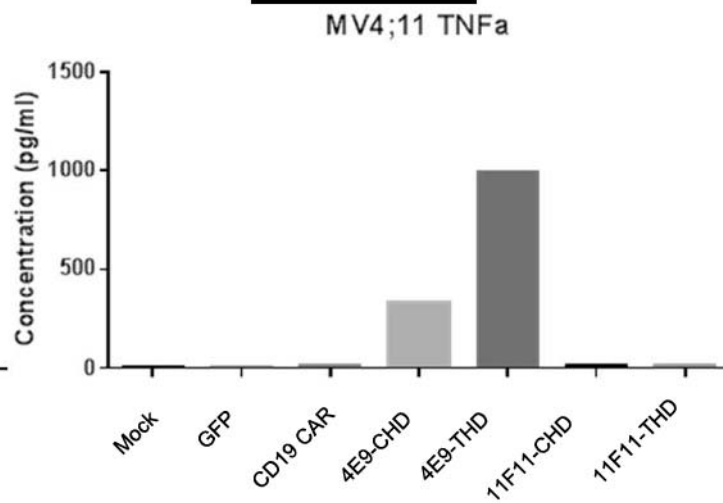
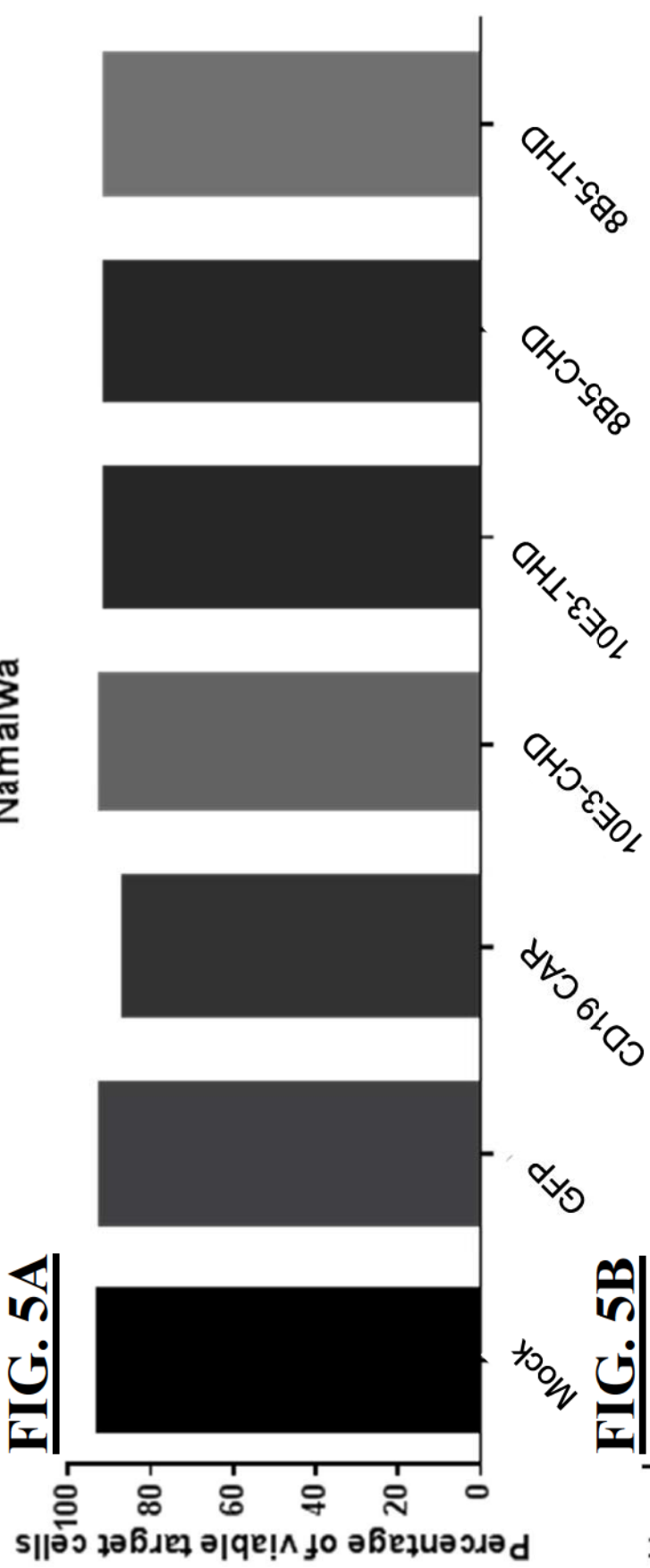


FIG. 4X



Namalwa

FIG. 5A



11/49

FIG. 5B

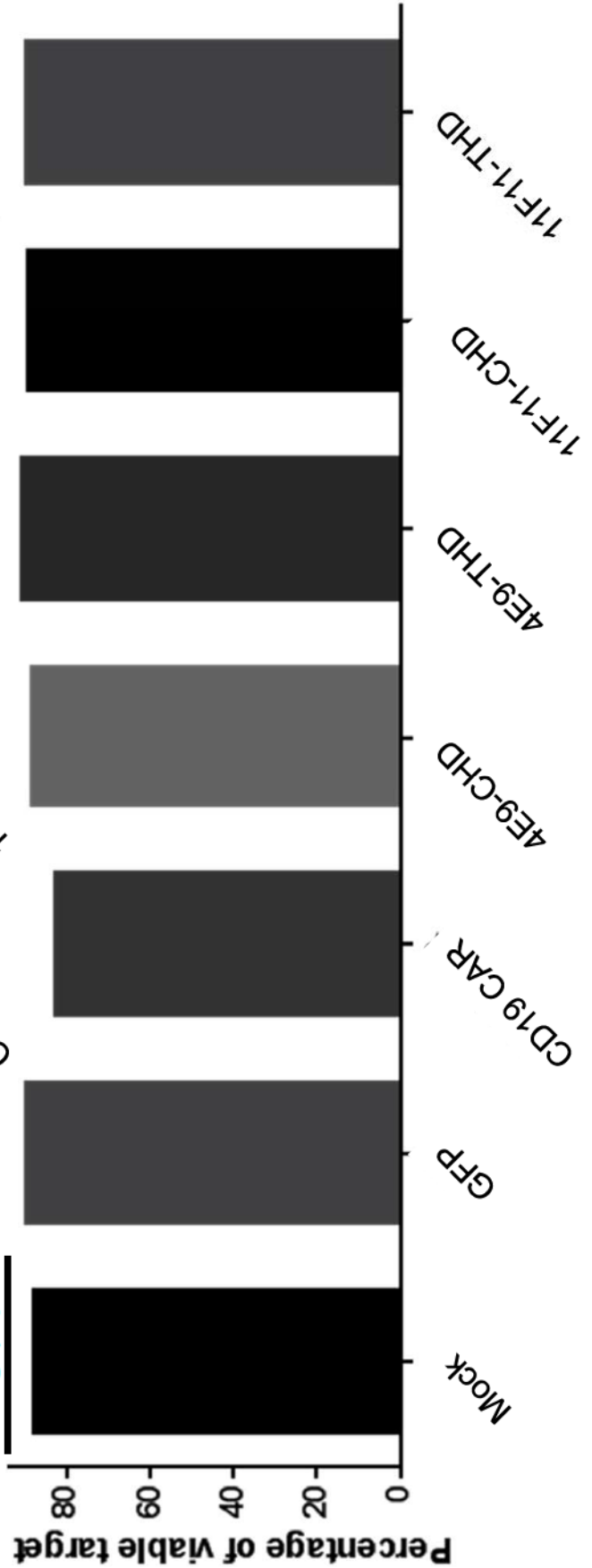


FIG. 5C

EoL1

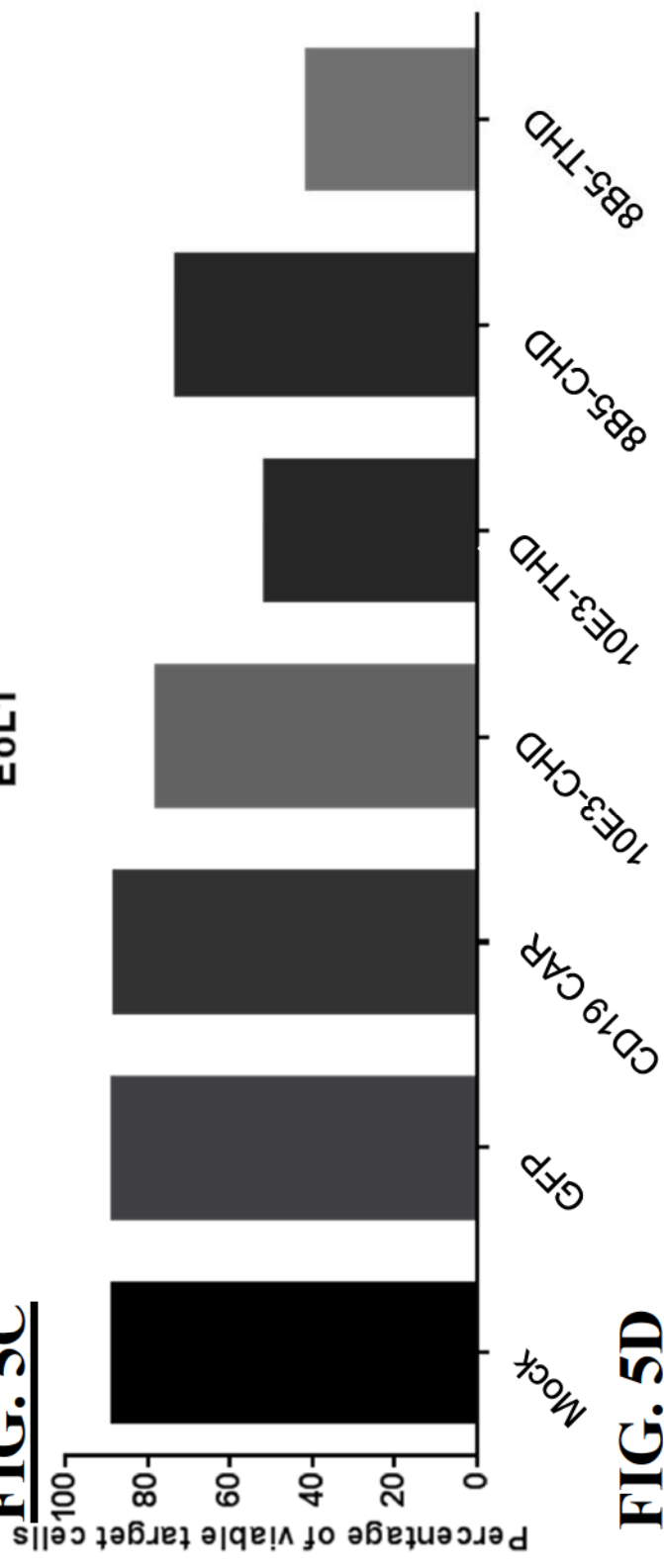


FIG. 5D

EoL1

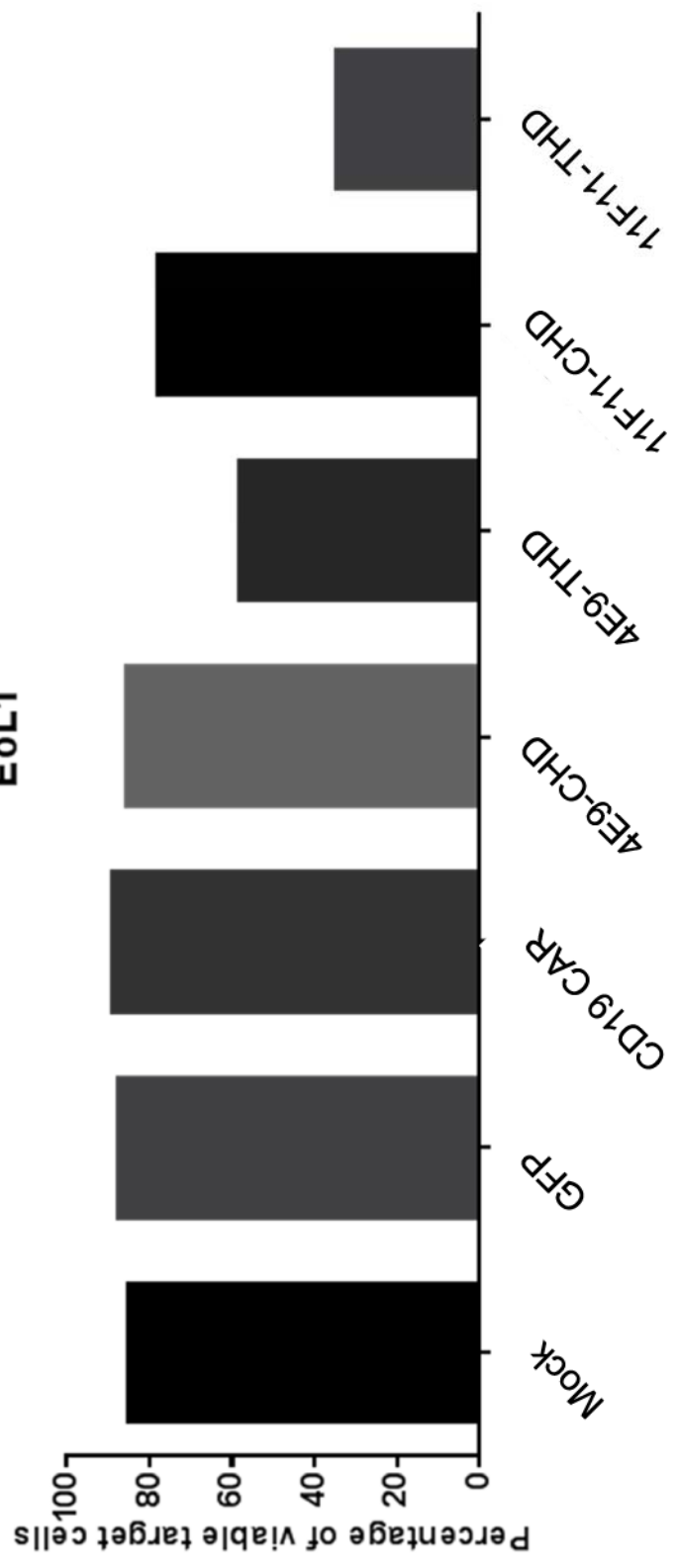


FIG. 5E

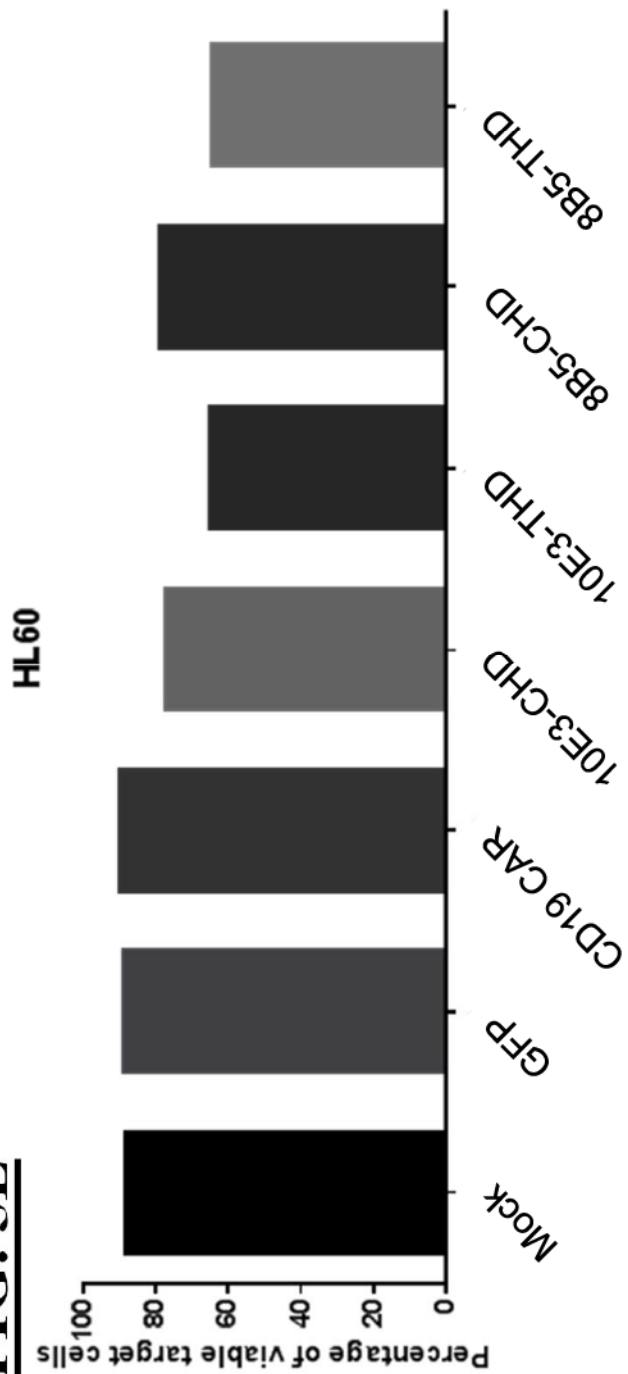


FIG. 5F

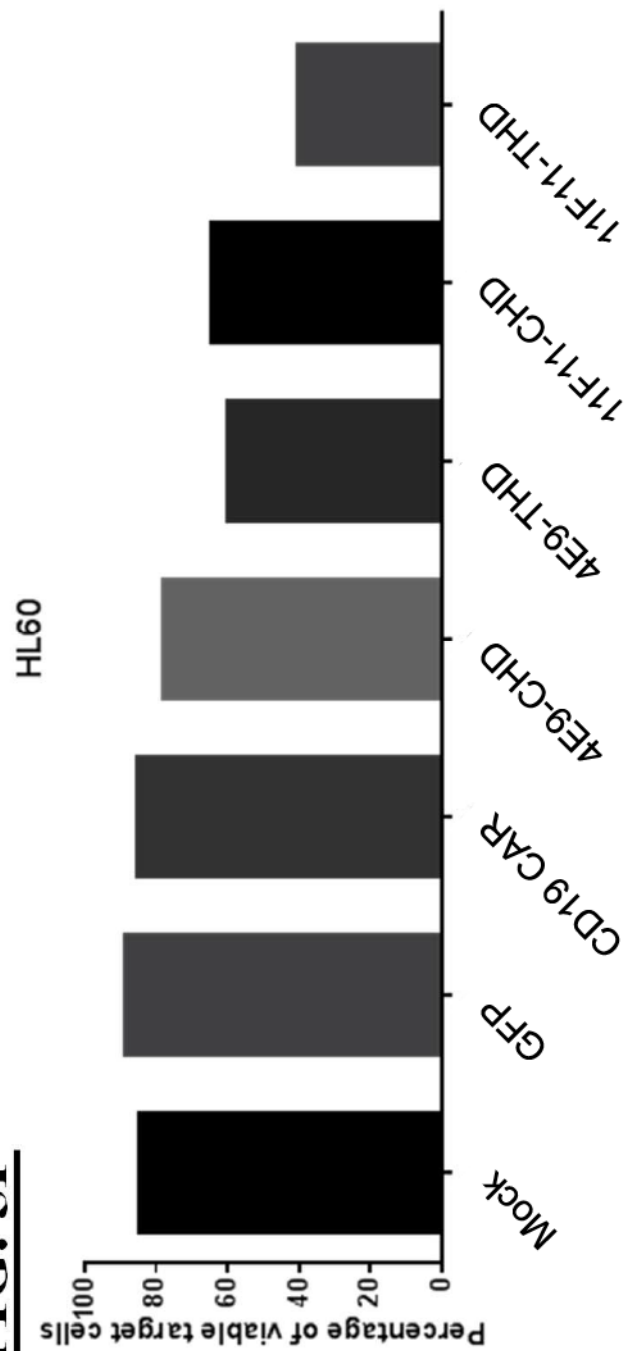
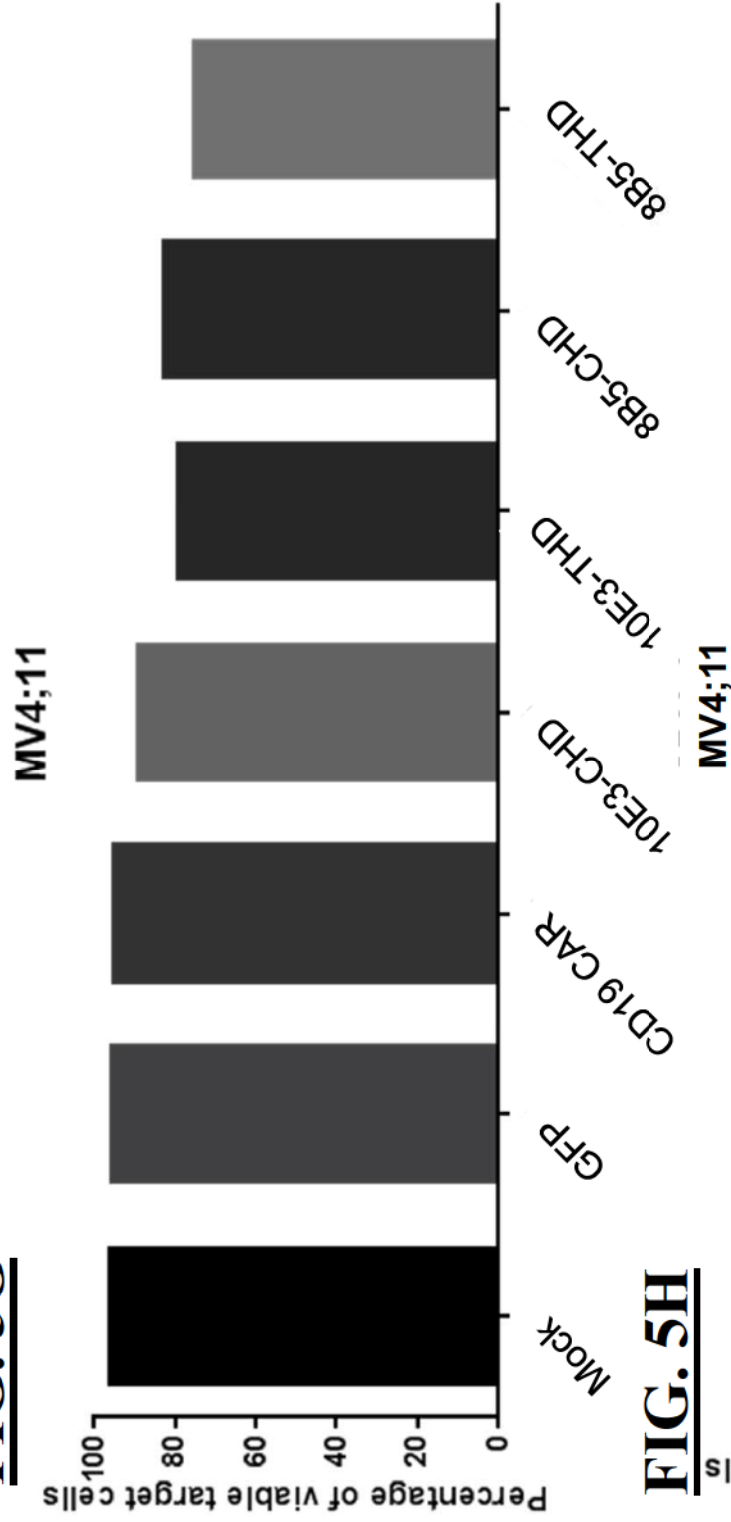


FIG. 5G



14/49

FIG. 5H

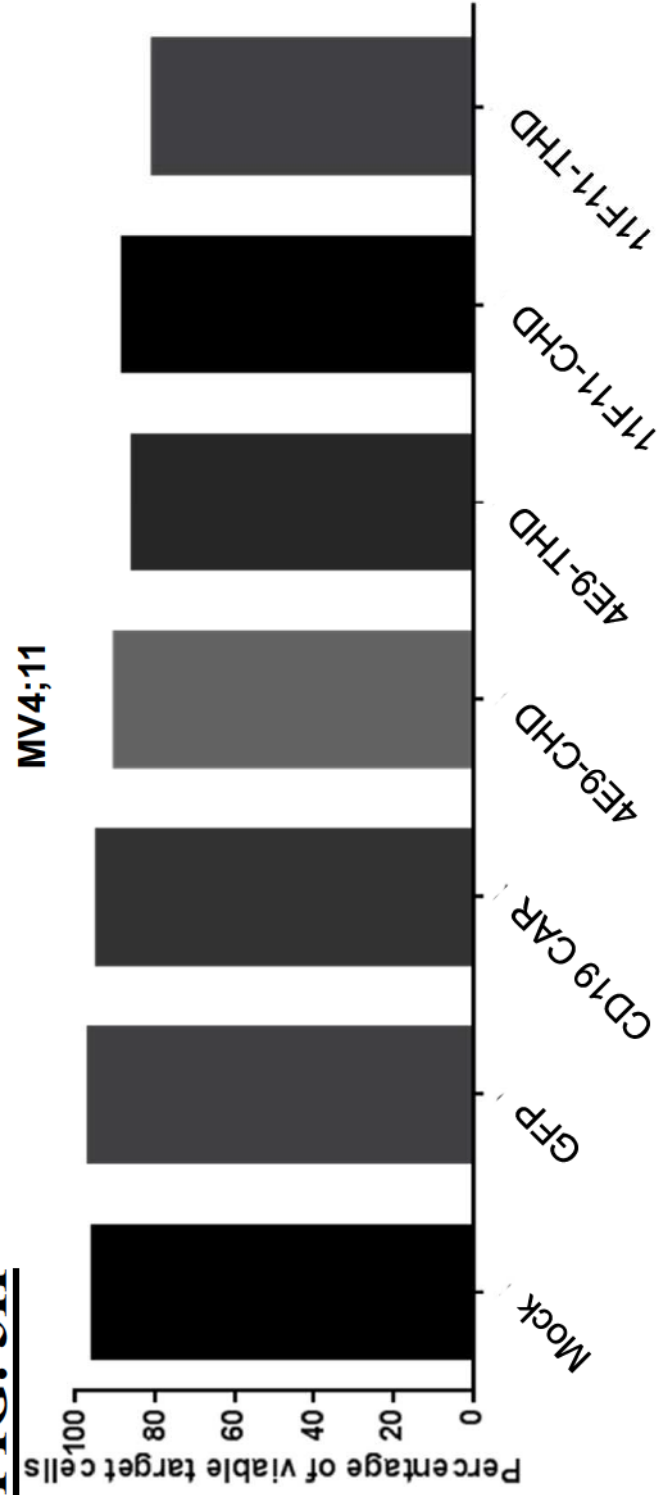


FIG. 6A

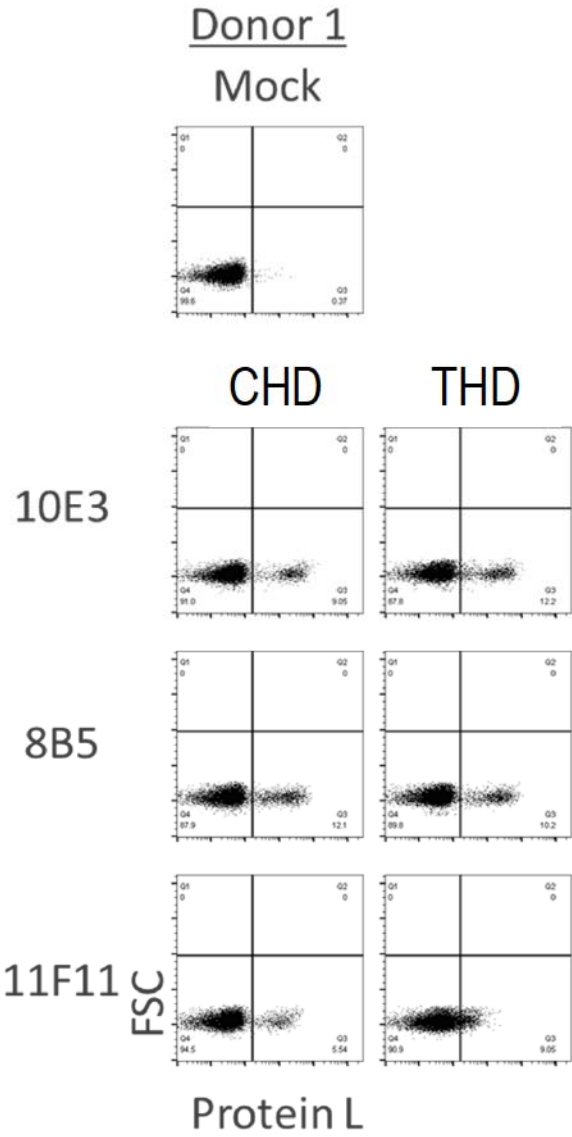


FIG. 6B

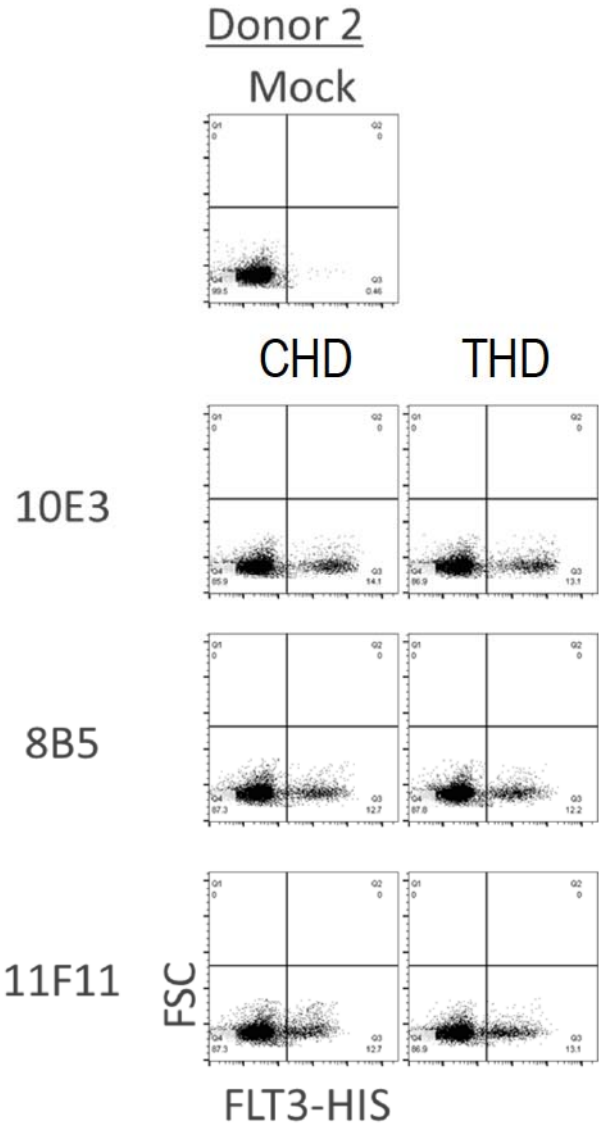


FIG. 7A

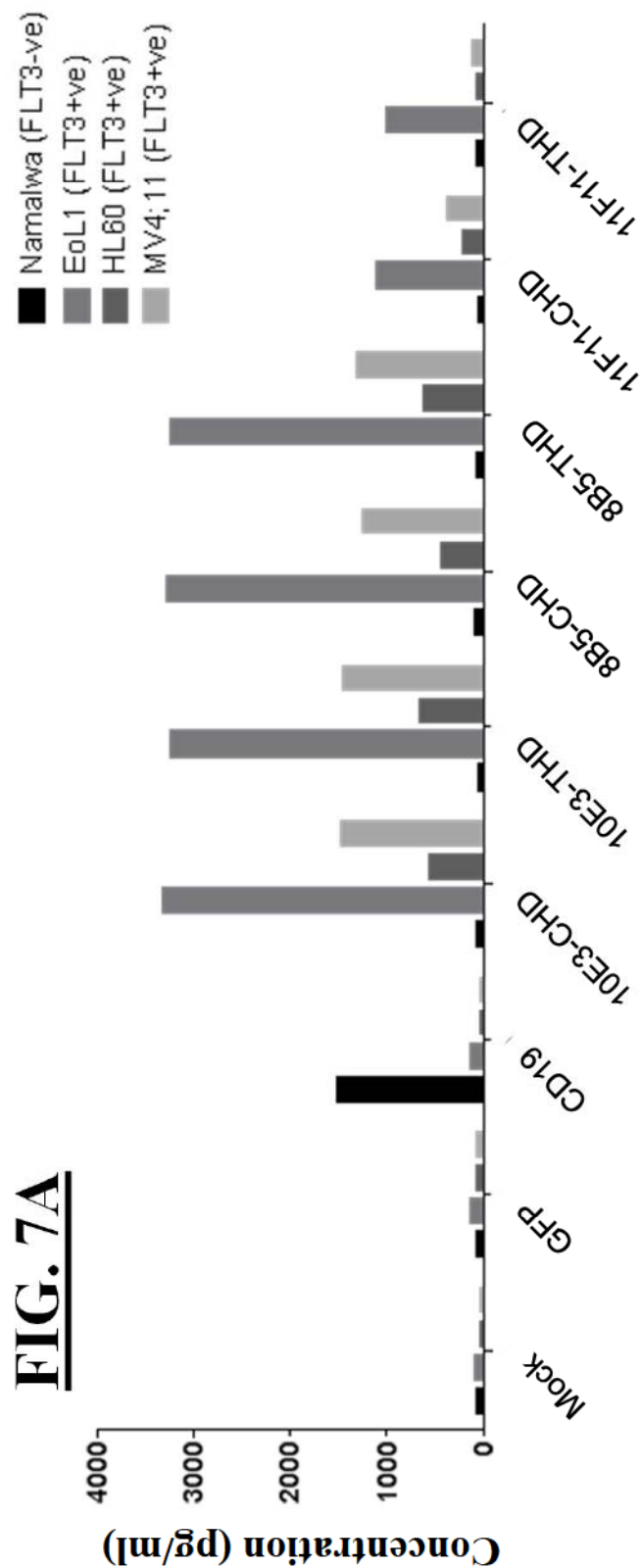


FIG. 7B

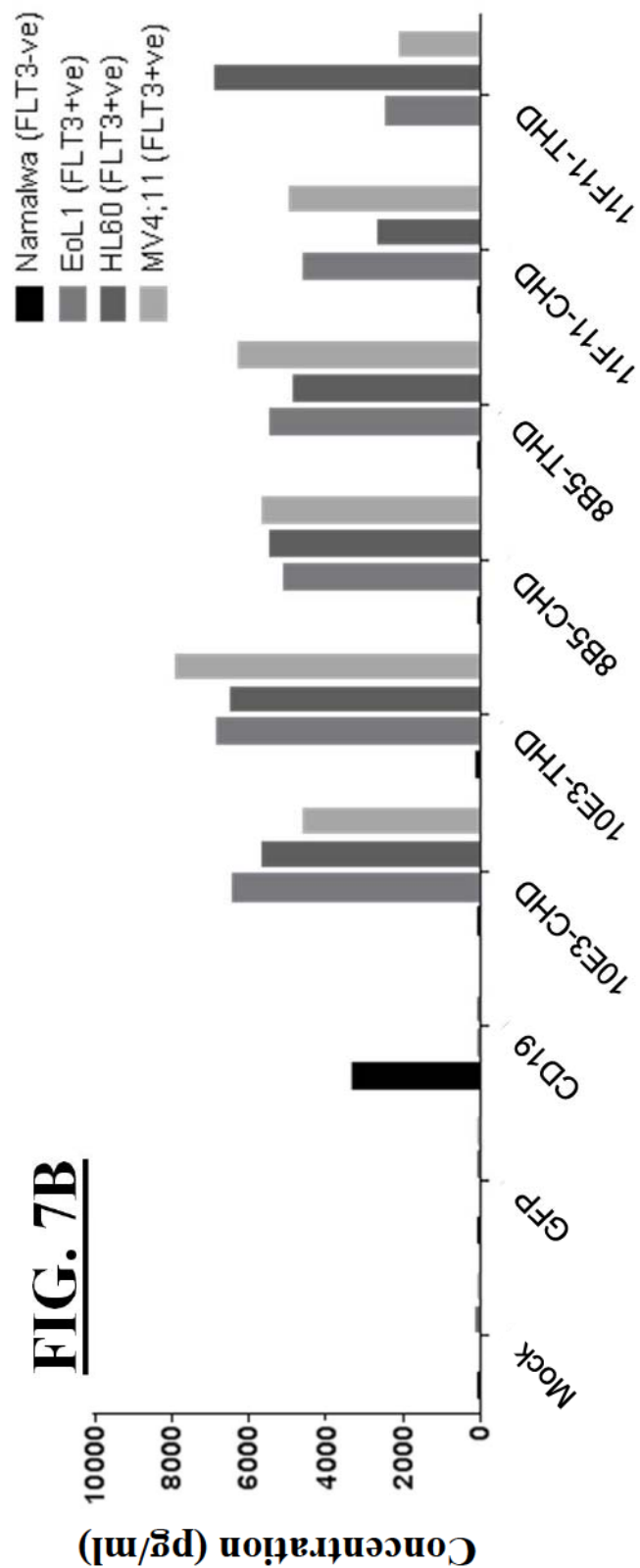


FIG. 7C

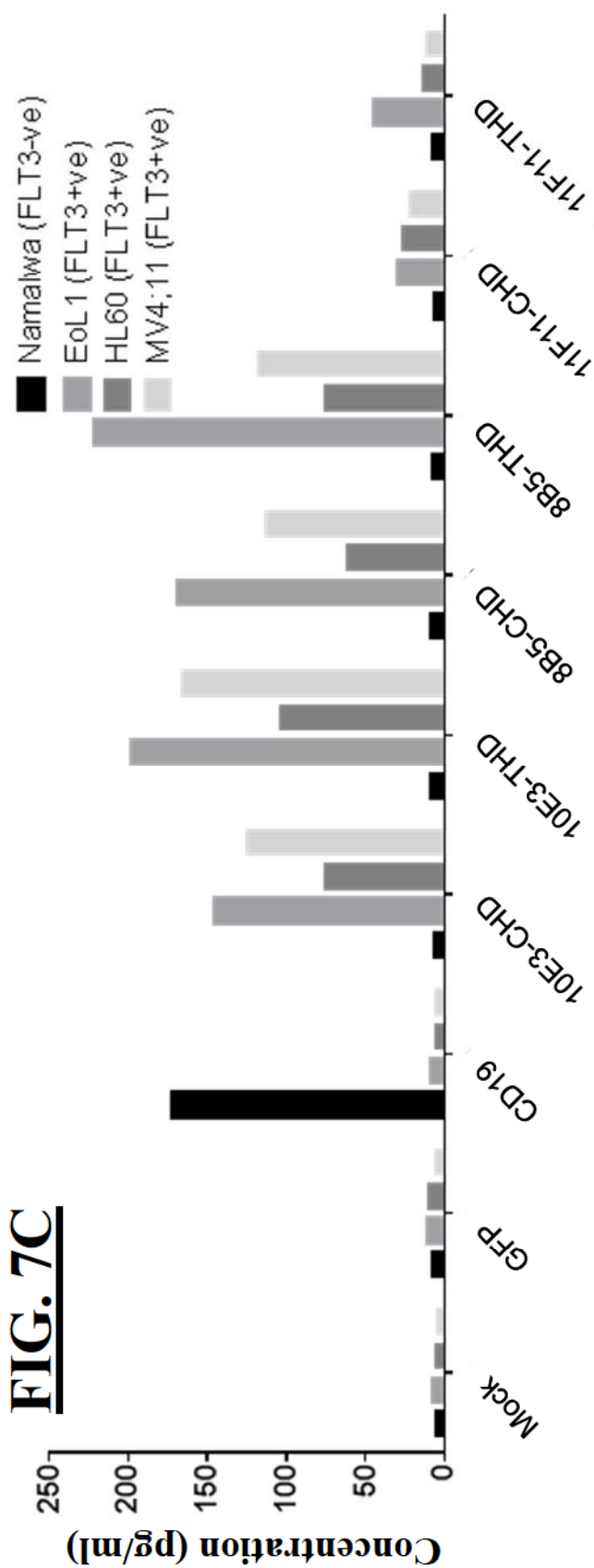


FIG. 7D

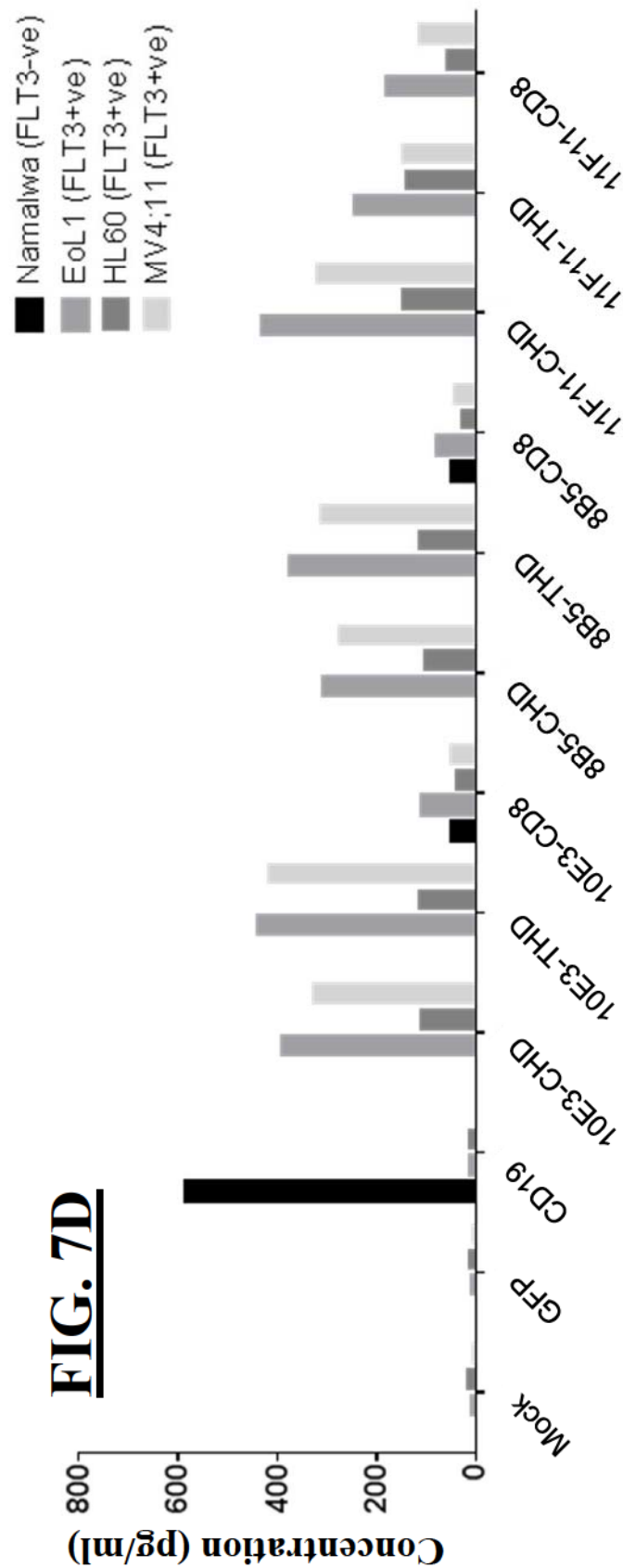


FIG. 7E

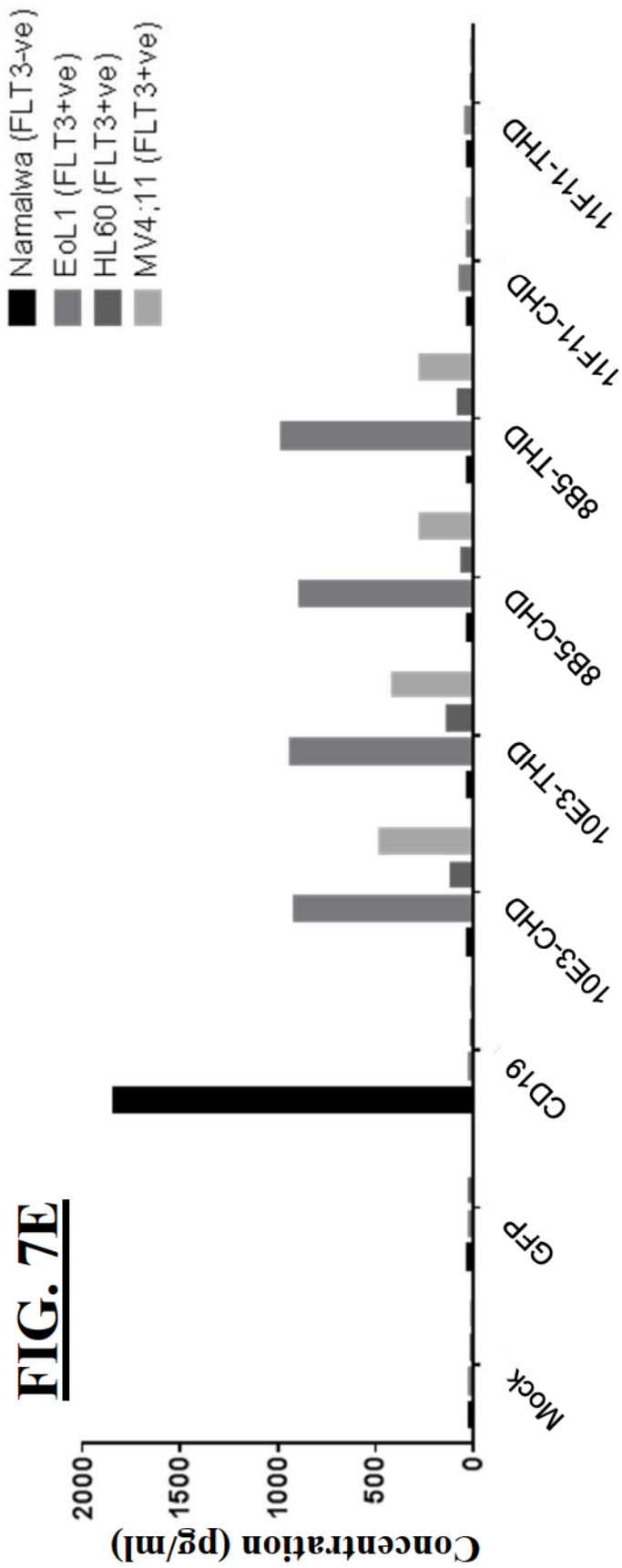


FIG. 7F

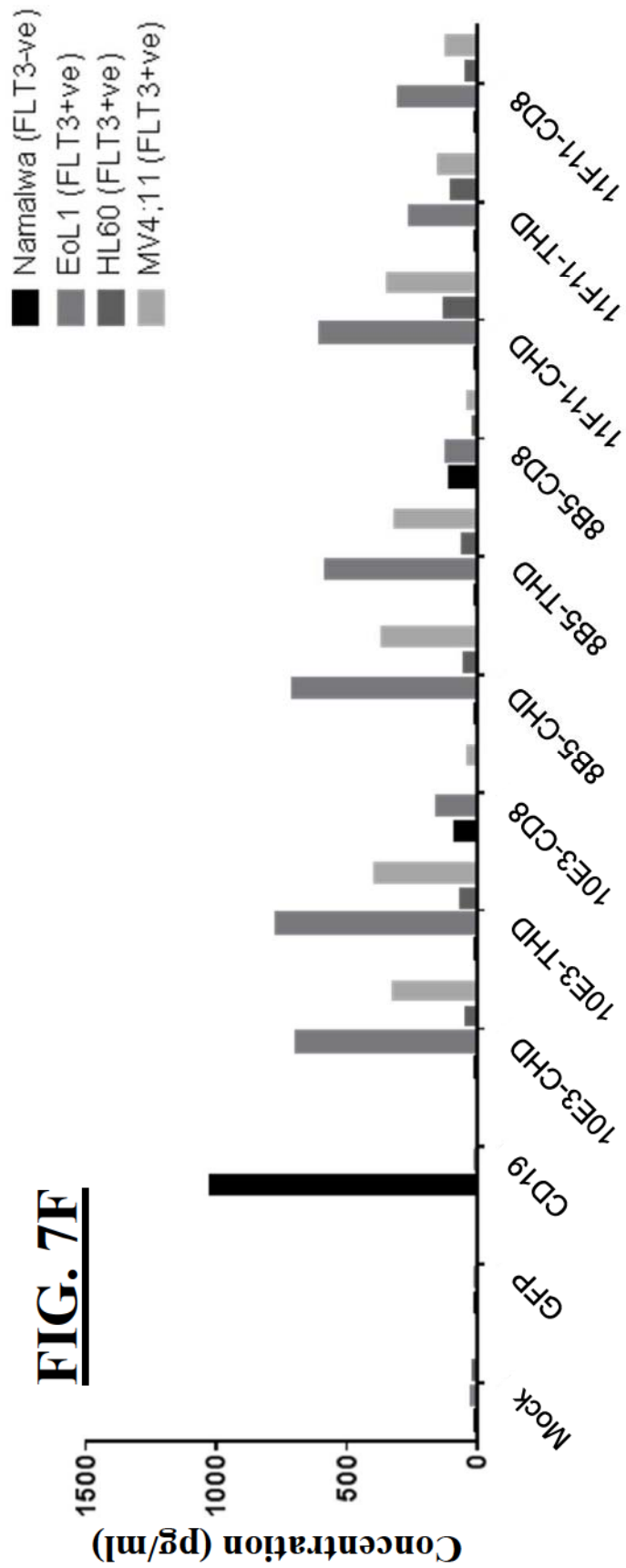


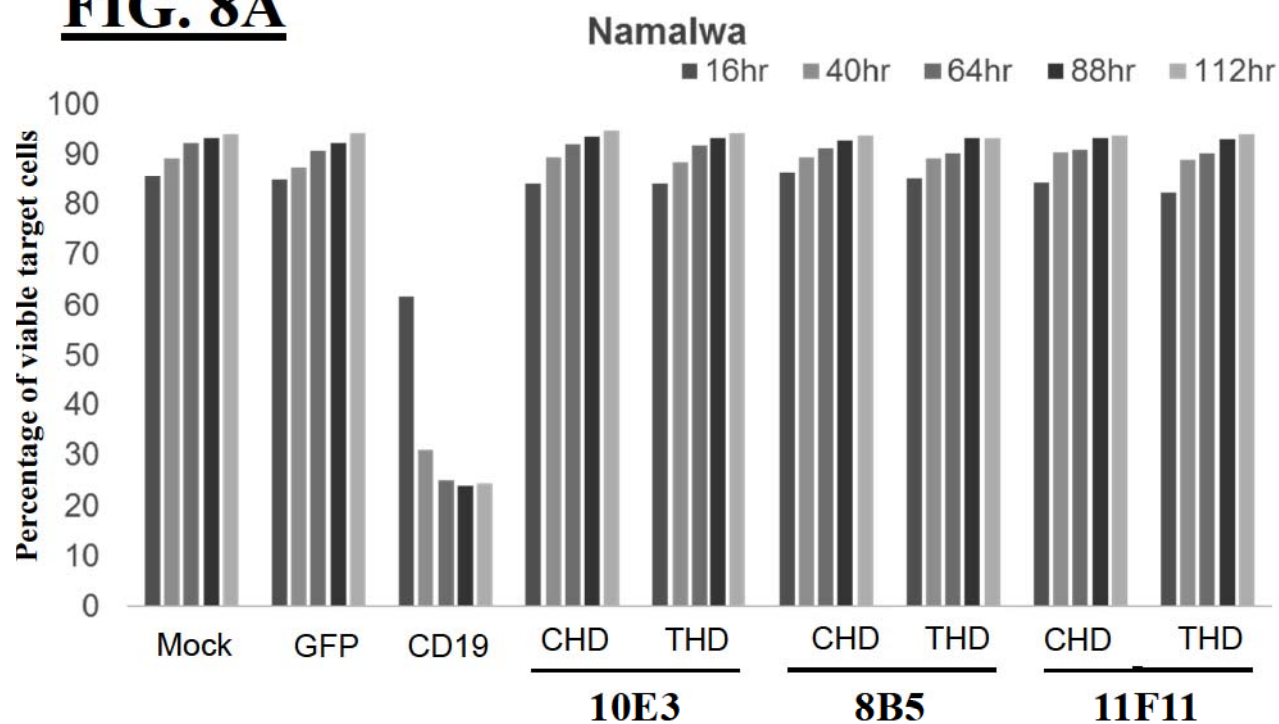
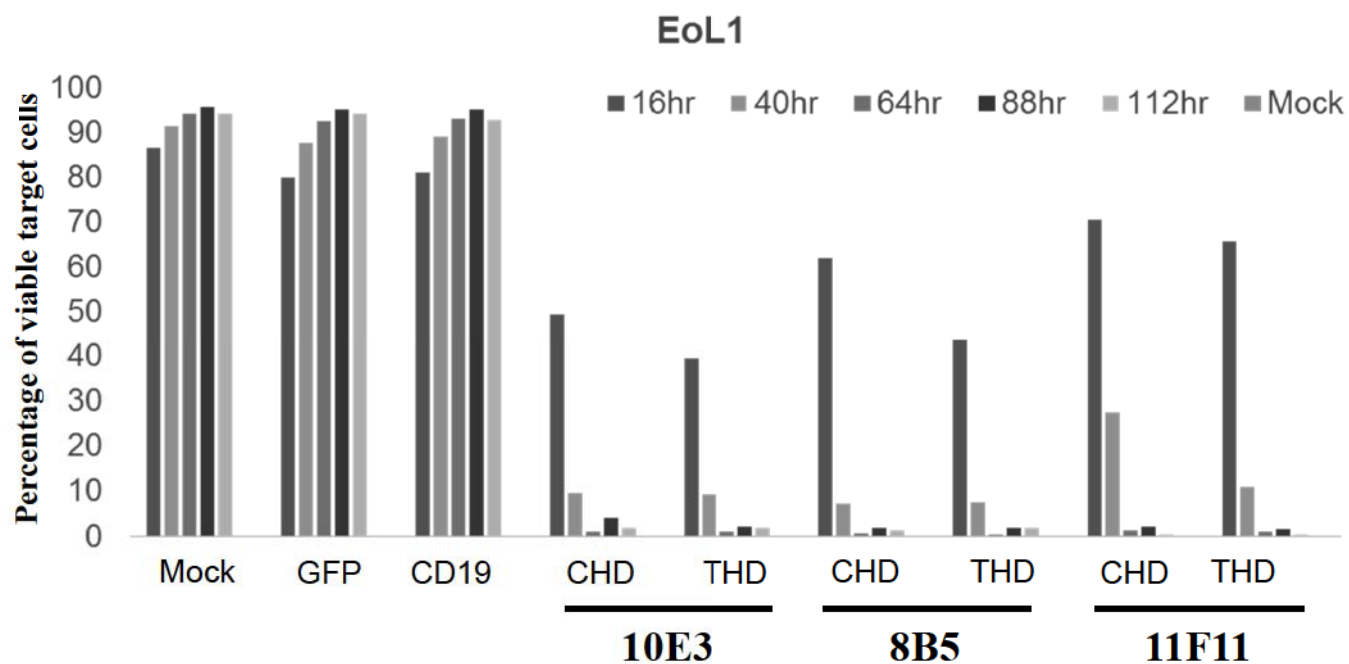
FIG. 8A**FIG. 8B**

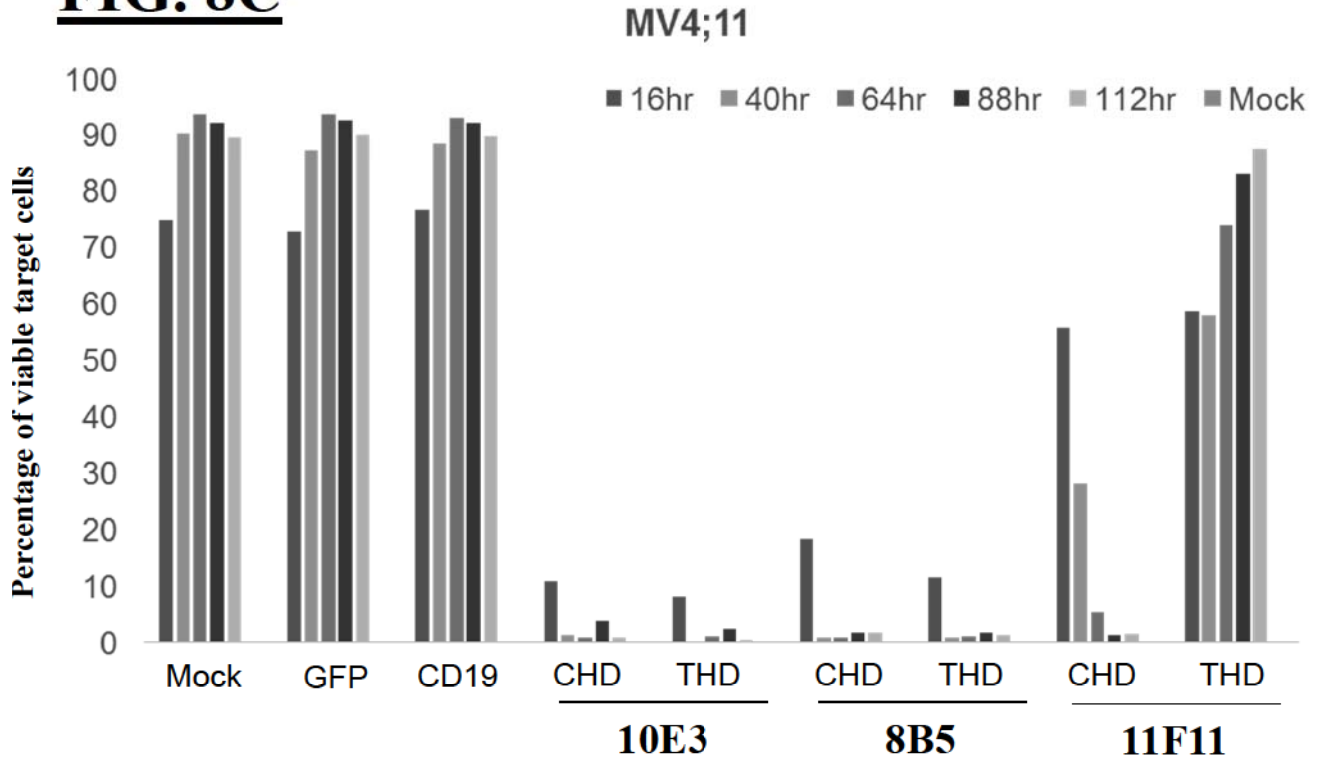
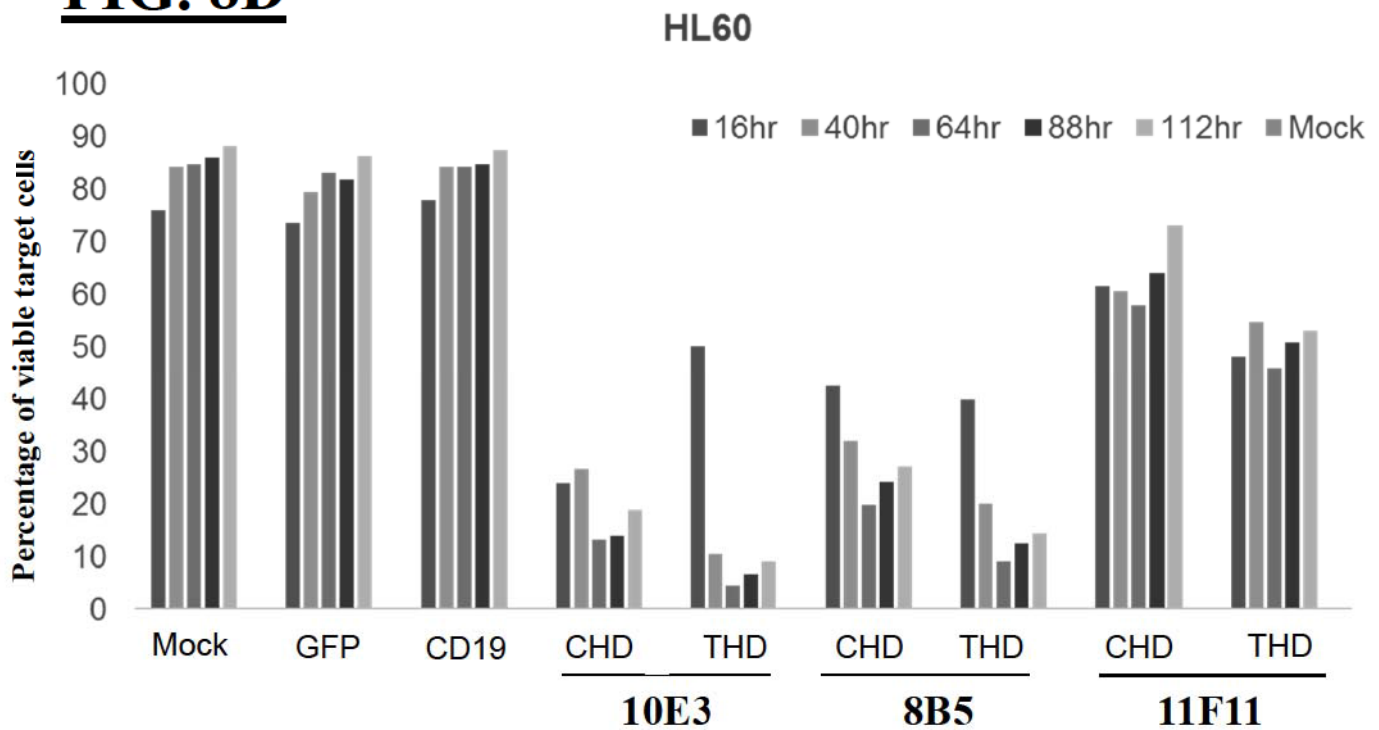
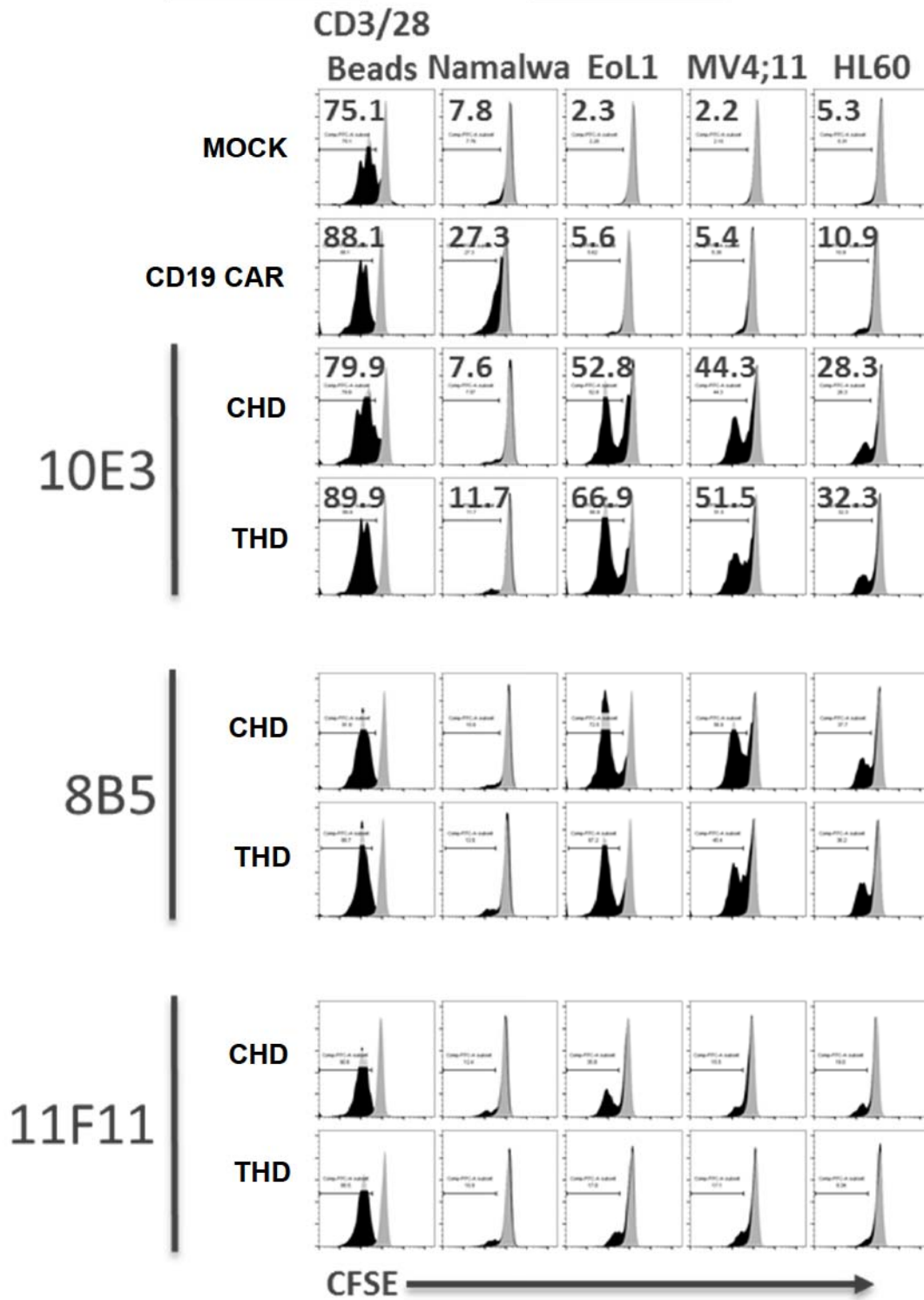
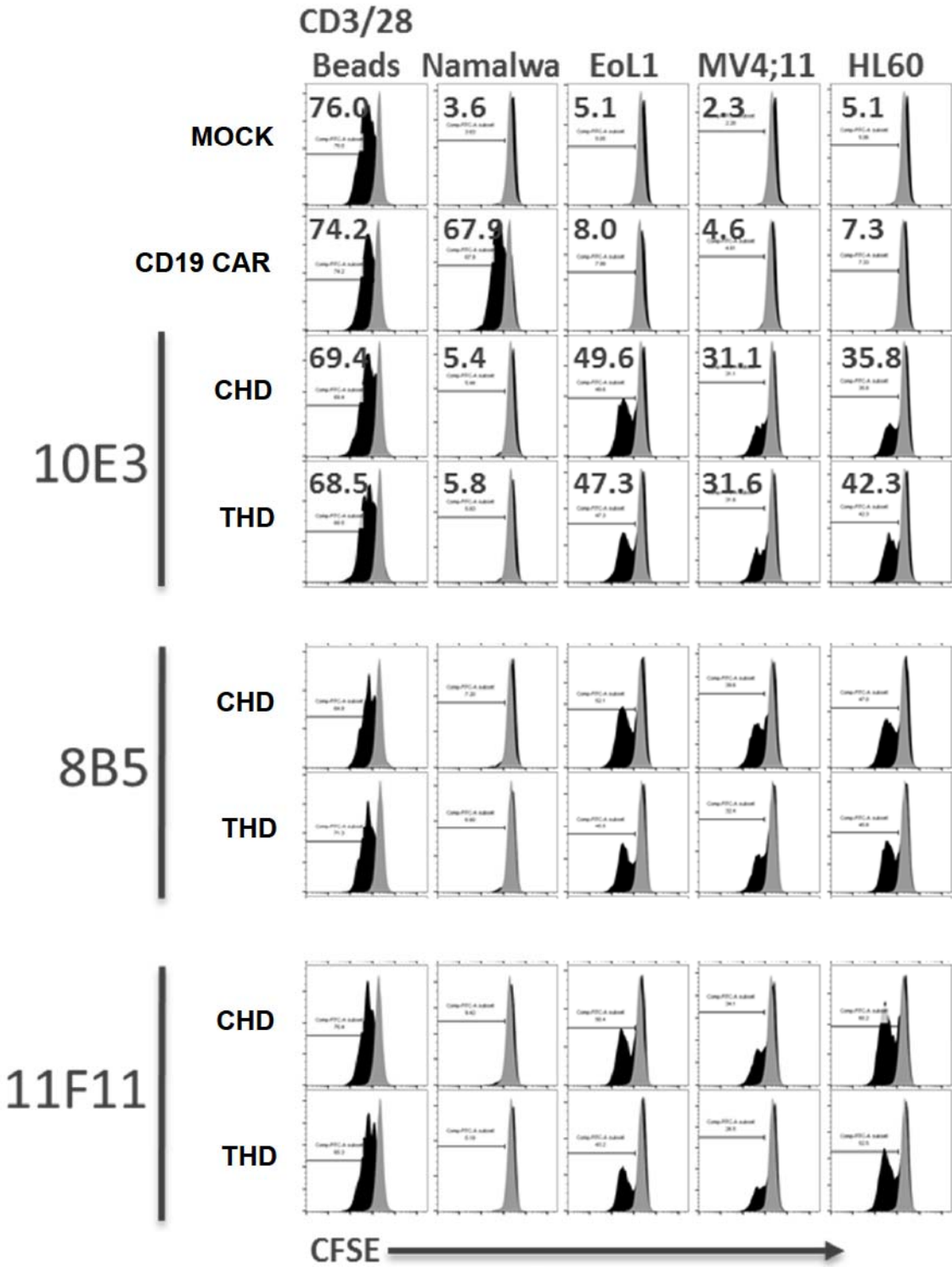
FIG. 8C**FIG. 8D**

FIG. 9A**Donor 1**

■ Unstimulated T cells ■ T cells + indicated stimulus

FIG. 9B **Donor 2**



■ Unstimulated T cells ■ T cells + indicated stimulus

FIG. 10A

Mock

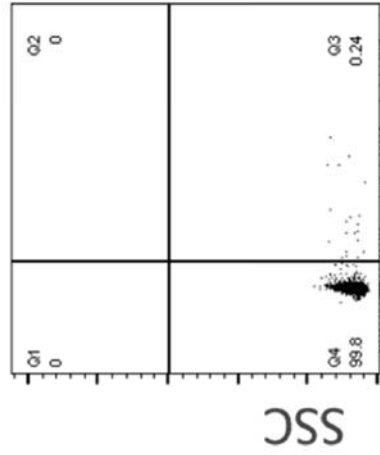


FIG. 10B

10E3-CHD

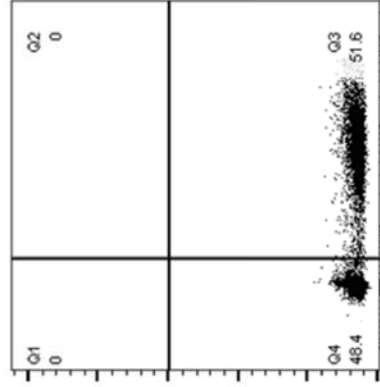


FIG. 10C

10E3-THD

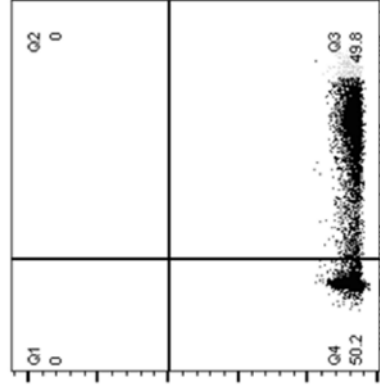


FIG. 10D

8B5-THD

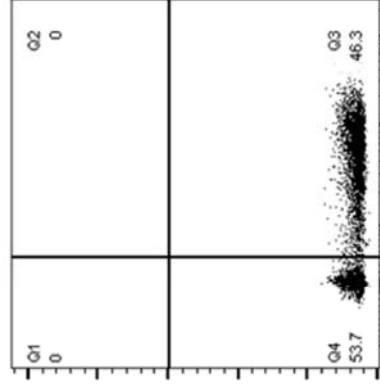


FIG. 10E

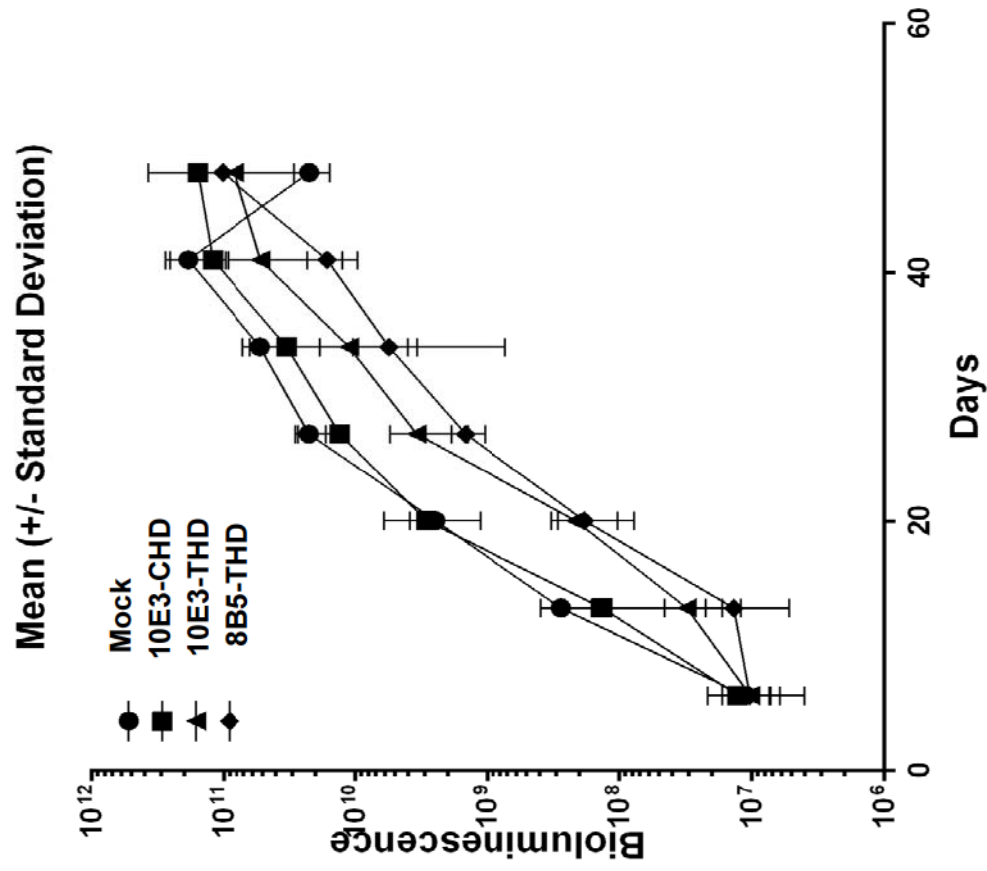


FIG. 10F

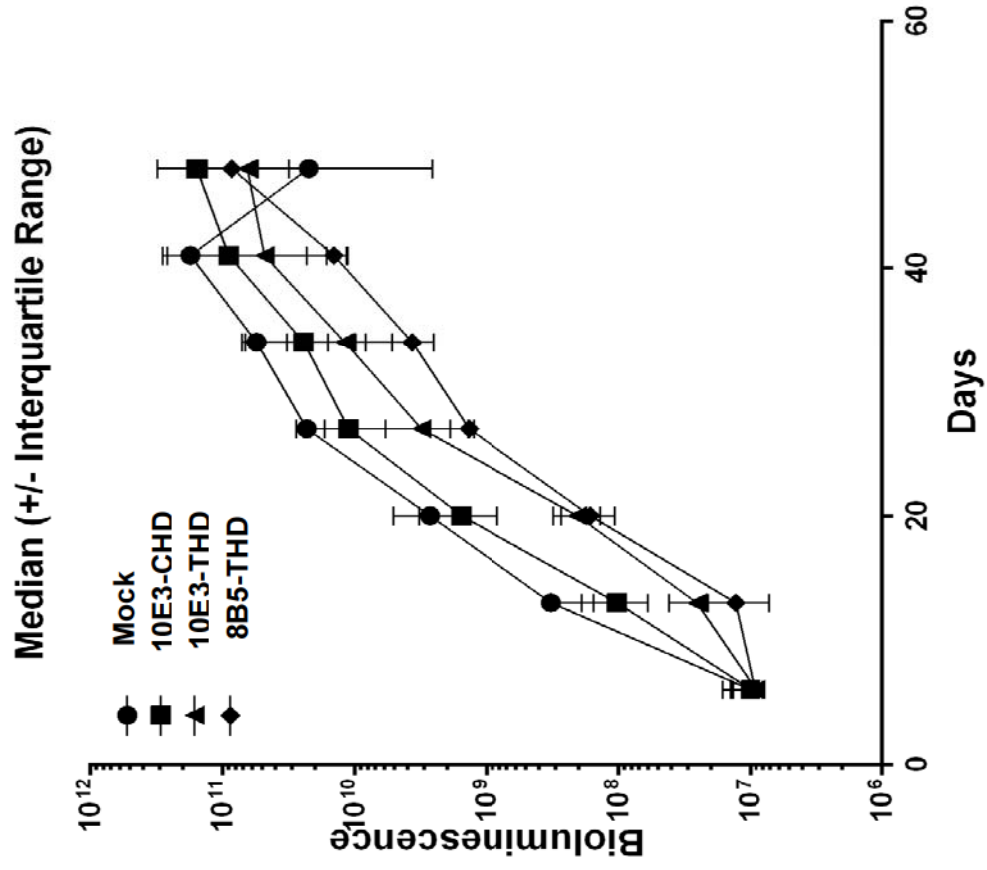


FIG. 10G

Day	Mock vs 10E3-CHD	Mock vs 10E3-THD	Mock vs 8B5-THD	10E3-THD vs 8B5-THD
6	0.756	0.657	0.690	0.959
13	0.067	0.0004	0.0002	0.028
20	0.777	0.0022	0.0020	0.639
27	0.158	<0.0001	<0.0001	0.042
34	0.200	0.0004	0.0001	0.142
41	0.376	0.0072	0.0009	0.054

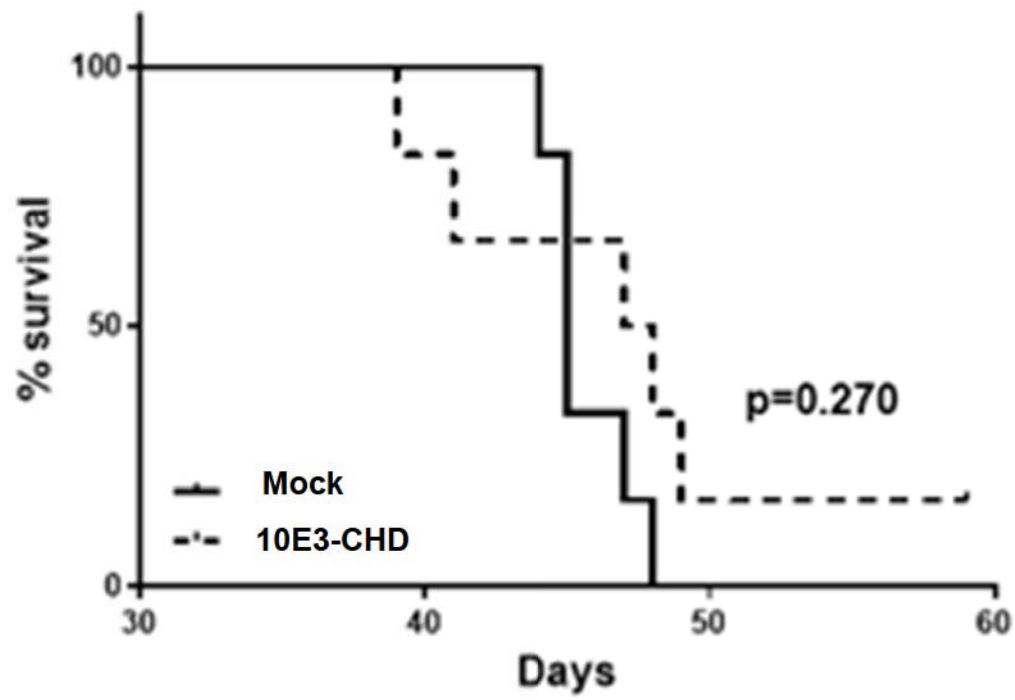
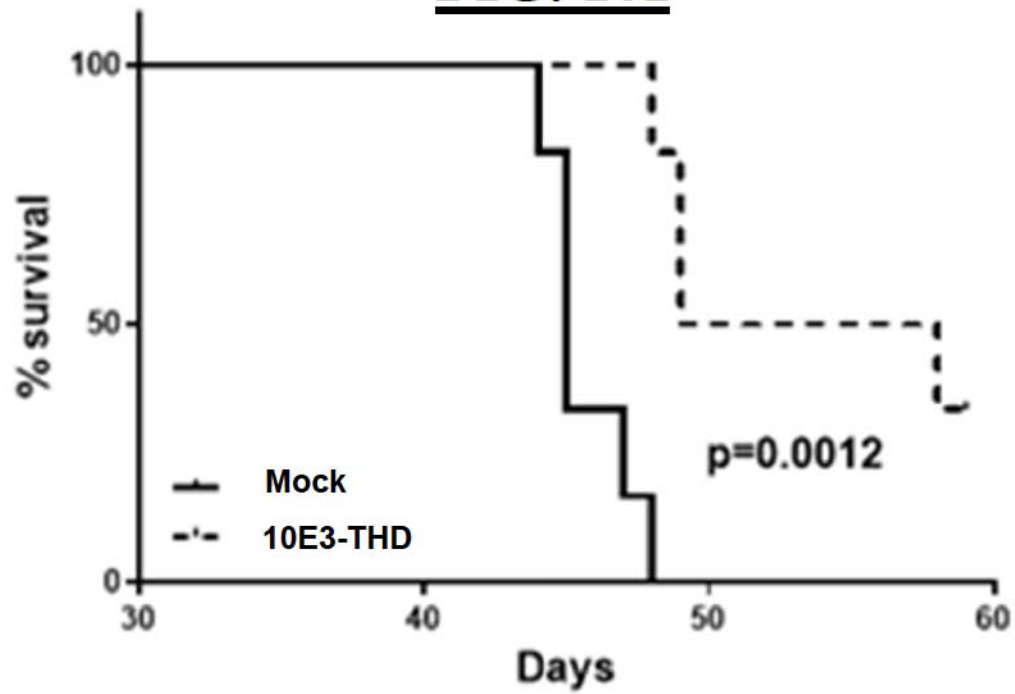
FIG. 10H**FIG. 10I**

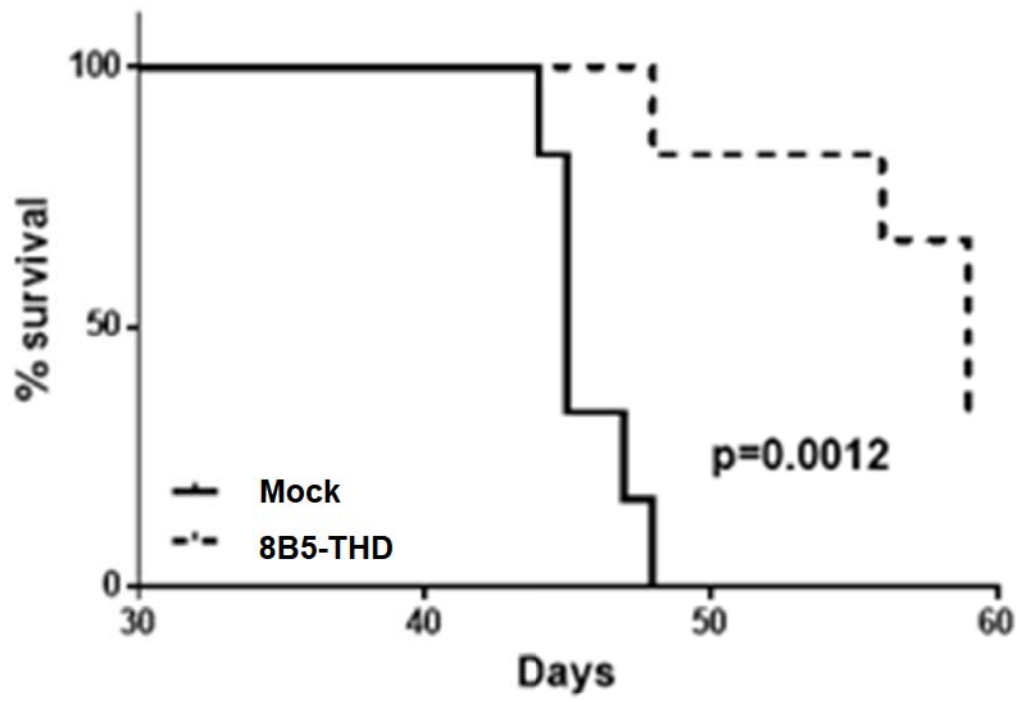
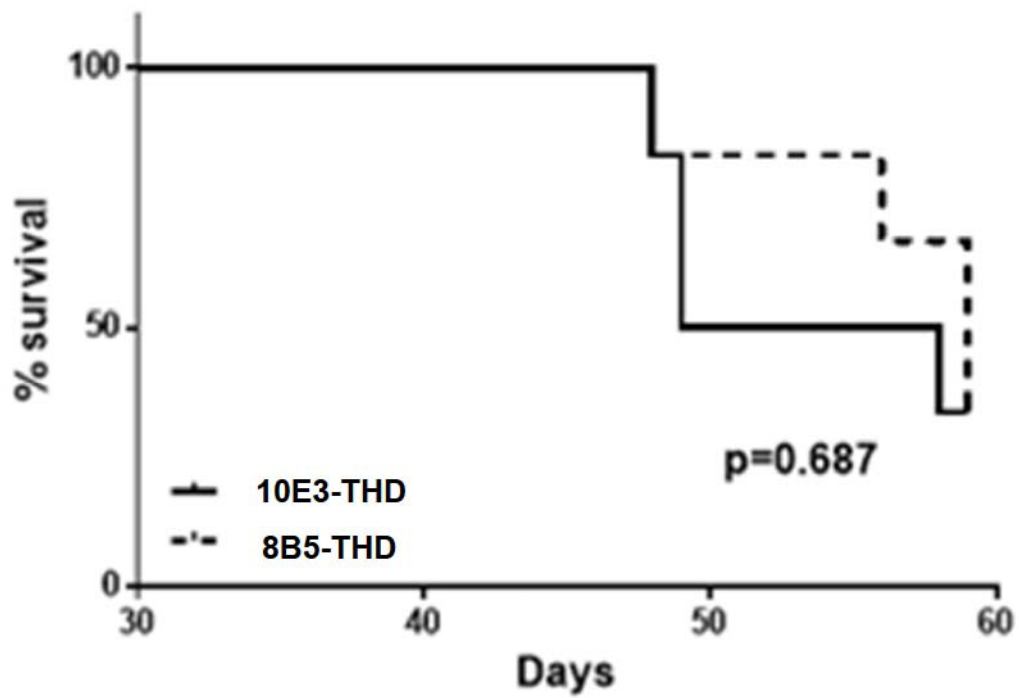
FIG. 10J**FIG. 10K**

FIG. 11A

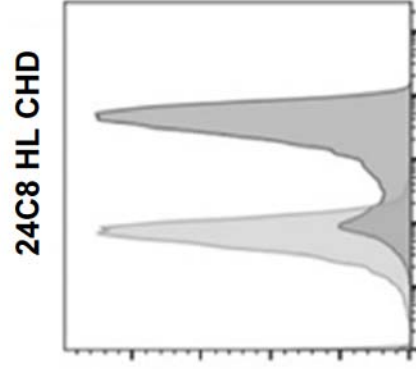
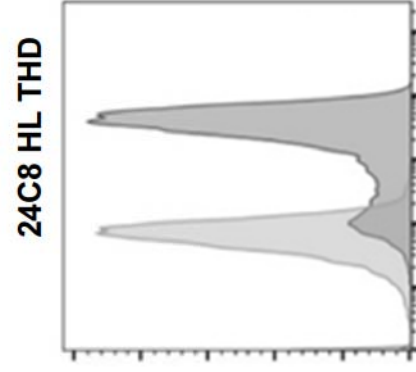


FIG. 11B



Protein L

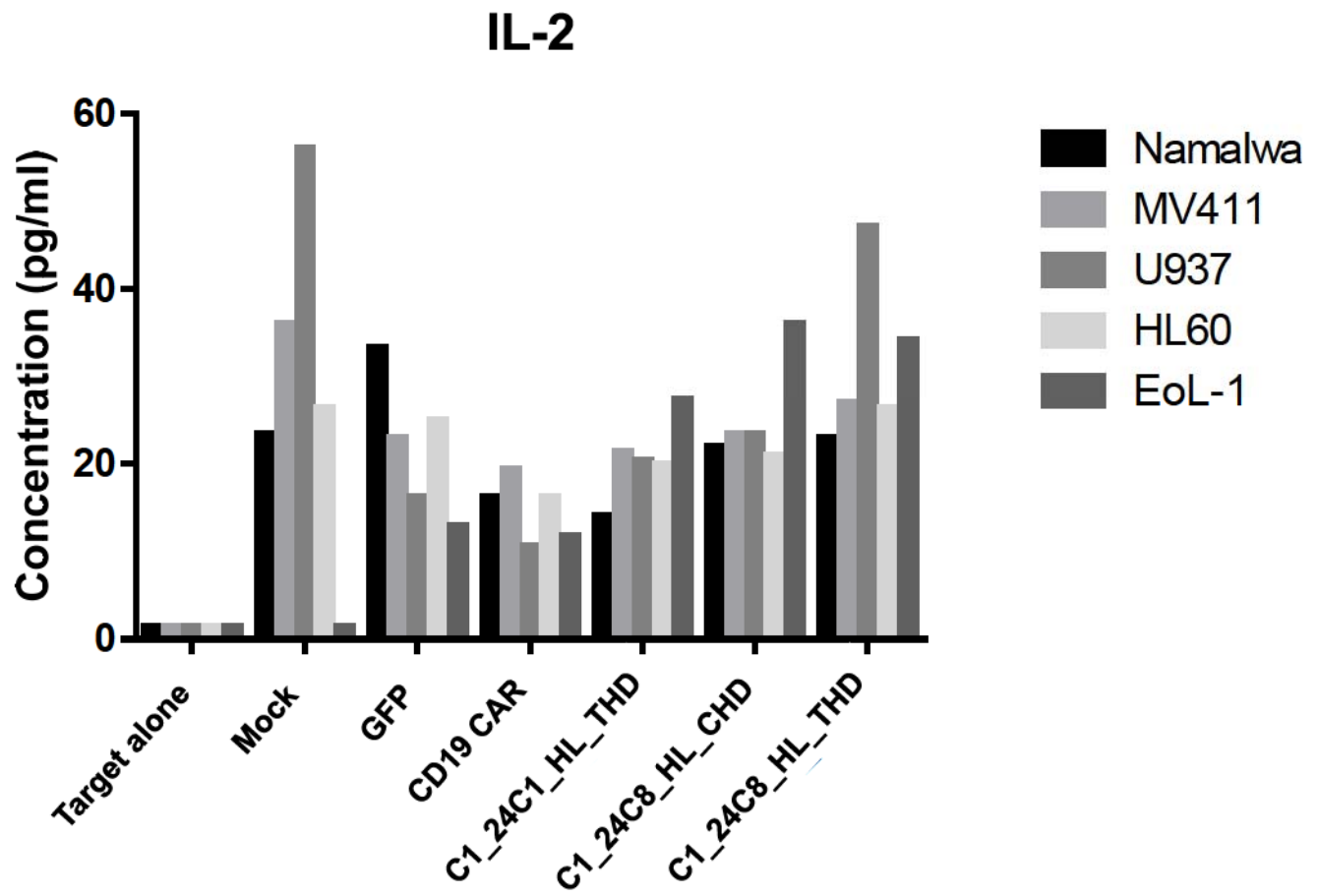
FIG. 12A

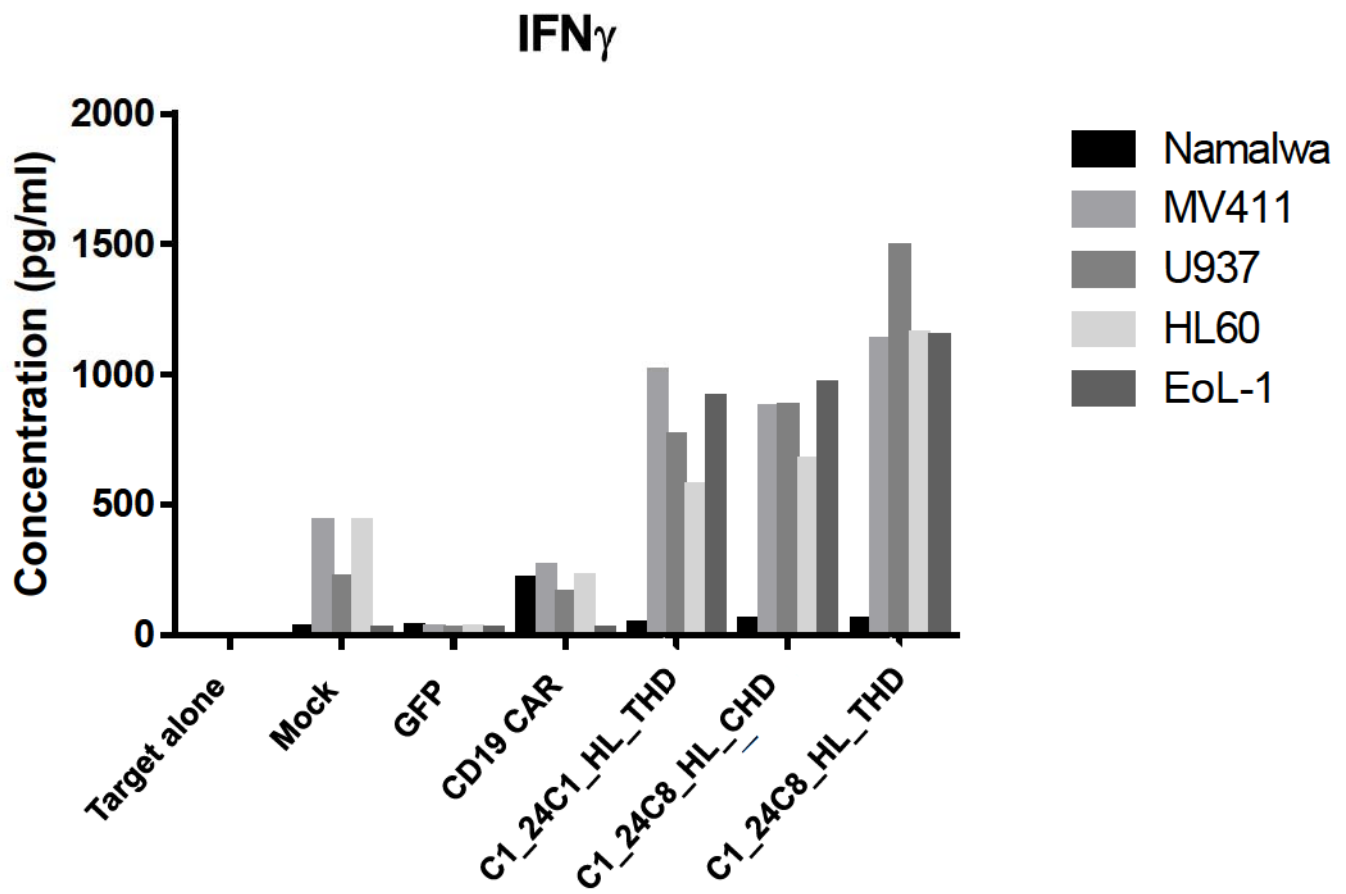
FIG. 12B

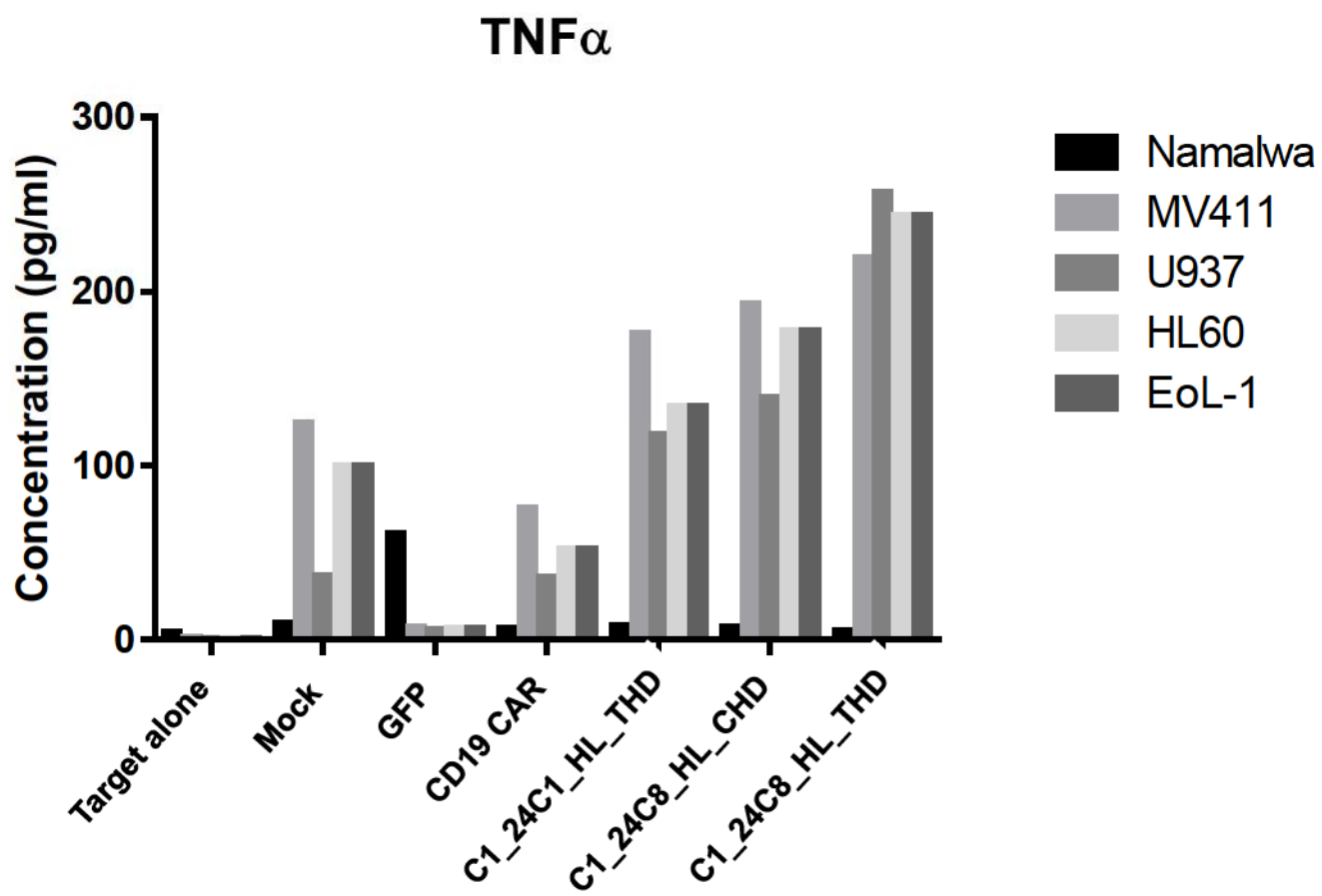
FIG. 12C

FIG. 13A

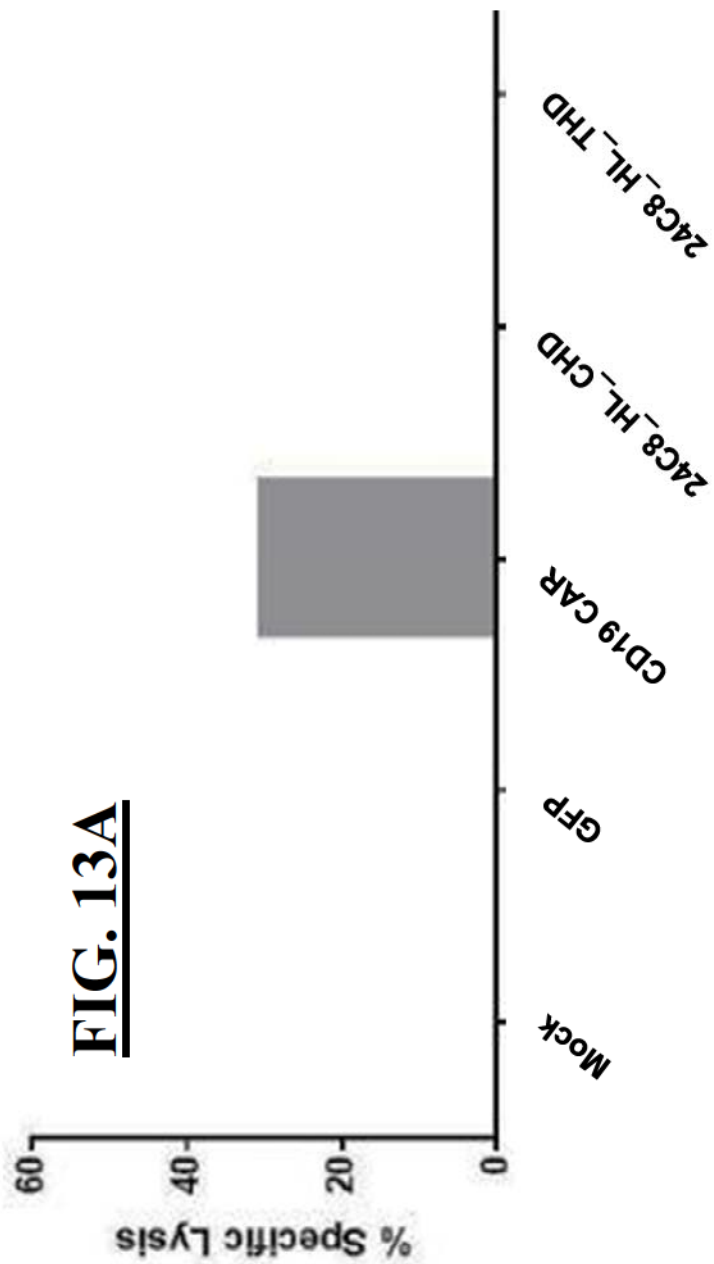


FIG. 13B

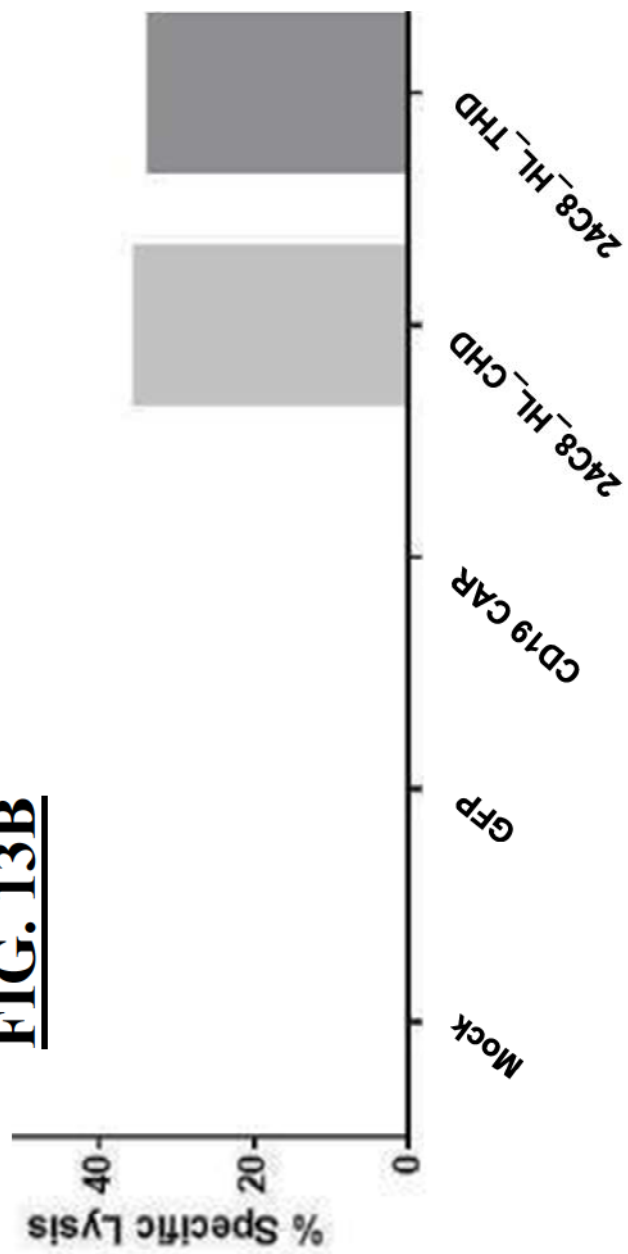


FIG. 13C

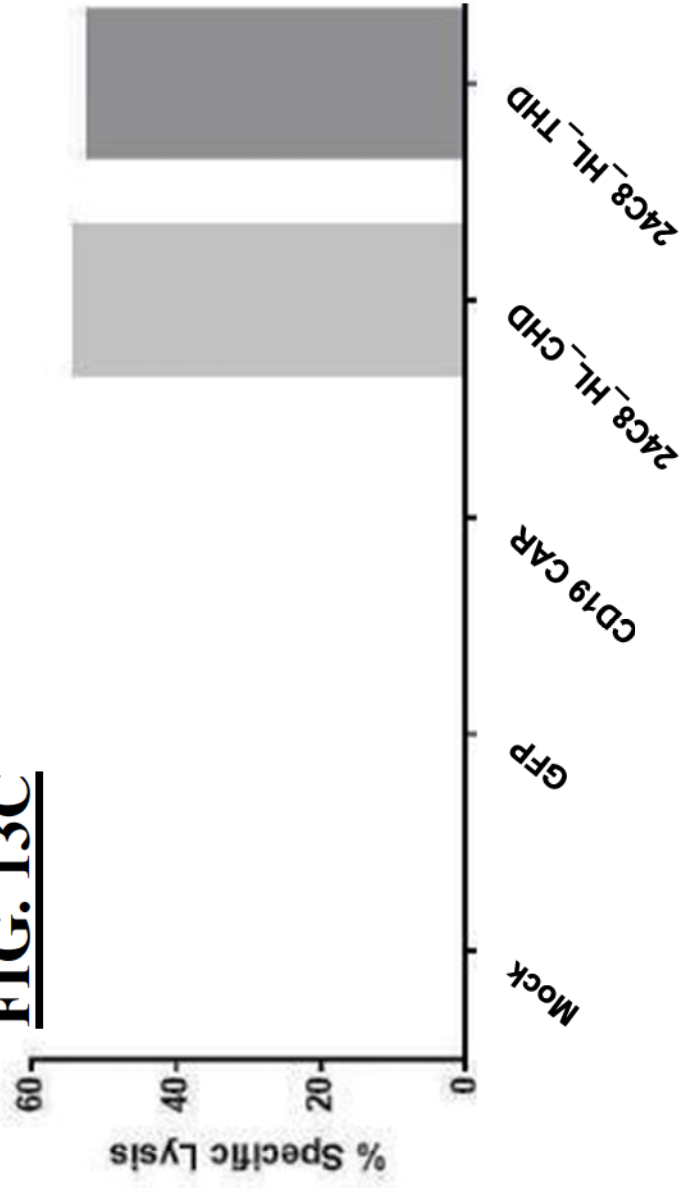


FIG. 13D

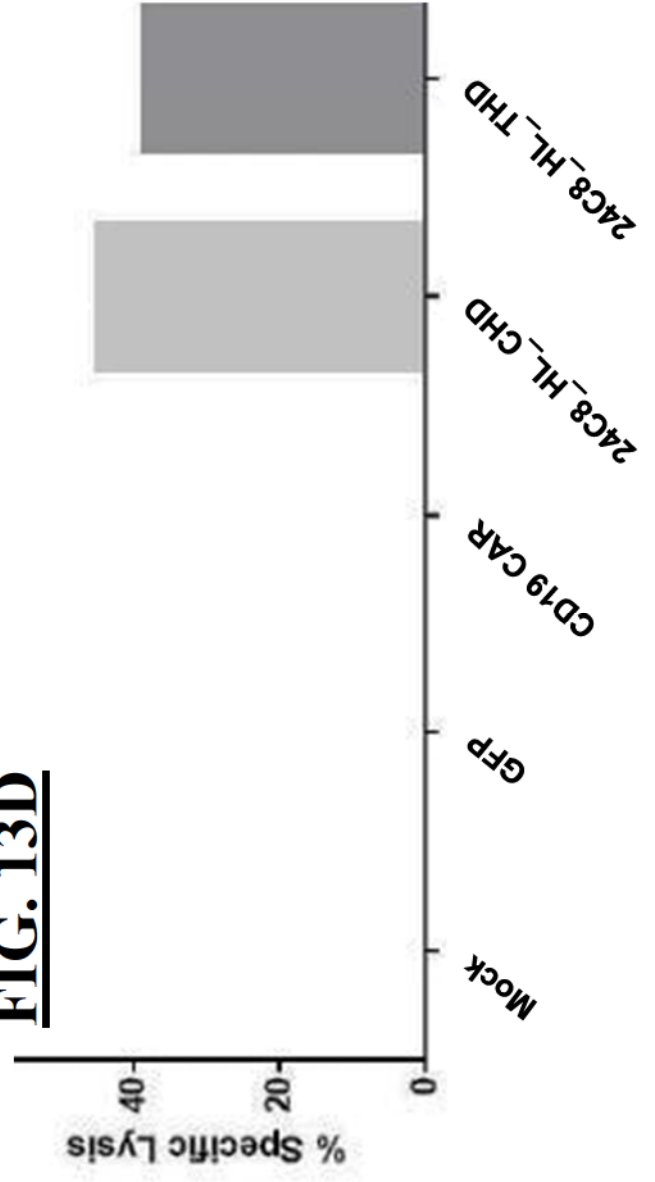


FIG. 13E

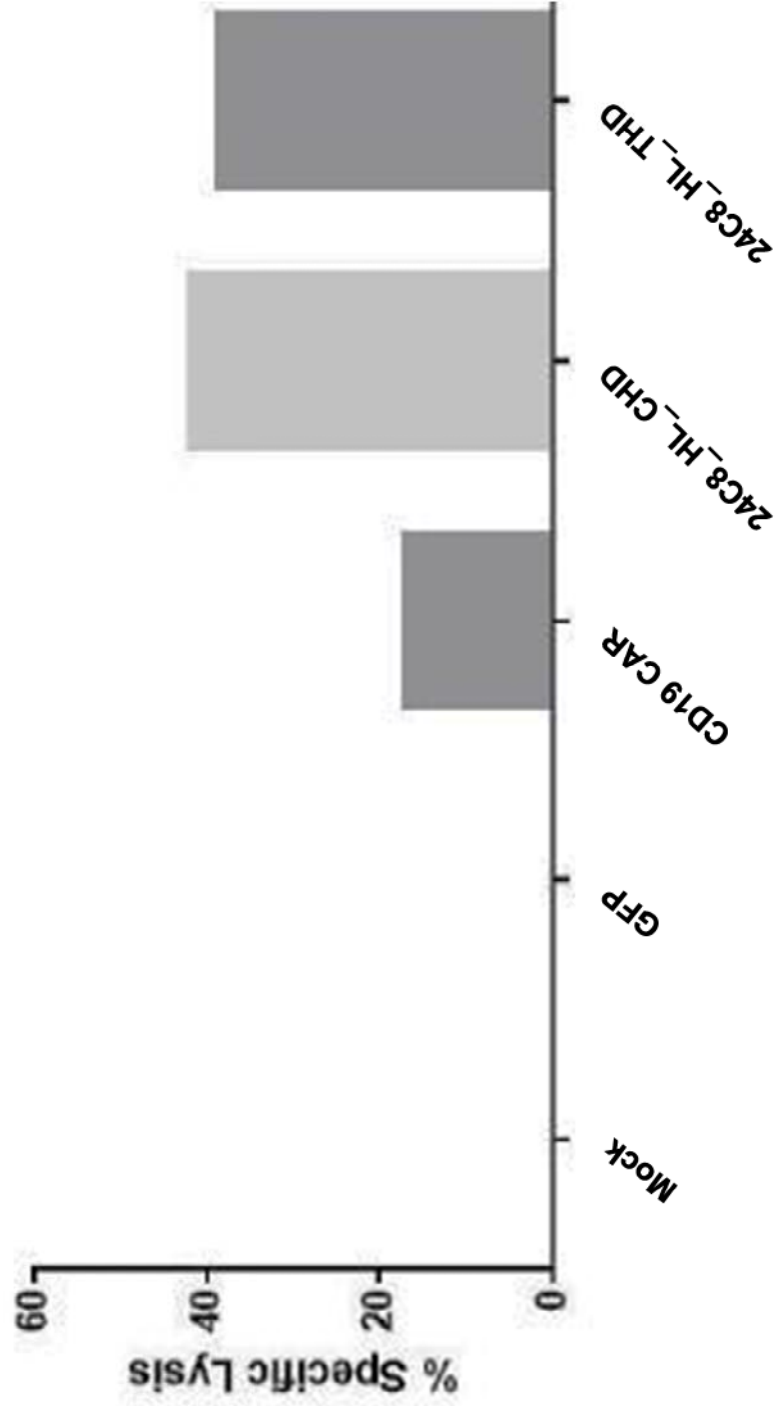


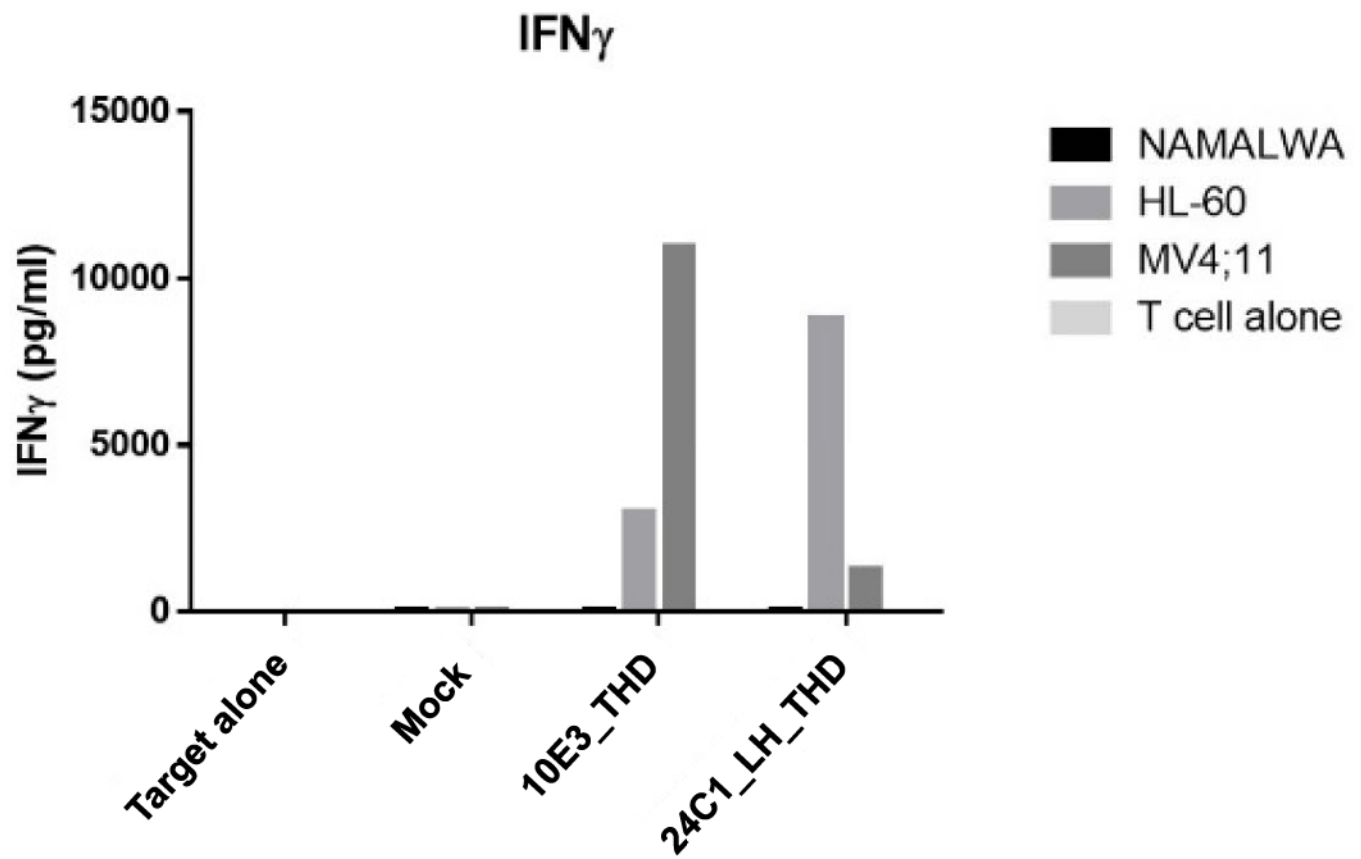
FIG. 14A

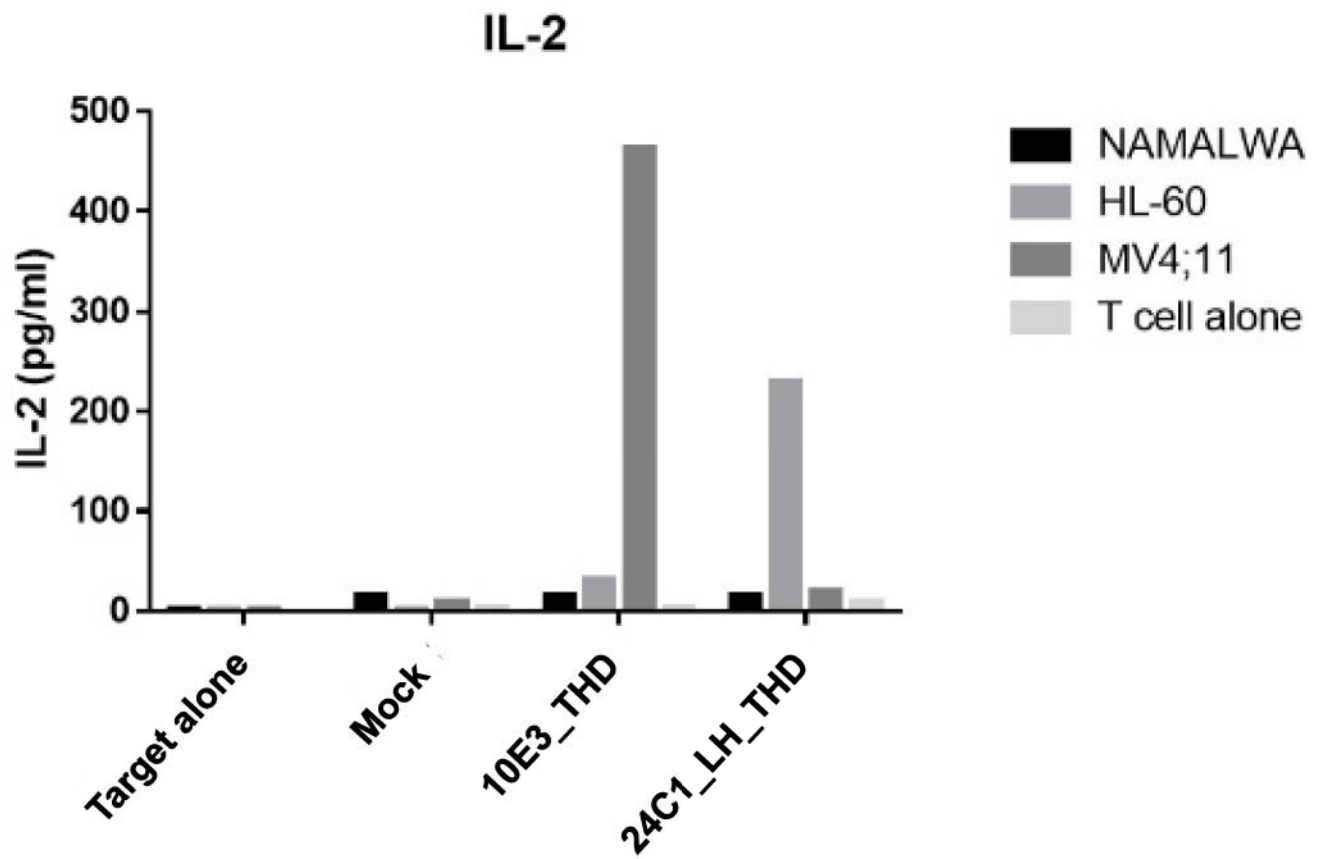
FIG. 14B

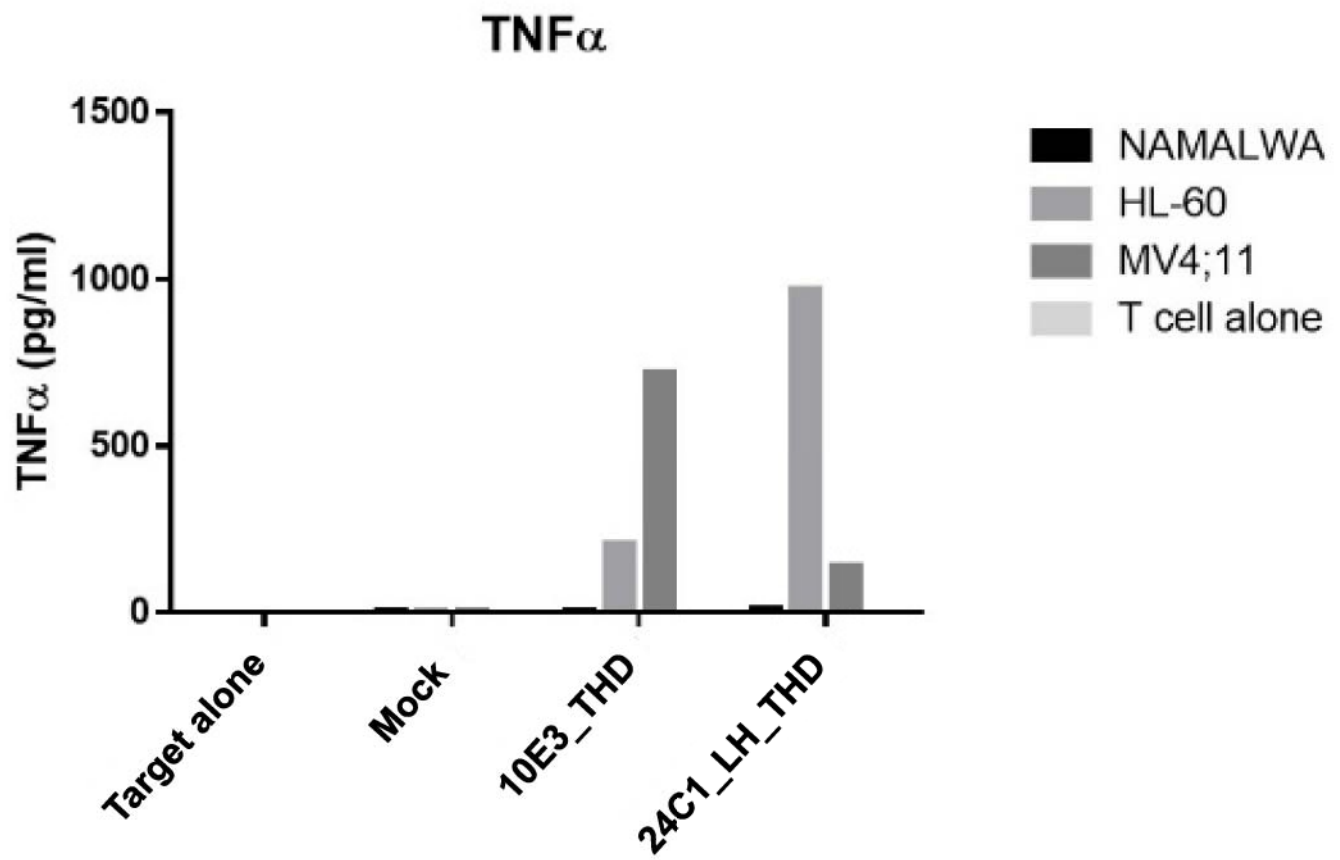
FIG. 14C

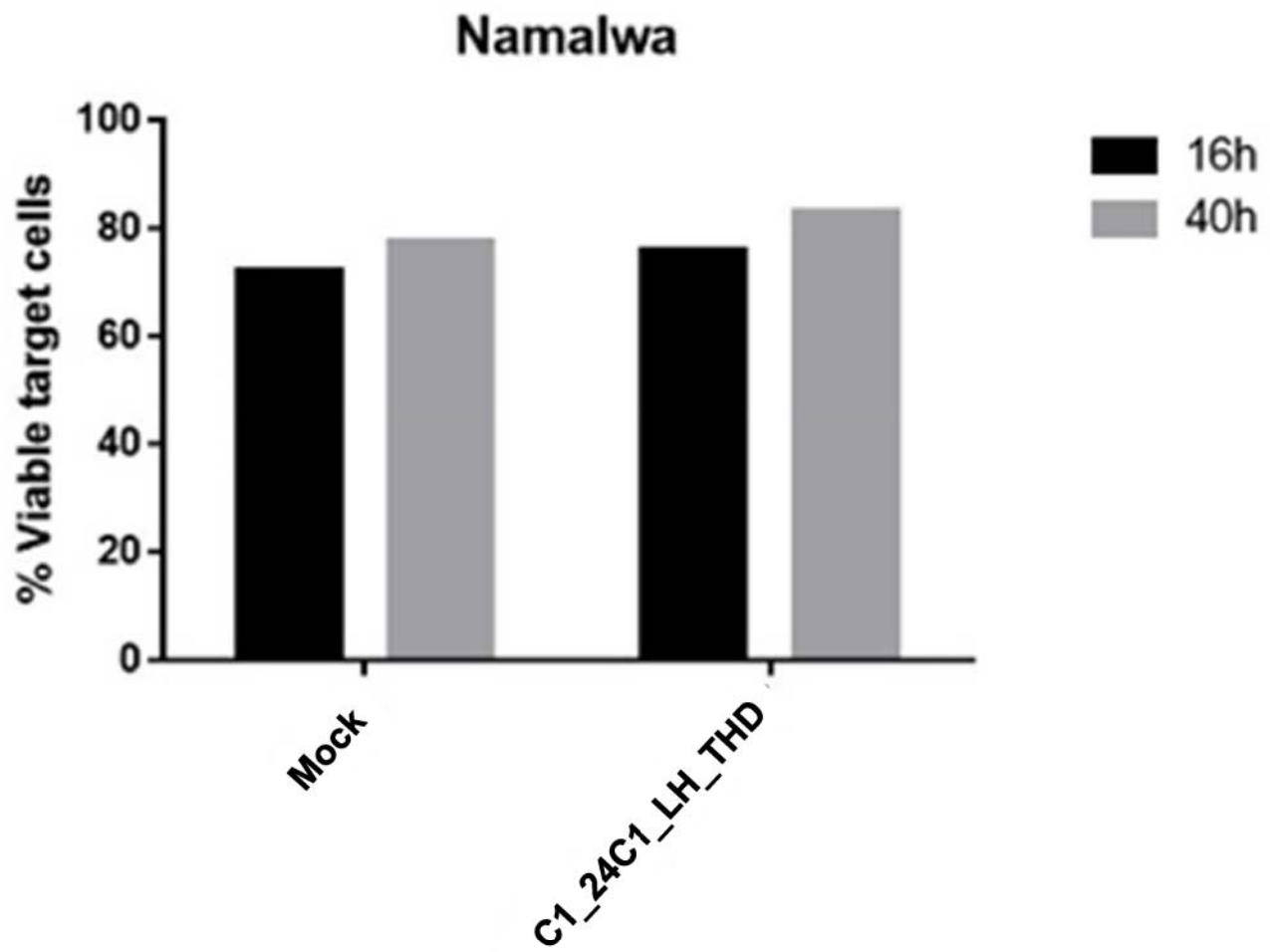
FIG. 15A

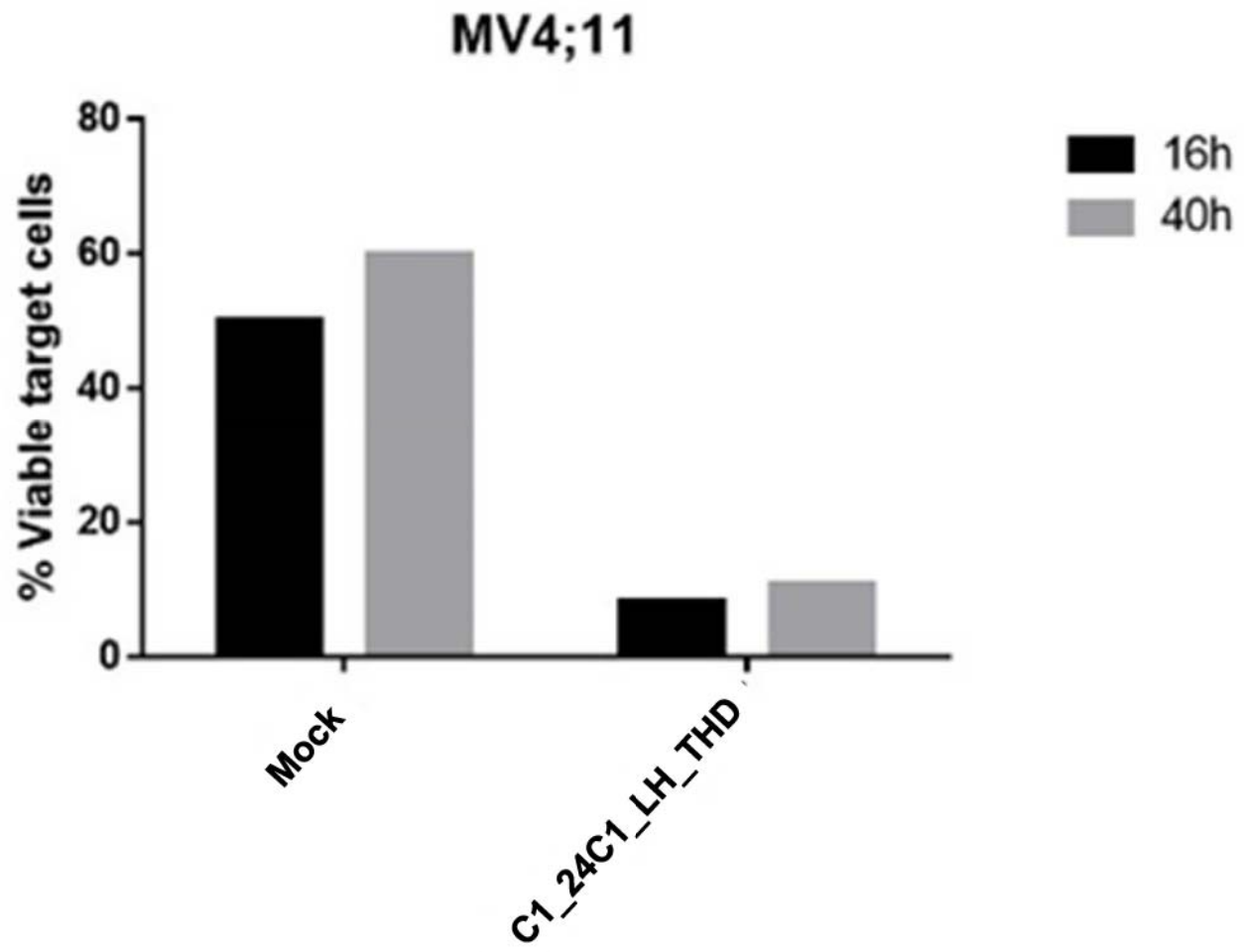
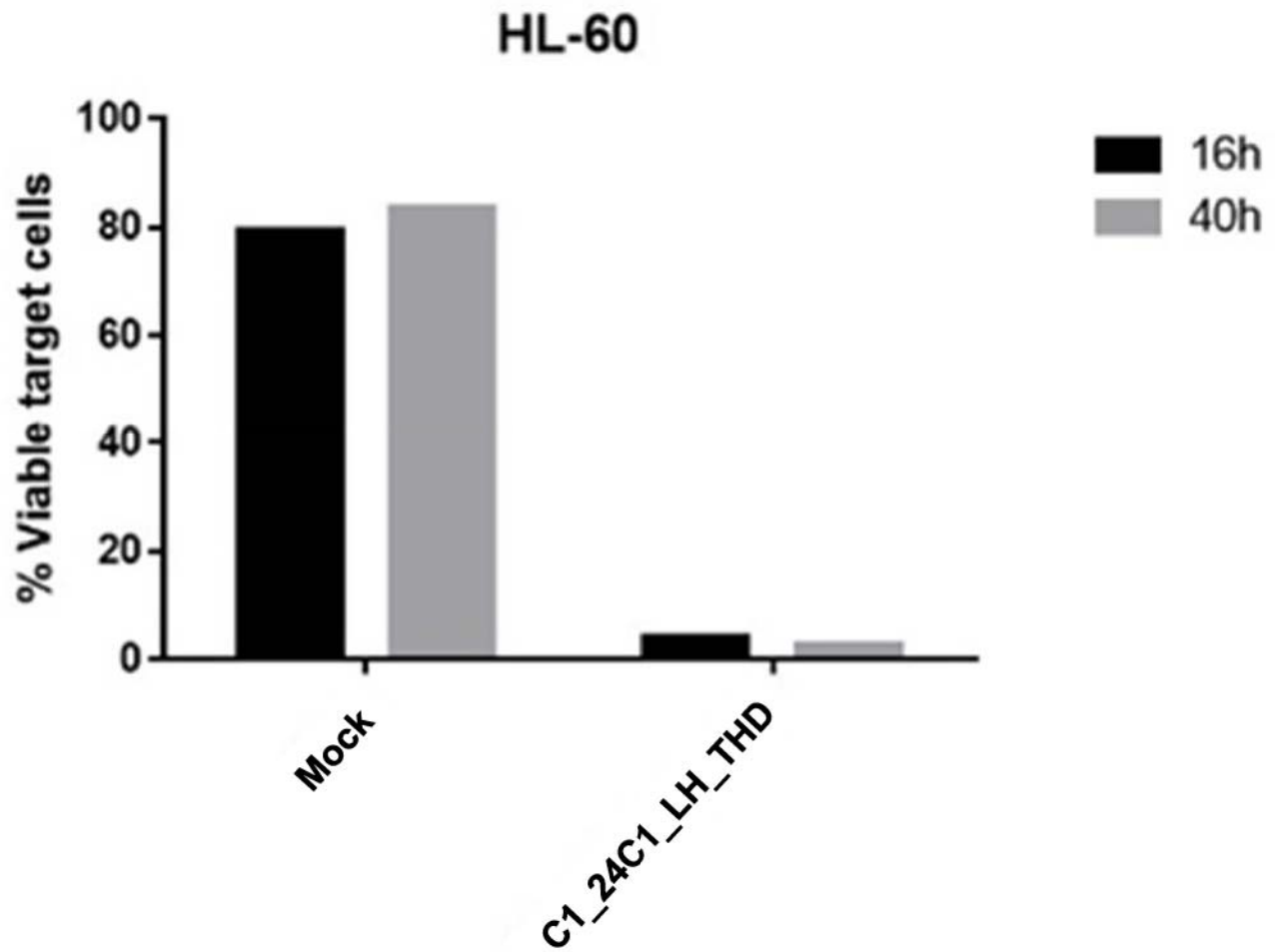
FIG. 15B

FIG. 15C

2017240667 23 Sep 2019

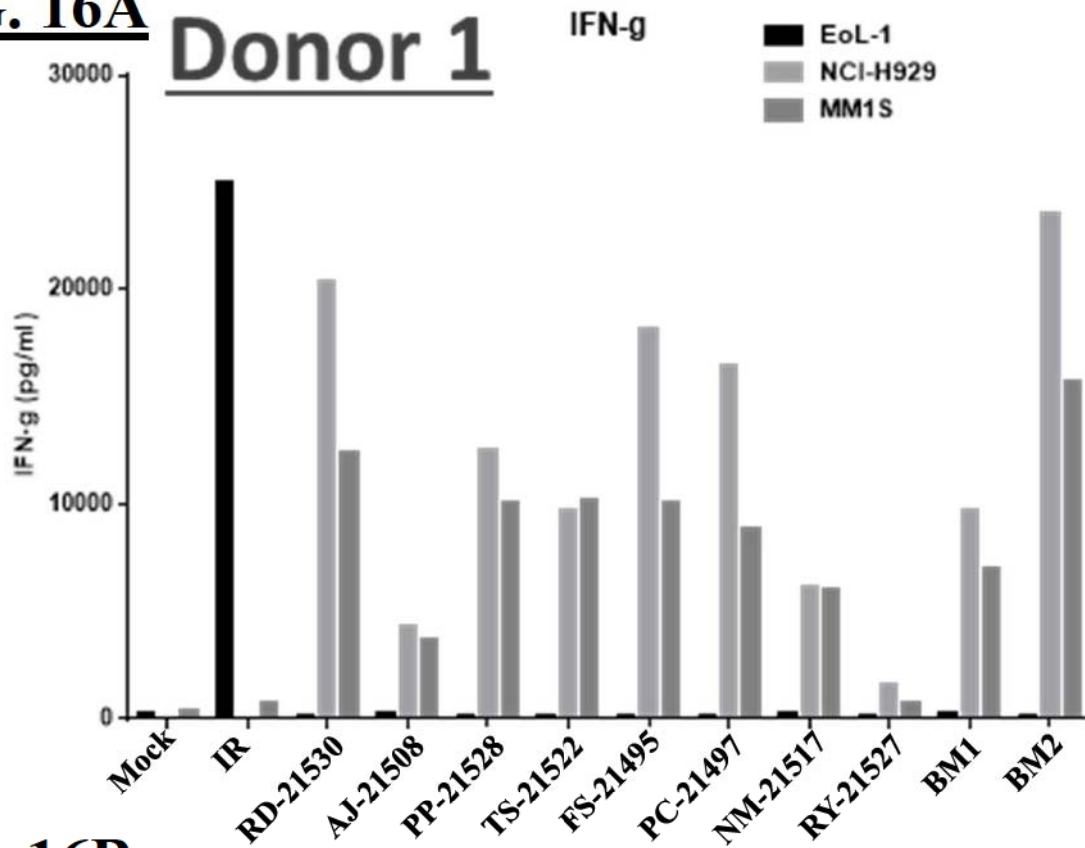
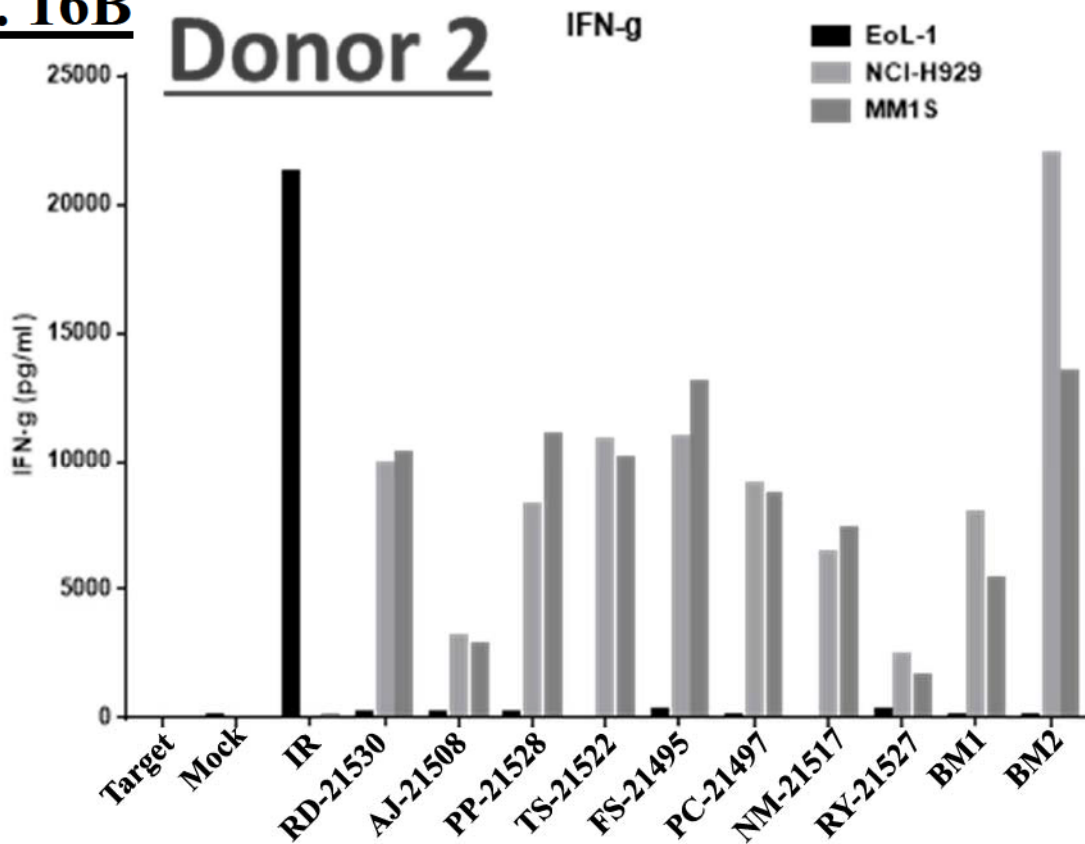
FIG. 16A**FIG. 16B**

FIG. 16C

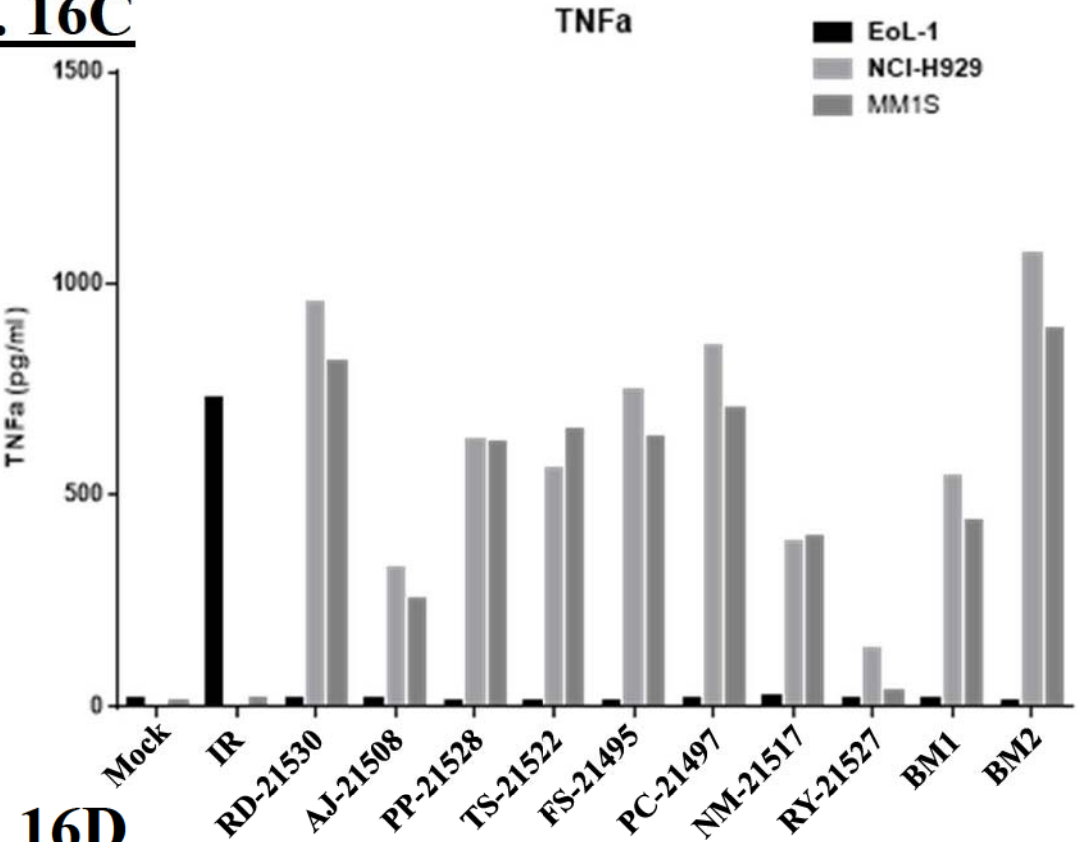


FIG. 16D

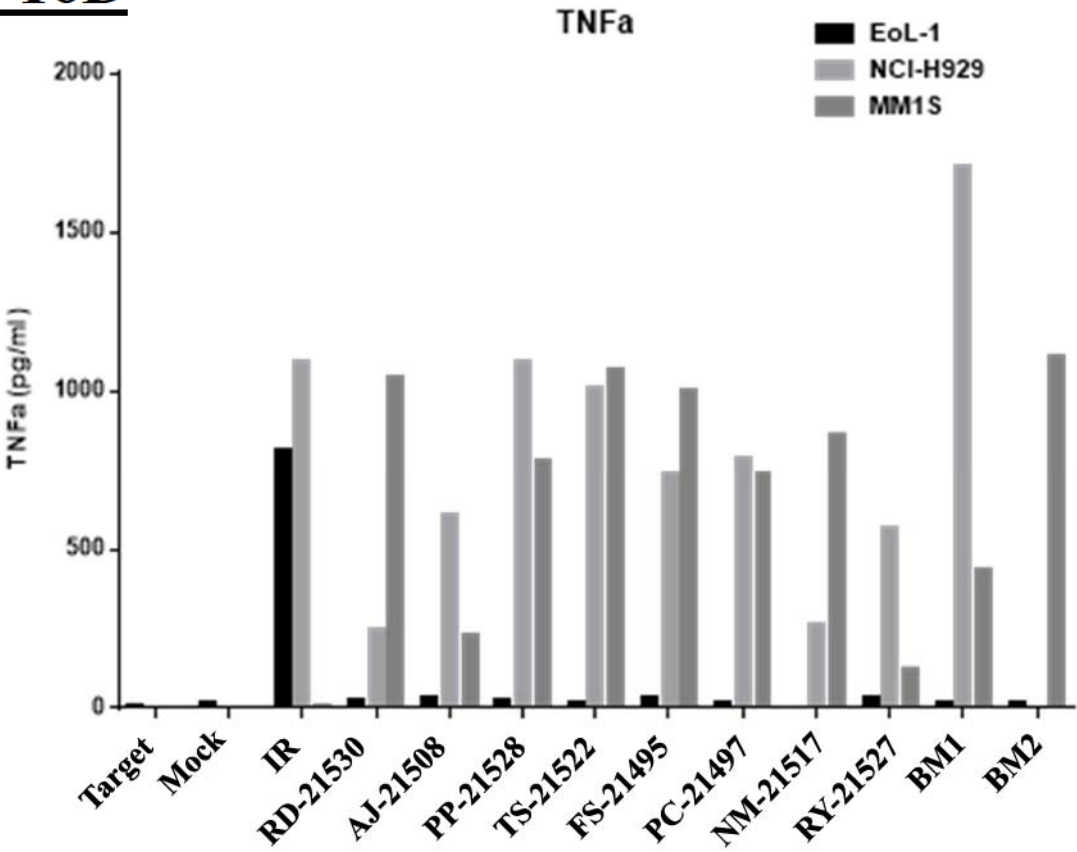


FIG. 16E

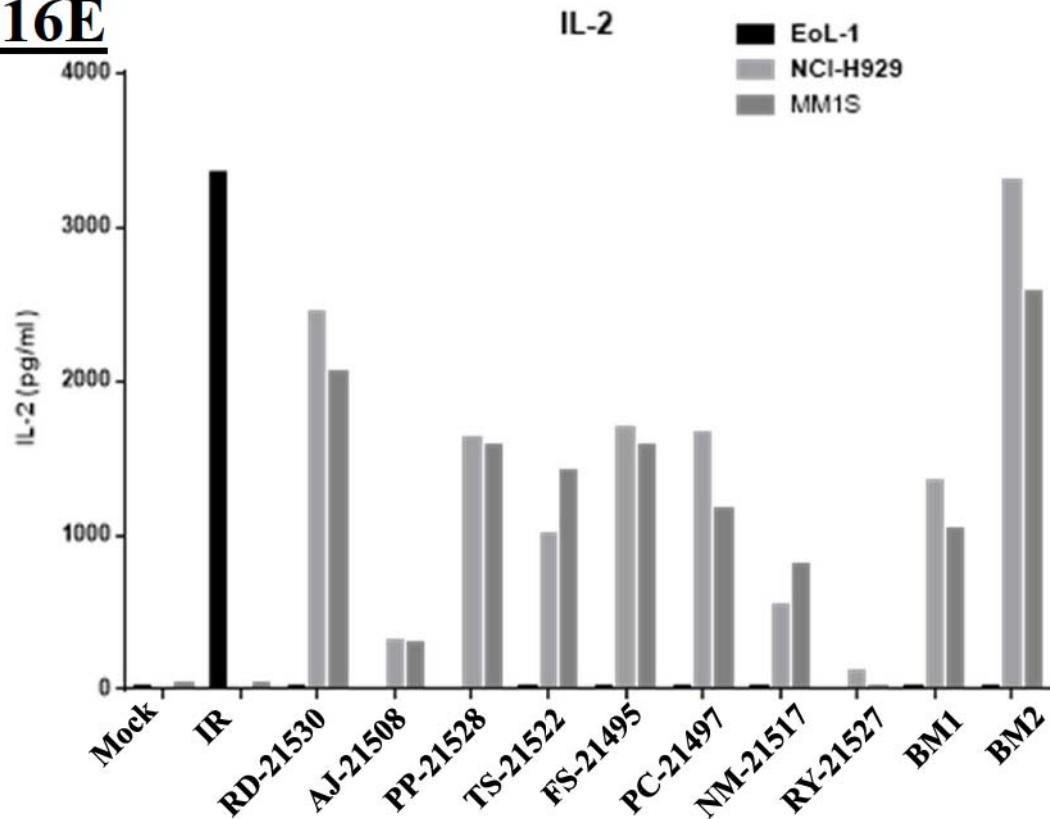


FIG. 16F

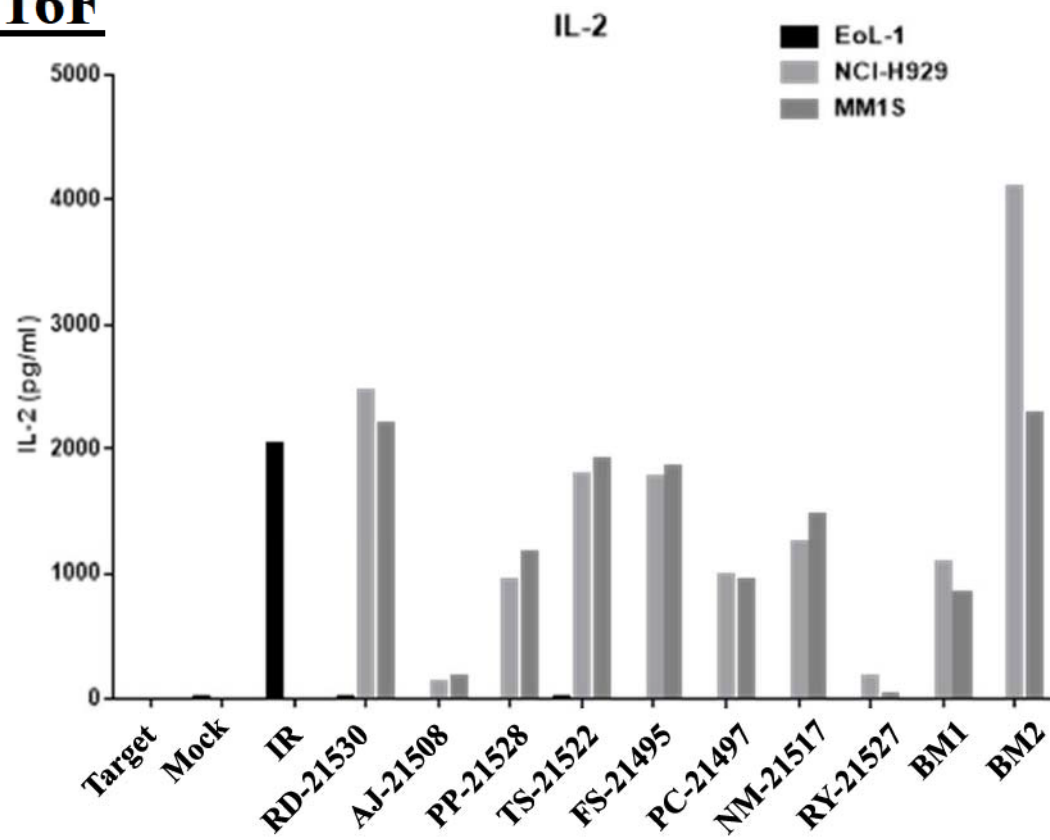


FIG. 17A

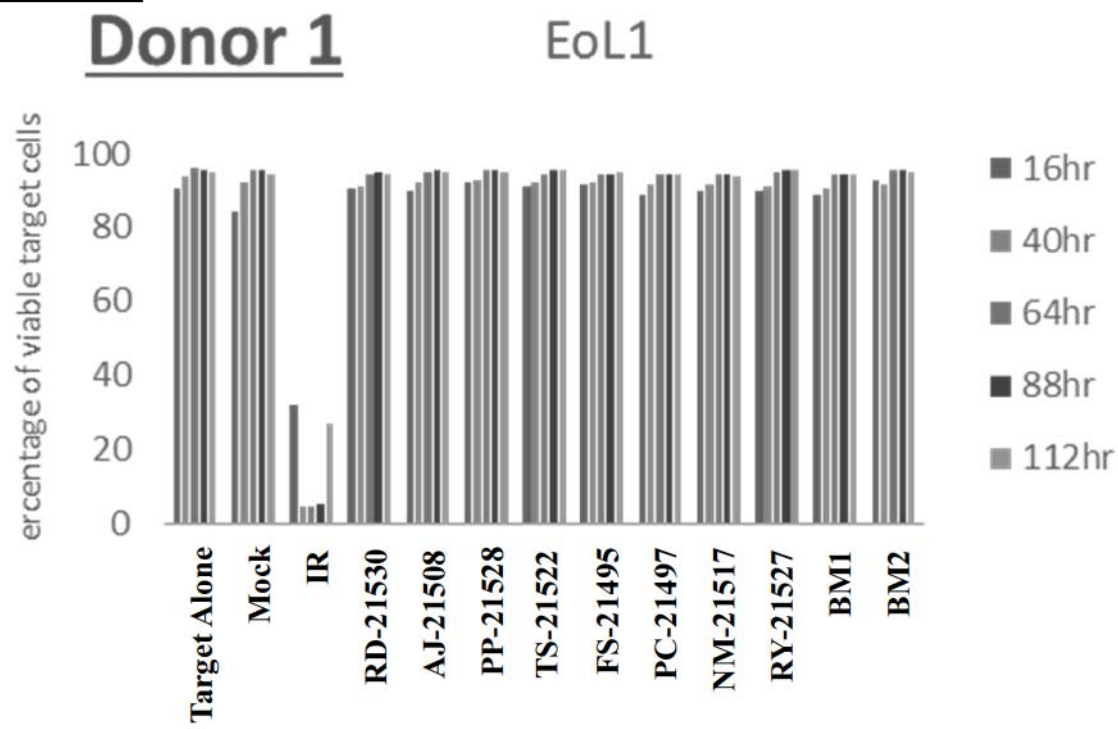


FIG. 17B

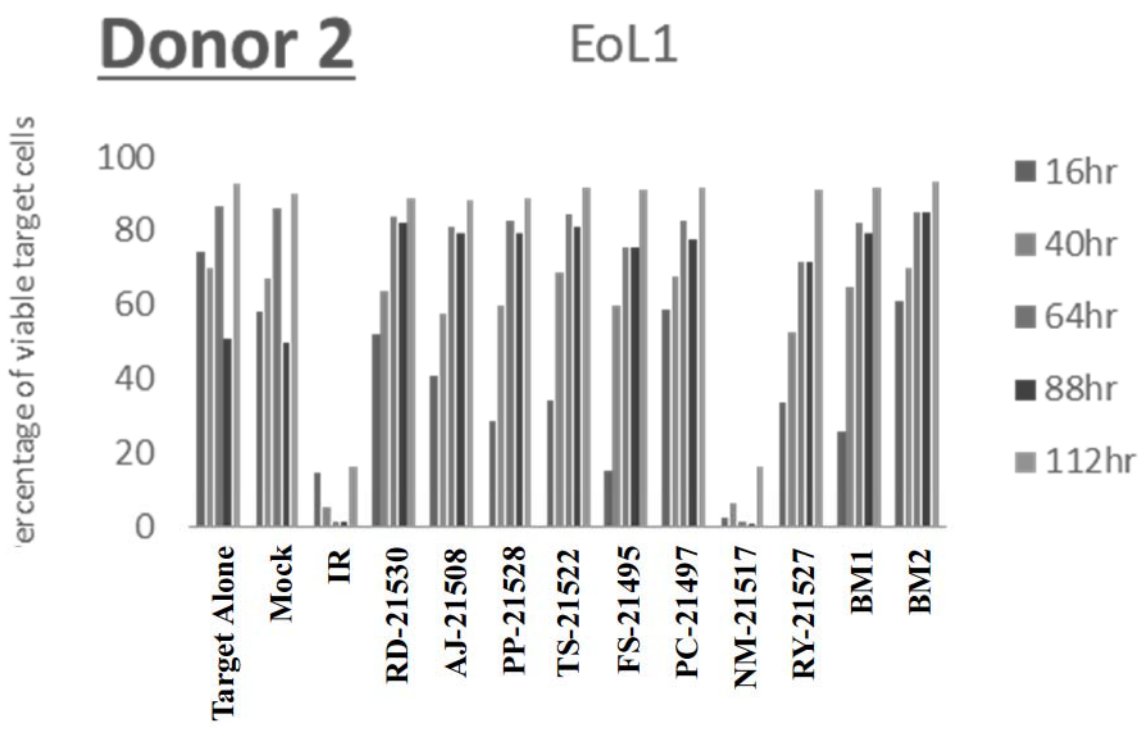


FIG. 17C

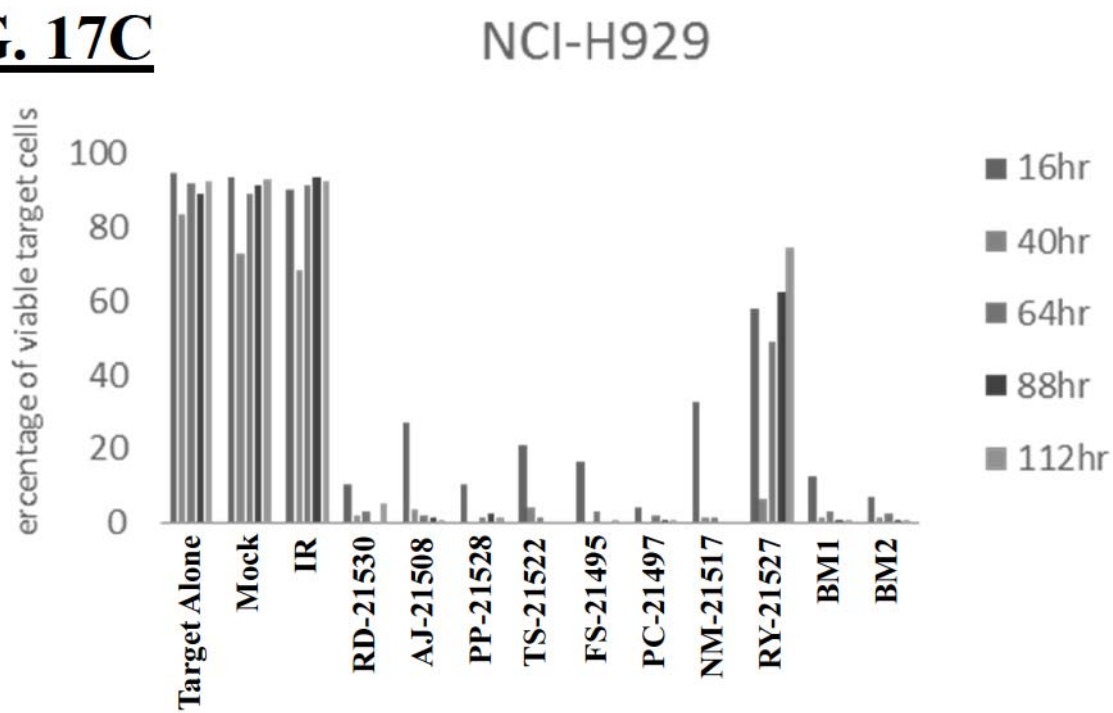


FIG. 17D

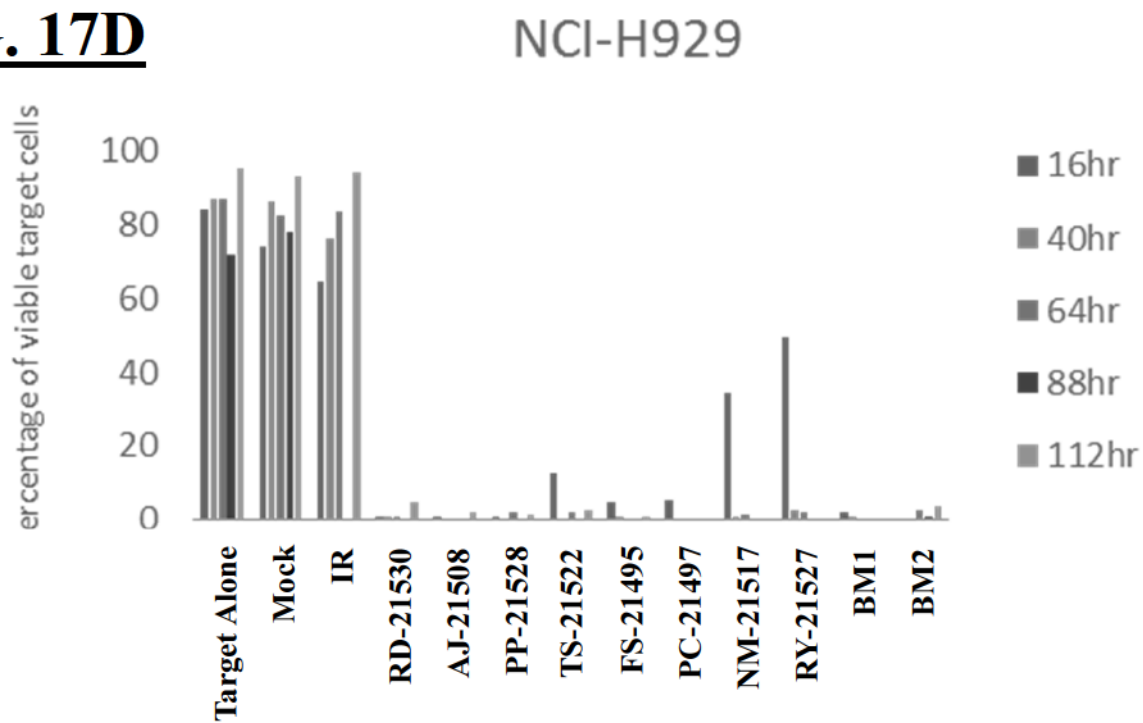


FIG. 17E

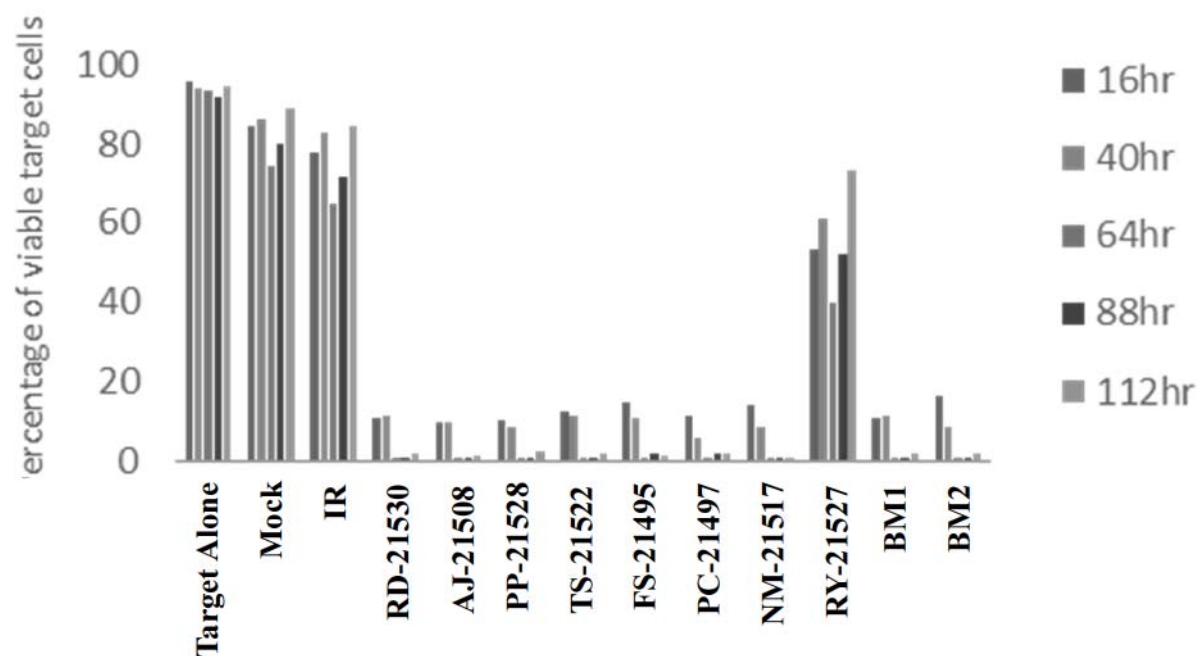


FIG. 17F

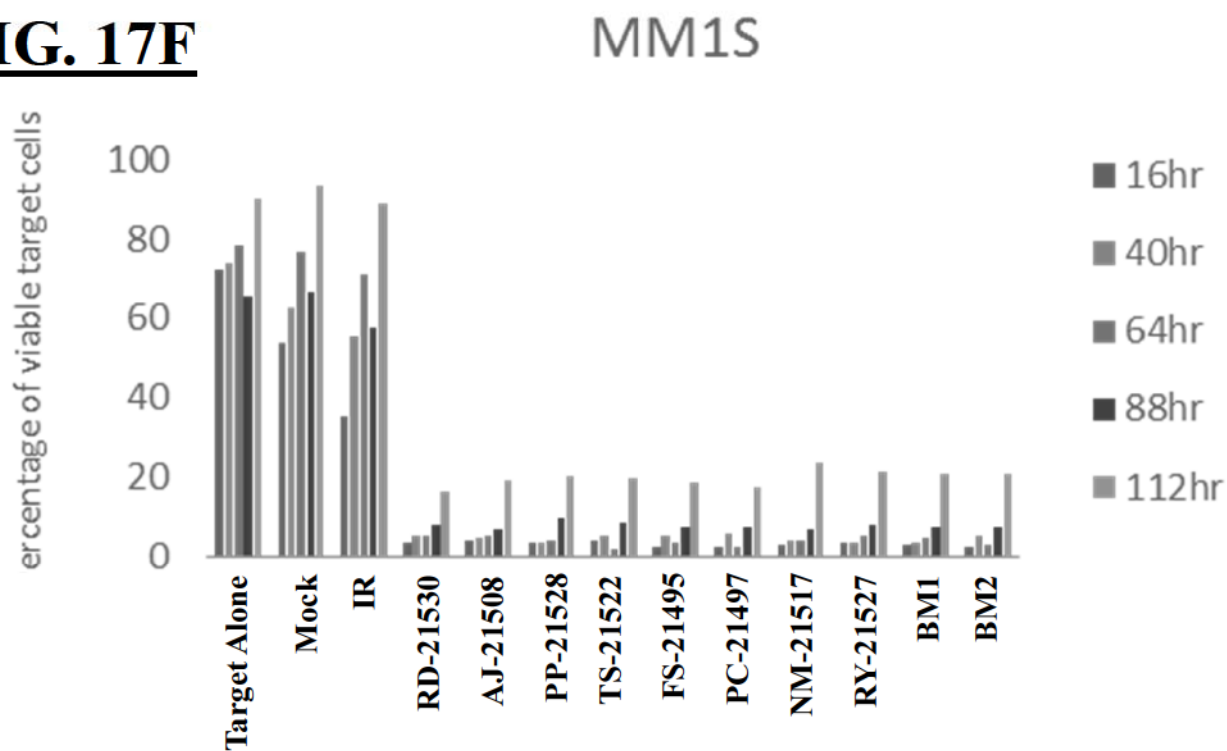


FIG. 18A

Donor 1

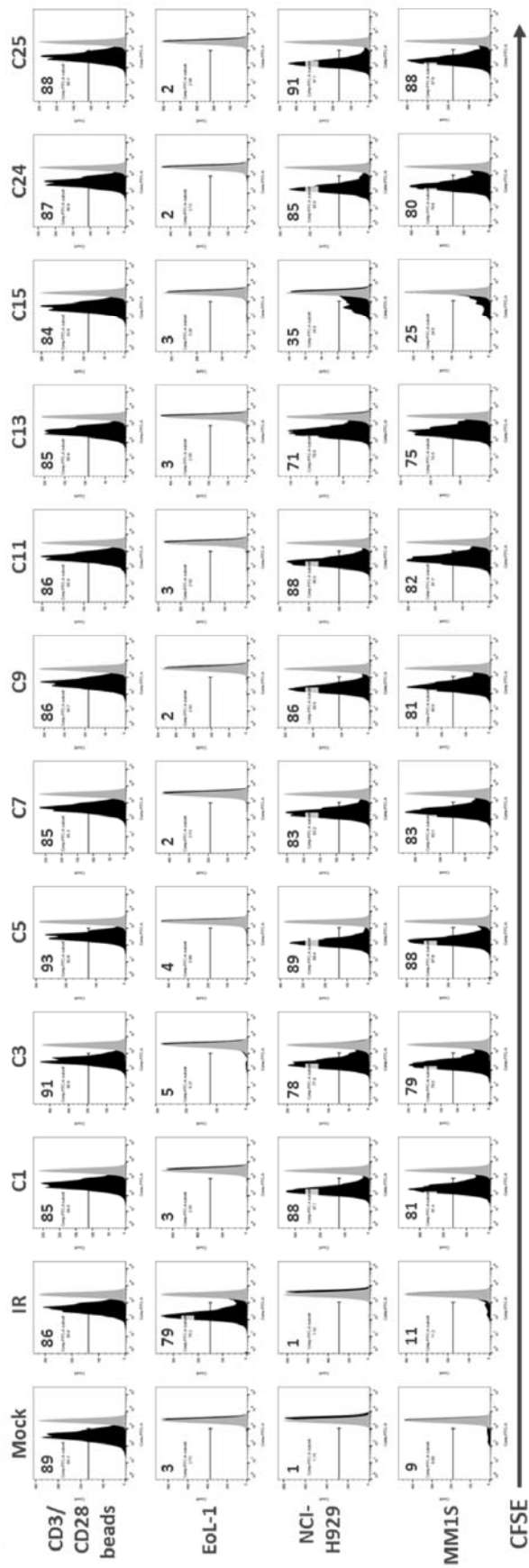
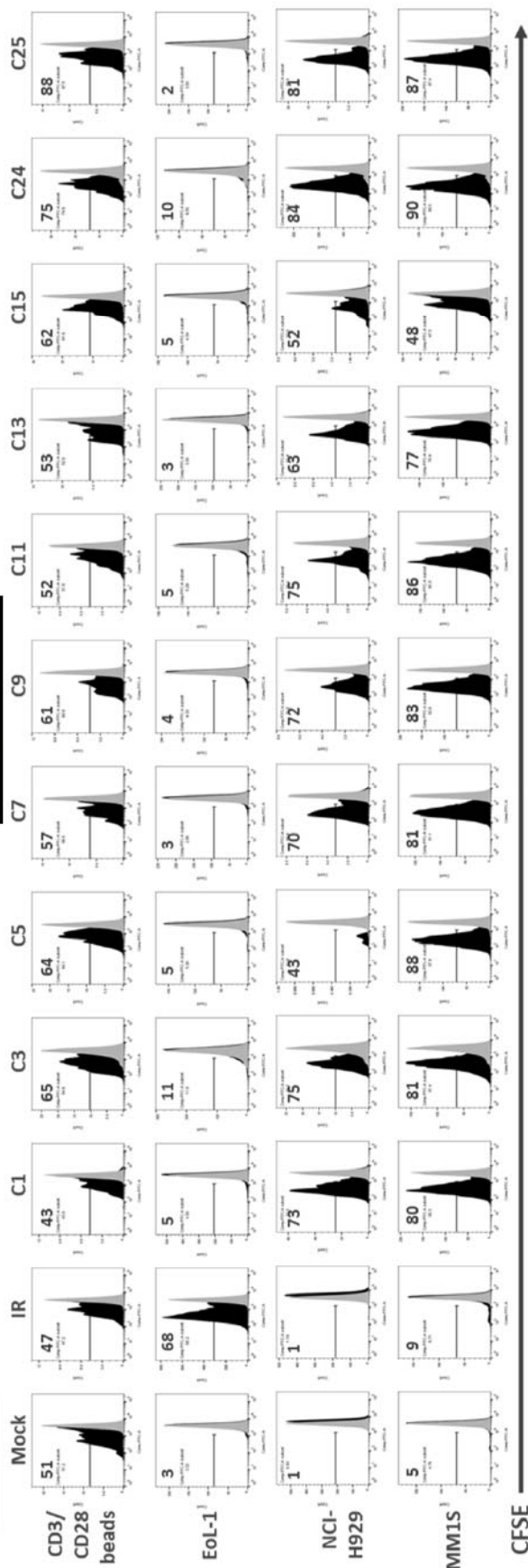
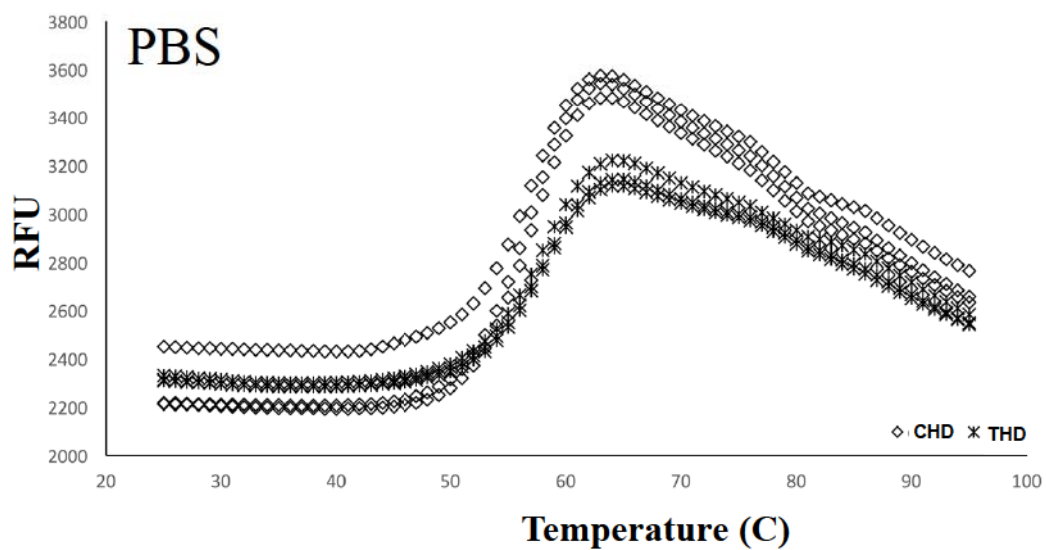
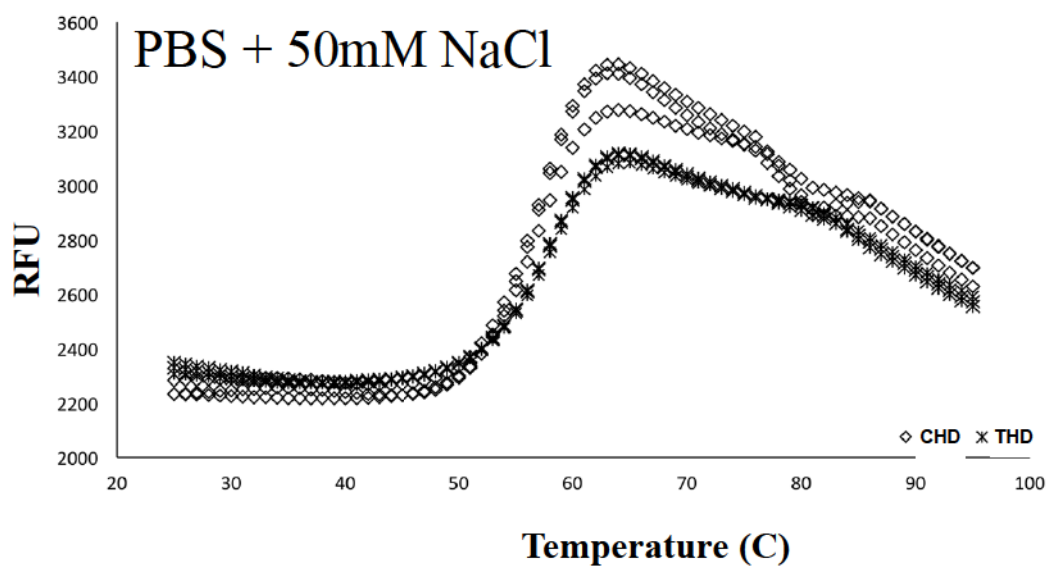


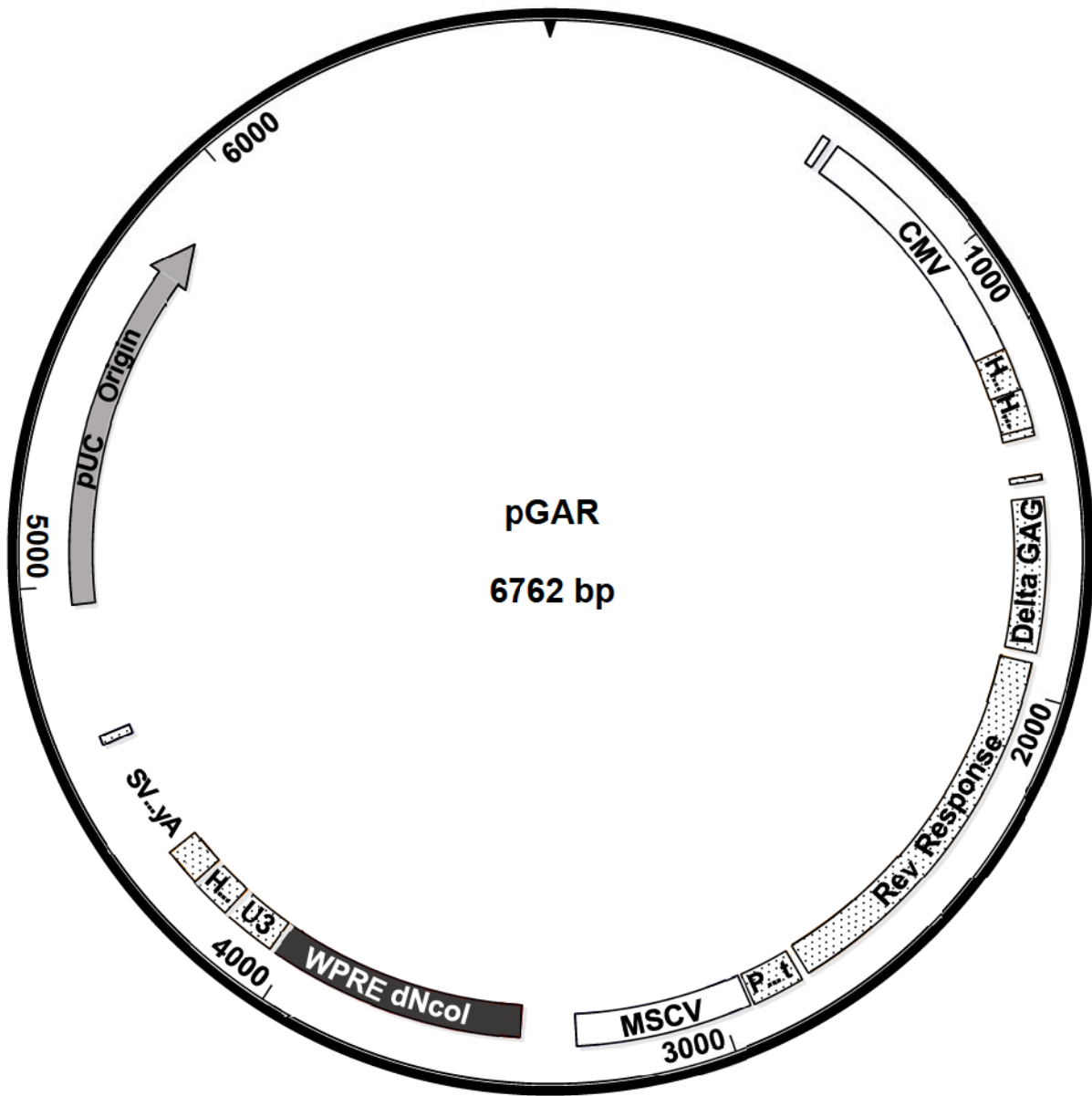
FIG. 18B

Donor 2



Unstimulated T cells ■ T cells + indicated stimulus

FIG. 19A**FIG. 19B**

**FIG. 20**

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<120> CHIMERIC ANTIGEN AND T CELL RECEPTORS AND METHODS OF USE

<130> K-1031.02US

<140> 15/475,681

<141> 2017-03-31

<150> 62/317,258

<151> 2016-04-01

<160> 284

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20 25 30

Asp Asn Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser
35 40 45

Arg Glu Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu
50 55 60

Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser
65 70 75 80

Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr
85 90 95

Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys
100 105 110

Lys Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser
115 120 125

Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
130 135 140

Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
145 150 155 160

Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
165 170 175

Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
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Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
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Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
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tcacccttgt tccctgggtcc atccaagcca 90

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polypeptide

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His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro
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gcttttataa tcttctgggt t 81

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Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
20 25

<210> 6

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 Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
 20 25 30
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 35 40

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cgggaccctg agatgggtgg caaaccaaga cgaaaaaacc cccaggagggg tctctataat      180
gagctgcaga aggataagat ggctgaagcc tattctgaaa taggcatgaa aggagagcgg      240
agaaggggaa aagggcacga cggtttgtac caggggactca gcactgctac gaaggatact      300
tatgacgctc tccacatgca agccctgcca cctagg                                     336

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Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
 20 25 30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
 35 40 45

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
 50 55 60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
 65 70 75 80

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
 85 90 95

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 100 105 110

31 Jul 2019
2017240667

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<213> Artificial Sequence

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oligonucleotide

<220>
<223> Signal (leader) Peptide

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ccg 63

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peptide

<220>
<223> Signal (leader) Peptide

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His Ala Ala Arg Pro
20

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peptide

<220>
<223> Linker

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

<210> 13

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1 5

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<220>

<223> VH CDR1

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Phe Thr Phe Ser Ser Tyr
1 5

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<223> VH CDR1

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Gly Tyr Thr Phe Thr Ser Tyr

2017240667 31 Jul 2019

1 5

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1 5

<210> 18
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1 5 10

31 Jul 2019 2017240667

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<210> 23

<211> 6

<212> PRT

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<220>

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<220>

<223> VH CDR2

<400> 23

Asn	Pro	Gly	Gly	Gly	Ser
1				5	

<210> 24

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<223> VH CDR2

<400> 24

Ser	Tyr	Ser	Gly	Ser
1			5	

<210> 25

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<223> VH CDR2

<400> 25

Ser Ser Ser Ser Ser Thr
1 5

<210> 26

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<223> VH CDR2

<400> 26

Ser Tyr Asp Gly Ser Asn
1 5

<210> 27

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<223> VH CDR2

<400> 27

Ile Pro Ile Phe Gly Thr
1 5

<210> 28

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<223> VH CDR2

<400> 28

Ser Tyr Asp Gly Ser Asn
1 5

<210> 29

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<223> VH CDR3

<400> 29

Ala Glu Met Gly Ala Val Phe Asp Ile
1 5

<210> 30

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<223> VH CDR3

<400> 30

Asp Gly Thr Tyr Leu Gly Gly Leu Trp Tyr Phe Asp Leu
1 5 10

<210> 31

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<223> VH CDR3

<400> 31
Glu Ser Trp Pro Met Asp Val
1 5

<210> 32
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<223> VH CDR3

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

<210> 33
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<223> VH CDR3

<400> 33
Gly Ser Gln Glu His Leu Ile Phe Asp Tyr
1 5 10

<210> 34
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<223> VH CDR3

<400> 34
Thr Asp Phe Trp Ser Gly Ser Pro Pro Gly Leu Asp Tyr
1 5 10

<210> 35
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<220>
 <223> VH CDR3

<400> 35
 Thr Pro Glu Tyr Ser Ser Ser Ile Trp His Tyr Tyr Tyr Gly Met Asp
 1 5 10 15

Val

<210> 36
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<220>
 <223> VH CDR3

<400> 36
 Gly Pro Leu Gln Glu Pro Pro Tyr Asp Tyr Gly Met Asp Val
 1 5 10

<210> 37
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<220>
 <223> VL CDR1

<400> 37
 Arg Ala Ser Gln Ser Val Ser Arg Tyr Leu Ala

1	5	10
<210> 38		
<211> 16		
<212> PRT		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic peptide		
<220>		
<223> VL CDR1		
<400> 38		
Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp		
1	5	10 15
<210> 39		
<211> 11		
<212> PRT		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic peptide		
<220>		
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<400> 39		
Arg Ala Ser Gln Ser Val Ser Ser Asn Leu Ala		
1	5	10
<210> 40		
<211> 11		
<212> PRT		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic peptide		
<220>		
<223> VL CDR1		
<400> 40		
Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala		
1	5	10

31 Jul 2019 2017240667

<210> 41
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<223> VL CDR1

<400> 41
Arg Ala Ser Gln Ser Val Ser Arg Tyr Leu Ala
1 5 10

<210> 42
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<223> VL CDR1

<400> 42
Arg Ala Ser Gln Gly Ile Ser Ser Trp Leu Ala
1 5 10

<210> 43
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<223> VL CDR1

<400> 43
Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 44
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<220>
 <223> VL CDR1

<400> 44
 Arg Ala Ser Gln Ser Val Ser Ser Asn Leu Ala
 1 5 10

<210> 45
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<220>
 <223> VL CDR2

<400> 45
 Asp Ala Ser Asn Arg Ala Thr
 1 5

<210> 46
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<220>
 <223> VL CDR2

<400> 46
 Leu Gly Ser Asn Arg Ala Ser
 1 5

<210> 47
 <211> 7

<212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic peptide

 <220>
 <223> VL CDR2

 <400> 47
 Gly Ala Ser Thr Arg Ala Thr
 1 5

 <210> 48
 <211> 7
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic peptide

 <220>
 <223> VL CDR2

 <400> 48
 Asp Ala Ser Asn Arg Ala Thr
 1 5

 <210> 49
 <211> 7
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic peptide

 <220>
 <223> VL CDR2

 <400> 49
 Asp Ala Ser Asn Arg Ala Thr
 1 5

 <210> 50
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<223> VL CDR2

<400> 50
Gly Ala Ser Ser Leu Gln Ser
1 5

<210> 51
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<223> VL CDR2

<400> 51
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 52
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<223> VL CDR2

<400> 52
Ser Ala Ser Thr Arg Ala Thr
1 5

<210> 53
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>

<223> VL CDR3

<400> 53

Gln Gln Arg Ile Ser Trp Pro Phe Thr
1 5

<210> 54

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<223> VL CDR3

<400> 54

Met Gln Gly Leu Gly Leu Pro Leu Thr
1 5

<210> 55

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<223> VL CDR3

<400> 55

Gln Gln Tyr Ala Ala Tyr Pro Thr
1 5

<210> 56

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<223> VL CDR3

<400> 56
Gln Gln Arg His Val Trp Pro Pro Thr
1 5

<210> 57
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<223> VL CDR3

<400> 57
Gln Gln Arg Phe Tyr Tyr Pro Trp Thr
1 5

<210> 58
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<223> VL CDR3

<400> 58
Gln Gln Ile Tyr Thr Phe Pro Phe Thr
1 5

<210> 59
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<223> VL CDR3

<400> 59
Gln Gln Phe Ala His Thr Pro Phe Thr

1 5

<210> 60
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<220>
 <223> VL CDR3

<400> 60
 Gln Gln His His Val Trp Pro Leu Thr
 1 5

<210> 61
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
 <223> VH DNA

<400> 61
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct 120
 ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgag agccgaggac acggcgggtg actactgcgc aagagccgag 300
 atgggagccg tattcgacat atgggggtcag ggtacaatgg tcaccgtctc ctca 354

<210> 62
 <211> 366
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> VH DNA

<400> 62

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc	60
tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct	120
ccaggcaagg ggctggagtg ggtggcagtt atatcgtatg atggaagtaa taaatactat	180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcaaata acagcctgag agccgaggac acggcggtgt actactgcgc cagagacggt	300
acttatctag gtggtctctg gtacttcgac ttatggggga gaggtacctt ggtcaccgtc	360
tcctca	366

<210> 63

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> VH DNA

<400> 63

caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaagggt	60
tcctgcaagg catctggata caccttcacc agctactata tgcactgggt gcgacaggcc	120
cctggacaag ggcttgagtg gatgggaata atcaaccctg gtggtggtag cacaagctac	180
gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac	240
atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc cagagagagt	300
tggccaatgg acgtatgggg ccaggaaca actgtcaccg tctcctca	348

<210> 64

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> VH DNA

<400> 64

cagctgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc	60
acctgcactg tctctggtgg ctccatcagc agtagtagtt actactgggg ctggatccgc	120
cagccccag ggaaggggct ggagtggatt gggagtatct cctatagtgg gagcacctac	180
tacaaccctg ccctcaagag tcgagtcacc atatccgtag acacgtccaa gaaccagttc	240
tccctgaagc tgagttctgt gaccgccgca gacacggcgg tgtactactg cgccagaggc	300
aggggatatg caaccagctt agccttcgat atctgggggtc aggttacaat ggtcaccgtc	360
tcctca	366

<210> 65

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> VH DNA

<400> 65

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc	60
tcctgtgcag cctctggatt caccttcagt agctatagca tgaactgggt ccgccaggct	120
ccagggaagg ggctggagtg ggtttcaacc attagtagta gtagtagtac catatactac	180
gcagactctg tgaagggccg attcaccatc tccagagaca atgccaagaa ctcaactgtat	240
ctgcaaatac acagcctgag agctgaggac acggcgggtgt actactgcgc cagaggttct	300
caggagcacc tgattttcga ttattgggga cagggtacat tggtcaccgt ctctca	357

<210> 66

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> VH DNA

<400> 66

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggct cctgagactc 60

tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatcgtatg atggaagtaa taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaata acagcctgag agccgaggac acggcggtgt actactgcgc cagaactgac 300

ttctggagcg gatccccctc aggcttagat tactggggac aggttacatt ggtcaccgtc 360

tcctca 366

<210> 67

<211> 378

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> VH DNA

<400> 67

caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggct 60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc cagaactcct 300

gaatactcct ccagcatatg gcactattac tacggcatgg acgtatgggg ccagggaaca 360

actgtcaccg tctcctca 378

<210> 68

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> VH DNA

<400> 68

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc	60
tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct	120
ccaggcaagg ggctggagtg ggtggcagtt atatcgtatg atggaagtaa taaatactat	180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcaaatac acagcctgag agccgaggac acggcggtgt actactgcgt caaggggccc	300
ttgcaggagc cgccatacga ttatggaatg gacgtatggg gccagggaac aactgtcacc	360
gtctcctca	369

<210> 69

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> VL DNA

<400> 69

gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc	60
ctctcctgca gggccagtca gagtgttagc aggtacttag cctggtacca acagaaacct	120
ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc	180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct	240
gaagattttg cagtttatta ctgtcagcag agaattctct ggcctttcac ttttggcgga	300
gggaccaagg ttgagatcaa a	321

<210> 70

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> VL DNA

<400> 70

gatattgtga tgactcagtc tccactctcc ctgcccgtca cccctggaga gccggcctcc	60
atctcctgca ggtctagtca gagcctcctg catagtaatg gatacaacta tttggattgg	120
tacctgcaga agccagggca gtctccacag ctctgatct atttgggttc taatcgggcc	180
tccgggggtcc ctgacaggtt cagtggcagt ggatcaggca cagattttac actgaaaatc	240
agcagagtgg aggctgagga tgttgggggtt tattactgca tgcagggact cggcctcctt	300
ctcacttttg gcggagggac caaggttgag atcaaa	336

<210> 71

<211> 318

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> VL DNA

<400> 71

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc	60
ctctcctgca gggccagtca gagtgttagc agcaacttag cctggtacca gcagaaacct	120
ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc	180
aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct	240
gaagattttg cagtttatta ctgtcagcag tacgccgcct accctacttt tggcggaggg	300
accaaggttg agatcaaa	318

<210> 72

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> VL DNA

<400> 72

gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agctacttag cctggtacca acagaaacct 120

ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 180

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 240

gaagattttg cagtttatta ctgtcagcag agacacgtct gcctcctac ttttggcgga 300

gggaccaagg ttgagatcaa a 321

<210> 73

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> VL DNA

<400> 73

gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc aggtacttag cctggtacca acagaaacct 120

ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 180

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 240

gaagattttg cagtttatta ctgtcagcag agattctact acccttggac ttttggcgga 300

gggaccaagg ttgagatcaa a 321

<210> 74

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> VL DNA

<400> 74

gacatccagt tgaccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc	60
atcacttgtc gggcgagtca ggggtattagc agctgggttag cctgggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatggt gcatccagtt tgcaaagtgg ggtcccatca	180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct	240
gaagattttg caacttatta ctgtcagcag atatacacct tccctttcac ttttggcgga	300
gggaccaagg ttgagatcaa a	321

<210> 75

<211> 339

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> VL DNA

<400> 75

gacatcgtga tgaccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc	60
atcaactgca agtccagcca gagtgtttta tacagctcca acaataagaa ctacttagct	120
tggtaccagc agaaaccagg acagcctcct aagctgtctca tttactgggc atctaccgg	180
gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc	240
atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcagtt cgcccacact	300
cctttcactt ttggcggagg gaccaagggtt gagatcaaa	339

<210> 76

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> VL DNA

<400> 76
gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgtagc agcaacttag cctggtacca gcagaaacct 120
ggccaggctc ccaggctcct catctatagc gcatccacca gggccactgg tatcccagcc 180
aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240
gaagattttg cagtttatta ctgtcagcag caccacgtct ggcctctcac ttttggcgga 300
gggaccaagg ttgagatcaa a 321

<210> 77
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<223> VH Protein

<400> 77
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ala Glu Met Gly Ala Val Phe Asp Ile Trp Gly Gln Gly Thr
100 105 110

Met Val Thr Val Ser Ser
115

<210> 78

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<223> VH Protein

<400> 78

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Thr Tyr Leu Gly Gly Leu Trp Tyr Phe Asp Leu Trp
100 105 110

Gly Arg Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 79

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<223> VH Protein

<400> 79

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Gly Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Ser Trp Pro Met Asp Val Trp Gly Gln Gly Thr Thr Val
100 105 110

Thr Val Ser Ser
115

<210> 80

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<223> VH Protein

<400> 80

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser
20 25 30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Ser Ile Ser Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Gly Arg Gly Tyr Ala Thr Ser Leu Ala Phe Asp Ile Trp
100 105 110

Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 81
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> VH Protein

<400> 81
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Thr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Ser Gln Glu His Leu Ile Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 82
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> VH Protein

<400> 82
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Thr Asp Phe Trp Ser Gly Ser Pro Pro Gly Leu Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 83

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<223> VH Protein

<400> 83

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Thr Pro Glu Tyr Ser Ser Ser Ile Trp His Tyr Tyr Tyr Gly
100 105 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 84
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<223> VH Protein

<400> 84
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Val Lys Gly Pro Leu Gln Glu Pro Pro Tyr Asp Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 85
<211> 107
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<223> VL Protein

<400> 85

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Arg Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ile Ser Trp Pro Phe
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 86

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<223> VL Protein

<400> 86

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly
85 90 95

Leu Gly Leu Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 87

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<223> VL Protein

<400> 87

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser

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65              70              75              80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ala Ala Tyr Pro Thr
      85              90              95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
      100              105

<210> 88
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<220>
<223> VL Protein

<400> 88
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1              5              10              15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
      20              25              30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
      35              40              45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
      50              55              60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65              70              75              80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg His Val Trp Pro Pro
      85              90              95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
      100              105

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<210> 89
<211> 107

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<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<223> VL Protein

<400> 89

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Arg Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Phe Tyr Tyr Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 90

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<223> VL Protein

<400> 90

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ile Tyr Thr Phe Pro Phe
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 91

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>

<223> VL Protein

<400> 91

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Phe Ala His Thr Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 92

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<223> VL Protein

<400> 92

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln His His Val Trp Pro Leu
85 90 95

31 Jul 2019
2017240667

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 93
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<223> VH CDR1

<400> 93
Gly Gly Ser Ile Ser Ser Tyr
1 5

<210> 94
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<223> VH CDR1

<400> 94
Gly Gly Ser Ile Ser Ser Gly Gly Phe
1 5

<210> 95
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<223> VH CDR1

<400> 95
Gly Tyr Thr Leu Thr Glu Leu
1 5

<210> 96
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<220>
 <223> VH CDR1

<400> 96
 Gly Phe Thr Phe Ser Ser Tyr
 1 5

<210> 97
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<220>
 <223> VH CDR2

<400> 97
 Tyr Tyr Ser Gly Ser
 1 5

<210> 98
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<220>
 <223> VH CDR2

<400> 98
 His His Ser Gly Ser
 1 5

<210> 99
 <211> 6


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<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<220>
<223> VH CDR2

<400> 99
Asp Pro Glu Asp Gly Glu
1          5

<210> 100
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<220>
<223> VH CDR2

<400> 100
Ser Tyr Asp Gly Ser Asp
1          5

<210> 101
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<220>
<223> VH CDR3

<400> 101
Leu Val Tyr Cys Gly Gly Asp Cys Tyr Ser Gly Phe Asp Tyr
1          5          10

<210> 102
<211> 14
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
        peptide

<220>
<223> VH CDR3

<400> 102
Leu Val Tyr Cys Gly Gly Asp Cys Tyr Ser Gly Phe Asp Tyr
1          5          10

<210> 103
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        peptide

<220>
<223> VH CDR3

<400> 103
Glu Ser Arg Gly Ile Gly Trp Pro Tyr Phe Asp Tyr
1          5          10

<210> 104
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        peptide

<220>
<223> VH CDR3

<400> 104
Glu Arg Tyr Ser Gly Arg Asp Tyr
1          5

<210> 105
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        peptide

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<220>

<223> VL CDR1

<400> 105

Gln Ala Ser Gln Asp Ile Asn Asn Phe Leu Asn
1 5 10

<210> 106

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<223> VL CDR1

<400> 106

Gln Ala Ser Gln Asp Ile Asn Asn Phe Leu Asn
1 5 10

<210> 107

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<223> VL CDR1

<400> 107

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

<210> 108

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<223> VL CDR1

<400> 108
 Arg Ala Ser Gln Ser Val Ser Ser Leu Leu Thr
 1 5 10

<210> 109
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<220>
 <223> VL CDR2

<400> 109
 Asp Ala Ser Asn Leu Glu Thr
 1 5

<210> 110
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<220>
 <223> VL CDR2

<400> 110
 Asp Ala Ser Asn Leu Glu Thr
 1 5

<210> 111
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<220>
 <223> VL CDR2

<400> 111
 Gly Ala Ser Ser Leu Lys Ser

1	5
<210> 112	
<211> 7	
<212> PRT	
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<220>	
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<223> VL CDR2	
<400> 112	
Gly Ala Ser Thr Arg Ala Thr	
1	5
<210> 113	
<211> 9	
<212> PRT	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic peptide	
<220>	
<223> VL CDR3	
<400> 113	
Gln Gln Tyr Gly Asn Leu Pro Phe Thr	
1	5
<210> 114	
<211> 9	
<212> PRT	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic peptide	
<220>	
<223> VL CDR3	
<400> 114	
Gln Gln Tyr Gly Asn Leu Pro Phe Thr	
1	5

<210> 115
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<223> VL CDR3

<400> 115
Gln Gln Ser Tyr Ser Thr Pro Ile Thr
1 5

<210> 116
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<223> VL CDR3

<400> 116
Gln Gln Tyr Asp Thr Trp Pro Phe Thr
1 5

<210> 117
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> VH DNA

<400> 117
caggtgcagc tgcaggaatc cggaccgggg ctggtgaagc ccagcgagac tctgagtctc 60
acgtgtacag tttctggagg tagcattagc tcctactatt ggtcatggat aaggcagccc 120
cccgggaagg gattggaatg gatcggctat atttactaca gtgggagcac caattacaac 180
ccctcactga agtctagagt tacaatcagc gttgacacct caaagaatca gttcagtttg 240

aaattgtcta gcgtcacagc agctgataca gccgtctatt atttgttttc tctgggtctat 300
 tgcggtgggg attgttacag tggctttgac tattgggggc aggggtactct ggttacagtt 360
 tctttcc 366

<210> 118
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<220>
 <223> VH DNA

<400> 118
 caggtacagc tgcaggaatc tgggcccgga cttgtcaagc caagtcagac actttctctt 60
 acatgtaccg tgagcggcgg aagtataagc agtggaggct tttactggtc ttggatacgg 120
 cagcaccag gcaaaggctt ggagtggatt ggatacattc atcattcagg atctacacac 180
 tataatccat cccttaagtc ccgggtcacc attagcattg atacgtctaa gaatctgttc 240
 agtctcaggc tgtcctccgt cactgctgcc gacacagccg tgtactactg cgcctccttg 300
 gtttactgcg gaggcgactg ttatagcggc tttgattatt gggggcaggg gaccctcgta 360
 accgtgagct ct 372

<210> 119
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<220>
 <223> VH DNA

<400> 119
 caggtccaac tgggtgcagtc cggagccgaa gtcaagaaac caggtgcctc cgtaaagtg 60
 agttgcaaag tctctggata cactctgacc gagctctcta tgcactgggt ccggcaggcc 120
 cccggcaagg gattggaatg gatgggcggg ttcgatcctg aggacggaga gactatctac 180

gctcaaaaat tccagggacg agtgactgtg accgaagaca ctagtaccga cactgcctac 240
atggaacttt cctctctgcg atcagaagat accgcagtgt actactgtgc tactgaatct 300
aggggcattg gatggcccta cttcgattac tggggtcagg gaactctggt gactgtctcc 360
agc 363

<210> 120
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> VH DNA

<400> 120
caggtccagt tggtcgaaag tggcgggtggt gtagtgcagc cgggccgcag tttgaggctt 60
tcctgtgctg cttcaggctt tactttttcc agctatggaa tgcactgggt gcggcaggcc 120
cccggcaaag gacttgagtg ggtggccgtc atttcttatg acggatcaga taagtactac 180
gtggacagcg tcaagggcag attcaccatc tctagggaca acagtaaaaa tagactctac 240
ctccagatga atagcctcag agctgaagac acggccgtct actattgtgc tcgggagcgg 300
tatagtggca gagactactg ggggcagggc acactcgтта cagtgagtag c 351

<210> 121
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> VL DNA

<400> 121
gacatccagt tgacacagag cccgagttcc ttgtccgcct ccgtcgggga tagagtgtca 60
tttacctgtc aggctctca ggatattaat aactttctga attggtatca gcaaaagccc 120
ggaaaggcac ccaagctggt gatttacgac gccagtaacc tggagacagg cgtgccctcc 180

cggttttagtg gtagcggaag cggtagcgat tttagcttta ctatcagctc tctccaaccc 240
gaagacattg caacctacta ttgtcaacaa tatggaaacc tgccttttac atttggcggc 300
ggcaccaagg tggagattaa gcgg 324

<210> 122
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> VL DNA

<400> 122
gatatccagc tcaactcaaag cccctctagt ctctctgcct cagtggggga tcgggtcagt 60
tttacttgtc aagcttcaca ggatatcaac aacttcctta attggtatca gcagaagcca 120
ggaaaagcac ccaagctgct catctatgat gcctcaaatt tggagacggg tgttcccagt 180
cgattctctg ggtaggggtc cgggaccgac tttagcttta cgatctcctc tctgcagccc 240
gaagacatcg ccacatacta ttgtcaacag tacggcaact tgcctttcac atttgggggc 300
gggactaagg ttgaaatcaa gagg 324

<210> 123
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> VL DNA

<400> 123
gatattcaga tgactcaatc tccttcttct ctgtccgctt ccgtgggcga tagagtgacc 60
attacttgta gggcgtccca gtcaatctcc agttatttga attggtatca gcagaagccc 120
gggaaagcac ctaagctgtt gatcagcggg gcttctagcc tgaagagtgg ggtaccttca 180
cggttcagcg gaagcggaag cggaaccgat ttcaccctga ctatcagcag cctgccacct 240

gaggactttg caacttacta ctgccaacag tcatacagca ctccgatcac tttcggccag 300

ggcaccgggc tcgaaatcaa gcgc 324

<210> 124

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> VL DNA

<400> 124

gagattgtta tgaccagag tcctgagacc ctctcagtca gccccgggga gcgcgcaact 60

ttgtcttgca gagctagtca gtccgtgtcc tctcttctga catggtacca gcaaaagccc 120

gggcaggctc cgcgctttt gatctttggg gcttcaacaa gagccactgg gattcccgca 180

cgattctctg gtcggggag cggtagtgtt ttcacctga cgattagcag tctccagagc 240

gaggacttcg ccgtatacta ctgccagcag tacgatacgt ggccattcac ttttggacca 300

gggactaaag tggattttaa gcgc 324

<210> 125

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<223> VH AA

<400> 125

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile

35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Val
85 90 95

Ser Leu Val Tyr Cys Gly Gly Asp Cys Tyr Ser Gly Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

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<210> 126
<211> 124
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<223> VH AA

<400> 126
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Phe Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile His His Ser Gly Ser Thr His Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Leu Phe
65 70 75 80

Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Ser Leu Val Tyr Cys Gly Gly Asp Cys Tyr Ser Gly Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 127

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>

<223> VH AA

<400> 127

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

Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Glu Leu
20 25 30

Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Gly Phe Asp Pro Glu Asp Gly Glu Thr Ile Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Val Thr Glu Asp Thr Ser Thr Asp Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Thr Glu Ser Arg Gly Ile Gly Trp Pro Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 128
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<223> VH AA

<400> 128
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asp Lys Tyr Tyr Val Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Arg Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

Val Thr Val Ser Ser
115

<210> 129
<211> 108
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<223> VL AA

<400> 129

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

Asp Arg Val Ser Phe Thr Cys Gln Ala Ser Gln Asp Ile Asn Asn Phe
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Gly Asn Leu Pro Phe
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 130

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<223> VL AA

<400> 130

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

Asp Arg Val Ser Phe Thr Cys Gln Ala Ser Gln Asp Ile Asn Asn Phe
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Gly Asn Leu Pro Phe
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 131

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<223> VL AA

<400> 131

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Ser Gly Ala Ser Ser Leu Lys Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Pro Pro

65					70						75					80
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Ser	Thr	Pro	Ile	
				85					90					95		
Thr	Phe	Gly	Gln	Gly	Thr	Arg	Leu	Glu	Ile	Lys	Arg					
			100					105								
<210> 132																
<211> 108																
<212> PRT																
<213> Artificial Sequence																
<220>																
<223> Description of Artificial Sequence: Synthetic polypeptide																
<220>																
<223> VL AA																
<400> 132																
Glu	Ile	Val	Met	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Val	Ser	Pro	Gly	
1				5					10					15		
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Leu	
			20					25					30			
Leu	Thr	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	
			35				40					45				
Phe	Gly	Ala	Ser	Thr	Arg	Ala	Thr	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly	
	50					55					60					
Ser	Gly	Ser	Gly	Thr	Gly	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Ser	
65					70					75				80		
Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Asp	Thr	Trp	Pro	Phe	
				85					90					95		
Thr	Phe	Gly	Pro	Gly	Thr	Lys	Val	Asp	Phe	Lys	Arg					
			100					105								

<210> 133
 <211> 1437

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> FS-21495CARDNAHxL

<400> 133

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ctctcctgtg cagcctctgg attcaccttt agcagctatg ccatgagctg ggtccgccag	180
gctccaggga aggggctgga gtgggtctca gctattagtg gtagtggtgg tagcacatac	240
tacgcagact ccgtgaaggg ccggttcacc atctccagag acaattccaa gaacacgctg	300
tatctgcaaa tgaacagcct gagagccgag gacacggcgg tgtactactg cgcaagagcc	360
gagatgggag ccgtattcga catatggggg cagggtacaa tggtcaccgt ctctcaggg	420
tctacatccg gctccgggaa gcccggaggt ggcgaaggta gtacaaaggg ggaaattgtg	480
ttgacacagt ctccagccac cctgtctttg tctccagggg aaagagccac cctctcctgc	540
agggccagtc agagtgttag caggtactta gcctgggtacc aacagaaacc tggccaggct	600
cccagggtcc tcatctatga tgcattcaac agggccactg gcatcccagc cagggttcagt	660
ggcagtgggt ctgggacaga cttcactctc accatcagca gcctagagcc tgaagatttt	720
gcagtttatt actgtcagca gagaatctcc tggcctttca cttttggcgg agggaccaag	780
gttgagatca aacgggccgc tgcccttgat aatgaaaagt caaacggaac aatcattcac	840
gtgaagggca agcacctctg tccgtcacc ttgttccctg gtccatccaa gccattctgg	900
gtgttggtcg tagtgggtgg agtcctcgct tgttactctc tgctcgtcac cgtggctttt	960
ataatcttct gggttagatc caaaagaagc cgctgctcc atagcgatta catgaatatg	1020
actccacgcc gccctggccc cacaaggaaa cactaccagc cttacgcacc acctagagat	1080
ttcgctgcct atcggagcag ggtgaagttt tccagatctg cagatgcacc agcgtatcag	1140
cagggccaga accaactgta taacgagctc aacctgggac gcagggaaga gtatgacgtt	1200
ttggacaagc gcagaggacg ggaccctgag atgggtggca aaccaagacg aaaaaacccc	1260
caggagggtc tctataatga gctgcagaag gataagatgg ctgaagccta ttctgaaata	1320

ggcatgaaag gagagcggag aaggggaaaa gggcacgacg gtttgtacca gggactcagc 1380

actgctacga aggatactta tgacgctctc cacatgcaag ccctgccacc taggtaa 1437

<210> 134

<211> 478

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<223> FS-21495CARHxL

<400> 134

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu
20 25 30

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr
65 70 75 80

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
85 90 95

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Arg Ala Glu Met Gly Ala Val Phe Asp Ile
115 120 125

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Ser Thr Ser Gly
130 135 140

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Ile Val
145 150 155 160

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
165 170 175

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Arg Tyr Leu Ala Trp
180 185 190

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala
195 200 205

Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
210 215 220

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
225 230 235 240

Ala Val Tyr Tyr Cys Gln Gln Arg Ile Ser Trp Pro Phe Thr Phe Gly
245 250 255

Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala Ala Leu Asp Asn Glu
260 265 270

Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro
275 280 285

Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val
290 295 300

Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe
305 310 315 320

Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
325 330 335

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
340 345 350

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val

355		360		365
Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn				
370		375		380
Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val				
385		390		400
Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg				
	405		410	415
Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys				
	420		425	430
Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg				
	435		440	445
Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys				
	450		455	460
Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg				
465		470		475

<210> 135
 <211> 1437
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
 <223> FS-21495CARDNALxH

<400> 135	
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ccggaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg ggaaagagcc	120
accctctcct gcagggccag tcagagtgtt agcaggtact tagcctggta ccaacagaaa	180
cctggccagg ctcccaggct cctcatctat gatgcatcca acagggccac tggcatcca	240
gccaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagcctagag	300

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cctgaagatt ttgcagttta ttactgtcag cagagaatct cctggccttt cacttttggc      360
ggagggacca aggttagat caaacggggg tctacatccg gctccgggaa gcccggaagt      420
ggcgaaggta gtacaaaggg ggaggtgcag ctgttggagt ctgggggagg cttggtacag      480
cctgggggggt ccctgagact ctctgtgca gcctctggat tcaccttag cagctatgcc      540
atgagctggg tccgccaggc tccagggaag gggctggagt gggctctcagc tattagtgg      600
agtggtaggt gcacatacta cgcagactcc gtgaagggcc gggtcaccat ctccagagac      660
aattccaaga acacgctgta tctgcaaatg aacagcctga gagccgagga cacggcgggtg      720
tactactgcg caagagccga gatgggagcc gtattcgaca tatgggggtca gggtagaatg      780
gtcaccgtct cctcagccgc tgcccttgat aatgaaaagt caaacggaac aatcattcac      840
gtgaagggca agcacctctg tccgtcacc ttgttccctg gtccatcaa gccattctgg      900
gtgttggtcg tagtggtgg agtcctcgct tgttactctc tgctcgtcac cgtggctttt      960
ataatcttct gggtagatc caaaagaagc cgcctgctcc atagcgatta catgaatatg     1020
actccacgcc gccctggccc cacaaggaaa cactaccagc cttacgcacc acctagagat     1080
ttcgctgcct atcggagcag ggtgaagttt tccagatctg cagatgcacc agcgtatcag     1140
cagggccaga accaactgta taacgagctc aacctgggac gcagggaaga gtatgacgtt     1200
ttggacaagc gcagaggacg ggaccctgag atgggtggca aaccaagacg aaaaaacccc     1260
caggagggtc tctataatga gctgcagaag gataagatgg ctgaagccta ttctgaaata     1320
ggcatgaaag gagagcggag aaggggaaaa gggcacgacg gtttgtacca gggactcagc     1380
actgctacga aggatactta tgacgtctc cacatgcaag ccctgccacc taggtaa      1437

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<210> 136
 <211> 478
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polypeptide

<220>
 <223> FS-21495CARLxH

<400> 136
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

31 Jul 2019
2017240667

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

Thr 225	Leu	Tyr	Leu	Gln	Met 230	Asn	Ser	Leu	Arg	Ala 235	Glu	Asp	Thr	Ala	Val 240
Tyr	Tyr	Cys	Ala	Arg 245	Ala	Glu	Met	Gly	Ala 250	Val	Phe	Asp	Ile	Trp 255	Gly
Gln	Gly	Thr	Met 260	Val	Thr	Val	Ser	Ser 265	Ala	Ala	Ala	Leu	Asp 270	Asn	Glu
Lys	Ser	Asn 275	Gly	Thr	Ile	Ile	His 280	Val	Lys	Gly	Lys	His 285	Leu	Cys	Pro
Ser	Pro 290	Leu	Phe	Pro	Gly	Pro 295	Ser	Lys	Pro	Phe	Trp 300	Val	Leu	Val	Val
Val 305	Gly	Gly	Val	Leu	Ala 310	Cys	Tyr	Ser	Leu	Leu 315	Val	Thr	Val	Ala	Phe 320
Ile	Ile	Phe	Trp	Val 325	Arg	Ser	Lys	Arg	Ser 330	Arg	Leu	Leu	His	Ser 335	Asp
Tyr	Met	Asn	Met 340	Thr	Pro	Arg	Arg	Pro 345	Gly	Pro	Thr	Arg	Lys 350	His	Tyr
Gln	Pro	Tyr 355	Ala	Pro	Pro	Arg	Asp 360	Phe	Ala	Ala	Tyr	Arg 365	Ser	Arg	Val
Lys 370	Phe	Ser	Arg	Ser	Ala	Asp 375	Ala	Pro	Ala	Tyr	Gln 380	Gln	Gly	Gln	Asn
Gln 385	Leu	Tyr	Asn	Glu	Leu 390	Asn	Leu	Gly	Arg	Arg 395	Glu	Glu	Tyr	Asp	Val 400
Leu	Asp	Lys	Arg	Arg 405	Gly	Arg	Asp	Pro	Glu 410	Met	Gly	Gly	Lys	Pro 415	Arg
Arg	Lys	Asn	Pro 420	Gln	Glu	Gly	Leu	Tyr 425	Asn	Glu	Leu	Gln	Lys 430	Asp	Lys
Met	Ala	Glu 435	Ala	Tyr	Ser	Glu	Ile 440	Gly	Met	Lys	Gly	Glu 445	Arg	Arg	Arg

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
450 455 460

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
465 470 475

<210> 137

<211> 1464

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> PC-21497CARDNAHxL

<400> 137

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ctctcctgtg cagcgtctgg attcaccttc agtagctatg gcatgcactg ggtccgccag	180
gctccaggca aggggctgga gtgggtggca gttatatcgt atgatggaag taataaatac	240
tatgcagact ccgtgaaggg ccgattcacc atctccagag acaattccaa gaacacgctg	300
tatctgcaaa tgaacagcct gagagccgag gacacggcgg tgtactactg cgccagagac	360
ggtacttatc taggtggtct ctggtacttc gacttatggg ggagaggtag cttggtcacc	420
gtctcctcag ggtctacatc cggctccggg aagcccggaa gtggcgaagg tagtacaaag	480
ggggatattg tgatgactca gtctccactc tccctgcccg tcacccttgg agagccggcc	540
tccatctcct gcaggtctag tcagagcctc ctgcatagta atggatacaa ctatttggat	600
tggtacctgc agaagccagg gcagtctcca cagctcctga tctatttggg ttctaatacgg	660
gcctccgggg tccctgacag gttcagtggc agtggatcag gcacagattt tacactgaaa	720
atcagcagag tggaggctga ggatgttggg gtttattact gcatgcaggg actcggcctc	780
cctctcactt ttggcggagg gaccaagggt gagatcaaac gggccgctgc ctttgataat	840
gaaaagtcaa acggaacaat cattcacgtg aagggaagc acctctgtcc gtcacccttg	900
ttccctggtc catccaagcc attctgggtg ttggctgtag tgggtggagt cctcgcttgt	960

tactctctgc tcgtcaccgt ggctttttata atcttctggg ttagatccaa aagaagccgc 1020
 ctgctccata gcgattacat gaatatgact ccacgccgcc ctggcccccac aaggaaacac 1080
 taccagcctt acgcaccacc tagagatttc gctgcctatc ggagcagggt gaagttttcc 1140
 agatctgcag atgcaccagc gtatcagcag ggccagaacc aactgtataa cgagctcaac 1200
 ctgggacgca gggaagagta tgacgttttg gacaagcgca gaggacggga ccctgagatg 1260
 ggtggcaaac caagacgaaa aaacccccag gagggctctct ataatgagct gcagaaggat 1320
 aagatggctg aagcctattc tgaaataggc atgaaaggag agcggagaag gggaaaaggg 1380
 cacgacgggt tgtaccaggg actcagcact gctacgaagg atacttatga cgctctccac 1440
 atgcaagccc tgccacctag gtaa 1464

<210> 138
 <211> 487
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<220>
 <223> PC-21497CARHxL

<400> 138
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val
 20 25 30

Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
 35 40 45

Thr Phe Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys
 50 55 60

Gly Leu Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr
 65 70 75 80

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser

31 Jul 2019

90

Ala Val Tyr Tyr Cys Ala Arg Asp Gly Thr Tyr Leu Gly Gly Leu Trp
115 120 125

Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys
145 150 155 160

Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His
180 185 190

Ser Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln
195 200 205

Ser Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val
210 215 220

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
225 230 235 240

Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln
245 250 255

Gly Leu Gly Leu Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
260 265 270

Lys Arg Ala Ala Ala Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile
275 280 285

His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro
290 295 300

Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys
305 310 315 320

Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser
325 330 335

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
340 345 350

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
355 360 365

Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp
370 375 380

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
385 390 395 400

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
405 410 415

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
420 425 430

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
435 440 445

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
450 455 460

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
465 470 475 480

Met Gln Ala Leu Pro Pro Arg
485

<210> 139
<211> 1464
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
        polynucleotide

<220>
<223> PC-21497CARDNALxH

<400> 139
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ccggatattg tgatgactca gtctccactc tccctgcccc tcacccctgg agagccggcc      120
tccatctcct gcaggtctag tcagagcctc ctgcatagta atggatacaa ctatttggat      180
tggtacctgc agaagccagg gcagtctcca cagctcctga tctatttggg ttctaatacg      240
gcctccgggg tccctgacag gttcagtggc agtggatcag gcacagattt tacactgaaa      300
atcagcagag tggaggctga ggatgttggg gtttattact gcatgcaggg actcggcctc      360
cctctcactt ttggcggagg gaccaagggt gagatcaaac ggggggtctac atccggctcc      420
gggaagcccc gaagtggcga aggtagtaca aaggggcagg tgcagctggg ggagtctggg      480
ggaggcgtgg tccagcctgg gaggtccctg agactctcct gtgcagcgtc tggattcacc      540
ttcagtagct atggcatgca ctgggtccgc caggctccag gcaaggggct ggagtgggtg      600
gcagttatat cgtatgatgg aagtaataaa tactatgcag actccgtgaa gggccgattc      660
accatctcca gagacaattc caagaacacg ctgtatctgc aaatgaacag cctgagagcc      720
gaggacacgg cgggtgtacta ctgcgccaga gacggtactt atctaggtgg tctctggtac      780
ttcgacttat gggggagagg taccttggtc accgtctcct cagccgctgc ctttgataat      840
gaaaagtcaa acggaacaat cattcacgtg aagggcaagc acctctgtcc gtcacccttg      900
ttccctggtc catccaagcc attctgggtg ttggctgtag tgggtggagt cctcgcttgt      960
tactctctgc tcgtcaccgt ggcttttata atcttctggg ttagatccaa aagaagccgc     1020
ctgctccata gcgattacat gaatatgact ccacgccgcc ctggccccac aaggaaacac     1080
taccagcctt acgcaccacc tagagatttc gctgcctatc ggagcagggt gaagttttcc     1140
agatctgcag atgcaccagc gtatcagcag ggccagaacc aactgtataa cgagctcaac     1200
ctgggacgca gggaagagta tgacgttttg gacaagcgca gaggacggga ccctgagatg     1260
ggtggcaaac caagacgaaa aaacccccag gagggctctt ataatagagct gcagaaggat     1320
aagatggctg aagcctattc tgaaataggc atgaaaggag agcggagaag gggaaaaggg     1380

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cacgacgggtt tgtaccaggg actcagcact gctacgaagg atacttatga cgctctccac 1440
atgcaagccc tgccacctag gtaa 1464

<210> 140
<211> 487
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<223> PC-21497CARHxL

<400> 140
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu
20 25 30

Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln
35 40 45

Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln
50 55 60

Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg
65 70 75 80

Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85 90 95

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr
100 105 110

Tyr Cys Met Gln Gly Leu Gly Leu Pro Leu Thr Phe Gly Gly Gly Thr
115 120 125

Lys Val Glu Ile Lys Arg Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly
130 135 140

Ser	Gly	Glu	Gly	Ser	Thr	Lys	Gly	Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	145	150	155	160
Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	165	170	175	
Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Gly	Met	His	Trp	Val	Arg	Gln	Ala	180	185	190	
Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Val	Ile	Ser	Tyr	Asp	Gly	Ser	195	200	205	
Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	210	215	220	
Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	225	230	235	240
Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Asp	Gly	Thr	Tyr	Leu	Gly	245	250	255	
Gly	Leu	Trp	Tyr	Phe	Asp	Leu	Trp	Gly	Arg	Gly	Thr	Leu	Val	Thr	Val	260	265	270	
Ser	Ser	Ala	Ala	Ala	Leu	Asp	Asn	Glu	Lys	Ser	Asn	Gly	Thr	Ile	Ile	275	280	285	
His	Val	Lys	Gly	Lys	His	Leu	Cys	Pro	Ser	Pro	Leu	Phe	Pro	Gly	Pro	290	295	300	
Ser	Lys	Pro	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	Cys	305	310	315	320
Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Phe	Trp	Val	Arg	Ser	325	330	335	
Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro	Arg	340	345	350	
Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	Arg	355	360	365	

Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp
370 375 380

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
385 390 395 400

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
405 410 415

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
420 425 430

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
435 440 445

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
450 455 460

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
465 470 475 480

Met Gln Ala Leu Pro Pro Arg
485

<210> 141
<211> 1428
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> AJ-21508CARDNAHxL

<400> 141
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60
ccgcaggtgc agctggtgca gtctggggct gaggtgaaga agcctggggc ctcagtgaag 120
gtttcctgca aggcattctgg atacaccttc accagctact atatgcactg ggtgcgacag 180
gcccctggac aagggttga gtggatggga ataatacaacc ctggtggtgg tagcacaagc 240

tacgcacaga agttccaggg cagagtcacc atgaccaggg acacgtccac gagcacagtc	300
tacatggagc tgagcagcct gagatctgag gacacggcgg tgtactactg cgccagagag	360
agttggccaa tggacgtatg gggccagggg acaactgtca ccgtctcctc aggggtctaca	420
tccggctccg ggaagcccgg aagtggcgaa ggtagtataa aggggggaaat agtgatgacg	480
cagtctccag ccaccctgtc tgtgtctcca ggggaaagag ccaccctctc ctgcaggggc	540
agtcagagtg ttagcagcaa cttagcctgg taccagcaga aacctggcca ggctcccagg	600
ctcctcatct atgggtgcatc caccaggggc actggatatcc cagccagggtt cagtggcagt	660
gggtctggga cagagtccac tctcaccatc agcagcctgc agtctgaaga ttttgagtt	720
tattactgtc agcagtagcg cgcctaccct acttttggcg gagggaccaaa gggtgagatc	780
aaacggggccg ctgcccttga taatgaaaag tcaaacggaa caatcattca cgtgaagggc	840
aagcacctct gtccgtcacc cttgttcctt ggtccatcca agccattctg ggtgttggtc	900
gtagtgggtg gagtccctgc ttgttactct ctgctcgtca ccgtggcttt tataatcttc	960
tgggttagat ccaaaagaag cgcctgctc catagcgatt acatgaatat gactccacgc	1020
cgccctggcc ccacaaggaa acactaccag ctttacgcac cacctagaga tttcgctgcc	1080
tatcgagca gggatgaagt ttccagatct gcagatgcac cagcgtatca gcagggccag	1140
aaccaactgt ataacgagct caacctggga cgcagggaag agtatgacgt tttggacaag	1200
cgcagaggac gggaccctga gatgggtggc aaaccaagac gaaaaaaccc ccaggagggt	1260
ctctataatg agctgcagaa ggataagatg gctgaagcct attctgaaat aggcatgaaa	1320
ggagagcgga gaaggggaaa agggcacgac ggtttgtacc agggactcag cactgctacg	1380
aaggatactt atgacgtctt ccacatgcaa gccctgccac ctaggtaa	1428

<210> 142

<211> 475

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<223> AJ-21508CARHxL

<400> 142
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15
His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30
Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
35 40 45
Thr Phe Thr Ser Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln
50 55 60
Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Gly Gly Gly Ser Thr Ser
65 70 75 80
Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
85 90 95
Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
100 105 110
Ala Val Tyr Tyr Cys Ala Arg Glu Ser Trp Pro Met Asp Val Trp Gly
115 120 125
Gln Gly Thr Thr Val Thr Val Ser Ser Gly Ser Thr Ser Gly Ser Gly
130 135 140
Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Ile Val Met Thr
145 150 155 160
Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu
165 170 175
Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln
180 185 190
Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr
195 200 205
Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr

2017240667 31 Jul 2019

210		215		220
Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val				
225		230		235
Tyr Tyr Cys Gln Gln Tyr Ala Ala Tyr Pro Thr Phe Gly Gly Gly Thr				
		245		250
Lys Val Glu Ile Lys Arg Ala Ala Ala Leu Asp Asn Glu Lys Ser Asn				
		260		265
Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu				
		275		280
Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly				
		290		295
Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe				
305		310		315
Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn				
		325		330
Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr				
		340		345
Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser				
		355		360
Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr				
		370		375
Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys				
385		390		395
Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn				
		405		410
Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu				
		420		425
				430

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
 435 440 445

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
 450 455 460

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 465 470 475

<210> 143

<211> 1428

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> AJ-21508CARDNALxH

<400> 143

atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc	60
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accctctcct gcagggccag tcagagtgtt agcagcaact tagcctggta ccagcagaaa	180
cctggccagg ctcccaggct cctcatctat ggtgcatcca ccagggccac tggatatcca	240
gccagggttca gtggcagtgg gtctgggaca gagttcactc tcaccatcag cagcctgcag	300
tctgaagatt ttgcagttta ttactgtcag cagtacgccg cctaccctac ttttggcgga	360
gggaccaagg ttgagatcaa acgggggtct acatccggct ccgggaagcc cggaagtggc	420
gaaggtagta caaaggggca ggtgcagctg gtgcagtctg gggctgaggt gaagaagcct	480
ggggcctcag tgaaggtttc ctgcaaggca tctggataca ccttcaccag ctactatatg	540
cactgggtgc gacaggcccc tggacaaggg cttgagtgga tgggaataat caaccctggt	600
ggtggtagca caagctacgc acagaagttc cagggcagag tcaccatgac cagggaacacg	660
tccacgagca cagtctacat ggagctgagc agcctgagat ctgaggacac ggcggtgtac	720
tactgcgcca gagagagttg gccaatggac gtatggggcc agggaacaac tgtcaccgtc	780
tcctcagccg ctgcccttga taatgaaaag tcaaacggaa caatcattca cgtgaagggc	840

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aagcacctct gtccgtcacc cttgttcctt ggtccatcca agccattctg ggtgttggtc      900
gtagtgggtg gtagtctcgc ttgttactct ctgctcgtca ccgtggcttt tataatcttc      960
tgggttagat ccaaaagaag cgcctgctc catagcgatt acatgaatat gactccacgc     1020
cgccctggcc ccacaaggaa aactaccag ccttacgcac cacctagaga tttcgctgcc     1080
tatcggagca ggtgaagtt ttccagatct gcagatgcac cagcgtatca gcagggccag     1140
aaccaactgt ataacgagct caacctggga cgcagggaag agtatgacgt tttggacaag     1200
cgcagaggac gggaccctga gatgggtggc aaaccaagac gaaaaaaccc ccaggagggt     1260
ctctataatg agctgcagaa ggataagatg gctgaagcct attctgaaat aggcatgaaa     1320
ggagagcgga gaaggggaaa agggcacgac ggtttgtacc agggactcag cactgctacg     1380
aaggatactt atgacgctct ccacatgcaa gccctgccac ctaggtaa                     1428

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<210> 144
 <211> 475
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polypeptide

<220>
 <223> AJ-21508CARLxH

<400> 144
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu
 20 25 30

Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
 35 40 45

Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
 50 55 60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro
 65 70 75 80

Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	
				85					90					95		
Ser	Ser	Leu	Gln	Ser	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	
			100					105					110			
Ala	Ala	Tyr	Pro	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	
		115					120					125				
Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys	Pro	Gly	Ser	Gly	Glu	Gly	Ser	Thr	
	130					135					140					
Lys	Gly	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	
145					150					155					160	
Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	
				165					170					175		
Ser	Tyr	Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	
			180					185					190			
Trp	Met	Gly	Ile	Ile	Asn	Pro	Gly	Gly	Gly	Ser	Thr	Ser	Tyr	Ala	Gln	
		195					200					205				
Lys	Phe	Gln	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	Ser	Thr	Ser	Thr	
	210					215					220					
Val	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	
225					230					235					240	
Tyr	Cys	Ala	Arg	Glu	Ser	Trp	Pro	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr	
				245					250					255		
Thr	Val	Thr	Val	Ser	Ser	Ala	Ala	Ala	Leu	Asp	Asn	Glu	Lys	Ser	Asn	
			260					265					270			
Gly	Thr	Ile	Ile	His	Val	Lys	Gly	Lys	His	Leu	Cys	Pro	Ser	Pro	Leu	
		275					280					285				
Phe	Pro	Gly	Pro	Ser	Lys	Pro	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	
	290					295					300					

31 Jul 2019
2017240667

Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe
305 310 315 320

Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn
325 330 335

Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr
340 345 350

Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser
355 360 365

Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr
370 375 380

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
385 390 395 400

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
405 410 415

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
420 425 430

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
435 440 445

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
450 455 460

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
465 470 475

<210> 145

<211> 1449

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>

<223> NM-21517CARDNAHxL

<400> 145

atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc	60
ccgcagctgc agctgcagga gtcggggccca ggactgggtga agccttcgga gaccctgtcc	120
ctcacctgca ctgtctctgg tggctccatc agcagtagta gttactactg gggctggatc	180
cgccagcccc cagggaaggg gctggagtgg attgggagta tctcctatag tgggagcacc	240
tactacaacc cgtccctcaa gagtcgagtc accatatccg tagacacgtc caagaaccag	300
ttctccctga agctgagttc tgtgaccgcc gcagacacgg cgggtgtacta ctgcgccaga	360
ggcaggggat atgcaaccag cttagccttc gatatctggg gtcagggtac aatggtcacc	420
gtctcctcag ggtctacatc cggctccggg aagcccggaa gtggcgaagg tagtaciaaag	480
ggggaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg ggaaagagcc	540
accctctcct gcagggccag tcagagtgtt agcagctact tagcctggta ccaacagaaa	600
cctggccagg ctcccaggct cctcatctat gatgcatcca acagggccac tggcatccca	660
gccaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagcctagag	720
cctgaagatt ttgcagttta ttactgtcag cagagacacg tctggcctcc tacttttggc	780
ggagggacca aggttagat caaacgggcc gctgcccttg ataataaaaa gtcaaacgga	840
acaatcattc acgtgaaggg caagcacctc tgtccgtcac cttgttccc tgggtccatcc	900
aagccattct ggggtgttggc cgtagtgggt ggagtcctcg cttgttactc tctgctcgtc	960
accgtggctt ttataatctt ctgggttaga tccaaaagaa gccgcctgct ccatagcgat	1020
tacatgaata tgactccacg ccgccctggc cccacaagga aacactacca gccttacgca	1080
ccacctagag atttcgctgc ctatcgagc aggggtgaagt tttccagatc tgcagatgca	1140
ccagcgtatc agcagggcca gaaccaactg tataacgagc tcaacctggg acgcaggga	1200
gagtatgacg ttttggacaa gcgcagagga cgggaccctg agatgggtgg caaaccaaga	1260
cgaaaaaacc cccaggaggg tctctataat gagctgcaga aggataagat ggctgaagcc	1320
tattctgaaa taggcatgaa aggagagcgg agaaggggaa aagggcacga cggtttgtac	1380
cagggactca gactgctac gaaggatact tatgacgctc tccacatgca agccctgcca	1440
cctaggtaa	1449

<210> 146
 <211> 482
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<220>
 <223> NM-21517CARHxL

<400> 146
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu
 20 25 30

Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly
 35 40 45

Ser Ile Ser Ser Ser Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro
 50 55 60

Gly Lys Gly Leu Glu Trp Ile Gly Ser Ile Ser Tyr Ser Gly Ser Thr
 65 70 75 80

Tyr Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr
 85 90 95

Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp
 100 105 110

Thr Ala Val Tyr Tyr Cys Ala Arg Gly Arg Gly Tyr Ala Thr Ser Leu
 115 120 125

Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly
 130 135 140

Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys
 145 150 155 160

Gly	Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	165	170	175
Gly	Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	180	185	190
Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	195	200	205
Ile	Tyr	Asp	Ala	Ser	Asn	Arg	Ala	Thr	Gly	Ile	Pro	Ala	Arg	Phe	Ser	210	215	220
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Glu	225	230	235
Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Arg	His	Val	Trp	Pro	245	250	255
Pro	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Ala	Ala	Ala	260	265	270
Leu	Asp	Asn	Glu	Lys	Ser	Asn	Gly	Thr	Ile	Ile	His	Val	Lys	Gly	Lys	275	280	285
His	Leu	Cys	Pro	Ser	Pro	Leu	Phe	Pro	Gly	Pro	Ser	Lys	Pro	Phe	Trp	290	295	300
Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	Cys	Tyr	Ser	Leu	Leu	Val	305	310	315
Thr	Val	Ala	Phe	Ile	Ile	Phe	Trp	Val	Arg	Ser	Lys	Arg	Ser	Arg	Leu	325	330	335
Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro	Arg	Arg	Pro	Gly	Pro	Thr	340	345	350
Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	Arg	Asp	Phe	Ala	Ala	Tyr	355	360	365
Arg	Ser	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln			

370 375 380

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
385 390 395 400

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
405 410 415

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
420 425 430

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
435 440 445

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
450 455 460

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
465 470 475 480

Pro Arg

<210> 147
<211> 1449
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> NM-21517CARDNALxH

<400> 147
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60
ccggaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg ggaaagagcc 120
accctctcct gcagggccag tcagagtgtt agcagctact tagcctggta ccaacagaaa 180
cctggccagg ctcccaggct cctcatctat gatgcatcca acagggccac tggcatccca 240
gccaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagcctagag 300

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cctgaagatt ttgcagttta ttactgtcag cagagacacg tctggcctcc tacttttggc      360
ggagggacca aggttgagat caaacggggg tctacatccg gctccgggaa gcccgggaagt      420
ggcgaaggta gtacaaaggg gcagctgcag ctgcaggagt cgggcccagg actggtgaag      480
ccttcggaga ccctgtccct cacctgcact gtctctggtg gctccatcag cagtagtagt      540
tactactggg gctggatccg ccagccccc a g g g a a g g g g c t g g a g t g g a t t g g g a g t a t c      600
tcctatagtg ggagcaccta ctacaacccg tccctcaaga gtcgagtcac catatccgta      660
gacacgtcca agaaccagtt ctccctgaag ctgagttctg tgaccgccgc agacacggcg      720
gtgtactact gcgccagagg caggggatat gcaaccagct tagccttcga tatctgggggt      780
caggggtacaa tgggtcacctg ctctcagcc gctgcccttg ataataaaaa gtcaaacgga      840
acaatcattc acgtgaaggg caagcacctc tgtccgtcac ccttgttccc tgggtccatcc      900
aagccattct ggggtgttggg cgtagtgggt ggagtcctcg cttgttactc tctgctcgtc      960
accgtggctt ttataatctt ctgggttaga tccaaaagaa gccgcctgct ccatagcgat     1020
tacatgaata tgactccacg ccgccctggc cccacaagga aacactacca gccttacgca     1080
ccacctagag atttcgctgc ctatcgagc aggggtgaagt tttccagatc tgcagatgca     1140
ccagcgtatc agcagggcc a gaaccaactg tataacgagc tcaacctggg acgcagggaa     1200
gagtatgacg ttttggacaa gcgcagagga cgggaccctg agatgggtgg caaaccaaga     1260
cgaaaaaacc cccaggaggg tctctataat gagctgcaga aggataagat ggctgaagcc     1320
tattctgaaa taggcatgaa aggagagcgg agaaggggaa aagggcacga cggtttgtac     1380
cagggactca gactgctac gaaggatact tatgacgctc tccacatgca agccctgcca     1440
cctaggtaa                                         1449

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<210> 148

<211> 482

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<223> NM-21517CARLxH

<400> 148

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

31 Jul 2019
2017240667

Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
225 230 235 240

Val Tyr Tyr Cys Ala Arg Gly Arg Gly Tyr Ala Thr Ser Leu Ala Phe
245 250 255

Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ala Ala
260 265 270

Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys
275 280 285

His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp
290 295 300

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
305 310 315 320

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu
325 330 335

Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr
340 345 350

Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr
355 360 365

Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
370 375 380

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
385 390 395 400

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
405 410 415

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
420 425 430

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
435 440 445

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
450 455 460

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
465 470 475 480

Pro Arg

<210> 149

<211> 1440

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> TS-21522CARDNAHxL

<400> 149

atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc	60
ccggagggtgc agctggtgga gtctggggga ggcttggtac agcctggggg gtccctgaga	120
ctctcctgtg cagcctctgg attcaccttc agtagctata gcatgaactg ggtccgccag	180
gctccaggga aggggctgga gtgggtttca accattagta gtagtagtag taccatatac	240
tacgcagact ctgtgaaggg ccgattcacc atctccagag acaatgcaa gaactcactg	300
tatctgcaaa tgaacagcct gagagctgag gacacggcgg tgtactactg cgccagaggt	360
tctcaggagc acctgatttt cgattattgg ggacagggta cattgggtcac cgtctcctca	420
gggtctacat ccggctccgg gaagcccgga agtggcgaag gtagtacaaa gggggaaatt	480
gtgttgacac agtctccagc caccctgtct ttgtctccag gggaaagagc caccctctcc	540
tgcagggccca gtcagagtgt tagcaggtag ttagcctggg accaacagaa acctggccag	600
gctcccaggc tcctcatcta tgatgcatcc aacagggccca ctggcatccc agccagggtc	660
agtggcagtg ggtctgggac agacttcact ctcacatca gcagcctaga gcctgaagat	720
tttgagttt attactgtca gcagagattc tactaccctt ggacttttgg cggaggggacc	780

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aaggttgaga tcaaacgggc cgctgccctt gataatgaaa agtcaaacgg aacaatcatt      840
cacgtgaagg gcaagcacct ctgtccgtca cccttgttcc ctggtccatc caagccattc      900
tgggtgttgg tcgtagtggg tggagtcctc gcttgttact ctctgctcgt caccgtggct      960
tttataatct tctgggtag atccaaaaga agccgcctgc tccatagcga ttacatgaat     1020
atgactccac gccgccctgg cccacaagg aaacactacc agccttacgc accacctaga     1080
gatttcgctg cctatcggag cagggtgaag ttttccagat ctgcagatgc accagcgtat     1140
cagcagggcc agaaccaact gtataacgag ctcaacctgg gacgcaggga agagtatgac     1200
gttttggaca agcgagagg acgggaccct gagatgggtg gcaaaccaag acgaaaaaac     1260
ccccaggagg gtctctataa tgagctgcag aaggataaga tggctgaagc ctattctgaa     1320
ataggcatga aaggagagcg gagaagggga aaagggcacg acggtttgta ccagggactc     1380
agcactgcta cgaaggatac ttatgacgct ctccacatgc aagccctgcc acctaggtaa     1440

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<210> 150
 <211> 479
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polypeptide

<220>
 <223> TS-21522CARHxL

<400> 150
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
 20 25 30

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
 35 40 45

Thr Phe Ser Ser Tyr Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys
 50 55 60

Gly Leu Glu Trp Val Ser Thr Ile Ser Ser Ser Ser Ser Thr Ile Tyr

65					70					75					80
Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala
				85					90					95	
Lys	Asn	Ser	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr
			100					105					110		
Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Gly	Ser	Gln	Glu	His	Leu	Ile	Phe	Asp
		115					120					125			
Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Ser	Thr	Ser
	130					135					140				
Gly	Ser	Gly	Lys	Pro	Gly	Ser	Gly	Glu	Gly	Ser	Thr	Lys	Gly	Glu	Ile
145					150					155					160
Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly	Glu	Arg
				165					170					175	
Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Arg	Tyr	Leu	Ala
			180					185					190		
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	Tyr	Asp
		195					200					205			
Ala	Ser	Asn	Arg	Ala	Thr	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly
	210					215					220				
Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Glu	Pro	Glu	Asp
225					230					235					240
Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Arg	Phe	Tyr	Tyr	Pro	Trp	Thr	Phe
				245					250					255	
Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Ala	Ala	Ala	Leu	Asp	Asn
			260					265					270		
Glu	Lys	Ser	Asn	Gly	Thr	Ile	Ile	His	Val	Lys	Gly	Lys	His	Leu	Cys
		275					280					285			

31 Jul 2019 2017240667

Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val
290 295 300

Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
305 310 315 320

Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser
325 330 335

Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His
340 345 350

Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg
355 360 365

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
370 375 380

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
385 390 395 400

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
405 410 415

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
420 425 430

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
435 440 445

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
450 455 460

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
465 470 475

<210> 151

<211> 1440

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> TS-21522CARDNALxH

<400> 151

atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc	60
ccggaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg ggaaagagcc	120
accctctcct gcagggccag tcagagtgtt agcagggtact tagcctggta ccaacagaaa	180
cctggccagg ctcccaggct cctcatctat gatgcatcca acagggccac tggcatccca	240
gccaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagcctagag	300
cctgaagatt ttgcagttta ttactgtcag cagagattct actacccttg gacttttggc	360
ggagggacca aggttagat caaacggggg tctacatccg gctccgggaa gcccggaaagt	420
ggcgaaggta gtacaaaggg ggaggtgcag ctggtggagt ctgggggagg cttggtacag	480
cctgggggggt ccctgagact ctctgtgca gcctctggat tcaccttcag tagctatagc	540
atgaactggg tccgccaggc tccagggaag gggctggagt gggtttcaac cattagtagt	600
agtagtagta ccatatacta cgcagactct gtgaagggcc gattcaccat ctccagagac	660
aatgccaaga actcactgta tctgcaaatg aacagcctga gagctgagga cacggcggtg	720
tactactgcg ccagaggttc tcaggagcac ctgattttcg attattgggg acaggggtaca	780
ttggtcaccg tctcctcagc cgctgccctt gataatgaaa agtcaaacgg aacaatcatt	840
cacgtgaagg gcaagcacct ctgtccgtca cccttgttcc ctggtccatc caagccattc	900
tgggtgttgg tcgtagtggg tggagtcctc gcttgttact ctctgctcgt caccgtggct	960
tttataatct tctgggttag atccaaaaga agccgcctgc tccatagcga ttacatgaat	1020
atgactccac gccgccctgg cccacaagg aaacactacc agccttacgc accacctaga	1080
gatttcgctg cctatcgag cagggtgaag ttttccagat ctgcagatgc accagcgtat	1140
cagcagggcc agaaccaact gtataacgag ctcaacctgg gacgcaggga agagtatgac	1200
gttttggaca agcgcagagg acgggaccct gagatgggtg gcaaaccaag acgaaaaaac	1260
ccccaggagg gtctctataa tgagctgcag aaggataaga tggctgaagc ctattctgaa	1320
ataggcatga aaggagagcg gagaagggga aaagggcacg acggtttgta ccagggactc	1380

agcactgcta cgaaggatac ttatgacgct ctccacatgc aagccctgcc acctaggtaa 1440

<210> 152
 <211> 479
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<220>
 <223> TS-21522CARLxH

<400> 152
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu
 20 25 30

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
 35 40 45

Ser Val Ser Arg Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
 50 55 60

Pro Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro
 65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
 85 90 95

Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg
 100 105 110

Phe Tyr Tyr Pro Trp Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 115 120 125

Arg Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser
 130 135 140

Thr Lys Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
 145 150 155 160

31 Jul 2019
2017240667

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
165 170 175

Ser Ser Tyr Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
180 185 190

Glu Trp Val Ser Thr Ile Ser Ser Ser Ser Thr Ile Tyr Tyr Ala
195 200 205

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
210 215 220

Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
225 230 235 240

Tyr Tyr Cys Ala Arg Gly Ser Gln Glu His Leu Ile Phe Asp Tyr Trp
245 250 255

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ala Ala Leu Asp Asn
260 265 270

Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys
275 280 285

Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val
290 295 300

Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
305 310 315 320

Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser
325 330 335

Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His
340 345 350

Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg
355 360 365

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
370 375 380

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
385 390 395 400

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
405 410 415

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
420 425 430

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
435 440 445

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
450 455 460

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
465 470 475

<210> 153

<211> 1449

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> RY-21527CARDNAHxL

<400> 153

atggcactcc ccgtaactgc tctgctgctg ccgttgcat tgctcctgca cgccgcacgc	60
ccgcaggtgc agctggtgga gtctggggga ggcgtggtcc agcctgggag gtccctgaga	120
ctctcctgtg cagcgtctgg attcaccttc agtagctatg gcatgcactg ggtccgccag	180
gctccaggca aggggctgga gtgggtggca gttatatcgt atgatggaag taataaatac	240
tatgcagact ccgtgaaggg ccgattcacc atctccagag acaattccaa gaacacgctg	300
tatctgcaaa tgaacagcct gagagccgag gacacggcgg tgtactactg cgccagaact	360
gacttctgga gcggatcccc tccaggctta gattactggg gacagggtac attggtcacc	420

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gtctcctcag ggtctacatc cggctccggg aagcccggaa gtggcgaagg tagtacaaag      480
ggggacatcc agttgaccca gtctccatct tccgtgtctg catctgtagg agacagagtc      540
accatcactt gtcgggagcg tcagggtatt agcagctggg tagcctggta tcagcagaaa      600
ccagggaag cccctaagct cctgatctat ggtgcatcca gtttgcaaag tgggggtcca      660
tcaaggttca gcggcagtgg atctgggaca gatttcactc tcacatcag cagcctgcag      720
cctgaagatt ttgcaactta ttactgtcag cagatataca cttcccttt cacttttggc      780
ggagggacca aggttgagat caaacgggcc gctgcccttg ataataaaaa gtcaaacgga      840
acaatcattc acgtgaaggg caagcacctc tgtccgtcac cttgttccc tgggtccatcc      900
aagccattct ggggtgttggg cgtagtgggt ggagtcctcg cttgttactc tctgctcgtc      960
accgtggctt ttataatctt ctgggttaga tccaaaagaa gccgcctgct ccatagcgat     1020
tacatgaata tgactccacg ccgccctggc cccacaagga aacactacca gccttacgca     1080
ccacctagag atttcgctgc ctatcggagc aggggtgaagt tttccagatc tgcagatgca     1140
ccagcgtatc agcagggccca gaaccaactg tataacgagc tcaacctggg acgcagggaa     1200
gagtatgacg ttttggacaa gcgcagagga cgggaccctg agatgggtgg caaaccaaga     1260
cgaaaaaacc cccaggaggg tctctataat gagctgcaga aggataagat ggctgaagcc     1320
tattctgaaa taggcatgaa aggagagcgg agaaggggaa aagggcacga cggtttgtac     1380
cagggactca gcaactgtac gaaggatact tatgacgctc tccacatgca agccctgcca     1440
cctaggtaa                                         1449

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<210> 154
 <211> 482
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polypeptide

<220>
 <223> RY-21527CARHxL

<400> 154
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

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

225					230					235					240
Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ile	Tyr	Thr	Phe	Pro
				245					250					255	
Phe	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Ala	Ala	Ala
			260					265					270		
Leu	Asp	Asn	Glu	Lys	Ser	Asn	Gly	Thr	Ile	Ile	His	Val	Lys	Gly	Lys
		275					280					285			
His	Leu	Cys	Pro	Ser	Pro	Leu	Phe	Pro	Gly	Pro	Ser	Lys	Pro	Phe	Trp
	290					295					300				
Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	Cys	Tyr	Ser	Leu	Leu	Val
305					310					315					320
Thr	Val	Ala	Phe	Ile	Ile	Phe	Trp	Val	Arg	Ser	Lys	Arg	Ser	Arg	Leu
				325					330					335	
Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro	Arg	Arg	Pro	Gly	Pro	Thr
			340					345					350		
Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	Arg	Asp	Phe	Ala	Ala	Tyr
		355					360					365			
Arg	Ser	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln
	370					375					380				
Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu
385					390					395					400
Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly
				405					410					415	
Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu
			420					425					430		
Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly
		435					440					445			

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
450 455 460

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
465 470 475 480

Pro Arg

<210> 155

<211> 1449

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> RY-21527CARDNALxH

<400> 155

atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc	60
ccggacatcc agttgaccca gtctccatct tccgtgtctg catctgtagg agacagagtc	120
accatcactt gtcgggcgag tcagggtatt agcagctggg tagcctggta tcagcagaaa	180
ccagggaaaag cccctaagct cctgatctat ggtgcatcca gtttgcaaag tgggggtccca	240
tcaagggttca gcggcagtggt atctgggaca gatttcactc tcacatcag cagcctgcag	300
cctgaagatt ttgcaactta ttactgtcag cagatatata ccttcccttt cacttttggc	360
ggagggacca aggttgagat caaacggggg tctacatccg gctccgggaa gcccggaagt	420
ggcgaaggta gtacaaaggg gcaggtgcag ctggtggagt ctgggggagg cgtgggtccag	480
cctgggaggt ccctgagact ctctgtgca gcgtctggat tcaccttcag tagctatggc	540
atgcactggg tccgccaggc tccaggcaag gggctggagt ggggtggcagt tatatcgtat	600
gatggaagta ataaatacta tgcagactcc gtgaagggcc gattcaccat ctccagagac	660
aattccaaga acacgctgta tctgcaaattg aacagcctga gagccgagga cacggcggtg	720
tactactgcg ccagaactga cttctggagc ggatcccctc caggcttaga ttactgggga	780
caggggtacat tggtcaccgt ctctcagcc gctgcccttg ataataaaaa gtcaaacgga	840

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acaatcattc acgtgaaggg caagcacctc tgtccgtcac cttgttccc tgggtccatcc      900
aagccattct ggggtgttggg cgtagtgggt ggagtcctcg cttgttactc tctgctcgtc      960
accgtggcctt ttataatctt ctgggttaga tccaaaagaa gccgcctgct ccatagcgat     1020
tacatgaata tgactccacg ccgccctggc cccacaagga aacactacca gccttacgca     1080
ccacctagag atttcgctgc ctatcggagc aggggtgaagt tttccagatc tgcagatgca     1140
ccagcgtatc agcagggcca gaaccaactg tataacgagc tcaacctggg acgcagggaa     1200
gagtatgacg ttttggacaa gcgcagagga cgggaccctg agatgggtgg caaaccaaga     1260
cgaaaaaacc cccaggaggg tctctataat gagctgcaga aggataagat ggctgaagcc     1320
tattctgaaa taggcatgaa aggagagcgg agaaggggaa aagggcacga cggtttgtac     1380
cagggactca gcactgctac gaaggatact tatgacgctc tccacatgca agccctgcca     1440
cctaggtaa                                           1449

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<210> 156
 <211> 482
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polypeptide

<220>
 <223> RY-21527CARLxH

<400> 156
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Val
 20 25 30

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
 35 40 45

Gly Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala
 50 55 60

Pro Lys Leu Leu Ile Tyr Gly Ala Ser Ser Leu Gln Ser Gly Val Pro
 65 70 75 80

31 Jul 2019
2017240667

Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	85	90	95
Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ile	100	105	110
Tyr	Thr	Phe	Pro	Phe	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	115	120	125
Arg	Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys	Pro	Gly	Ser	Gly	Glu	Gly	Ser	130	135	140
Thr	Lys	Gly	Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	145	150	155
Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	165	170	175
Ser	Ser	Tyr	Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	180	185	190
Glu	Trp	Val	Ala	Val	Ile	Ser	Tyr	Asp	Gly	Ser	Asn	Lys	Tyr	Tyr	Ala	195	200	205
Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	210	215	220
Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	225	230	235
Tyr	Tyr	Cys	Ala	Arg	Thr	Asp	Phe	Trp	Ser	Gly	Ser	Pro	Pro	Gly	Leu	245	250	255
Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ala	Ala	260	265	270
Leu	Asp	Asn	Glu	Lys	Ser	Asn	Gly	Thr	Ile	Ile	His	Val	Lys	Gly	Lys	275	280	285

His	Leu	Cys	Pro	Ser	Pro	Leu	Phe	Pro	Gly	Pro	Ser	Lys	Pro	Phe	Trp
290						295					300				
Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	Cys	Tyr	Ser	Leu	Leu	Val
305					310					315					320
Thr	Val	Ala	Phe	Ile	Ile	Phe	Trp	Val	Arg	Ser	Lys	Arg	Ser	Arg	Leu
				325					330					335	
Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro	Arg	Arg	Pro	Gly	Pro	Thr
			340					345					350		
Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	Arg	Asp	Phe	Ala	Ala	Tyr
		355					360					365			
Arg	Ser	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln
	370					375					380				
Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu
385					390					395					400
Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly
				405					410					415	
Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu
			420					425					430		
Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly
		435					440					445			
Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser
	450					455					460				
Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro
465					470					475					480
Pro	Arg														

<210> 157
<211> 1479

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> PP-21528CARDNAHxL

<400> 157

atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc	60
ccgcaggtgc agctggtgca gtctggggct gaggtgaaga agcctgggtc ctcggtgaag	120
gtctcctgca aggcttctgg aggcaccttc agcagctatg ctatcagctg ggtgcgacag	180
gcccctggac aagggttga gtggatggga gggatcatcc ctatctttgg tacagcaaac	240
tacgcacaga agttccaggg cagagtcacg attaccgcgg acgaatccac gagcacagcc	300
tacatggagc tgagcagcct gagatctgag gacacggcgg tgtactactg cgccagaact	360
cctgaatact cctccagcat atggcactat tactacggca tggacgtatg gggccaggga	420
acaactgtca ccgtctcctc agggctctaca tccggctccg ggaagcccgg aagtggcgaa	480
ggtagtaciaa agggggacat cgtgatgacc cagtctccag actccctggc tgtgtctctg	540
ggcgagaggg ccaccatcaa ctgcaagtcc agccagagtg ttttatacag ctccaacaat	600
aagaactact tagcttggtgta ccagcagaaa ccaggacagc ctcctaagct gctcatttac	660
tgggcatcta cccgggaatc cgggggtccct gaccgattca gtggcagcgg gtctgggaca	720
gatttcactc tcaccatcag cagcctgcag gctgaagatg tggcagttta ttactgtcag	780
cagttcgccc acactccttt cacttttggc ggagggacca aggttgagat caaacgggcc	840
gctgcccttg ataataaaaa gtcaaacgga acaatcattc acgtgaaggg caagcacctc	900
tgtccgtcac cttgtttccc tgggtccatcc aagccattct gggtgttggt cgtagtgggt	960
ggagtcctcg cttgttactc tctgctcgtc accgtggctt ttataatctt ctgggttaga	1020
tcacaaaagaa gccgcctgct ccatagcgat tacatgaata tgactccacg ccgccctggc	1080
cccacaagga aacactacca gccttacgca ccacctagag atttcgctgc ctatcggagc	1140
agggtgaagt tttccagatc tgcagatgca ccagcgtatc agcagggcca gaaccaactg	1200
tataacgagc tcaacctggg acgcagggaa gagtatgacg ttttggacaa gcgcagagga	1260
cgggaccctg agatgggtgg caaaccaaga cgaacaaacc cccaggaggg tctctataat	1320

gagctgcaga aggataagat ggctgaagcc tattctgaaa taggcatgaa aggagagcgg 1380
 agaaggggaa aagggcacga cggtttgtac cagggactca gcaactgctac gaaggatact 1440
 tatgacgctc tccacatgca agccctgcca cctaggtaa 1479

<210> 158
 <211> 492
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<220>
 <223> PP-21528CARHxL

<400> 158
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
 20 25 30

Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly
 35 40 45

Thr Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln
 50 55 60

Gly Leu Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn
 65 70 75 80

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser
 85 90 95

Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
 100 105 110

Ala Val Tyr Tyr Cys Ala Arg Thr Pro Glu Tyr Ser Ser Ser Ile Trp
 115 120 125

His Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr

130	135	140
Val 145 Ser Ser Gly Ser Thr 150 Ser Gly Ser Gly Lys 155 Pro Gly Ser Gly Glu 160		
Gly Ser Thr Lys 165 Gly Asp Ile Val Met Thr 170 Gln Ser Pro Asp Ser 175 Leu		
Ala Val Ser 180 Leu Gly Glu Arg Ala Thr 185 Ile Asn Cys Lys Ser Ser Gln		
Ser Val 195 Leu Tyr Ser Ser Asn 200 Asn Lys Asn Tyr Leu Ala Trp Tyr Gln		
Gln Lys 210 Pro Gly Gln Pro 215 Pro Lys Leu Leu Ile Tyr 220 Trp Ala Ser Thr		
Arg Glu Ser Gly Val 230 Pro Asp Arg Phe Ser Gly 235 Ser Gly Ser Gly Thr 240		
Asp Phe Thr Leu Thr 245 Ile Ser Ser Leu Gln 250 Ala Glu Asp Val Ala Val 255		
Tyr Tyr Cys Gln 260 Gln Phe Ala His Thr 265 Pro Phe Thr Phe Gly 270 Gly Gly Gly		
Thr Lys 275 Val Glu Ile Lys Arg Ala 280 Ala Ala Leu Asp Asn 285 Glu Lys Ser		
Asn Gly 290 Thr Ile Ile His Val 295 Lys Gly Lys His Leu 300 Cys Pro Ser Pro		
Leu Phe Pro Gly Pro 310 Ser Lys Pro Phe Trp Val 315 Leu Val Val Val Gly 320		
Gly Val Leu Ala Cys 325 Tyr Ser Leu Leu Val 330 Thr Val Ala Phe Ile Ile 335		
Phe Trp Val 340 Arg Ser Lys Arg Ser Arg 345 Leu Leu His Ser Asp 350 Tyr Met		

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
355 360 365

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe
370 375 380

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
385 390 395 400

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
405 410 415

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
420 425 430

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
435 440 445

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
450 455 460

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
465 470 475 480

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 159
<211> 1479
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> PP-21528CARDNALxH

<400> 159
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60
ccggacatcg tgatgaccga gtctccagac tccctggctg tgtctctggg cgagagggcc 120

accatcaact gcaagtccag ccagagtgtt ttatacagct ccaacaataa gaactactta	180
gcttgggtacc agcagaaaacc aggacagcct cctaagctgc tcattttactg ggcatctacc	240
cgggaatccg ggggtccctga ccgattcagt ggcagcgggt ctgggacaga tttcactctc	300
accatcagca gcctgcaggc tgaagatgtg gcagttttatt actgtcagca gttcgcccac	360
actcctttca cttttggcgg agggaccaag gttgagatca aacgggggtc tacatccggc	420
tccgggaagc ccggaagtgg cgaaggtagt acaaaggggc aggtgcagct ggtgcagtct	480
ggggctgagg tgaagaagcc tgggtcctcg gtgaaggtct cctgcaaggc ttctggaggc	540
accttcagca gctatgctat cagctgggtg cgacaggccc ctggacaagg gcttgagtgg	600
atgggaggga tcatccctat ctttgggtaca gcaaactacg cacagaagtt ccagggcaga	660
gtcacgatta ccgcggacga atccacgagc acagcctaca tggagctgag cagcctgaga	720
tctgaggaca cggcgggtgta ctactgcgcc agaactcctg aatactcctc cagcatatgg	780
cactattact acggcatgga cgtatggggc cagggaacaa ctgtcaccgt ctcctcagcc	840
gctgcccttg ataataaaaa gtcaaacgga acaatcattc acgtgaaggg caagcacctc	900
tgtccgtcac ctttgttccc tgggtccatcc aagccattct ggggtgttggc cgtagtgggt	960
ggagtcctcg cttgttactc tctgctcgtc accgtggctt ttataatctt ctgggttaga	1020
tccaaaagaa gccgcctgct ccatagcgat tacatgaata tgactccacg ccgccctggc	1080
cccacaagga aacactacca gccttacgca ccacctagag atttcgctgc ctatcggagc	1140
agggtgaagt tttccagatc tgcagatgca ccagcgtatc agcagggccca gaaccaactg	1200
tataacgagc tcaacctggg acgcaggga gagtatgacg ttttggacaa gcgcagagga	1260
cgggaccctg agatgggtgg caaaccaaga cgaaaaaacc cccaggaggg tctctataat	1320
gagctgcaga aggataagat ggctgaagcc tattctgaaa taggcatgaa aggagagcgg	1380
agaaggggaa aagggcacga cggtttgtac cagggactca gcactgctac gaaggatact	1440
tatgacgctc tccacatgca agccctgcc cctaggtaa	1479

<210> 160

<211> 492

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

polypeptide

<220>

<223> PP-21528CARLxH

<400> 160

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu
20 25 30

Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln
35 40 45

Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln
50 55 60

Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr
65 70 75 80

Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
85 90 95

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val
100 105 110

Tyr Tyr Cys Gln Gln Phe Ala His Thr Pro Phe Thr Phe Gly Gly Gly
115 120 125

Thr Lys Val Glu Ile Lys Arg Gly Ser Thr Ser Gly Ser Gly Lys Pro
130 135 140

Gly Ser Gly Glu Gly Ser Thr Lys Gly Gln Val Gln Leu Val Gln Ser
145 150 155 160

Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys
165 170 175

Ala Ser Gly Gly Thr Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln
180 185 190

Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	Gly	Gly	Ile	Ile	Pro	Ile	Phe	195	200	205
Gly	Thr	Ala	Asn	Tyr	Ala	Gln	Lys	Phe	Gln	Gly	Arg	Val	Thr	Ile	Thr	210	215	220
Ala	Asp	Glu	Ser	Thr	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	225	230	235
Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Thr	Pro	Glu	Tyr	Ser	245	250	255
Ser	Ser	Ile	Trp	His	Tyr	Tyr	Tyr	Gly	Met	Asp	Val	Trp	Gly	Gln	Gly	260	265	270
Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ala	Ala	Leu	Asp	Asn	Glu	Lys	Ser	275	280	285
Asn	Gly	Thr	Ile	Ile	His	Val	Lys	Gly	Lys	His	Leu	Cys	Pro	Ser	Pro	290	295	300
Leu	Phe	Pro	Gly	Pro	Ser	Lys	Pro	Phe	Trp	Val	Leu	Val	Val	Val	Gly	305	310	315
Gly	Val	Leu	Ala	Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	325	330	335
Phe	Trp	Val	Arg	Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	340	345	350
Asn	Met	Thr	Pro	Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	355	360	365
Tyr	Ala	Pro	Pro	Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser	Arg	Val	Lys	Phe	370	375	380
Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	385	390	395
Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	405	410	415

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
420 425 430

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
435 440 445

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
450 455 460

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
465 470 475 480

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 161
<211> 1452
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> RD-21530CARDNAHxL

<400> 161
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60
ccgcaggtgc agctggtgga gtctggggga ggcgtggtcc agcctgggag gtccctgaga 120
ctctcctgtg cagcgtctgg attcaccttc agtagctatg gcatgcactg ggtccgccag 180
gctccaggca aggggctgga gtgggtggca gttatatcgt atgatggaag taataaatac 240
tatgcagact ccgtgaaggg ccgattcacc atctccagag acaattccaa gaacacgctg 300
tatctgcaaa tgaacagcct gagagccgag gacacggcgg tgtactactg cgtcaagggg 360
ccgttgcagg agccgccata cgattatgga atggacgtat ggggccaggg aacaactgtc 420
accgtctcct cagggtctac atccggctcc gggaagcccg gaagtggcga aggtagtaca 480
aagggggaaa tagtgatgac gcagtctcca gccaccctgt ctgtgtctcc aggggaaaga 540
gccaccctct cctgcagggc cagtcagagt gttagcagca acttagcctg gtaccagcag 600

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aaacctggcc aggctcccag gtcctcatc tatagcgcac ccaccagggc cactggtatc      660
ccagccaggt tcagtggcag tgggtctggg acagagttca ctctcaccat cagcagcctg      720
cagtctgaag attttgcagt ttattactgt cagcagcacc acgtctggcc tctcactttt      780
ggcggaggga ccaaggttga gatcaaacgg gccgctgccc ttgataatga aaagtcaaac      840
ggaacaatca ttcacgtgaa gggcaagcac ctctgtccgt cacccttggt ccctggtcca      900
tccaagccat tctgggtggt ggtcgtagt ggtggagtcc tcgcttggtta ctctctgctc      960
gtcaccgtgg cttttataat cttctgggtt agatccaaaa gaagccgcct gtcctatagc     1020
gattacatga atatgactcc acgccgccct ggccccacaa ggaaacacta ccagccttac     1080
gcaccaccta gagatttcgc tgcctatcgg agcagggtga agttttccag atctgcagat     1140
gcaccagcgt atcagcaggg ccagaaccaa ctgtataacg agctcaacct gggacgcagg     1200
gaagagtatg acgttttgga caagcgcaga ggacgggacc ctgagatggg tggcaaacca     1260
agacgaaaaa acccccagga gggctctctat aatgagctgc agaaggataa gatggctgaa     1320
gcctattctg aaatagggcat gaaaggagag cggagaaggg gaaaagggca cgacggtttg     1380
taccagggac tcagcactgc tacgaaggat acttatgacg ctctccacat gcaagccctg     1440
ccacctaggt aa                                                              1452

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<210> 162
 <211> 483
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<220>
 <223> RD-21530CARHxL

<400> 162
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val
 20 25 30

Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe

		35				40				45							
Thr	Phe	Ser	Ser	Tyr	Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys		
	50					55					60						
Gly	Leu	Glu	Trp	Val	Ala	Val	Ile	Ser	Tyr	Asp	Gly	Ser	Asn	Lys	Tyr		
65					70					75				80			
Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser		
				85					90					95			
Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr		
			100					105					110				
Ala	Val	Tyr	Tyr	Cys	Val	Lys	Gly	Pro	Leu	Gln	Glu	Pro	Pro	Tyr	Asp		
		115					120					125					
Tyr	Gly	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser		
	130					135					140						
Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys	Pro	Gly	Ser	Gly	Glu	Gly	Ser	Thr		
145					150					155					160		
Lys	Gly	Glu	Ile	Val	Met	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Val	Ser		
				165					170					175			
Pro	Gly	Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser		
			180					185					190				
Ser	Asn	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu		
		195					200					205					
Leu	Ile	Tyr	Ser	Ala	Ser	Thr	Arg	Ala	Thr	Gly	Ile	Pro	Ala	Arg	Phe		
	210					215					220						
Ser	Gly	Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu		
225					230					235					240		
Gln	Ser	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	His	His	Val	Trp		
				245					250					255			

Pro	Leu	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Ala	Ala	
			260					265					270			
Ala	Leu	Asp	Asn	Glu	Lys	Ser	Asn	Gly	Thr	Ile	Ile	His	Val	Lys	Gly	
		275					280					285				
Lys	His	Leu	Cys	Pro	Ser	Pro	Leu	Phe	Pro	Gly	Pro	Ser	Lys	Pro	Phe	
	290					295					300					
Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	Cys	Tyr	Ser	Leu	Leu	
305					310					315					320	
Val	Thr	Val	Ala	Phe	Ile	Ile	Phe	Trp	Val	Arg	Ser	Lys	Arg	Ser	Arg	
			325						330					335		
Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro	Arg	Arg	Pro	Gly	Pro	
			340					345					350			
Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	Arg	Asp	Phe	Ala	Ala	
		355					360					365				
Tyr	Arg	Ser	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	
	370					375					380					
Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	
385					390					395					400	
Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	
			405						410					415		
Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	
			420					425					430			
Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	
		435					440					445				
Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	
	450					455					460					
Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	

465	470	475	480
Pro	Pro	Arg	
<210> 163 <211> 1452 <212> DNA <213> Artificial Sequence			
<220> <223> Description of Artificial Sequence: Synthetic polynucleotide			
<220> <223> RD-21530CARDNALxH			
<400> 163			
atggcactcc	ccgtaactgc	tctgctgctg	ccgttggcat
tgctcctgca	cgccgcacgc	60	
ccggaaatag	tgatgacgca	gtctccagcc	accctgtctg
tgtctccagg	ggaaagagcc	120	
accctctcct	gcagggccag	tcagagtgtt	agcagcaact
tagcctggta	ccagcagaaa	180	
cctggccagg	ctcccaggct	cctcatctat	agcgcattcca
ccagggccac	tggtatccca	240	
gccaggttca	gtggcagtgg	gtctgggaca	gagttcactc
tcaccatcag	cagcctgcag	300	
tctgaagatt	ttgcagttta	ttactgtcag	cagcaccacg
tctggcctct	cacttttggc	360	
ggagggacca	aggttgagat	caaacggggg	tctacatccg
gctccgggaa	gcccggaagt	420	
ggcgaaggta	gtacaaaggg	gcaggtgcag	ctgggtggagt
ctgggggagg	cgtgggtccag	480	
cctgggaggt	ccctgagact	ctcctgtgca	gcgtctggat
tcaccttcag	tagctatggc	540	
atgcactggg	tccgccaggc	tccaggcaag	gggctggagt
gggtggcagt	tatatcgtat	600	
gatggaagta	ataaatacta	tgagactcc	gtgaagggcc
gattcaccat	ctccagagac	660	
aattccaaga	acacgctgta	tctgcaaatg	aacagcctga
gagccgagga	cacggcggtg	720	
tactactgcg	tcaaggggcc	gttgacaggag	ccgccatacg
attatggaat	ggacgtatgg	780	
ggccagggaa	caactgtcac	cgtctcctca	gccgctgccc
ttgataatga	aaagtcaaac	840	
ggaacaatca	ttcacgtgaa	gggcaagcac	ctctgtccgt
cacccttggt	ccctgggtcca	900	
tccaagccat	tctgggtggt	ggtcgtagtg	ggtggagtcc
tcgcttggtta	ctctctgctc	960	
gtcaccgtgg	cttttataat	cttctggggt	agatccaaaa
gaagccgcct	gctccatagc	1020	

gattacatga atatgactcc acgccgccct ggccccacaa ggaaacacta ccagccttac 1080
gcaccaccta gagatttcgc tgcctatcgg agcagggtga agttttccag atctgcagat 1140
gcaccagcgt atcagcaggg ccagaaccaa ctgtataacg agctcaacct gggacgcagg 1200
gaagagtatg acgtttttgga caagcgcaga ggacgggacc ctgagatggg tggcaaacca 1260
agacgaaaaa acccccagga gggctctctat aatgagctgc agaaggataa gatggctgaa 1320
gcctattctg aaatagggcat gaaaggagag cggagaaggg gaaaagggca cgacggtttg 1380
taccagggac tcagcactgc tacgaaggat acttatgacg ctctccacat gcaagccctg 1440
ccacctaggt aa 1452

<210> 164
<211> 483
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<223> RD-21530CARLxH

<400> 164
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu
20 25 30

Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
35 40 45

Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr Ser Ala Ser Thr Arg Ala Thr Gly Ile Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
85 90 95

Ser	Ser	Leu	Gln	Ser	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	His	100	105	110
His	Val	Trp	Pro	Leu	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	115	120	125
Arg	Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys	Pro	Gly	Ser	Gly	Glu	Gly	Ser	130	135	140
Thr	Lys	Gly	Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	145	150	155
Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	165	170	175
Ser	Ser	Tyr	Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	180	185	190
Glu	Trp	Val	Ala	Val	Ile	Ser	Tyr	Asp	Gly	Ser	Asn	Lys	Tyr	Tyr	Ala	195	200	205
Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	210	215	220
Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	225	230	235
Tyr	Tyr	Cys	Val	Lys	Gly	Pro	Leu	Gln	Glu	Pro	Pro	Tyr	Asp	Tyr	Gly	245	250	255
Met	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ala	260	265	270
Ala	Leu	Asp	Asn	Glu	Lys	Ser	Asn	Gly	Thr	Ile	Ile	His	Val	Lys	Gly	275	280	285
Lys	His	Leu	Cys	Pro	Ser	Pro	Leu	Phe	Pro	Gly	Pro	Ser	Lys	Pro	Phe	290	295	300
Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	Cys	Tyr	Ser	Leu	Leu	305	310	315
																		320

31 Jul 2019
2017240667

Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
325 330 335

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
340 345 350

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
355 360 365

Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
370 375 380

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
385 390 395 400

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
405 410 415

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
420 425 430

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
435 440 445

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
450 455 460

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
465 470 475 480

Pro Pro Arg

<210> 165

<211> 1440

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>

<223> anti-CLL-1 CAR construct

<400> 165

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ctgacgtgca cggtcagtgg cggctccatc tcctcctatt attggtcatg gatacgacaa	180
ccccaggtta agggcctgga atggattggc tatatctact attcaggaag cacgaactac	240
aatcccagcc tgaagtcccg agtgacaatt tcagtagata ccagtaaaaa ccagttcagt	300
cttaaaactgt caagcgtgac agctgccgac accgctgtgt attactgcgt ctactggtg	360
tattgtggag gggattgtta tagcgggttc gattattggg gacaggggaac cctggtgact	420
gtatcttccg gcggcggcgg ctcaggggggt ggcggtagtg gcggtggggg ttccgatatt	480
caactgacac aatccccag ctactcagc gccagcgtgg gggacagggt tagctttacc	540
tgtcaagcct ctcaggatat aaataacttt ctgaactggt atcaacagaa gcctgggaag	600
gcgcccaaac tcctgatcta tgatgcgtcc aacctggaaa ctggcgtgcc ttcacgcttt	660
agcggctctg gcagtggtag agacttcact tttaccatct cttcacttca gccggaggac	720
atgccacat attactgtca acagtacgga aacttgccct ttacttttgg aggcggcacc	780
aaagttgaaa tcaaaagggc cgctgccctg gataacgaaa agagcaatgg gactataata	840
catgttaaag gaaaacacct gtgtccatct cccctgttcc ctggaccgtc aaagccattt	900
tgggtgctcg tggttgtcgg tggcgttctc gcctgttata gcttgctggt gacagtagcc	960
ttcattatct tttgggtgag atccaaaaga agccgcctgc tccatagcga ttacatgaat	1020
atgactccac gccgccctgg cccacaagg aaactactacc agccttacgc accacctaga	1080
gatttcgctg cctatcggag cagggtgaag ttttccagat ctgcagatgc accagcgtat	1140
cagcagggcc agaaccaact gtataacgag ctcaacctgg gacgcaggga agagtatgac	1200
gttttggaca agcgcagagg acgggaccct gagatgggtg gcaaaccaag acgaaaaaac	1260
ccccaggagg gtctctataa tgagctgcag aaggataaga tggctgaagc ctattctgaa	1320
ataggcatga aaggagagcg gagaagggga aaagggcacg acggtttgta ccagggactc	1380
agcactgcta cgaaggatac ttatgacgct ctccacatgc aagccctgcc acctaggtaa	1440

<210> 166
 <211> 479
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<220>
 <223> anti-CLL-1 CAR construct

<400> 166
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu
 20 25 30

Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly
 35 40 45

Ser Ile Ser Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys
 50 55 60

Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr
 65 70 75 80

Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys
 85 90 95

Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
 100 105 110

Val Tyr Tyr Cys Val Ser Leu Val Tyr Cys Gly Gly Asp Cys Tyr Ser
 115 120 125

Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
 130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
 145 150 155 160

Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg

				165					170					175			
Val	Ser	Phe	Thr	Cys	Gln	Ala	Ser	Gln	Asp	Ile	Asn	Asn	Phe	Leu	Asn		
			180					185					190				
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Asp		
		195					200					205					
Ala	Ser	Asn	Leu	Glu	Thr	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly		
	210					215					220						
Ser	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp		
225					230				235						240		
Ile	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr	Gly	Asn	Leu	Pro	Phe	Thr	Phe		
				245					250					255			
Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Ala	Ala	Ala	Leu	Asp	Asn		
			260					265					270				
Glu	Lys	Ser	Asn	Gly	Thr	Ile	Ile	His	Val	Lys	Gly	Lys	His	Leu	Cys		
		275					280					285					
Pro	Ser	Pro	Leu	Phe	Pro	Gly	Pro	Ser	Lys	Pro	Phe	Trp	Val	Leu	Val		
	290					295					300						
Val	Val	Gly	Gly	Val	Leu	Ala	Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala		
305					310					315					320		
Phe	Ile	Ile	Phe	Trp	Val	Arg	Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser		
				325					330					335			
Asp	Tyr	Met	Asn	Met	Thr	Pro	Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His		
			340					345					350				
Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser	Arg		
		355					360					365					
Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln		
	370					375					380						

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
385 390 395 400

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
405 410 415

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
420 425 430

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
435 440 445

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
450 455 460

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
465 470 475

<210> 167
<211> 1374
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 167
caggtccaac tgcaagaaag cggacccgga ctggtgaagc cttctgagac acttagtctg 60
acgtgcacgg tcagtggcgg ctccatctcc tcctattatt ggtcatggat acgacaaccc 120
ccaggtaagg gcctggaatg gattggctat atctactatt caggaagcac gaactacaat 180
cccagcctga agtcccgagt gacaatttca gtagatacca gtaaaaacca gttcagtctt 240
aaactgtcaa gcgtgacagc tgccgacacc gctgtgtatt actgcgtctc actggtgtat 300
tgtggagggg attgttatag cgggttcgat tattggggac agggaaccct ggtgactgta 360
tcttccggcg gcggcggctc agggggtggc ggtagtggcg gtgggggttc cgatattcaa 420
ctgacacaat ccccagctc actcagcgcc agcgtggggg acagggttag ctttacctgt 480

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caagcctctc aggatataaa taactttctg aactggtatc aacagaagcc tgggaaggcg      540
cccaaactcc tgatctatga tgcgtccaac ctggaaactg gcgtgccttc acgctttagc      600
ggctctggca gtggtacaga cttcactttt accatctctt cacttcagcc ggaggacatc      660
gccacatatt actgtcaaca gtacggaaac ttgcccttta cttttggagg cggcaccaaa      720
gttgaaatca aaagggccgc tgccctggat aacgaaaaga gcaatgggac tataatacat      780
gttaaaggaa aacacctgtg tccatctccc ctgttccttg gaccgtcaaa gccattttgg      840
gtgctcgtgg ttgtcgggtg cgttctcgcc tgttatagct tgctggtgac agtagccttc      900
attatctttt gggtgagatc caaaagaagc cgctgctcc atagcgatta catgaatatg      960
actccacgcc gccctggccc cacaaggaaa cactaccagc cttacgcacc acctagagat     1020
ttcgctgcct atcggagcag ggtgaagttt tccagatctg cagatgcacc agcgtatcag     1080
cagggccaga accaactgta taacgagctc aacctgggac gcaggggaaga gtatgacgtt     1140
ttggacaagc gcagaggacg ggaccctgag atgggtggca aaccaagacg aaaaaacccc     1200
caggagggtc tctataatga gctgcagaag gataagatgg ctgaagccta ttctgaaata     1260
ggcatgaaag gagagcggag aaggggaaaa gggcacgacg gtttgtacca gggactcagc     1320
actgctacga aggatactta tgacgctctc cacatgcaag ccctgccacc tagg           1374

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<210> 168
 <211> 458
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<220>
 <223> anti-CLL-1 CAR construct

<400> 168
 Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
 20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45

31 Jul 2019
2017240667

Gly	Tyr	Ile	Tyr	Tyr	Ser	Gly	Ser	Thr	Asn	Tyr	Asn	Pro	Ser	Leu	Lys	50	55	60	
Ser	Arg	Val	Thr	Ile	Ser	Val	Asp	Thr	Ser	Lys	Asn	Gln	Phe	Ser	Leu	65	70	75	80
Lys	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Val	85	90	95	
Ser	Leu	Val	Tyr	Cys	Gly	Gly	Asp	Cys	Tyr	Ser	Gly	Phe	Asp	Tyr	Trp	100	105	110	
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	115	120	125	
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Gln	Leu	Thr	Gln	Ser	130	135	140	
Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Ser	Phe	Thr	Cys	145	150	155	160
Gln	Ala	Ser	Gln	Asp	Ile	Asn	Asn	Phe	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	165	170	175	
Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Asp	Ala	Ser	Asn	Leu	Glu	180	185	190	
Thr	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	195	200	205	
Thr	Phe	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	210	215	220	
Cys	Gln	Gln	Tyr	Gly	Asn	Leu	Pro	Phe	Thr	Phe	Gly	Gly	Gly	Thr	Lys	225	230	235	240
Val	Glu	Ile	Lys	Arg	Ala	Ala	Ala	Leu	Asp	Asn	Glu	Lys	Ser	Asn	Gly	245	250	255	

Thr	Ile	Ile	His	Val	Lys	Gly	Lys	His	Leu	Cys	Pro	Ser	Pro	Leu	Phe	
			260					265					270			
Pro	Gly	Pro	Ser	Lys	Pro	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	
		275					280					285				
Leu	Ala	Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Phe	Trp	
	290					295					300					
Val	Arg	Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	
305					310					315					320	
Thr	Pro	Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	
				325					330					335		
Pro	Pro	Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser	Arg	Val	Lys	Phe	Ser	Arg	
			340					345					350			
Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	
		355					360					365				
Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	
	370					375					380					
Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	
385					390					395					400	
Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	
				405					410					415		
Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	
			420					425					430			
Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	
		435					440					445				
Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg							
	450					455										

<210> 169

<211> 1467

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> anti-CLL-1 CAR construct

<400> 169

atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc	60
ccgcaggtgc agctgcagga atccggaccg gggctggtga agcccagcga gactctgagt	120
ctcacgtgta cagtttctgg aggtagcatt agctcctact attggtcatg gataaggcag	180
ccccccggga agggattgga atggatcggc tatatttact acagtgggag caccaattac	240
aaccctcac tgaagtctag agttacaatc agcgttgaca cctcaaagaa tcagttcagt	300
ttgaaattgt ctagcgtcac agcagctgat acagccgtct attattgtgt ttctctggtc	360
tattgcggtg gggattgtta cagtggcttt gactattggg ggcagggtac tctggttaca	420
gtttcttccg gggggggagg ctctgggggc ggaggctcag gtggtggagg cagcgacatc	480
cagttgacac agagcccagag ttccttgtcc gcctccgtcg gggatagagt gtcatttacc	540
tgtaggcct ctcaggatat taataacttt ctgaattggt atcagcaaaa gcccggaaag	600
gcaccaagc tgttgattta cgacgccagt aacctggaga caggcgtgcc ctcccgttt	660
agtggtagcg gaagcggtag ggattttacc ttactatca gctctctcca acccgaagac	720
attgcaacct actattgtca acaatatgga aacctgcctt ttacatttgg cggcggcacc	780
aaggtggaga ttaagcgggc ggcagctatt gaggtgatgt atccaccgcc ttacctggat	840
aacgaaaaga gtaacggtac catcattcac gtgaaaggta aacacctgtg tccttctccc	900
ctcttccccg ggccatcaaa gcccttctgg gttcttgtgg tcgtgggagg cgtgcttgct	960
tggtattctc tgctcgttac cgtggcgctt atcatttttt gggtttagatc caaaagaagc	1020
cgctgctcc atagcgatta catgaatatg actccacgcc gccctggccc cacaaggaaa	1080
cactaccagc cttacgcacc acctagagat ttcgctgcct atcggagcag ggtgaagttt	1140
tccagatctg cagatgcacc agcgtatcag cagggccaga accaactgta taacgagctc	1200
aacctgggac gcagggaaga gtatgacgtt ttggacaagc gcagaggacg ggaccctgag	1260
atgggtggca aaccaagacg aaaaaacccc caggagggtc tctataatga gctgcagaag	1320

gataagatgg ctgaagccta ttctgaaata ggcatgaaag gagagcggag aaggggaaaa 1380
 gggcacgacg gtttgtacca gggactcagc actgctacga aggatactta tgacgctctc 1440
 cacatgcaag ccctgccacc taggtaa 1467

<210> 170
 <211> 488
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<220>
 <223> anti-CLL-1 CAR construct

<400> 170
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu
 20 25 30

Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly
 35 40 45

Ser Ile Ser Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys
 50 55 60

Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr
 65 70 75 80

Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys
 85 90 95

Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
 100 105 110

Val Tyr Tyr Cys Val Ser Leu Val Tyr Cys Gly Gly Asp Cys Tyr Ser
 115 120 125

Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly

130		135		140
Gly 145	Gly	Gly	Gly	Gly
Gly	Ser	Gly	Gly	Gly
Gly	Ser	Gly	Gly	Gly
Ser	Gly	Gly	Gly	Ser
Ser	Gly	Gly	Gly	Asp
Ser	Gly	Gly	Gly	Ile 160
Gln	Leu	Thr	Gln	Ser
Leu	Thr	Gln	Ser	Pro
Thr	Gln	Ser	Pro	Ser
Gln	Ser	Pro	Ser	Leu
Ser	Pro	Ser	Leu	Ser
Pro	Ser	Leu	Ser	Ala
Ser	Leu	Ser	Ala	Ser
Leu	Ser	Ala	Ser	Val
Ser	Ala	Ser	Val	Gly
Ala	Ser	Val	Gly	Asp
Ser	Val	Gly	Asp	Arg
Val	Gly	Asp	Arg	
Gly	Asp	Arg		
Asp	Arg			
Ile	Asn	Asn	Phe	Leu
Asn	Phe	Leu	Asn	
Phe	Leu	Asn		
Leu	Asn			
Asn				
Val	Ser	Phe	Thr	Cys
Ser	Phe	Thr	Cys	Gln
Phe	Thr	Cys	Gln	Ala
Thr	Cys	Gln	Ala	Ser
Cys	Gln	Ala	Ser	Gln
Gln	Ala	Ser	Gln	Asp
Ala	Ser	Gln	Asp	Ile
Ser	Gln	Asp	Ile	Asn
Gln	Asp	Ile	Asn	Asn
Asp	Ile	Asn	Asn	Phe
Ile	Asn	Asn	Phe	Leu
Asn	Phe	Leu	Asn	
Phe	Leu	Asn		
Leu	Asn			
Asn				
Trp	Tyr	Gln	Gln	Lys
Tyr	Gln	Lys	Pro	Gly
Gln	Lys	Pro	Gly	Lys
Lys	Pro	Gly	Lys	Ala
Pro	Gly	Lys	Ala	Pro
Ala	Pro	Lys	Leu	Leu
Pro	Lys	Leu	Leu	Ile
Lys	Leu	Ile	Tyr	Asp
Leu	Ile	Tyr	Asp	
Ile	Tyr	Asp		
Tyr	Asp			
Asp				
Ala	Ser	Asn	Leu	Glu
Ser	Asn	Leu	Glu	Thr
Asn	Leu	Glu	Thr	Gly
Leu	Glu	Thr	Gly	Val
Glu	Thr	Gly	Val	Pro
Thr	Gly	Val	Pro	Ser
Gly	Val	Pro	Ser	Arg
Val	Pro	Ser	Arg	Phe
Pro	Ser	Arg	Phe	Ser
Ser	Arg	Phe	Ser	Gly
Arg	Phe	Ser	Gly	Ser
Phe	Ser	Gly	Ser	Gly
Ser	Gly	Ser	Gly	
Gly				
Ser	Gly	Thr	Asp	Phe
Gly	Thr	Asp	Phe	Thr
Thr	Asp	Phe	Thr	Ile
Asp	Phe	Thr	Ile	Ser
Phe	Thr	Ile	Ser	Ser
Thr	Ile	Ser	Ser	Leu
Ile	Ser	Leu	Gln	Pro
Ser	Leu	Gln	Pro	Glu
Leu	Gln	Pro	Glu	Asp
Gln	Pro	Glu	Asp	
Pro	Glu	Asp		
Glu	Asp			
Asp				
Ile	Ala	Thr	Tyr	Tyr
Ala	Thr	Tyr	Tyr	Cys
Thr	Tyr	Tyr	Cys	Gln
Tyr	Tyr	Cys	Gln	Gln
Tyr	Cys	Gln	Gln	Tyr
Cys	Gln	Gln	Tyr	Gly
Gln	Gln	Tyr	Gly	Asn
Gln	Tyr	Gly	Asn	Leu
Tyr	Gly	Asn	Leu	Pro
Gly	Asn	Leu	Pro	Phe
Asn	Leu	Pro	Phe	Thr
Leu	Pro	Phe	Thr	Phe
Pro	Phe	Thr	Phe	
Phe	Thr	Phe		
Thr	Phe			
Phe				
Gly	Gly	Gly	Thr	Lys
Gly	Thr	Lys	Val	Glu
Thr	Lys	Val	Glu	Ile
Lys	Val	Glu	Ile	Lys
Val	Glu	Ile	Lys	Arg
Glu	Ile	Lys	Arg	Ala
Ile	Lys	Arg	Ala	Ala
Lys	Arg	Ala	Ala	Ala
Arg	Ala	Ala	Ile	Glu
Ala	Ala	Ile	Glu	Val
Ala	Ile	Glu	Val	
Ile	Glu	Val		
Glu	Val			
Val				
Met	Tyr	Pro	Pro	Pro
Tyr	Pro	Pro	Tyr	Leu
Pro	Tyr	Leu	Asp	Asn
Pro	Leu	Asp	Asn	Glu
Tyr	Asp	Asn	Glu	Lys
Leu	Asn	Glu	Lys	Ser
Asp	Glu	Lys	Ser	Asn
Asn	Lys	Ser	Asn	Gly
Glu	Ser	Asn	Gly	Thr
Lys	Asn	Gly	Thr	Ile
Ser	Asn	Thr	Ile	
Asn	Thr	Ile		
Gly	Thr			
Thr				
Ile	His	Val	Lys	Gly
His	Val	Lys	Gly	Lys
Val	Lys	Gly	Lys	His
Lys	Gly	Lys	His	Leu
Gly	Lys	His	Leu	Cys
Lys	His	Leu	Cys	Pro
His	Leu	Cys	Pro	Ser
Leu	Cys	Pro	Ser	Pro
Cys	Pro	Ser	Pro	Leu
Pro	Ser	Pro	Leu	Phe
Ser	Pro	Leu	Phe	Pro
Pro	Leu	Phe	Pro	Gly
Leu	Phe	Pro	Gly	
Phe	Pro	Gly		
Pro	Gly			
Gly				
Pro	Ser	Lys	Pro	Phe
Ser	Lys	Pro	Phe	Trp
Lys	Pro	Phe	Trp	Val
Pro	Phe	Trp	Val	Leu
Phe	Trp	Val	Leu	Val
Trp	Val	Leu	Val	Val
Val	Leu	Val	Val	Gly
Val	Val	Gly	Gly	Val
Gly	Val	Val	Val	Leu
Val	Leu	Val	Leu	Ala
Leu	Ala	Leu	Ala	
Ala	Leu	Ala		
Cys	Tyr	Ser	Leu	Leu
Tyr	Ser	Leu	Leu	Val
Ser	Leu	Leu	Val	Thr
Leu	Leu	Val	Thr	Val
Leu	Val	Thr	Val	Ala
Val	Thr	Val	Ala	Phe
Thr	Val	Ala	Phe	Ile
Val	Ala	Phe	Ile	Ile
Ala	Phe	Ile	Ile	Phe
Phe	Ile	Ile	Phe	Trp
Ile	Trp	Val	Arg	
Trp	Val	Arg		
Val	Arg			
Arg				
Ser	Lys	Arg	Ser	Arg
Lys	Arg	Ser	Arg	Leu
Arg	Ser	Arg	Leu	Leu
Ser	Leu	Leu	His	Ser
Leu	Leu	His	Ser	Asp
His	Ser	Asp	Tyr	Met
Ser	Asp	Tyr	Met	Asn
Asp	Tyr	Met	Asn	Met
Tyr	Met	Asn	Met	Thr
Met	Asn	Met	Thr	Pro
Asn	Met	Thr	Pro	
Met	Thr	Pro		
Thr	Pro			
Pro				

Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
355 360 365

Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala
370 375 380

Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
385 390 395 400

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
405 410 415

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
420 425 430

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
435 440 445

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
450 455 460

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
465 470 475 480

His Met Gln Ala Leu Pro Pro Arg
485

<210> 171
<211> 1401
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 171
caggtgcagc tgcaggaatc cggaccgggg ctggtgaagc ccagcgagac tctgagtctc 60
acgtgtacag tttctggagg tagcattagc tcctactatt ggtcatggat aaggcagccc 120

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ccccgggaagg gattggaatg gatcggctat atttactaca gtgggagcac caattacaac      180
ccctcactga agtctagagt tacaatcagc gttgacacct caaagaatca gttcagtttg      240
aaattgtcta gcgtcacagc agctgataca gccgtctatt attgtgtttc tctgggtctat      300
tgcggtgggg attgttacag tggctttgac tattgggggc aggggtactct ggttacagtt      360
tcttccgggg ggggaggctc tgggggcgga ggctcagggtg gtggaggcag cgacatccag      420
ttgacacaga gcccagagttc cttgtccgcc tccgtcgggg atagagtgtc atttacctgt      480
caggcctctc aggatattaa taactttctg aattgggtatc agcaaaagcc cggaaaggca      540
cccaagctgt tgatttacga cgccagtaac ctggagacag gcgtgccctc ccggtttagt      600
ggtagcggaa gcggtacgga ttttaccttt actatcagct ctctccaacc cgaagacatt      660
gcaacctact attgtcaaca atatggaaac ctgcctttta catttggcgg cggcaccaag      720
gtggagatta agcgggcggc agctattgag gtgatgtatc caccgcctta cctggataac      780
gaaaagagta acggtaccat cattcacgtg aaaggtaaac acctgtgtcc ttctcccctc      840
ttccccgggc catcaaagcc cttctgggtt cttgtggtcg tgggaggcgt gcttgcttgt      900
tattctctgc tcgttaccgt ggcgtttatc attttttggg ttagatccaa aagaagccgc      960
ctgctcata gcgattacat gaatatgact ccacgccgcc ctggccccac aaggaaacac     1020
taccagcctt acgcaccacc tagagatttc gctgcctatc ggagcagggt gaagttttcc     1080
agatctgcag atgcaccagc gtatcagcag ggccagaacc aactgtataa cgagctcaac     1140
ctgggacgca gggaagagta tgacgttttg gacaagcgca gaggacggga ccctgagatg     1200
ggtggcaaac caagacgaaa aaacccccag gagggctctt ataatgagct gcagaaggat     1260
aagatggctg aagcctattc tgaaataggc atgaaaggag agcggagaag gggaaaaggg     1320
cacgacggtt tgtaccaggg actcagcact gctacgaagg atacttatga cgctctccac     1380
atgcaagccc tgccacctag g                                     1401

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<210> 172

<211> 467

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<223> anti-CLL-1 CAR construct

<400> 172

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Val
85 90 95

Ser Leu Val Tyr Cys Gly Gly Asp Cys Tyr Ser Gly Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser
130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Ser Phe Thr Cys
145 150 155 160

Gln Ala Ser Gln Asp Ile Asn Asn Phe Leu Asn Trp Tyr Gln Gln Lys
165 170 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu
180 185 190

Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
195 200 205

31 Jul 2019
2017240667

Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr
210 215 220

Cys Gln Gln Tyr Gly Asn Leu Pro Phe Thr Phe Gly Gly Gly Thr Lys
225 230 235 240

Val Glu Ile Lys Arg Ala Ala Ala Ile Glu Val Met Tyr Pro Pro Pro
245 250 255

Tyr Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly
260 265 270

Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe
275 280 285

Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
290 295 300

Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
305 310 315 320

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
325 330 335

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
340 345 350

Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
355 360 365

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
370 375 380

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
385 390 395 400

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
405 410 415

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
420 425 430

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
435 440 445

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
450 455 460

Pro Pro Arg
465

<210> 173
<211> 1548
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 173
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60
ccgcaggtgc aattgcaaga gtccggcccc ggactcgtta aaccagtgga gacgcttagc 120
ctgacctgta ccgtctcagg gggcagcatc tcctcttatt actggagctg gatcaggcag 180
cctccaggaa aaggccttga atggattggg tacatctact actctggctc aacaaattat 240
aatccatccc tgaagtcccg cgtgactatc tctgtggaca ccagcaagaa tcagttttca 300
ctgaagttgt ctagtggttac cgcggccgac accgccgtat actactgtgt gtctcttgtg 360
tactgtggcg gcgactgcta ttccgggttc gactactggg gccaagggac tctggtaacc 420
gtgtcctcag gcggcggcgg gtcaggagga ggcggcagtg gaggtggcgg ctccgacatc 480
cagctgacac aatcaccatc ttccctttca gcttcagtcg gggacagagt gtccttcaca 540
tgccaggcca gccaggatat caataacttc ctgaactggg accaacagaa acccggaag 600
gtccaaagc tcctgatcta tgatgcttcc aacctggaga ccggcgtgcc ctccagggtc 660
agtggttcag gatcaggcac tgactttacg ttcaccatat ccagtcttca gcccgaagac 720
attgcaacct attactgcca acaatacggg aaccttcctt ttacattcgg aggcggcacc 780

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aaggtggaaa tcaaaagggc tgcagcattg agcaactcaa taatgtatTT tagtcacttt      840
gtaccagtgt tcttgccggc taagcctact accacacccg ctccacggcc acctacccca      900
gctcctacca tcgcttcaca gcctctgtcc ctgcgcccag aggcttgccg accggccgca      960
gggggcgctg ttcataccag aggactggat ttgcctgctg atatctatat ctgggcaccc     1020
ctggccggaa cctgcggcgt actcctgctg tccctgggtca tcacgctcta ttgtaatcac     1080
aggaacagat ccaaaagaag cgcctgctc catagcgatt acatgaatat gactccacgc     1140
cgccctggcc ccacaaggaa aactaccag cttacgcac cacctagaga tttcgctgcc     1200
tatcggagca gggatgaagt ttccagatct gcagatgcac cagcgatatca gcagggccag     1260
aaccaactgt ataacgagct caacctggga cgcagggaag agtatgacgt tttggacaag     1320
cgcagaggac gggaccctga gatgggtggc aaaccaagac gaaaaaaccc ccaggagggt     1380
ctctataatg agctgcagaa ggataagatg gctgaagcct attctgaaat aggcatgaaa     1440
ggagagcgga gaaggggaaa agggcacgac ggtttgtacc agggactcag cactgctacg     1500
aaggatactt atgacgctct ccacatgcaa gccctgccac ctaggtaa                     1548

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<210> 174
 <211> 515
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<220>
 <223> anti-CLL-1 CAR construct

<400> 174
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu
 20 25 30

Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly
 35 40 45

Ser Ile Ser Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys

31 Jul 2019

2017240667

50					55					60					
Gly 65	Leu	Glu	Trp	Ile	Gly 70	Tyr	Ile	Tyr	Tyr	Ser 75	Gly	Ser	Thr	Asn	Tyr 80
Asn	Pro	Ser	Leu	Lys 85	Ser	Arg	Val	Thr	Ile 90	Ser	Val	Asp	Thr	Ser	Lys
Asn	Gln	Phe	Ser 100	Leu	Lys	Leu	Ser	Ser 105	Val	Thr	Ala	Ala	Asp 110	Thr	Ala
Val	Tyr	Tyr 115	Cys	Val	Ser	Leu	Val 120	Tyr	Cys	Gly	Gly	Asp 125	Cys	Tyr	Ser
Gly	Phe 130	Asp	Tyr	Trp	Gly	Gln 135	Gly	Thr	Leu	Val	Thr 140	Val	Ser	Ser	Gly
Gly 145	Gly	Gly	Ser	Gly	Gly 150	Gly	Gly	Ser	Gly	Gly 155	Gly	Gly	Ser	Asp	Ile 160
Gln	Leu	Thr	Gln	Ser 165	Pro	Ser	Ser	Leu	Ser 170	Ala	Ser	Val	Gly	Asp 175	Arg
Val	Ser	Phe	Thr 180	Cys	Gln	Ala	Ser	Gln 185	Asp	Ile	Asn	Asn	Phe 190	Leu	Asn
Trp	Tyr	Gln 195	Gln	Lys	Pro	Gly	Lys 200	Ala	Pro	Lys	Leu	Leu 205	Ile	Tyr	Asp
Ala	Ser 210	Asn	Leu	Glu	Thr	Gly 215	Val	Pro	Ser	Arg	Phe 220	Ser	Gly	Ser	Gly
Ser 225	Gly	Thr	Asp	Phe	Thr 230	Phe	Thr	Ile	Ser	Ser 235	Leu	Gln	Pro	Glu	Asp 240
Ile	Ala	Thr	Tyr	Tyr 245	Cys	Gln	Gln	Tyr	Gly 250	Asn	Leu	Pro	Phe	Thr 255	Phe
Gly	Gly	Gly	Thr 260	Lys	Val	Glu	Ile	Lys 265	Arg	Ala	Ala	Ala	Leu	Ser	Asn

Ser Ile Met Tyr Phe Ser His Phe Val Pro Val Phe Leu Pro Ala Lys
275 280 285

Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
290 295 300

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
305 310 315 320

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
325 330 335

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
340 345 350

Val Ile Thr Leu Tyr Cys Asn His Arg Asn Arg Ser Lys Arg Ser Arg
355 360 365

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
370 375 380

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
385 390 395 400

Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
405 410 415

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
420 425 430

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
435 440 445

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
450 455 460

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
465 470 475 480

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu

485

490

495

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
500 505 510

Pro Pro Arg
515

<210> 175
<211> 1482
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 175
caggtgcaat tgcaagagtc cggccccgga ctcgttaaac ccagtgagac gcttagcctg 60
acctgtaccg tctcaggggg cagcatctcc tcttattact ggagctggat caggcagcct 120
ccaggaaaag gccttgaatg gattgggtac atctactact ctggctcaac aaattataat 180
ccatccctga agtcccgcgt gactatctct gtggacacca gcaagaatca gttttcactg 240
aagttgtcta gtgttaccgc ggccgacacc gccgtatact actgtgtgtc tcttgtgtac 300
tgtggcggcg actgctattc cgggttcgac tactggggcc aagggactct ggtaaccgtg 360
tcctcaggcg gcggcgggtc aggaggaggc ggcagtggag gtggcggctc cgacatccag 420
ctgacacaat caccatcttc cttttcagct tcagtcgggg acagagtgtc cttcacatgc 480
caggccagcc aggatatcaa taacttcctg aactgggtacc aacagaaacc cggaaaggct 540
ccaaagctcc tgatctatga tgcttccaac ctggagaccg gcgtgccctc caggttcagt 600
ggttcaggat caggcactga ctttacgttc accatatcca gtcttcagcc cgaagacatt 660
gcaacctatt actgccaaca atacgggaac cttcccttta cattcggagg cggcaccaag 720
gtggaaatca aaagggtgc agcattgagc aactcaataa tgtatttttag tcactttgta 780
ccagtgttct tgccggctaa gcctactacc acaccgctc cacggccacc taccagct 840
cctaccatcg cttcacagcc tctgtccctg cgcccagagg cttgccgacc ggccgcaggg 900

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ggcgctgttc ataccagagg actggatttc gcctgcgata tctatatctg ggcacccctg      960
gccggaacct gcggcggtact cctgctgtcc ctgggtcatca cgctctattg taatcacagg    1020
aacagatcca aaagaagccg cctgctccat agcgattaca tgaatatgac tccacgccgc      1080
cctggcccca caaggaaaca ctaccagcct tacgcaccac ctagagattt cgctgcctat     1140
cggagcaggg tgaagttttc cagatctgca gatgcaccag cgtatcagca gggccagaac     1200
caactgtata acgagctcaa cctgggacgc aggggaagagt atgacgtttt ggacaagcgc     1260
agaggacggg accctgagat ggggtggcaaa ccaagacgaa aaaaccccca ggagggtctc     1320
tataatgagc tgcagaagga taagatggct gaagcctatt ctgaaatagg catgaaagga     1380
gagcggagaa ggggaaaagg gcacgacggt ttgtaccagg gactcagcac tgctacgaag     1440
gatacttatg acgctctcca catgcaagcc ctgccaccta gg                          1482

```

<210> 176
 <211> 494
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polypeptide

<220>
 <223> anti-CLL-1 CAR construct

<400> 176
 Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
 20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
 50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80

Lys	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Val	85	90	95	
Ser	Leu	Val	Tyr	Cys	Gly	Gly	Asp	Cys	Tyr	Ser	Gly	Phe	Asp	Tyr	Trp	100	105	110	
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	115	120	125	
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Gln	Leu	Thr	Gln	Ser	130	135	140	
Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Ser	Phe	Thr	Cys	145	150	155	160
Gln	Ala	Ser	Gln	Asp	Ile	Asn	Asn	Phe	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	165	170	175	
Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Asp	Ala	Ser	Asn	Leu	Glu	180	185	190	
Thr	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	195	200	205	
Thr	Phe	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	210	215	220	
Cys	Gln	Gln	Tyr	Gly	Asn	Leu	Pro	Phe	Thr	Phe	Gly	Gly	Gly	Thr	Lys	225	230	235	240
Val	Glu	Ile	Lys	Arg	Ala	Ala	Ala	Leu	Ser	Asn	Ser	Ile	Met	Tyr	Phe	245	250	255	
Ser	His	Phe	Val	Pro	Val	Phe	Leu	Pro	Ala	Lys	Pro	Thr	Thr	Thr	Pro	260	265	270	
Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	275	280	285	
Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	290	295	300	

31 Jul 2019
2017240667

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
305 310 315 320

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
325 330 335

Cys Asn His Arg Asn Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
340 345 350

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
355 360 365

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val
370 375 380

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
385 390 395 400

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
405 410 415

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
420 425 430

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
435 440 445

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
450 455 460

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
465 470 475 480

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 177

<211> 1440

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> anti-CLL-1 CAR construct

<400> 177

atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc	60
ccggatatcc agctcacgca atccccctca agcttgagtg cctccgtggg cgaccgggtg	120
tccttcacat gtcaggcaag ccaagacata aataatttcc tgaattggta ccaacaaaaa	180
cccggcaagg ctcccaaact cctgatttat gatgcctcca atctggagac cggggtcctt	240
tctagattca gcggaagtgg cagcggcaca gactttacat ttactatctc ttctctgcaa	300
ccagaggaca tcgccacata ctattgccag caatacggca atctgccctt caccttcgga	360
ggcggaaacca aggtagaaat taaaaggggc ggtggaggct ccggaggggg gggctctggc	420
ggagggggct cccaagtaca attgcaggag tcagggcctg gactcgtgaa gccttcagaa	480
actttgtcac tgacatgtac agtgtccggc ggaagcattt ccagttacta ttggctctgg	540
attagacagc caccggcaa aggactggaa tggattggat atatctacta ctctggatct	600
acaaactata atcccagcct caaatccagg gtcactatta gtgtggatac atcaaagaat	660
cagttctcct tgaagctgag ctcagtcact gctgccgaca ccgcagtga ctattgtgtg	720
agcctgggtct actgcggcgg agattgctac agcggtttcg attactgggg ccagggcacc	780
ctggttaccg ttagttccgc ggctgctctt gataacgaga agtccaacgg tacgattatc	840
cacgttaagg gtaagcacct ttgccctagc ccgctgttcc caggccccag taagcccttt	900
tgggtcctcg ttgtggtagg tgggggtactc gcctgctact ccctgctcgt cactgtcgca	960
ttcatcatct tctgggtcag atccaaaaga agccgcctgc tccatagcga ttacatgaat	1020
atgactccac gccgccctgg cccacaagg aaacactacc agccttacgc accacctaga	1080
gatttcgctg cctatcggag cagggtgaag ttttccagat ctgcagatgc accagcgtat	1140
cagcagggcc agaaccaact gtataacgag ctcaacctgg gacgcaggga agagtatgac	1200
gttttggaca agcgcagagg acgggaccct gagatgggtg gcaaaccaag acgaaaaaac	1260
ccccaggagg gtctctataa tgagctgcag aaggataaga tggctgaagc ctattctgaa	1320
ataggcatga aaggagagcg gagaagggga aaagggcacg acggtttgta ccagggactc	1380

agcactgcta cgaaggatac ttatgacgct ctccacatgc aagccctgcc acctaggtaa 1440

<210> 178
<211> 479
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 178
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu
20 25 30

Ser Ala Ser Val Gly Asp Arg Val Ser Phe Thr Cys Gln Ala Ser Gln
35 40 45

Asp Ile Asn Asn Phe Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
50 55 60

Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro
65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile
85 90 95

Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr
100 105 110

Gly Asn Leu Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
115 120 125

Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

145					150					155					160
Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Gly	Ser	Ile	Ser	Ser	Tyr
				165					170					175	
Tyr	Trp	Ser	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile
			180					185					190		
Gly	Tyr	Ile	Tyr	Tyr	Ser	Gly	Ser	Thr	Asn	Tyr	Asn	Pro	Ser	Leu	Lys
		195					200					205			
Ser	Arg	Val	Thr	Ile	Ser	Val	Asp	Thr	Ser	Lys	Asn	Gln	Phe	Ser	Leu
	210					215					220				
Lys	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Val
225					230					235					240
Ser	Leu	Val	Tyr	Cys	Gly	Gly	Asp	Cys	Tyr	Ser	Gly	Phe	Asp	Tyr	Trp
				245					250					255	
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ala	Ala	Leu	Asp	Asn
			260					265					270		
Glu	Lys	Ser	Asn	Gly	Thr	Ile	Ile	His	Val	Lys	Gly	Lys	His	Leu	Cys
		275					280					285			
Pro	Ser	Pro	Leu	Phe	Pro	Gly	Pro	Ser	Lys	Pro	Phe	Trp	Val	Leu	Val
	290					295					300				
Val	Val	Gly	Gly	Val	Leu	Ala	Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala
305					310					315					320
Phe	Ile	Ile	Phe	Trp	Val	Arg	Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser
				325					330					335	
Asp	Tyr	Met	Asn	Met	Thr	Pro	Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His
			340					345					350		
Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser	Arg
		355					360					365			

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
370 375 380

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
385 390 395 400

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
405 410 415

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
420 425 430

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
435 440 445

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
450 455 460

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
465 470 475

<210> 179

<211> 1374

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> anti-CLL-1 CAR construct

<400> 179

gatatccagc tcacgcaatc cccctcaagc ttgagtgcct ccgtgggcga ccgggtgtcc	60
ttcacatgtc aggcaagcca agacataaat aatttcctga attggtacca acaaaaaccc	120
ggcaaggctc ccaaactcct gatttatgat gcctccaatc tggagaccgg ggtcccttct	180
agattcagcg gaagtggcag cggcacagac ttacattta ctatctcttc tctgcaacca	240
gaggacatcg ccacatacta ttgccagcaa tacggcaatc tgcccttcac cttcggaggc	300
ggaaccaagg tagaaattaa aaggggcggt ggaggctccg gagggggggg ctctggcgga	360

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gggggctccc aagtacaatt gcaggagtca gggcctggac tcgtgaagcc ttcagaaact      420
ttgtcactga catgtacagt gtccggcgga agcattttcca gttactattg gtcctggatt      480
agacagccac ccggcaaagg actggaatgg attggatata tctactactc tggatctaca      540
aactataatc ccagcctcaa atccagggtc actattagtg tggatacatc aaagaatcag      600
ttctccttga agctgagctc agtcactgct gccgacaccg cagtgtacta ttgtgtgagc      660
ctggcttact gcggcggaga ttgctacagc ggtttcgatt actggggcca gggcaccttg      720
gttaccgtta gttccgcggc tgctcttgat aacgagaagt ccaacggtag gattatccac      780
gttaagggtg agcacctttg ccctagcccg ctgttcccag gccccagtaa gcccttttgg      840
gtcctcgttg tggtaggtgg ggtactcgcc tgctactccc tgctcgtcac tgtcgcattc      900
atcatcttct gggtcagatc caaaagaagc cgcctgctcc atagcgatta catgaatatg      960
actccacgcc gccctggccc cacaaggaaa cactaccagc cttacgcacc acctagagat     1020
ttcgctgcct atcggagcag ggtgaagttt tccagatctg cagatgcacc agcgtatcag     1080
cagggccaga accaactgta taacgagctc aacctgggac gcagggaaga gtatgacgtt     1140
ttggacaagc gcagaggacg ggaccctgag atgggtggca aaccaagacg aaaaaacccc     1200
caggagggtc tctataatga gctgcagaag gataagatgg ctgaagccta ttctgaaata     1260
ggcatgaaag gagagcggag aaggggaaaa gggcacgacg gtttgtacca gggactcagc     1320
actgctacga aggatactta tgacgctctc cacatgcaag ccctgccacc tagg           1374

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<210> 180

<211> 458

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<223> anti-CLL-1 CAR construct

<400> 180

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

```

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Asp Arg Val Ser Phe Thr Cys Gln Ala Ser Gln Asp Ile Asn Asn Phe
          20          25          30

```

31 Jul 2019
2017240667

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

Val	Thr	Val	Ser	Ser	Ala	Ala	Ala	Leu	Asp	Asn	Glu	Lys	Ser	Asn	Gly	
				245					250					255		
Thr	Ile	Ile	His	Val	Lys	Gly	Lys	His	Leu	Cys	Pro	Ser	Pro	Leu	Phe	
			260					265					270			
Pro	Gly	Pro	Ser	Lys	Pro	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	
		275					280					285				
Leu	Ala	Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Phe	Trp	
	290					295					300					
Val	Arg	Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	
305					310					315					320	
Thr	Pro	Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	
				325					330					335		
Pro	Pro	Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser	Arg	Val	Lys	Phe	Ser	Arg	
			340					345					350			
Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	
		355					360					365				
Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	
	370					375					380					
Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	
385					390					395					400	
Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	
				405					410					415		
Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	
			420					425					430			
Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	
		435					440					445				
Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg							
	450					455										

<210> 181
 <211> 1467
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
 <223> anti-CLL-1 CAR construct

<400> 181
 atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60
 ccggatatcc agctgaccca gtctccatcc tctttgagtg cctccgtggg tgaccgcgtc 120
 tctttcactt gccaaagccag ccaagacatc aacaactttc tgaattggta ccagcagaaa 180
 ccaggcaaag caccaaagct cctcatctac gacgcctcca acctggaaac cgggggtgcc 240
 agcaggttta gcgggagcgg ttctggcacg gattttacgt tcaccatctc ctctctgcag 300
 cccgaggata tagctactta ttactgtcag cagtacggga atctgccatt tacttttggg 360
 ggtggaacta aggtggaaat caaaaggggc ggcgggggaa gcgggggcgg gggctcaggt 420
 ggcggaggga gccaggtgca actccaggaa agtggcccag gattggtgaa gcccagcgag 480
 accctttccc ttacttgtac tgttagcggg ggcagcataa gcagctacta ttggtcctgg 540
 atcagacagc caccagggaag agggcttgaa tggattggct acatttacta ttccgggtcc 600
 accaactaca acccatccct caagtcccgc gtgacaattt ccgtcgacac aagcaagaac 660
 cagttctccc tgaaacttag tagcgtcact gctgcagata cagcagtgtg ctattgtgtc 720
 agccttgtct actgtggcgg cgactgctac agtggctttg attactgggg acagggcacg 780
 ctcgtgacag tgtccagcgc tgcggctatc gaggtaatgt atccgccacc gtatctggac 840
 aacgagaagt ctaatgggac aatcattcac gtgaagggga agcacctgtg tccatcccc 900
 ctgtttccgg gtcccagtaa acccttctgg gtgcttggtg tcgttggcgg ggtgctggcc 960
 tgctattccc tgctgggtgac cgtcgcgttt attattttct gggttagatc caaaagaagc 1020
 cgcttgctcc atagcgatta catgaatatg actccacgcc gccctggccc cacaaggaaa 1080
 cactaccagc cttacgcacc acctagagat ttcgctgcct atcgagcag ggtgaagttt 1140
 tccagatctg cagatgcacc agcgtatcag cagggccaga accaactgta taacgagctc 1200

```

aacctgggac gcagggaaga gtatgacgtt ttggacaagc gcagaggacg ggaccctgag      1260
atgggtggca aaccaagacg aaaaaacccc caggagggtc tctataatga gctgcagaag      1320
gataagatgg ctgaagccta ttctgaaata ggcatgaaag gagagcggag aaggggaaaa      1380
gggcacgacg gtttgtacca gggactcagc actgctacga aggatactta tgacgctctc      1440
cacatgcaag ccctgccacc taggtaa                                          1467

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```

<210> 182
<211> 488
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

```

```

<220>
<223> anti-CLL-1 CAR construct

```

```

<400> 182
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1              5              10              15

```

```

His Ala Ala Arg Pro Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu
      20              25              30

```

```

Ser Ala Ser Val Gly Asp Arg Val Ser Phe Thr Cys Gln Ala Ser Gln
      35              40              45

```

```

Asp Ile Asn Asn Phe Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
      50              55              60

```

```

Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro
      65              70              75              80

```

```

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile
      85              90              95

```

```

Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr
      100             105             110

```

```

Gly Asn Leu Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

```

	115		120		125												
Arg	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser		
	130					135					140						
Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu		
145					150					155					160		
Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Gly	Ser	Ile	Ser	Ser	Tyr		
				165					170					175			
Tyr	Trp	Ser	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile		
			180					185					190				
Gly	Tyr	Ile	Tyr	Tyr	Ser	Gly	Ser	Thr	Asn	Tyr	Asn	Pro	Ser	Leu	Lys		
		195					200					205					
Ser	Arg	Val	Thr	Ile	Ser	Val	Asp	Thr	Ser	Lys	Asn	Gln	Phe	Ser	Leu		
	210					215					220						
Lys	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Val		
225					230					235					240		
Ser	Leu	Val	Tyr	Cys	Gly	Gly	Asp	Cys	Tyr	Ser	Gly	Phe	Asp	Tyr	Trp		
				245					250					255			
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ala	Ala	Ile	Glu	Val		
			260					265					270				
Met	Tyr	Pro	Pro	Pro	Tyr	Leu	Asp	Asn	Glu	Lys	Ser	Asn	Gly	Thr	Ile		
		275					280					285					
Ile	His	Val	Lys	Gly	Lys	His	Leu	Cys	Pro	Ser	Pro	Leu	Phe	Pro	Gly		
	290					295					300						
Pro	Ser	Lys	Pro	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala		
305					310					315					320		
Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Phe	Trp	Val	Arg		
				325					330					335			

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Ser  Lys  Arg  Ser  Arg  Leu  Leu  His  Ser  Asp  Tyr  Met  Asn  Met  Thr  Pro
      340                      345                      350

Arg  Arg  Pro  Gly  Pro  Thr  Arg  Lys  His  Tyr  Gln  Pro  Tyr  Ala  Pro  Pro
      355                      360                      365

Arg  Asp  Phe  Ala  Ala  Tyr  Arg  Ser  Arg  Val  Lys  Phe  Ser  Arg  Ser  Ala
      370                      375                      380

Asp  Ala  Pro  Ala  Tyr  Gln  Gln  Gly  Gln  Asn  Gln  Leu  Tyr  Asn  Glu  Leu
      385                      390                      395                      400

Asn  Leu  Gly  Arg  Arg  Glu  Glu  Tyr  Asp  Val  Leu  Asp  Lys  Arg  Arg  Gly
      405                      410                      415

Arg  Asp  Pro  Glu  Met  Gly  Gly  Lys  Pro  Arg  Arg  Lys  Asn  Pro  Gln  Glu
      420                      425                      430

Gly  Leu  Tyr  Asn  Glu  Leu  Gln  Lys  Asp  Lys  Met  Ala  Glu  Ala  Tyr  Ser
      435                      440                      445

Glu  Ile  Gly  Met  Lys  Gly  Glu  Arg  Arg  Arg  Gly  Lys  Gly  His  Asp  Gly
      450                      455                      460

Leu  Tyr  Gln  Gly  Leu  Ser  Thr  Ala  Thr  Lys  Asp  Thr  Tyr  Asp  Ala  Leu
      465                      470                      475                      480

His  Met  Gln  Ala  Leu  Pro  Pro  Arg
      485

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<210> 183

<211> 1401

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> anti-CLL-1 CAR construct

<400> 183

gatatccagc tgacccagtc tccatcctct ttgagtgcct ccgtgggtga ccgctctct	60
ttcacttgcc aagccagcca agacatcaac aacttttctga attggtacca gcagaaacca	120
ggcaaagcac caaagctcct catctacgac gcctccaacc tggaaaccgg ggtgcccagc	180
aggttttagcg ggagcggttc tggcacggat tttacgttca ccatctcctc tctgcagccc	240
gaggatatag ctacttatta ctgtcagcag tacgggaatc tgccatttac ttttgggggt	300
ggaactaagg tggaaatcaa aaggggcggc gggggaagcg ggggcggggg ctgaggtggc	360
ggagggagcc aggtgcaact ccaggaaagt ggcccaggat tggatgaagcc cagcgagacc	420
ctttccctta cttgtactgt tagcggaggc agcataagca gctactattg gtcctggatc	480
agacagccac cagggaaagg gcttgaatgg attggctaca ttactattc cgggtccacc	540
aactacaacc catccctcaa gtcccgcgtg acaatttccg tcgacacaag caagaaccag	600
ttctccctga aacttagtag cgtcactgct gcagatacag cagtgtacta ttgtgtcagc	660
cttgtctact gtggcggcga ctgctacagt ggctttgatt actggggaca gggcacgctc	720
gtgacagtgt ccagcgtgc ggctatcgag gtaatgtatc cgccaccgta tctggacaac	780
gagaagtcta atgggacaat cattcacgtg aaggggaagc acctgtgtcc atccccctg	840
tttccgggtc ccagtaaacc cttctgggtg cttgttgtcg ttggcggggg gctggcctgc	900
tattccctgc tggatgaccgt cgcgtttatt attttctggg ttagatccaa aagaagccgc	960
ctgctccata gcgattacat gaatatgact ccacgccgcc ctggccccac aaggaaacac	1020
taccagcctt acgcaccacc tagagatttc gctgcctatc ggagcagggt gaagttttcc	1080
agatctgcag atgcaccagc gtatcagcag ggccagaacc aactgtataa cgagctcaac	1140
ctgggacgca gggaagagta tgacgttttg gacaagcgca gaggacggga ccctgagatg	1200
ggtggcaaac caagacgaaa aaacccccag gaggttctct ataattgagct gcagaaggat	1260
aagatggctg aagcctattc tgaaataggc atgaaaggag agcggagaag gggaaaaggg	1320
cacgacggtt tgtaccaggg actcagcact gctacgaagg atacttatga cgctctccac	1380
atgcaagccc tgccacctag g	1401

<210> 184

<211> 467

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<223> anti-CLL-1 CAR construct

<400> 184

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

Asp Arg Val Ser Phe Thr Cys Gln Ala Ser Gln Asp Ile Asn Asn Phe
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Gly Asn Leu Pro Phe
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly
100 105 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
115 120 125

Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr
130 135 140

Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr Tyr Trp Ser Trp Ile
145 150 155 160

Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr
165 170 175

Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile
180 185 190

31 Jul 2019
2017240667

Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
195 200 205

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Val Ser Leu Val Tyr Cys
210 215 220

Gly Gly Asp Cys Tyr Ser Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu
225 230 235 240

Val Thr Val Ser Ser Ala Ala Ala Ile Glu Val Met Tyr Pro Pro Pro
245 250 255

Tyr Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly
260 265 270

Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe
275 280 285

Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
290 295 300

Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
305 310 315 320

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
325 330 335

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
340 345 350

Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
355 360 365

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
370 375 380

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
385 390 395 400

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
405 410 415

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
420 425 430

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
435 440 445

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
450 455 460

Pro Pro Arg
465

<210> 185
<211> 1548
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 185
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60
ccggacattc aattgaccca gtcccctagc agtctctcag caagtgtggg agatagggtg 120
tcattcacct gtcaggcttc acaggacatc aacaacttcc tcaattggta tcagcagaag 180
ccagggaagg caccaaagct gtcatatat gacgcttcaa accttgaaac cggagtacct 240
agccgcttca gcggaagcgg atcagggact gacttcactt ttaccatctc ttactgcag 300
cccgaagaca tcgccacata ctactgccag cagtacggaa acttgccttt tacatttggg 360
ggcggcacca aagtggagat taagcgaggg ggaggcggct caggaggcgg tggctccgga 420
ggcggggggtt cccaggtcca gctccaggaa tccggcccag gtctgggtaa gccagtgaa 480
actttgtccc tcacgtgtac tgtgagcggg ggttcaatct cctcatacta ttgggtcttg 540
atacggcaac ctcttgaaa gggcctcgag tggatcggct atatctacta tagtggctcc 600
actaattaca acccttcctt caagtccaga gtcaccattt ccgtggacac atctaagaac 660


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cagttcagtc tgaagttgtc cagcgttaca gccgcagaca cagccgttta ttactgtgtg      720
tctcttgttt actgcggggg agactgttat agcggcttcg attactgggg ccagggcacc      780
ttggtcacag tctcttccgc ggccgccctc tctaacagta ttatgtactt ttctcathtt      840
gtacccgtgt tccttccgc taagccaact actaccccg cccacggcc gcctaccct      900
gcaccacaa tagccagtca gcctttgagc ctgagacctg aggcttgctg gccggctgct      960
gggggtgcag tgcacacacg aggtcttgat tttgcttgcg acatatacat ctgggcccct     1020
ctggccggga cctgtggggg gctgcttctg agcttgggtca tcacgctcta ttgcaaccat     1080
cgcaacagat ccaaaagaag cgcctgctc catagcgatt acatgaatat gactccacgc     1140
cgccctggcc ccacaaggaa aactaccag ctttacgcac cacctagaga tttcgctgcc     1200
tatcggagca ggggtgaagt ttccagatct gcagatgcac cagcgatatca gcagggccag     1260
aaccaactgt ataacgagct caacctggga cgcagggaag agtatgacgt tttggacaag     1320
cgcagaggac gggaccctga gatgggtggc aaaccaagac gaaaaaaccc ccaggagggt     1380
ctctataatg agctgcagaa ggataagatg gctgaagcct attctgaaat aggcataaaa     1440
ggagagcgga gaaggggaaa agggcacgac ggtttgtacc agggactcag cactgctacg     1500
aaggatactt atgacgctct ccacatgcaa gccctgccac ctaggtaa                     1548

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<210> 186
 <211> 515
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<220>
 <223> anti-CLL-1 CAR construct

<400> 186
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu
 20 25 30

Ser Ala Ser Val Gly Asp Arg Val Ser Phe Thr Cys Gln Ala Ser Gln

31 Jul 2019

2017240667

	35					40					45				
Asp	Ile	Asn	Asn	Phe	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala
	50					55					60				
Pro	Lys	Leu	Leu	Ile	Tyr	Asp	Ala	Ser	Asn	Leu	Glu	Thr	Gly	Val	Pro
65					70					75					80
Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile
				85					90					95	
Ser	Ser	Leu	Gln	Pro	Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr
			100					105					110		
Gly	Asn	Leu	Pro	Phe	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys
		115					120					125			
Arg	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
	130					135					140				
Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu
145					150					155					160
Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Gly	Ser	Ile	Ser	Ser	Tyr
				165					170					175	
Tyr	Trp	Ser	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile
			180				185						190		
Gly	Tyr	Ile	Tyr	Tyr	Ser	Gly	Ser	Thr	Asn	Tyr	Asn	Pro	Ser	Leu	Lys
		195					200					205			
Ser	Arg	Val	Thr	Ile	Ser	Val	Asp	Thr	Ser	Lys	Asn	Gln	Phe	Ser	Leu
	210					215					220				
Lys	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Val
225					230					235					240
Ser	Leu	Val	Tyr	Cys	Gly	Gly	Asp	Cys	Tyr	Ser	Gly	Phe	Asp	Tyr	Trp
				245					250					255	

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ala Ala Leu Ser Asn
260 265 270

Ser Ile Met Tyr Phe Ser His Phe Val Pro Val Phe Leu Pro Ala Lys
275 280 285

Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
290 295 300

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
305 310 315 320

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
325 330 335

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
340 345 350

Val Ile Thr Leu Tyr Cys Asn His Arg Asn Arg Ser Lys Arg Ser Arg
355 360 365

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
370 375 380

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
385 390 395 400

Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
405 410 415

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
420 425 430

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
435 440 445

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
450 455 460

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys

2017240667

465 470 475 480

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
485 490 495

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
500 505 510

Pro Pro Arg
515

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<210> 187
<211> 1482
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 187						
gacattcaat	tgacccagtc	ccctagcagt	ctctcagcaa	gtgtgggaga	taggggtgtca	60
ttcacctgtc	aggcttcaca	ggacatcaac	aacttcctca	attggtatca	gcagaagcca	120
gggaaggcac	caaagctgct	catatatgac	gcttcaaacc	ttgaaaccgg	agtacctagc	180
cgcttcagcg	gaagcggatc	agggactgac	ttcactttta	ccatctcttc	actgcagccc	240
gaagacatcg	ccacatacta	ctgccagcag	tacggaaact	tgccttttac	atttgggggc	300
ggcaccaaag	tggagattaa	gcgaggggga	ggcggctcag	gaggcgggtg	ctccggaggc	360
gggggttccc	aggtccagct	ccaggaatcc	ggcccaggtc	tggttaagcc	cagtgaaact	420
ttgtccctca	cgtgtactgt	gagcgggtgt	tcaatctcct	catactattg	gtcttggata	480
cggcaacctc	ctggaaaggg	cctcgagtgg	atcggctata	tctactatag	tggctccact	540
aattacaacc	cttccctcaa	gtccagagtc	accatttccg	tggacacatc	taagaaccag	600
ttcagtctga	agttgtccag	cgttacagcc	gcagacacag	ccgtttatta	ctgtgtgtct	660
cttgtttact	gcggggggaga	ctgtttatagc	ggcttcgatt	actggggcca	gggcaccttg	720
gtcacagtct	cttccgcggc	cgcctctctt	aacagtatta	tgtacttttc	tcattttgta	780

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cccggtgttcc ttcccgctaa gccaaactact accccggccc cacggccgcc tacccctgca      840
cccacaatag ccagtcagcc tttagacctg agacctgagg cttgtcggcc ggctgctggg      900
gggtgcagtgc acacacgagg tcttgatttt gcttgcgaca tatacatctg ggcccctctg      960
gccgggacct gtgggggtgct gcttctgagc ttgggtcatca cgctctattg caaccatcgc     1020
aacagatcca aaagaagccg cctgctccat agcgattaca tgaatatgac tccacgccgc      1080
cctggcccca caaggaaaca ctaccagcct tacgcaccac ctagagattt cgctgcctat      1140
cggagcaggg tgaagttttc cagatctgca gatgcaccag cgatatcagca gggccagaac     1200
caactgtata acgagctcaa cctgggacgc aggggaagagt atgacgtttt ggacaagcgc     1260
agaggacggg accctgagat gggtggcaaa ccaagacgaa aaaaccccca ggagggtctc     1320
tataatgagc tgcagaagga taagatggct gaagcctatt ctgaaatagg catgaaagga     1380
gagcggagaa ggggaaaagg gcacgacggt ttgtaccagg gactcagcac tgctacgaag     1440
gatacttatg acgctctcca catgcaagcc ctgccaccta gg                          1482

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<210> 188
 <211> 494
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<220>
 <223> anti-CLL-1 CAR construct

<400> 188
 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Ser Phe Thr Cys Gln Ala Ser Gln Asp Ile Asn Asn Phe
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser 65	Gly	Ser	Gly	Thr	Asp 70	Phe	Thr	Phe	Thr	Ile 75	Ser	Ser	Leu	Gln	Pro 80
Glu	Asp	Ile	Ala	Thr 85	Tyr	Tyr	Cys	Gln	Gln 90	Tyr	Gly	Asn	Leu	Pro 95	Phe
Thr	Phe	Gly	Gly 100	Gly	Thr	Lys	Val	Glu 105	Ile	Lys	Arg	Gly	Gly 110	Gly	Gly
Ser	Gly	Gly 115	Gly	Gly	Ser	Gly	Gly 120	Gly	Gly	Ser	Gln	Val	Gln	Leu	Gln
Glu 130	Ser	Gly	Pro	Gly	Leu	Val 135	Lys	Pro	Ser	Glu	Thr 140	Leu	Ser	Leu	Thr
Cys 145	Thr	Val	Ser	Gly	Gly 150	Ser	Ile	Ser	Ser	Tyr 155	Tyr	Trp	Ser	Trp	Ile 160
Arg	Gln	Pro	Pro	Gly 165	Lys	Gly	Leu	Glu	Trp 170	Ile	Gly	Tyr	Ile	Tyr 175	Tyr
Ser	Gly	Ser	Thr	Asn 180	Tyr	Asn	Pro	Ser 185	Leu	Lys	Ser	Arg	Val 190	Thr	Ile
Ser	Val	Asp 195	Thr	Ser	Lys	Asn	Gln 200	Phe	Ser	Leu	Lys	Leu 205	Ser	Ser	Val
Thr 210	Ala	Ala	Asp	Thr	Ala	Val 215	Tyr	Tyr	Cys	Val 220	Ser	Leu	Val	Tyr	Cys
Gly 225	Gly	Asp	Cys	Tyr	Ser 230	Gly	Phe	Asp	Tyr	Trp 235	Gly	Gln	Gly	Thr	Leu 240
Val	Thr	Val	Ser	Ser 245	Ala	Ala	Ala	Leu	Ser 250	Asn	Ser	Ile	Met	Tyr 255	Phe
Ser	His	Phe	Val	Pro 260	Val	Phe	Leu	Pro 265	Ala	Lys	Pro	Thr	Thr 270	Thr	Pro
Ala	Pro	Arg 275	Pro	Pro	Thr	Pro	Ala 280	Pro	Thr	Ile	Ala	Ser 285	Gln	Pro	Leu

31 Jul 2019
2017240667

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
290 295 300

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
305 310 315 320

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
325 330 335

Cys Asn His Arg Asn Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
340 345 350

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
355 360 365

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val
370 375 380

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
385 390 395 400

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
405 410 415

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
420 425 430

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
435 440 445

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
450 455 460

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
465 470 475 480

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 189
<211> 1446
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 189
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60
ccgcaggtac agctgcagga atctgggccc ggacttgtca agccaagtca gacactttct 120
cttacatgta ccgtgagcgg cggaagtata agcagtggag gcttttactg gtcttggata 180
cggcagcacc caggcaaagg cttggagtgg attggataca ttcatcattc aggatctaca 240
cactataatc catcccttaa gtcccgggtc accattagca ttgatacgtc taagaatctg 300
ttcagtctca ggctgtcctc cgtcactgct gccgacacag ccgtgtacta ctgcgcctcc 360
ttggtttact gcggaggcga ctgttatagc ggctttgatt attgggggca ggggacctc 420
gtaaccgtga gctctggagg gggtgggagc gggggaggag gttcaggggg gggcggctcc 480
gatatccagc tactcaaag cccctctagt ctctctgcct cagtggggga tcgggtcagt 540
tttacttgtc aagcttcaca ggatatcaac aacttcctta attggtatca gcagaagcca 600
ggaaaagcac ccaagctgct catctatgat gcctcaaatt tggagacggg tgttcccagt 660
cgattctctg ggtcagggtc cgggaccgac tttacgttta cgatctcctc tctgcagccc 720
gaagacatcg ccacatacta ttgtcaacag tacggcaact tgcctttcac atttgggggc 780
gggactaagg ttgaaatcaa gagggccgct gcactggaca atgagaagtc caacggcacc 840
atcatccacg tgaagggcaa gcacctgtgc ctagtcctc tgttcccagg cccatccaaa 900
cctttttggg ttcttgttgt ggtcgggggg gtgctggcct gctattctct gctggtcacg 960
gtggccttca taattttctg ggtagatcc aaaagaagcc gcctgctcca tagcgattac 1020
atgaatatga ctccacgccg ccctggcccc acaaggaaac actaccagcc ttacgcacca 1080
cctagagatt tcgctgccta tcggagcagg gtgaagtttt ccagatctgc agatgcacca 1140
gcgtatcagc agggccagaa ccaactgtat aacgagctca acctgggacg cagggaagag 1200
tatgacgttt tggacaagcg cagaggacgg gaccctgaga tgggtggcaa accaagacga 1260


```

aaaaaccccc aggagggtct ctataatgag ctgcagaagg ataagatggc tgaagcctat      1320
tctgaaatag gcatgaaagg agagcggaga aggggaaaag ggcacgacgg tttgtaccag      1380
ggactcagca ctgctacgaa ggatacttat gacgctctcc acatgcaagc cctgccacct      1440
aggtaa                                           1446

```

```

<210> 190
<211> 481
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

```

```

<220>
<223> anti-CLL-1 CAR construct

```

```

<400> 190
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1             5             10             15

```

```

His Ala Ala Arg Pro Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu
      20             25             30

```

```

Val Lys Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly
      35             40             45

```

```

Ser Ile Ser Ser Gly Gly Phe Tyr Trp Ser Trp Ile Arg Gln His Pro
      50             55             60

```

```

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile His His Ser Gly Ser Thr
      65             70             75             80

```

```

His Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Ile Asp Thr
      85             90             95

```

```

Ser Lys Asn Leu Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp
      100            105            110

```

```

Thr Ala Val Tyr Tyr Cys Ala Ser Leu Val Tyr Cys Gly Gly Asp Cys
      115            120            125

```

Tyr	Ser	Gly	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	
	130					135					140					
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	
145					150					155					160	
Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	
				165					170					175		
Asp	Arg	Val	Ser	Phe	Thr	Cys	Gln	Ala	Ser	Gln	Asp	Ile	Asn	Asn	Phe	
			180					185					190			
Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	
		195					200					205				
Tyr	Asp	Ala	Ser	Asn	Leu	Glu	Thr	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	
	210					215					220					
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Ser	Leu	Gln	Pro	
225					230					235					240	
Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr	Gly	Asn	Leu	Pro	Phe	
				245					250					255		
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Ala	Ala	Ala	Leu	
			260					265					270			
Asp	Asn	Glu	Lys	Ser	Asn	Gly	Thr	Ile	Ile	His	Val	Lys	Gly	Lys	His	
		275					280					285				
Leu	Cys	Pro	Ser	Pro	Leu	Phe	Pro	Gly	Pro	Ser	Lys	Pro	Phe	Trp	Val	
	290					295					300					
Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	Cys	Tyr	Ser	Leu	Leu	Val	Thr	
305					310					315					320	
Val	Ala	Phe	Ile	Ile	Phe	Trp	Val	Arg	Ser	Lys	Arg	Ser	Arg	Leu	Leu	
			325						330					335		
His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro	Arg	Arg	Pro	Gly	Pro	Thr	Arg	

				340						345							350
Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	Arg	Asp	Phe	Ala	Ala	Tyr	Arg		
		355					360					365					
Ser	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln		
	370					375					380						
Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu		
385					390				395						400		
Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly		
				405					410					415			
Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln		
			420					425					430				
Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu		
		435					440					445					
Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr		
	450					455					460						
Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro		
465					470					475					480		

Arg

<210> 191
 <211> 1380
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
 <223> anti-CLL-1 CAR construct

<400> 191
 caggtacagc tgcaggaatc tgggcccgga cttgtcaagc caagtcagac actttctctt

60

```

acatgtaccg tgagcggcgg aagtataagc agtggaggct tttactggtc ttggatacgg      120
cagcaccag gcaaaggctt ggagtggatt ggatacattc atcattcagg atctacacac      180
tataatccat cccttaagtc ccgggtcacc attagcattg atacgtctaa gaatctgttc      240
agtctcaggc tgtcctccgt cactgctgcc gacacagccg tgtactactg cgcctccttg      300
gtttactgcg gaggcgactg ttatagcggc tttgattatt gggggcaggg gaccctcgta      360
accgtgagct ctggaggggg tgggagcggg ggaggagggt cagggggggg cggctccgat      420
atccagctca ctcaaagccc ctctagtctc tctgcctcag tgggggatcg ggtcagtttt      480
acttgtcaag cttcacagga tatcaacaac ttccttaatt ggtatcagca gaagccagga      540
aaagcaccca agctgctcat ctatgatgcc tcaaatttgg agacgggtgt tcccagtcga      600
ttctctgggt caggggtccgg gaccgacttt acgtttacga tctcctctct gcagcccgaa      660
gacatcgcca catactattg tcaacagtac ggcaacttgc ctttcacatt tgggggcggg      720
actaagggtg aaatcaagag ggccgctgca ctggacaatg agaagtcaa cggcaccatc      780
atccacgtga agggcaagca cctgtgccct agtcctctgt tcccaggccc atccaaacct      840
ttttgggttc ttgttgtggt cgggggggtg ctggcctgct attctctgct ggtcacggtg      900
gccttcataa ttttctgggt tagatccaaa agaagccgcc tgctccatag cgattacatg      960
aatatgactc cacgccgccc tggccccaca aggaaacact accagcctta cgcaccacct     1020
agagatttcg ctgcctatcg gagcagggtg aagttttcca gatctgcaga tgcaccagcg     1080
tatcagcagg gccagaacca actgtataac gagctcaacc tgggacgcag ggaagagtat     1140
gacgttttgg acaagcgag aggacgggac cctgagatgg gtggcaaacc aagacgaaaa     1200
aacccccagg agggctctcta taatgagctg cagaaggata agatggctga agcctattct     1260
gaaataggca tgaaaggaga gcggagaagg ggaaaagggc acgacggttt gtaccaggga     1320
ctcagcactg ctacgaagga tacttatgac gctctccaca tgcaagccct gccacctagg     1380

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<210> 192

<211> 460

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<223> anti-CLL-1 CAR construct

<400> 192

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Phe Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile His His Ser Gly Ser Thr His Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Leu Phe
65 70 75 80

Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Ser Leu Val Tyr Cys Gly Gly Asp Cys Tyr Ser Gly Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
130 135 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Ser Phe
145 150 155 160

Thr Cys Gln Ala Ser Gln Asp Ile Asn Asn Phe Leu Asn Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn
180 185 190

Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

31 Jul 2019
2017240667

Asp	Phe	Thr	Phe	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Ile	Ala	Thr	
	210					215					220					
Tyr	Tyr	Cys	Gln	Gln	Tyr	Gly	Asn	Leu	Pro	Phe	Thr	Phe	Gly	Gly	Gly	
225					230					235					240	
Thr	Lys	Val	Glu	Ile	Lys	Arg	Ala	Ala	Ala	Leu	Asp	Asn	Glu	Lys	Ser	
				245					250					255		
Asn	Gly	Thr	Ile	Ile	His	Val	Lys	Gly	Lys	His	Leu	Cys	Pro	Ser	Pro	
			260					265					270			
Leu	Phe	Pro	Gly	Pro	Ser	Lys	Pro	Phe	Trp	Val	Leu	Val	Val	Val	Gly	
		275					280					285				
Gly	Val	Leu	Ala	Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	
	290					295					300					
Phe	Trp	Val	Arg	Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	
305					310					315					320	
Asn	Met	Thr	Pro	Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	
				325					330					335		
Tyr	Ala	Pro	Pro	Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser	Arg	Val	Lys	Phe	
			340					345					350			
Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	
		355					360					365				
Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	
	370					375					380					
Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	
385					390					395					400	
Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	
				405					410					415		

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
 420 425 430

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
 435 440 445

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 450 455 460

<210> 193

<211> 1473

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polynucleotide

<220>

<223> anti-CLL-1 CAR construct

<400> 193

atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc	60
ccgcaggtgc agctgcagga aagcggtccg ggacttgtca agccgtccca aacgctgagt	120
ctgacgtgta ctgtctctgg tggctctatt tcttccgggg gcttttattg gtcttggatc	180
agacaacacc ctggcaaagg gctggagtgg atagggtata ttcaccactc tgggtccact	240
cactacaacc catcattgaa atccagagtg actatctcaa tcgacacatc caagaacctt	300
ttcagcctga ggttgtcatc agttaccgcc gctgacaccg cgggtgtatta ttg'gcctct	360
ctcgtgtact gcggtggcga ttgttatagt ggctttgact actgggggca ggggacattg	420
gttaccgttt caagtggagg cgggtgggtct ggcgggggcg gtagcggagg tggggggagc	480
gacatacagc ttacgcagag cccctccagc ctttcagcct ccgtggggga taggggtgtcc	540
tttacctgcc aggcttccca ggacataaac aacttcctca attggtatca gcaaaagccc	600
gggaaagcac caaagctgct catctacgat gccagcaacc tggaaaccgg agtgccgtct	660
cgcttctctg gaagtggcag tgggaccgat ttcactttta caatctcaag tttgcagcca	720
gaagacattg caacatacta ctgtcaacag tacggcaatc tcccctttac atttgggggg	780
ggaactaaag tggagattaa gcgcgctgca gccattgaag ttatgtatcc gccccgtat	840
ctggataacg agaaatctaa tgggtaccata atacatgtga aggggaagca cctctgtcca	900

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tcaccgctgt tccccggccc ttcaaaacct ttctgggtac tcgttgctgt ggggtggagtt      960
ctggcctgct atagtctgct ggtgaccgtg gcgtttatca tcttctgggt aagatccaaa      1020
agaagccgcc tgctccatag cgattacatg aatatgactc cacgccgccc tggccccaca      1080
aggaaacact accagcctta cgcaccacct agagatttcg ctgcctatcg gagcagggtg      1140
aagttttcca gatctgcaga tgcaccagcg tatcagcagg gccagaacca actgtataac      1200
gagctcaacc tgggacgcag ggaagagtat gacgttttgg acaagcgcag aggacgggac      1260
cctgagatgg gtggcaaacc aagacgaaaa aacccccagg agggctctcta taatgagctg      1320
cagaaggata agatggctga agcctattct gaaataggca tgaaaggaga gcggagaagg      1380
ggaaaagggc acgacggttt gtaccaggga ctcagcactg ctacgaagga tacttatgac      1440
gctctccaca tgcaagccct gccacctagg taa                                     1473

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<210> 194
 <211> 490
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polypeptide

<220>
 <223> anti-CLL-1 CAR construct

<400> 194
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu
 20 25 30

Val Lys Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly
 35 40 45

Ser Ile Ser Ser Gly Gly Phe Tyr Trp Ser Trp Ile Arg Gln His Pro
 50 55 60

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile His His Ser Gly Ser Thr
 65 70 75 80

His	Tyr	Asn	Pro	Ser	Leu	Lys	Ser	Arg	Val	Thr	Ile	Ser	Ile	Asp	Thr	85	90	95
Ser	Lys	Asn	Leu	Phe	Ser	Leu	Arg	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	100	105	110
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ser	Leu	Val	Tyr	Cys	Gly	Gly	Asp	Cys	115	120	125
Tyr	Ser	Gly	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	130	135	140
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	145	150	155
Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	165	170	175
Asp	Arg	Val	Ser	Phe	Thr	Cys	Gln	Ala	Ser	Gln	Asp	Ile	Asn	Asn	Phe	180	185	190
Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	195	200	205
Tyr	Asp	Ala	Ser	Asn	Leu	Glu	Thr	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	210	215	220
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Ser	Leu	Gln	Pro	225	230	235
Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr	Gly	Asn	Leu	Pro	Phe	245	250	255
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Ala	Ala	Ala	Ile	260	265	270
Glu	Val	Met	Tyr	Pro	Pro	Pro	Tyr	Leu	Asp	Asn	Glu	Lys	Ser	Asn	Gly	275	280	285
Thr	Ile	Ile	His	Val	Lys	Gly	Lys	His	Leu	Cys	Pro	Ser	Pro	Leu	Phe			

2017240667 31 Jul 2019

290		295		300
Pro Gly Pro Ser Lys	Pro Phe Trp Val Leu	Val Val Val Gly Gly Val		
305	310	315		320
Leu Ala Cys Tyr Ser	Leu Leu Val Thr Val	Ala Phe Ile Ile Phe Trp		
	325	330		335
Val Arg Ser Lys Arg	Ser Arg Leu Leu His	Ser Asp Tyr Met Asn Met		
	340	345		350
Thr Pro Arg Arg Pro	Gly Pro Thr Arg Lys	His Tyr Gln Pro Tyr Ala		
	355	360		365
Pro Pro Arg Asp Phe	Ala Ala Tyr Arg Ser	Arg Val Lys Phe Ser Arg		
	370	375		380
Ser Ala Asp Ala Pro	Ala Tyr Gln Gln Gly	Gln Asn Gln Leu Tyr Asn		
385	390	395		400
Glu Leu Asn Leu Gly	Arg Arg Glu Glu Tyr	Asp Val Leu Asp Lys Arg		
	405	410		415
Arg Gly Arg Asp Pro	Glu Met Gly Gly Lys	Pro Arg Arg Lys Asn Pro		
	420	425		430
Gln Glu Gly Leu Tyr	Asn Glu Leu Gln Lys	Asp Lys Met Ala Glu Ala		
	435	440		445
Tyr Ser Glu Ile Gly	Met Lys Gly Glu Arg	Arg Arg Gly Lys Gly His		
	450	455		460
Asp Gly Leu Tyr Gln	Gly Leu Ser Thr Ala	Thr Lys Asp Thr Tyr Asp		
465	470	475		480
Ala Leu His Met Gln	Ala Leu Pro Pro Arg			
	485	490		

<210> 195
 <211> 1407
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> anti-CLL-1 CAR construct

<400> 195

caggtgcagc tgcaggaaag cgggtccggga cttgtcaagc cgtcccaaac gctgagtctg	60
acgtgtactg tctctggtgg ctctatttct tccgggggct tttattggtc ttggatcaga	120
caacaccctg gcaaagggtt ggagtggata ggggtatattc accactctgg gtccactcac	180
tacaacccat cattgaaatc cagagtgact atctcaatcg acacatccaa gaaccttttc	240
agcctgaggt tgtcatcagt taccgccgct gacaccgcgg tgtattattg cgcctctctc	300
gtgtactgcg gtggcgattg ttatagtggc ttgtactact gggggcaggg gacattgggt	360
accgtttcaa gtggaggcgg tgggtctggc gggggcggta gcggagggtg ggggagcgac	420
atacagctta cgcagagccc ctccagcctt tcagcctccg tgggggatat ggtgtccttt	480
acctgccagg cttcccagga cataaacaac ttcctcaatt ggtatcagca aaagcccggg	540
aaagcaccaa agctgctcat ctacgatgcc agcaacctgg aaaccggagt gccgtctcgc	600
ttctctggaa gtggcagtgg gaccgatttc actttttaca tctcaagttt gcagccagaa	660
gacattgcaa catactactg tcaacagtac ggcaatctcc cctttacatt tgggggggga	720
actaaagtgg agattaagcg cgctgcagcc attgaagtta tgtatccgcc cccgtatctg	780
gataacgaga aatctaattg taccataata catgtgaagg ggaagcacct ctgtccatca	840
ccgctgttcc ccggcccttc aaaacctttc tgggtactcg ttgtcgtggg tggagtcttg	900
gcctgctata gtctgctggt gaccgtggcg tttatcatct tctgggtaag atccaaaaga	960
agccgcctgc tccatagcga ttacatgaat atgactccac gccgccctgg cccacaagg	1020
aaacactacc agccttacgc accacctaga gatttcgctg cctatcggag cagggtgaag	1080
ttttccagat ctgcagatgc accagcgtat cagcagggcc agaaccaact gtataacgag	1140
ctcaacctgg gacgcaggga agagtatgac gtttttgaca agcgcagagg acgggaccct	1200
gagatgggtg gcaaaccaag acgaaaaaac ccccaggagg gtctctataa tgagctgcag	1260
aaggataaga tggctgaagc ctattctgaa ataggcatga aaggagagcg gagaagggga	1320

aaagggcacg acggtttgta ccagggactc agcactgcta cgaaggatac ttatgacgct 1380
ctccacatgc aagccctgcc acctagg 1407

<210> 196
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 196
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Phe Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile His His Ser Gly Ser Thr His Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Leu Phe
65 70 75 80

Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Ser Leu Val Tyr Cys Gly Gly Asp Cys Tyr Ser Gly Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
130 135 140

Gln 145	Ser	Pro	Ser	Ser	Leu 150	Ser	Ala	Ser	Val	Gly 155	Asp	Arg	Val	Ser	Phe 160
Thr	Cys	Gln	Ala	Ser 165	Gln	Asp	Ile	Asn	Asn 170	Phe	Leu	Asn	Trp	Tyr 175	Gln
Gln	Lys	Pro	Gly 180	Lys	Ala	Pro	Lys	Leu 185	Leu	Ile	Tyr	Asp	Ala 190	Ser	Asn
Leu	Glu	Thr 195	Gly	Val	Pro	Ser	Arg 200	Phe	Ser	Gly	Ser	Gly 205	Ser	Gly	Thr
Asp	Phe 210	Thr	Phe	Thr	Ile	Ser 215	Ser	Leu	Gln	Pro	Glu 220	Asp	Ile	Ala	Thr
Tyr 225	Tyr	Cys	Gln	Gln	Tyr 230	Gly	Asn	Leu	Pro	Phe 235	Thr	Phe	Gly	Gly	Gly 240
Thr	Lys	Val	Glu	Ile 245	Lys	Arg	Ala	Ala	Ala 250	Ile	Glu	Val	Met	Tyr 255	Pro
Pro	Pro	Tyr	Leu 260	Asp	Asn	Glu	Lys	Ser 265	Asn	Gly	Thr	Ile	Ile 270	His	Val
Lys	Gly	Lys 275	His	Leu	Cys	Pro	Ser 280	Pro	Leu	Phe	Pro	Gly 285	Pro	Ser	Lys
Pro	Phe 290	Trp	Val	Leu	Val	Val 295	Val	Gly	Gly	Val	Leu 300	Ala	Cys	Tyr	Ser
Leu 305	Leu	Val	Thr	Val	Ala 310	Phe	Ile	Ile	Phe	Trp 315	Val	Arg	Ser	Lys	Arg 320
Ser	Arg	Leu	Leu	His 325	Ser	Asp	Tyr	Met	Asn 330	Met	Thr	Pro	Arg	Arg 335	Pro
Gly	Pro	Thr	Arg 340	Lys	His	Tyr	Gln	Pro 345	Tyr	Ala	Pro	Pro	Arg 350	Asp	Phe
Ala	Ala	Tyr 355	Arg	Ser	Arg	Val	Lys 360	Phe	Ser	Arg	Ser	Ala 365	Asp	Ala	Pro

31 Jul 2019
2017240667

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
370 375 380

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
385 390 395 400

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
405 410 415

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
420 425 430

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
435 440 445

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
450 455 460

Ala Leu Pro Pro Arg
465

<210> 197
<211> 1554
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 197
atggcactcc ccgtaactgc tctgctgctg ccgttgcat tgctcctgca cgccgcacgc 60
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ctgacatgca ctgtgtccgg cgggtccata tcttccgggg gtttttattg gtcctggata 180
cgccagcatc ccgggaaagg acttgaatgg attggatata tccaccattc cggaagcacc 240
cactacaatc caagccttaa atcccgggtg acaatctcca tcgacacctc aaagaatctt 300
ttttccctgc ggttgtcttc agtaactgcc gccgataccg ctgtgtacta ctgtgccagc 360

ctcgtctatt gcggcggaga ttgttattct gggttcgatt attgggggtca aggcacactg	420
gtaactgtca gcagcggagg cggcggttcc gggggcgggg gcagtggagg gggcggatct	480
gacattcagc ttacgcagtc cccatcttca cttagcgcca gcgttggcga tcgggtcagc	540
ttcacgtgtc aagcaagtca ggatatcaac aactttctta actggtacca gcagaagcca	600
ggcaaggcac ccaagttgct gattttacgat gcttctaacc tcgagacggg agtgcctagc	660
cgcttctccg ggagcggcag cggcacagac tttaccttta cgatttccag tctgcagcca	720
gaggatatag caacttatta ctgtcagcag tatggcaacc tcccttttac cttcggtggt	780
ggcacaaagg tcgagattaa aagagccgca gcgttgtcca actccataat gtatTTTTct	840
cattttgtgc ccgtctttct gcctgcaaaa cctaccacca ccccgcccc acgaccacct	900
actccagccc ccaccatcgc ctcccagccc ctcagcctga ggccagaggc ttgtcgccct	960
gctgcggggg gcgctgtcca taccagagga ctcgacttcg cctgcgatat ttatatatgg	1020
gccccctcg ccggcacctg cggagtcttg ctctgagcc ttgtgatcac gctttattgt	1080
aaccatcgga atagatccaa aagaagccgc ctgctccata gcgattacat gaatatgact	1140
ccacgccgcc ctggccccac aaggaaacac taccagcctt acgcaccacc tagagatttc	1200
gctgcctatc ggagcagggt gaagttttcc agatctgcag atgcaccagc gtatcagcag	1260
ggccagaacc aactgtataa cgagctcaac ctgggacgca gggaagagta tgacgttttg	1320
gacaagcgca gaggacggga ccctgagatg ggtggcaaac caagacgaaa aaacccccag	1380
gagggtctct ataatgagct gcagaaggat aagatggctg aagcctattc tgaaataggc	1440
atgaaaggag agcggagaag gggaaaaggg cacgacgggt tgtaccaggg actcagcact	1500
gctacgaagg atacttatga cgctctccac atgcaagccc tgccacctag gtaa	1554

<210> 198

<211> 517

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<223> anti-CLL-1 CAR construct

31 Jul 2019 2017240667

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<400> 198
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1      5      10      15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu
      20      25      30

Val Lys Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly
      35      40      45

Ser Ile Ser Ser Gly Gly Phe Tyr Trp Ser Trp Ile Arg Gln His Pro
      50      55      60

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile His His Ser Gly Ser Thr
65      70      75      80

His Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Ile Asp Thr
      85      90      95

Ser Lys Asn Leu Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp
      100      105      110

Thr Ala Val Tyr Tyr Cys Ala Ser Leu Val Tyr Cys Gly Gly Asp Cys
      115      120      125

Tyr Ser Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
      130      135      140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145      150      155      160

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
      165      170      175

Asp Arg Val Ser Phe Thr Cys Gln Ala Ser Gln Asp Ile Asn Asn Phe
      180      185      190

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
      195      200      205

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly

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210	215	220
Ser 225	Gly Ser Gly Thr Asp 230	Phe Thr Phe Thr Ile 235
		Ser Ser Leu Gln Pro 240
Glu	Asp Ile Ala Thr 245	Tyr Tyr Cys Gln 250
		Tyr Gly Asn Leu Pro Phe 255
Thr	Phe Gly Gly 260	Gly Thr Lys Val Glu 265
		Ile Lys Arg Ala Ala Leu 270
Ser	Asn Ser 275	Ile Met Tyr Phe Ser 280
		His Phe Val Pro Val Phe Leu Pro 285
Ala	Lys Pro Thr Thr Thr 295	Pro Ala Pro Arg Pro 300
		Thr Pro Ala Pro
Thr 305	Ile Ala Ser Gln 310	Pro Leu Ser Leu Arg Pro 315
		Glu Ala Cys Arg Pro 320
Ala	Ala Gly Gly Ala 325	Val His Thr Arg Gly 330
		Leu Asp Phe Ala Cys Asp 335
Ile	Tyr Ile Trp Ala 340	Pro Leu Ala Gly 345
		Thr Cys Gly Val Leu Leu Leu 350
Ser	Leu Val Ile Thr Leu Tyr 360	Cys Asn His Arg Asn 365
		Arg Ser Lys Arg
Ser	Arg Leu Leu His Ser 375	Asp Tyr Met Asn Met 380
		Thr Pro Arg Arg Pro
Gly 385	Pro Thr Arg Lys His Tyr 390	Gln Pro Tyr Ala 395
		Pro Pro Arg Asp Phe 400
Ala	Ala Tyr Arg Ser 405	Arg Val Lys Phe Ser 410
		Arg Ser Ala Asp Ala Pro 415
Ala	Tyr Gln Gln Gly Gln 420	Asn Gln Leu Tyr Asn 425
		Glu Leu Asn Leu Gly 430

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
435 440 445

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
450 455 460

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
465 470 475 480

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
485 490 495

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
500 505 510

Ala Leu Pro Pro Arg
515

<210> 199
<211> 1488
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 199
caggtgcagt tgcaggaaag cgggcctggc cttgtgaaac caagccagac actgagcctg 60
acatgcactg tgtccggcgg gtccatatct tccgggggtt tttattggtc ctggatacgc 120
cagcatcccg ggaaaggact tgaatggatt ggatatatcc accattccgg aagcaccac 180
tacaatccaa gccttaaadc ccgggtgaca atctccatcg acacctcaaa gaatcttttt 240
tccctgcggt tgtcttcagt aactgccgcc gataccgctg tgtactactg tgccagcctc 300
gtctattgcg gcggagattg ttattctggg ttcgattatt ggggtcaagg cacactggta 360
actgtcagca gcggaggcgg cggttccggg ggcgggggca gtggaggggg cggatctgac 420
attcagctta cgcagtcacc atcttcactt agcgcagcgt ttggcgatcg ggtcagcttc 480

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acgtgtcaag caagtcagga tatcaacaac tttcttaact ggtaccagca gaagccaggc      540
aaggcaccca agttgctgat ttacgatgct tctaacctcg agacgggagt gcctagccgc      600
ttctccggga gcggcagcgg cacagacttt acctttacga tttccagtct gcagccagag      660
gatatagcaa cttattactg tcagcagtat ggcaacctcc cttttacctt cggtggtggc      720
acaaaggtcg agattaaaag agccgcagcg ttgtccaact ccataatgta tttttctcat      780
tttgtgcccg tctttctgcc tgccaaacct accaccaccc ccgccccacg accacctact      840
ccagccccca ccatcgcctc ccagcccctc agcctgaggc cagaggcttg tcgccctgct      900
gcggggggcg ctgtccatac cagaggactc gacttcgcct gcgatattta tatatgggcc      960
cccctcgccg gcacctgcgg agtcttgctc ctgagccttg tgatcacgct ttattgtaac     1020
catcggaata gatccaaaag aagccgcctg ctccatagcg attaccatgaa tatgactcca     1080
cgccgccctg gccccacaag gaaacactac cagccttacg caccacctag agatttcgct     1140
gcctatcgga gcagggtgaa gttttccaga tctgcagatg caccagcgta tcagcagggc     1200
cagaaccaac tgtataacga gctcaacctg ggacgcaggg aagagtatga cgttttggac     1260
aagcgcagag gacgggaccc tgagatgggt ggcaaacc aa gacgaaaaaa cccccaggag     1320
ggctcttata atgagctgca gaaggataag atggctgaag cctattctga aataggcatg     1380
aaaggagagc ggagaagggg aaaagggcac gacggtttgt accaggggact cagcactgct     1440
acgaaggata cttatgacgc tctccacatg caagccctgc cacctagg                       1488

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<210> 200

<211> 496

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<223> anti-CLL-1 CAR construct

<400> 200

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

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Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
          20           25           30

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31 Jul 2019
2017240667

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

Thr	Lys	Val	Glu	Ile	Lys	Arg	Ala	Ala	Ala	Leu	Ser	Asn	Ser	Ile	Met	
				245					250					255		
Tyr	Phe	Ser	His	Phe	Val	Pro	Val	Phe	Leu	Pro	Ala	Lys	Pro	Thr	Thr	
			260					265					270			
Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	
		275					280					285				
Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	
	290					295					300					
Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	
305					310					315					320	
Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	
				325				330						335		
Leu	Tyr	Cys	Asn	His	Arg	Asn	Arg	Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	
			340					345					350			
Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro	Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	
		355					360					365				
His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser	
	370					375					380					
Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	
385					390					395					400	
Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	
				405					410					415		
Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	
			420					425					430			
Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	
		435					440					445				
Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	
	450					455					460					

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
465 470 475 480

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490 495

<210> 201
<211> 1437
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 201
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gtgagttgca aagtctctgg atacactctg accgagctct ctatgcactg ggtccggcag 180
gccccggca agggattgga atggatgggc gggttcgatc ctgaggacgg agagactatc 240
tacgctcaaa aattccaggg acgagtgact gtgaccgaag acactagtagc cgacactgcc 300
tacatggaac tttcctctct gcgatcagaa gataccgcag tgtactactg tgctactgaa 360
tctaggggca ttggatggcc ctacttcgat tactgggggtc aggggaactct ggtgactgtc 420
tccagcgggtg gaggtggcag cgggtggtggc ggaagcgggg ggggcggctc tgatattcag 480
atgactcaat ctccttcttc tctgtccgct tccgtgggcg atagagtgac cattacttgt 540
agggcgtccc agtcaatctc cagttatttg aattgggtatc agcagaagcc cgggaaagca 600
cctaagctgt tgatcagcgg ggcttctagc ctgaagagtg gggtagcttc acggttcagc 660
ggaagcggaa gcggaaccga tttcaccttg actatcagca gcctgccacc tgaggacttt 720
gcaacttact actgccaaca gtcatacagc actccgatca ctttcggcca gggcacccgg 780
ctcgaaatca agcgcgtgc tgctttggac aatgagaagt caaacggcac catcatacat 840
gttaaaggta aacatctgtg tccctccccg ctgttccccg gcccttccaa accgttctgg 900
gttctggtgg tggtcggagg cgtactcgct tgctatagtc tgctggtaac tgtcgccttc 960

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atcatctttt gggtgagatc caaaagaagc cgcctgctcc atagcgatta catgaatatg      1020
actccacgcc gccctggccc cacaaggaaa cactaccagc cttacgcacc acctagagat      1080
ttcgctgcct atcggagcag ggtgaagttt tccagatctg cagatgcacc agcgtatcag      1140
cagggccaga accaactgta taacgagctc aacctgggac gcagggaaga gtatgacgtt      1200
ttggacaagc gcagaggacg ggaccctgag atgggtggca aaccaagacg aaaaaacccc      1260
caggagggtc tctataatga gctgcagaag gataagatgg ctgaagccta ttctgaaata      1320
ggcatgaaag gagagcggag aaggggaaaa gggcacgacg gtttgtacca gggactcagc      1380
actgctacga aggatactta tgacgctctc cacatgcaag ccctgccacc taggtaa      1437

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<210> 202
 <211> 478
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<220>
 <223> anti-CLL-1 CAR construct

<400> 202
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
 20 25 30

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr
 35 40 45

Thr Leu Thr Glu Leu Ser Met His Trp Val Arg Gln Ala Pro Gly Lys
 50 55 60

Gly Leu Glu Trp Met Gly Gly Phe Asp Pro Glu Asp Gly Glu Thr Ile
 65 70 75 80

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Val Thr Glu Asp Thr Ser
 85 90 95

Thr	Asp	Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	100	105	110
Ala	Val	Tyr	Tyr	Cys	Ala	Thr	Glu	Ser	Arg	Gly	Ile	Gly	Trp	Pro	Tyr	115	120	125
Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	130	135	140
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Gln	145	150	155
Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	165	170	175
Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Ser	Ser	Tyr	Leu	Asn	Trp	180	185	190
Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Ser	Gly	Ala	195	200	205
Ser	Ser	Leu	Lys	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	210	215	220
Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Pro	Pro	Glu	Asp	Phe	225	230	235
Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Ser	Thr	Pro	Ile	Thr	Phe	Gly	245	250	255
Gln	Gly	Thr	Arg	Leu	Glu	Ile	Lys	Arg	Ala	Ala	Ala	Leu	Asp	Asn	Glu	260	265	270
Lys	Ser	Asn	Gly	Thr	Ile	Ile	His	Val	Lys	Gly	Lys	His	Leu	Cys	Pro	275	280	285
Ser	Pro	Leu	Phe	Pro	Gly	Pro	Ser	Lys	Pro	Phe	Trp	Val	Leu	Val	Val	290	295	300
Val	Gly	Gly	Val	Leu	Ala	Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe			

305		310		315		320
Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp						
	325			330		335
Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr						
	340			345		350
Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val						
	355			360		365
Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn						
	370			375		380
Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val						
	385			390		400
Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg						
	405			410		415
Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys						
	420			425		430
Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg						
	435			440		445
Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys						
	450			455		460
Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg						
	465			470		475

<210> 203
 <211> 1371
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
 <223> anti-CLL-1 CAR construct

<400> 203
caggtccaac tgggtgcagtc cggagccgaa gtcaagaaac caggtgcctc cgtaaagtg 60
agttgcaaag tctctggata cactctgacc gagctctcta tgcactgggt ccggcaggcc 120
cccggcaagg gattggaatg gatgggcggg ttcgatcctg aggacggaga gactatctac 180
gctcaaaaat tccagggacg agtgactgtg accgaagaca ctagtaccga cactgcctac 240
atggaacttt cctctctgcg atcagaagat accgcagtgt actactgtgc tactgaatct 300
aggggcattg gatggccta cttcgattac tggggtcagg gaactctggt gactgtctcc 360
agcgggtggag gtggcagcgg tgggtggcggg agcggggggg gcggctctga tattcagatg 420
actcaatctc cttcttctct gtccgcttcc gtgggcgata gagtgaccat tactttagg 480
gcgtcccagt caatctccag ttatttgaat tggtatcagc agaagcccgg gaaagcacct 540
aagctgttga tcagcggggc ttctagcctg aagagtgggg taccttcacg gttcagcggg 600
agcgggaagcg gaaccgattt caccctgact atcagcagcc tgccacctga ggactttgca 660
acttactact gccaacagtc atacagcact ccgatcactt tcggccaggg caccggctc 720
gaaatcaagc gcgctgctgc tttggacaat gagaagtcaa acggcaccat catacatgtt 780
aaaggtaaac atctgtgtcc ctccccgctg ttccccggcc cttccaaacc gttctgggtt 840
ctggtggtgg tcggaggcgt actcgcttgc tatagtctgc tggtaactgt cgccttcac 900
atcttttggg tgagatccaa aagaagccgc ctgctccata gcgattacat gaatatgact 960
ccacgccgcc ctggccccac aaggaaacac taccagcctt acgcaccacc tagagatttc 1020
gctgcctatc ggagcagggt gaagttttcc agatctgcag atgcaccagc gtatcagcag 1080
ggccagaacc aactgtataa cgagctcaac ctgggacgca gggaagagta tgacgttttg 1140
gacaagcgca gaggacggga ccctgagatg ggtggcaaac caagacgaaa aaacccccag 1200
gagggtctct ataatgagct gcagaaggat aagatggctg aagcctattc tgaaataggc 1260
atgaaaggag agcggagaag gggaaaaggg cacgacggtt tgtaccaggg actcagcact 1320
gctacgaagg atacttatga cgctctccac atgcaagccc tgccacctag g 1371

<210> 204
<211> 457
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<223> anti-CLL-1 CAR construct

<400> 204

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

Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Glu Leu
20 25 30

Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Gly Phe Asp Pro Glu Asp Gly Glu Thr Ile Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Val Thr Glu Asp Thr Ser Thr Asp Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Thr Glu Ser Arg Gly Ile Gly Trp Pro Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
130 135 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145 150 155 160

Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Leu Leu Ile Ser Gly Ala Ser Ser Leu Lys Ser
180 185 190

31 Jul 2019
2017240667

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Ser Leu Pro Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Ser Tyr Ser Thr Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu
225 230 235 240

Glu Ile Lys Arg Ala Ala Ala Leu Asp Asn Glu Lys Ser Asn Gly Thr
245 250 255

Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro
260 265 270

Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu
275 280 285

Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
290 295 300

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
305 310 315 320

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
325 330 335

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser
340 345 350

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
355 360 365

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
370 375 380

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
385 390 395 400

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
405 410 415

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
420 425 430

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
435 440 445

Leu His Met Gln Ala Leu Pro Pro Arg
450 455

<210> 205

<211> 1464

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> anti-CLL-1 CAR construct

<400> 205

atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc	60
ccgcaggtgc agcttgtgca gagcggggcc gaggtgaaga agcccggggc cagcgtcaaa	120
gtgtcctgta aggtcagcgg ttacaccctc accgagctga gcatgcactg ggtacggcag	180
gctcccggca aaggtcttga gtggatgggt ggatttgatc cagaagatgg agagactatc	240
tacgcccaga agttccaggg ccgggtcacc gtaacagaag acacctcaac tgacaccgct	300
tacatggagc tgagttcact gcggtccgag gacacggccg tgtattattg tgccaccgag	360
agccgcggaa tcggatggcc ttacttcgac tactggggac aggttacact tgttacagta	420
tcatccgggg gtggcggctc tgggtggggc ggctccggag ggggtggatc agatatccaa	480
atgactcaaa gtccaagttc cctgtctgcc tcagtcggag atagagtcac cataacctgc	540
agggcaagtc agtccatctc ctcttatctg aactgggtacc aacagaaacc tggaaaggcg	600
cctaagctcc tgatctccgg agcctcatct ttgaaatccg gtgtcccatc tcgcttcagt	660
ggctctggaa gcggtacaga ttttactttg accattagca gcctcccacc ggaagacttt	720
gctacatatt actgccagca gtcttactca accccaatca ccttcgggca aggcaccaga	780

```
ctcgaaataa aaagagcagc tgctatcgag gttatgtacc caccgccgta cttggataac      840
gaaaaaagca atgggaccat cattcatgtg aagggttaagc acctttgccc tagcccactg      900
tttcctggcc cgagtaaacc cttttgggta cttgtggtcg tcggcggcgt gctggcctgc      960
tactcactcc tggttaccgt cgcattcatc atcttttggg tgagatccaa aagaagccgc     1020
ctgctccata gcgattacat gaatatgact ccacgccgcc ctggcccccac aaggaaacac     1080
taccagcctt acgcaccacc tagagatttc gctgcctatc ggagcagggt gaagttttcc     1140
agatctgcag atgcaccagc gtatcagcag ggccagaacc aactgtataa cgagctcaac     1200
ctgggacgca gggaagagta tgacgttttg gacaagcgca gaggacggga ccctgagatg     1260
ggtggcaaac caagacgaaa aaacccccag gagggctctt ataatgagct gcagaaggat     1320
aagatggctg aagcctattc tgaaataggc atgaaaggag agcggagaag gggaaaaggg     1380
cacgacggtt tgtaccaggg actcagcact gctacgaagg atacttatga cgctctccac     1440
atgcaagccc tgccacctag gtaa                                           1464
```

<210> 206
 <211> 487
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<220>
 <223> anti-CLL-1 CAR construct

<400> 206
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
 20 25 30

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr
 35 40 45

Thr Leu Thr Glu Leu Ser Met His Trp Val Arg Gln Ala Pro Gly Lys
 50 55 60

Gly 65	Leu	Glu	Trp	Met	Gly 70	Gly	Phe	Asp	Pro	Glu 75	Asp	Gly	Glu	Thr	Ile 80
Tyr	Ala	Gln	Lys	Phe 85	Gln	Gly	Arg	Val	Thr 90	Val	Thr	Glu	Asp	Thr 95	Ser
Thr	Asp	Thr	Ala 100	Tyr	Met	Glu	Leu	Ser 105	Ser	Leu	Arg	Ser	Glu 110	Asp	Thr
Ala	Val	Tyr 115	Tyr	Cys	Ala	Thr	Glu 120	Ser	Arg	Gly	Ile	Gly 125	Trp	Pro	Tyr
Phe	Asp 130	Tyr	Trp	Gly	Gln	Gly 135	Thr	Leu	Val	Thr	Val 140	Ser	Ser	Gly	Gly
Gly 145	Gly	Ser	Gly	Gly	Gly 150	Gly	Ser	Gly	Gly	Gly 155	Gly	Ser	Asp	Ile	Gln 160
Met	Thr	Gln	Ser	Pro 165	Ser	Ser	Leu	Ser	Ala 170	Ser	Val	Gly	Asp	Arg	Val 175
Thr	Ile	Thr	Cys 180	Arg	Ala	Ser	Gln	Ser 185	Ile	Ser	Ser	Tyr	Leu	Asn	Trp 190
Tyr	Gln	Gln	Lys 195	Pro	Gly	Lys	Ala 200	Pro	Lys	Leu	Leu	Ile 205	Ser	Gly	Ala
Ser 210	Ser	Leu	Lys	Ser	Gly	Val 215	Pro	Ser	Arg	Phe	Ser 220	Gly	Ser	Gly	Ser
Gly 225	Thr	Asp	Phe	Thr	Leu 230	Thr	Ile	Ser	Ser	Leu 235	Pro	Pro	Glu	Asp	Phe 240
Ala	Thr	Tyr	Tyr	Cys 245	Gln	Gln	Ser	Tyr	Ser 250	Thr	Pro	Ile	Thr	Phe	Gly 255
Gln	Gly	Thr	Arg 260	Leu	Glu	Ile	Lys	Arg 265	Ala	Ala	Ala	Ile	Glu	Val	Met 270
Tyr	Pro	Pro	Pro	Tyr	Leu	Asp	Asn	Glu	Lys	Ser	Asn	Gly	Thr	Ile	Ile

	275		280		285												
His	Val	Lys	Gly	Lys	His	Leu	Cys	Pro	Ser	Pro	Leu	Phe	Pro	Gly	Pro		
	290					295					300						
Ser	Lys	Pro	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	Cys		
305					310					315					320		
Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Phe	Trp	Val	Arg	Ser		
				325					330					335			
Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro	Arg		
			340					345					350				
Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	Arg		
		355					360					365					
Asp	Phe	Ala	Ala	Tyr	Arg	Ser	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp		
	370					375					380						
Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn		
385					390					395					400		
Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg		
				405					410					415			
Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly		
			420					425					430				
Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu		
		435					440					445					
Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu		
	450					455					460						
Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His		
465					470					475					480		
Met	Gln	Ala	Leu	Pro	Pro	Arg											
				485													

<210> 207
 <211> 1398
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
 <223> anti-CLL-1 CAR construct

<400> 207
 cagggtgcagc ttgtgcagag cggggccgag gtgaagaagc ccggggccag cgtcaaagtg 60
 tcctgtaagg tcagcggtta caccctcacc gagctgagca tgcaactgggt acggcagggt 120
 cccggcaaag gtcttgagtg gatgggtgga tttgatccag aagatggaga gactatctac 180
 gcccagaagt tccagggccg ggtcaccgta acagaagaca cctcaactga caccgcttac 240
 atggagctga gttcactgcg gtccgaggac acggccgtgt attattgtgc caccgagagc 300
 cgcggaatcg gatggcctta cttcgactac tggggacagg gtacacttgt tacagtatca 360
 tccgggggtg gcggctctgg tgggggcggc tccggagggg gtggatcaga tatccaaatg 420
 actcaaagtc caagttccct gtctgcctca gtcggagata gagtcaccat aacctgcagg 480
 gcaagtcagt ccatctcctc ctatctgaac tggtagaac agaaacctgg aaaggcgcct 540
 aagctcctga tctccggagc ctcatctttg aaatccggtg tcccatctcg cttcagtggc 600
 tctggaagcg gtacagattt tactttgacc attagcagcc tcccaccgga agactttgct 660
 acatattact gccagcagtc ttactcaacc ccaatcacct tcgggcaagg caccagactc 720
 gaaataaaaa gagcagctgc tatcgagggt atgtaccac cgccgtactt ggataacgaa 780
 aaaagcaatg ggaccatcat tcatgtgaag ggtaagcacc tttgccctag cccactgttt 840
 cctggcccga gtaaaccctt ttgggtactt gtggctcgct gcggcgtgct ggcttgctac 900
 tcactcctgg ttaccgtcgc attcatcatc ttttgggtga gatccaaaag aagccgcctg 960
 ctccatagcg attacatgaa tatgactcca cgccgccctg gccccacaag gaaacactac 1020
 cagccttacg caccacctag agatttcgct gcctatcgga gcagggtgaa gttttccaga 1080
 tctgcagatg caccagcgta tcagcagggc cagaaccaac tgtataacga gctcaacctg 1140
 ggacgcaggg aagagtatga cgttttggac aagcgcagag gacgggaccc tgagatgggt 1200

```

ggcaaaccac gacgaaaaaa cccccaggag ggtctctata atgagctgca gaaggataag      1260
atggctgaag cctattctga aatagggcatg aaaggagagc ggagaagggg aaaaggggcac      1320
gacggtttgt accaggggact cagcactgct acgaaggata cttatgacgc tctccacatg      1380
caagccctgc cacctagg                                     1398

```

```

<210> 208
<211> 466
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

```

```

<220>
<223> anti-CLL-1 CAR construct

```

```

<400> 208
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1              5              10              15

```

```

Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Glu Leu
      20              25              30

```

```

Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
      35              40              45

```

```

Gly Gly Phe Asp Pro Glu Asp Gly Glu Thr Ile Tyr Ala Gln Lys Phe
      50              55              60

```

```

Gln Gly Arg Val Thr Val Thr Glu Asp Thr Ser Thr Asp Thr Ala Tyr
      65              70              75              80

```

```

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
      85              90              95

```

```

Ala Thr Glu Ser Arg Gly Ile Gly Trp Pro Tyr Phe Asp Tyr Trp Gly
      100             105             110

```

```

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
      115             120             125

```

Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	
130						135					140					
Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	
145					150					155					160	
Ala	Ser	Gln	Ser	Ile	Ser	Ser	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	
				165					170					175		
Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Ser	Gly	Ala	Ser	Ser	Leu	Lys	Ser	
			180					185					190			
Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	
		195					200					205				
Leu	Thr	Ile	Ser	Ser	Leu	Pro	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	
	210					215					220					
Gln	Gln	Ser	Tyr	Ser	Thr	Pro	Ile	Thr	Phe	Gly	Gln	Gly	Thr	Arg	Leu	
225					230					235					240	
Glu	Ile	Lys	Arg	Ala	Ala	Ala	Ile	Glu	Val	Met	Tyr	Pro	Pro	Pro	Tyr	
				245					250					255		
Leu	Asp	Asn	Glu	Lys	Ser	Asn	Gly	Thr	Ile	Ile	His	Val	Lys	Gly	Lys	
		260						265					270			
His	Leu	Cys	Pro	Ser	Pro	Leu	Phe	Pro	Gly	Pro	Ser	Lys	Pro	Phe	Trp	
		275					280					285				
Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	Cys	Tyr	Ser	Leu	Leu	Val	
	290					295					300					
Thr	Val	Ala	Phe	Ile	Ile	Phe	Trp	Val	Arg	Ser	Lys	Arg	Ser	Arg	Leu	
305					310					315					320	
Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro	Arg	Arg	Pro	Gly	Pro	Thr	
				325					330					335		
Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	Arg	Asp	Phe	Ala	Ala	Tyr	
			340					345					350			

Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
355 360 365

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
370 375 380

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
385 390 395 400

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
405 410 415

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
420 425 430

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
435 440 445

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
450 455 460

Pro Arg
465

<210> 209
<211> 1545
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 209
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60
ccgcagggtgc agttggtgca aagcggcgca gaagttaaga aacctggggc gtcagttaag 120
gtgtcttgca aagtatctgg ctataccctc actgagctgt ccatgcattg ggtaaggcag 180
gctcctggaa aggggctcga atggatggga ggatttgacc ctgaagacgg agagaccatc 240

tacgcccaga aattccaggg tagagtaaca gtgactgagg acactagcac tgacacagcg	300
tacatgggagc tgagtttctt gagaagttag gacacagccg tttactactg cgctaccgag	360
tccagaggta ttggctggcc atacttcgac tattgggggtc agggcaccct ggttacagt	420
agttcaggag gcgggggctc tggggggggc ggttccggag gggggggctc agatatacag	480
atgacgcaga gtccatcaag tctctcagcc agcgtgggag atcgcgtagc tattacttgc	540
cgcgccagcc agagtattag ctcttatctg aattgggtacc agcaaaagcc cgggaaggcc	600
cctaagcttc tgatttctgg cgctcctct ttgaagtcag gtgtgccaag cagatttagc	660
gggtctggaa gtggcactga ctttacactt actatctcca gcctgcccc agaggatttt	720
gccacatatt actgtcagca aagctactct actccaatca ctttcggcca gggcacaaga	780
ttggagatta agagggtgc cgcactttca aattccatca tgtatttcag ccattttgtg	840
cctgtttttt ttccggccaa acctacaacc actcccgccc cagccccacc tactcccgcc	900
cctaccattg cctcccagcc tctgtctctt agacctgagg cttgtagacc tgctgccggc	960
ggagccgtgc acactcgcg tctggacttc gcctgcgaca tctatatctg ggcccctctg	1020
gccggcacct gcggcgttct ctttctctca ctcgtaatca cactctattg caatcacagg	1080
aacagatcca aaagaagccg cctgctccat agcgattaca tgaatatgac tccacgccgc	1140
cctggcccca caaggaaaca ctaccagcct tacgcaccac ctagagattt cgctgcctat	1200
cggagcaggg tgaagttttc cagatctgca gatgcaccag cgtatcagca gggccagaac	1260
caactgtata acgagctcaa cctgggacgc aggggaagagt atgacgtttt ggacaagcgc	1320
agaggacggg accctgagat gggtggcaaa ccaagacgaa aaaaccccca ggagggtctc	1380
tataatgagc tgcagaagga taagatggct gaagcctatt ctgaaatagg catgaaagga	1440
gagcggagaa ggggaaaagg gcacgacggt ttgtaccagg gactcagcac tgctacgaag	1500
gatacttatg acgctctcca catgcaagcc ctgccaccta ggtaa	1545

<210> 210

<211> 514

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<223> anti-CLL-1 CAR construct

<400> 210

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr
35 40 45

Thr Leu Thr Glu Leu Ser Met His Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Met Gly Gly Phe Asp Pro Glu Asp Gly Glu Thr Ile
65 70 75 80

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Val Thr Glu Asp Thr Ser
85 90 95

Thr Asp Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Thr Glu Ser Arg Gly Ile Gly Trp Pro Tyr
115 120 125

Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
145 150 155 160

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
165 170 175

Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
180 185 190

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Ser Gly Ala

195					200					205					
Ser	Ser	Leu	Lys	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser
	210					215					220				
Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Pro	Pro	Glu	Asp	Phe
225					230					235					240
Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Ser	Thr	Pro	Ile	Thr	Phe	Gly
				245					250					255	
Gln	Gly	Thr	Arg	Leu	Glu	Ile	Lys	Arg	Ala	Ala	Ala	Leu	Ser	Asn	Ser
			260					265					270		
Ile	Met	Tyr	Phe	Ser	His	Phe	Val	Pro	Val	Phe	Leu	Pro	Ala	Lys	Pro
		275					280					285			
Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala
		290					295				300				
Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly
305					310					315					320
Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile
				325					330					335	
Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val
			340					345					350		
Ile	Thr	Leu	Tyr	Cys	Asn	His	Arg	Asn	Arg	Ser	Lys	Arg	Ser	Arg	Leu
		355					360					365			
Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro	Arg	Arg	Pro	Gly	Pro	Thr
		370					375					380			
Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	Arg	Asp	Phe	Ala	Ala	Tyr
385					390					395					400
Arg	Ser	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln
				405					410					415	

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
420 425 430

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
435 440 445

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
450 455 460

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
465 470 475 480

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
485 490 495

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
500 505 510

Pro Arg

<210> 211
<211> 1479
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 211
caggtgcagt tggtgcaaag cggcgcagaa gttaagaaac ctggggcgctc agttaaggtg 60
tcttgcaaag tatctggcta taccctcact gagctgtcca tgcattgggt aaggcaggct 120
cctggaaagg ggctcgaatg gatgggagga tttgaccctg aagacggaga gaccatctac 180
gccagaaat tccagggtag agtaacagtg actgaggaca ctagcactga cacagcgtac 240
atggagctga gttctctgag aagtgaggac acagccgttt actactgcgc taccgagtcc 300
agaggtattg gctggccata cttcgactat tggggtcagg gcaccctggt tacagtgagt 360

tcaggaggcg	ggggctctgg	ggggggcggt	tccggagggg	ggggctcaga	tatacagatg	420
acgcagagtc	catcaagtct	ctcagccagc	gtgggagatc	gcgtgactat	tacttgccgc	480
gccagccaga	gtattagctc	ctatctgaat	tggtaccagc	aaaagcccgg	gaaggcccct	540
aagcttctga	tttctggcgc	ctcctctttg	aagtcagggtg	tgccaagcag	atttagcggg	600
tctggaagtg	gcactgactt	tacacttact	atctccagcc	tgcccccaga	ggattttgcc	660
acatattact	gtcagcaaag	ctactctact	ccaatcactt	tcggccaggg	cacaagattg	720
gagattaaga	gggctgccgc	actttcaaat	tccatcatgt	atttcagcca	ttttgtgcct	780
gtttttcttc	cggccaaacc	tacaaccact	ccgccccac	gcccacctac	tcccgcccct	840
accattgcct	cccagcctct	gtctcttaga	cctgaggctt	gtagacctgc	tgccggcgga	900
gccgtgcaca	ctcgcggtct	ggacttcgcc	tgcgacatct	atatctgggc	ccctctggcc	960
ggcacctgcg	gcgttctcct	tctctcactc	gtaatcacac	tctattgcaa	tcacaggaac	1020
agatccaaaa	gaagccgcct	gctccatagc	gattacatga	atatgactcc	acgccgcctt	1080
ggccccacaa	ggaaacacta	ccagccttac	gcaccaccta	gagatttcgc	tgccctatcg	1140
agcagggtga	agttttccag	atctgcagat	gcaccagcgt	atcagcaggg	ccagaaccaa	1200
ctgtataacg	agctcaacct	gggacgcagg	gaagagtatg	acgttttgga	caagcgcaga	1260
ggacgggacc	ctgagatggg	tggcaaacca	agacgaaaaa	acccccagga	gggtctctat	1320
aatgagctgc	agaaggataa	gatggctgaa	gcctattctg	aaataggcat	gaaaggagag	1380
cggagaaggg	gaaaagggca	cgacggtttg	taccaggggac	tcagcactgc	tacgaaggat	1440
acttatgacg	ctctccacat	gcaagccctg	ccacctagg			1479

<210> 212

<211> 493

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<223> anti-CLL-1 CAR construct

<400> 212

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

31 Jul 2019
2017240667

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

Gln 225	Gln	Ser	Tyr	Ser	Thr 230	Pro	Ile	Thr	Phe	Gly 235	Gln	Gly	Thr	Arg	Leu 240
Glu	Ile	Lys	Arg	Ala 245	Ala	Ala	Leu	Ser	Asn 250	Ser	Ile	Met	Tyr	Phe 255	Ser
His	Phe	Val	Pro 260	Val	Phe	Leu	Pro	Ala 265	Lys	Pro	Thr	Thr	Thr	Pro	Ala
Pro	Arg	Pro 275	Pro	Thr	Pro	Ala	Pro	Thr 280	Ile	Ala	Ser	Gln 285	Pro	Leu	Ser
Leu	Arg 290	Pro	Glu	Ala	Cys	Arg 295	Pro	Ala	Ala	Gly	Gly 300	Ala	Val	His	Thr
Arg 305	Gly	Leu	Asp	Phe	Ala 310	Cys	Asp	Ile	Tyr	Ile 315	Trp	Ala	Pro	Leu	Ala 320
Gly	Thr	Cys	Gly	Val 325	Leu	Leu	Leu	Ser	Leu 330	Val	Ile	Thr	Leu	Tyr 335	Cys
Asn	His	Arg	Asn 340	Arg	Ser	Lys	Arg	Ser 345	Arg	Leu	Leu	His	Ser 350	Asp	Tyr
Met	Asn 355	Met	Thr	Pro	Arg	Arg	Pro 360	Gly	Pro	Thr	Arg	Lys 365	His	Tyr	Gln
Pro	Tyr 370	Ala	Pro	Pro	Arg	Asp 375	Phe	Ala	Ala	Tyr	Arg 380	Ser	Arg	Val	Lys
Phe 385	Ser	Arg	Ser	Ala	Asp 390	Ala	Pro	Ala	Tyr	Gln 395	Gln	Gly	Gln	Asn	Gln 400
Leu	Tyr	Asn	Glu 405	Leu	Asn	Leu	Gly	Arg	Arg 410	Glu	Glu	Tyr	Asp	Val 415	Leu
Asp	Lys	Arg	Arg 420	Gly	Arg	Asp	Pro	Glu 425	Met	Gly	Gly	Lys	Pro 430	Arg	Arg
Lys	Asn 435	Pro	Gln	Glu	Gly	Leu	Tyr 440	Asn	Glu	Leu	Gln	Lys 445	Asp	Lys	Met

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
450 455 460

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
465 470 475 480

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 213

<211> 1425

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>

<223> anti-CLL-1 CAR construct

<400> 213

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atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc      60
ccgcaggtcc agttggtcga aagtggcggt ggtgtagtgc agccgggccg cagtttgagg      120
ctttcctgtg cggcttcagg ctttactttt tccagctatg gaatgcactg ggtgcggcag      180
gccccgggca aaggacttga gtgggtggcc gtcatttctt atgacggatc agataagtac      240
tacgtggaca gcgtcaaggg cagattcacc atctctaggg acaacagtaa aaatagactc      300
tacctccaga tgaatagcct cagagctgaa gacacggccg tctactattg tgctcgggag      360
cggtatagtg gcagagacta ctgggggcag ggcacactcg ttacagttag tagcggcgga      420
ggagggagtg ggggcggtgg ctccggtgga ggaggttctg agattgttat gaccagagt      480
cctgcgaccc tctcagtcag ccccggggag cgcgcaactt tgtcttgtag agctagtcag      540
tccgtgtcct ctcttctgac atggtaccag caaaagcccc ggagggtcc gcgccttttg      600
atctttgggg cttcaacaag agccactggg attccgcac gattctctgg ctccgggagc      660
ggtactgggtt tcaccctgac gattagcagt ctccagagcg aggacttcgc cgtatactac      720
tgccagcagt acgatacgtg gccattcact tttggaccag ggactaaagt ggattttaag      780
cgcgccgccg ctctcgataa cgaaaagtca aatggcacca taatccacgt caaaggcaag      840
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cacctgtgcc cttccccgct cttccccgga cccagtaaac catttttgggt gctggttgtt      900
gtggggggcg tgctggcctg ctatagcctt ttggtcactg tagccttcat tatttttttg      960
gtcagatcca aaagaagccg cctgctccat agcgattaca tgaatatgac tccacgccgc     1020
cctggcccca caaggaaaca ctaccagcct tacgcaccac ctagagattt cgctgcctat     1080
cggagcaggg tgaagttttc cagatctgca gatgcaccag cgtatcagca gggccagaac     1140
caactgtata acgagctcaa cctgggacgc aggggaagagt atgacgtttt ggacaagcgc     1200
agaggacggg accctgagat gggtggcaaa ccaagacgaa aaaaccccca ggagggtctc     1260
tataatgagc tgcagaagga taagatggct gaagcctatt ctgaaatagg catgaaagga     1320
gagcggagaa ggggaaaagg gcacgacggg ttgtaccagg gactcagcac tgctacgaag     1380
gatacttatg acgctctcca catgcaagcc ctgccaccta ggtaa                        1425

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<210> 214
 <211> 474
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polypeptide

<220>
 <223> anti-CLL-1 CAR construct

<400> 214
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val
 20 25 30

Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
 35 40 45

Thr Phe Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys
 50 55 60

Gly Leu Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asp Lys Tyr
 65 70 75 80

Tyr	Val	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	
				85					90					95		
Lys	Asn	Arg	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	
			100					105					110			
Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Glu	Arg	Tyr	Ser	Gly	Arg	Asp	Tyr	Trp	
		115					120					125				
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	
	130					135					140					
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Ile	Val	Met	Thr	Gln	Ser	
145					150					155					160	
Pro	Ala	Thr	Leu	Ser	Val	Ser	Pro	Gly	Glu	Arg	Ala	Thr	Leu	Ser	Cys	
				165					170					175		
Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Leu	Leu	Thr	Trp	Tyr	Gln	Gln	Lys	
			180					185					190			
Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	Phe	Gly	Ala	Ser	Thr	Arg	Ala	
		195					200					205				
Thr	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Gly	Phe	
	210					215					220					
Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Ser	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	
225					230					235					240	
Cys	Gln	Gln	Tyr	Asp	Thr	Trp	Pro	Phe	Thr	Phe	Gly	Pro	Gly	Thr	Lys	
				245					250					255		
Val	Asp	Phe	Lys	Arg	Ala	Ala	Ala	Leu	Asp	Asn	Glu	Lys	Ser	Asn	Gly	
			260					265					270			
Thr	Ile	Ile	His	Val	Lys	Gly	Lys	His	Leu	Cys	Pro	Ser	Pro	Leu	Phe	
	275						280					285				
Pro	Gly	Pro	Ser	Lys	Pro	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	

290	295	300	
Leu Ala Cys Tyr Ser	Leu Leu Val Thr Val	Ala Phe Ile Ile Phe Trp	
305	310	315	320
Val Arg Ser Lys Arg	Ser Arg Leu Leu His Ser	Asp Tyr Met Asn Met	
325	330	335	
Thr Pro Arg Arg Pro	Gly Pro Thr Arg Lys His Tyr	Gln Pro Tyr Ala	
340	345	350	
Pro Pro Arg Asp Phe	Ala Ala Tyr Arg Ser Arg	Val Lys Phe Ser Arg	
355	360	365	
Ser Ala Asp Ala Pro	Ala Tyr Gln Gln Gly Gln	Asn Gln Leu Tyr Asn	
370	375	380	
Glu Leu Asn Leu Gly	Arg Arg Glu Glu Tyr Asp	Val Leu Asp Lys Arg	
385	390	395	400
Arg Gly Arg Asp Pro	Glu Met Gly Gly Lys Pro	Arg Arg Lys Asn Pro	
405	410	415	
Gln Glu Gly Leu Tyr	Asn Glu Leu Gln Lys Asp	Lys Met Ala Glu Ala	
420	425	430	
Tyr Ser Glu Ile Gly	Met Lys Gly Glu Arg Arg	Arg Gly Lys Gly His	
435	440	445	
Asp Gly Leu Tyr Gln	Gly Leu Ser Thr Ala Thr	Lys Asp Thr Tyr Asp	
450	455	460	
Ala Leu His Met Gln	Ala Leu Pro Pro Arg		
465	470		

<210> 215

<211> 1359

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

polynucleotide

<220>

<223> anti-CLL-1 CAR construct

<400> 215

caggtccagt	tggtcgaaag	tggcgggtggt	gtagtgcagc	cgggccgcag	tttgaggctt	60
tcctgtgcgg	cttcaggctt	tactttttcc	agctatggaa	tgactgggt	gcggcaggcc	120
cccggcaaag	gacttgagt	ggtggccgtc	atttcttatg	acggatcaga	taagtactac	180
gtggacagcg	tcaagggcag	attcaccatc	tctagggaca	acagtaaaaa	tagactctac	240
ctccagatga	atagcctcag	agctgaagac	acggccgtct	actattgtgc	tcgggagcgg	300
tatagtggca	gagactactg	ggggcagggc	acactcgtaa	cagttagtag	cggcggagga	360
gggagtgggg	gcgggtggctc	cgggtggagga	ggttctgaga	ttgttatgac	ccagagtcct	420
gcgaccctct	cagtcagccc	cggggagcgc	gcaactttgt	cttgacagagc	tagtcagtcc	480
gtgtcctctc	ttctgacatg	gtaccagcaa	aagcccgggc	aggctccgcg	ccttttgatc	540
tttggggctt	caacaagagc	caactgggatt	cccgcacgat	tctctggctc	cgggagcggg	600
actggtttca	ccctgacgat	tagcagtctc	cagagcgagg	acttcgccgt	atactactgc	660
cagcagtacg	atacgtggcc	attcactttt	ggaccaggga	ctaaagtgga	ttttaagcgc	720
gccgccgctc	tcgataacga	aaagtcaa	ggcaccataa	tccacgtcaa	aggcaagcac	780
ctgtgccctt	ccccgctctt	ccccggaccc	agtaaaccat	tttgggtgct	ggttgtttgt	840
ggggggcgtg	tggcctgcta	tagccttttg	gtcactgtag	ccttcattat	tttttgggtc	900
agatccaaaa	gaagccgcct	gctccatagc	gattacatga	atatgactcc	acgccgcctt	960
ggccccacaa	ggaaacacta	ccagccttac	gcaccaccta	gagatttcgc	tgccatcgg	1020
agcaggggtga	agttttccag	atctgcagat	gcaccagcgt	atcagcaggg	ccagaaccaa	1080
ctgtataacg	agctcaacct	gggacgcagg	gaagagtatg	acgttttgga	caagcgcaga	1140
ggacgggacc	ctgagatggg	tggcaaacca	agacgaaaaa	acccccagga	gggtctctat	1200
aatgagctgc	agaaggataa	gatggctgaa	gcctattctg	aaataggcat	gaaaggagag	1260
cggagaaggg	gaaaagggca	cgacggtttg	taccagggac	tcagcactgc	tacgaaggat	1320
acttatgacg	ctctccacat	gcaagccctg	ccacctagg			1359

<210> 216

<211> 453
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<220>
 <223> anti-CLL-1 CAR construct

<400> 216
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asp Lys Tyr Tyr Val Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Arg Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

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

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly
 115 120 125

Gly Gly Gly Ser Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser
 130 135 140

Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
 145 150 155 160

Val Ser Ser Leu Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
 165 170 175

31 Jul 2019
2017240667

Arg Leu Leu Ile Phe Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala
180 185 190

Arg Phe Ser Gly Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser
195 200 205

Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp
210 215 220

Thr Trp Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Phe Lys Arg
225 230 235 240

Ala Ala Ala Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val
245 250 255

Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys
260 265 270

Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
275 280 285

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
290 295 300

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
305 310 315 320

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
325 330 335

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
340 345 350

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
355 360 365

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
370 375 380

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
385 390 395 400

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
405 410 415

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
420 425 430

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
435 440 445

Ala Leu Pro Pro Arg
450

<210> 217
<211> 1452
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 217
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60
ccgcaggtgc agctcgtgga gtctggcggc ggcgtggtcc agcccggccg gtccctgcgc 120
ctgtcctgcg ccgccagcgg gtttactttt tcctcctacg gcatgcactg ggtgcgccag 180
gctcccggca agggcctcga gtgggtcgcc gtgatctcat acgatgggtc agacaaatac 240
tatgtcgatt ctgttaaagg gcggtttacc atttcaagag ataactctaa gaataggctg 300
tatttgcaga tgaacagcct gagggctgaa gataccgcag tgtactattg cgctagggag 360
cggtatagtg gccgcgatta ctggggacag ggtacactgg tgaccgtgag ctctgggggt 420
ggcgggaagcg ggggtggcgg aagcggcgga ggggtagtg aaattgtgat gaccagtcct 480
ccggctacac tttcagtctc ccctggggag agagctacac tgtcatgcag agcgtcccag 540
tccgtctctt ctctccttac ctggtatcag cagaagcccc gccaggctcc tcgactgctg 600
atcttcggtg cctccacaag ggcgaccggg attccagccc gcttctcagg ttctgggagc 660

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ggaactgggtt tcactttgac aatcagttca ctgcagtcag aggatttcgc cgtgtactac      720
tgccagcaat acgacacatg gccattcact ttcggaacccg gtaccaaagt cgatttcaag      780
agagccgcgg ccatcgaggt tatgtacca ccaccatatac tggacaatga aaaaagcaat      840
ggaaccatta tccatgtgaa gggtaaacac ctctgcccta gcccactttt ccctggccca      900
tcaaagccct tctgggtcct ggtggtcgtg ggggggtgtg tggcctgtta cagccttctg      960
gtgacgggtt ctttcattat cttctgggtt agatccaaaa gaagccgcct gctccatagc     1020
gattacatga atatgactcc acgccgccct ggccccacaa ggaaacacta ccagccttac     1080
gcaccaccta gagatttcgc tgcctatcgg agcagggtga agttttccag atctgcagat     1140
gcaccagcgt atcagcaggg ccagaaccaa ctgtataacg agctcaacct gggacgcagg     1200
gaagagtatg acgttttggg caagcgcaga ggacggggacc ctgagatggg tggcaaacca     1260
agacgaaaaa acccccagga gggctctctat aatgagctgc agaaggataa gatggctgaa     1320
gcctattctg aaataggcat gaaaggagag cggagaaggg gaaaagggca cgacggtttg     1380
taccaggggac tcagcactgc tacgaaggat acttatgacg ctctccacat gcaagccctg     1440
ccacctaggt aa                                                                1452

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<210> 218
 <211> 483
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<220>
 <223> anti-CLL-1 CAR construct

<400> 218
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val
 20 25 30

Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
 35 40 45

Thr	Phe	Ser	Ser	Tyr	Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	
	50					55					60					
Gly	Leu	Glu	Trp	Val	Ala	Val	Ile	Ser	Tyr	Asp	Gly	Ser	Asp	Lys	Tyr	
65					70					75					80	
Tyr	Val	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	
				85					90					95		
Lys	Asn	Arg	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	
			100					105					110			
Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Glu	Arg	Tyr	Ser	Gly	Arg	Asp	Tyr	Trp	
		115					120					125				
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	
	130					135					140					
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Ile	Val	Met	Thr	Gln	Ser	
145					150					155					160	
Pro	Ala	Thr	Leu	Ser	Val	Ser	Pro	Gly	Glu	Arg	Ala	Thr	Leu	Ser	Cys	
				165					170					175		
Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Leu	Leu	Thr	Trp	Tyr	Gln	Gln	Lys	
			180					185					190			
Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	Phe	Gly	Ala	Ser	Thr	Arg	Ala	
		195				200						205				
Thr	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Gly	Phe	
	210					215					220					
Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Ser	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	
225					230					235					240	
Cys	Gln	Gln	Tyr	Asp	Thr	Trp	Pro	Phe	Thr	Phe	Gly	Pro	Gly	Thr	Lys	
				245					250					255		
Val	Asp	Phe	Lys	Arg	Ala	Ala	Ala	Ile	Glu	Val	Met	Tyr	Pro	Pro	Pro	

	260	265	270
Tyr	Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly		
	275	280	285
Lys	His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe		
	290	295	300
Trp	Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu		
	305	310	315
Val	Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg		
	325	330	335
Leu	Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro		
	340	345	350
Thr	Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala		
	355	360	365
Tyr	Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr		
	370	375	380
Gln	Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg		
	385	390	395
Glu	Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met		
	405	410	415
Gly	Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu		
	420	425	430
Leu	Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys		
	435	440	445
Gly	Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu		
	450	455	460
Ser	Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu		
	465	470	475
			480

Pro Pro Arg

<210> 219

<211> 1386

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> anti-CLL-1 CAR construct

<400> 219

caggtgcagc tcgtggagtc tggcggcggc gtggtccagc ccggccggtc cctgcgctg	60
tcctgcgccg ccagcgggtt tactttttcc tcctacggca tgcactgggt gcgccaggct	120
cccggcaagg gcctcgagtg ggtcgccgtg atctcatagc atgggtcaga caaatactat	180
gtcgattctg ttaaagggcg gtttaccatt tcaagagata actctaagaa taggctgtat	240
ttgcagatga acagcctgag ggctgaagat accgcagtgt actattgcgc tagggagcgg	300
tatagtggcc gcgattactg gggacagggt aacttggtga ccgtgagctc tgggggtggc	360
ggaagcgggg gtggcgggaa cggcggaggg ggtagtgaaa ttgtgatgac ccagtctccg	420
gctacacttt cagtctcccc tggggagaga gctacactgt catgcagagc gtcccagtcc	480
gtctcttctc tccttacctg gtatcagcag aagcccggcc aggctcctcg actgctgac	540
ttcgggtgcct ccacaagggc gaccgggatt ccagcccgtc tctcagggtc tgggagcggg	600
actggtttca ctttgacaat cagttcactg cagtcagagg atttcgccgt gtactactgc	660
cagcaatacg acacatggcc attcactttc ggacccggta ccaaagtcga tttcaagaga	720
gccgcggcca tcgaggttat gtaccaccca ccatatctgg acaatgaaaa aagcaatgga	780
accattatcc atgtgaaggg taaacacctc tgccctagcc cactttttccc tggcccatca	840
aagcccttct gggctcttggg ggtcgtgggg ggtgtgctgg cctgttacag ccttctgggtg	900
acggttgctt tcattatctt ctgggttaga tccaaaagaa gccgcctgct ccatagcgat	960
tacatgaata tgactccacg ccgccctggc ccacaagga aacactacca gccttacgca	1020
ccacctagag atttcgctgc ctatcgagc aggggtgaagt tttccagatc tgcagatgca	1080

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ccagcgtatc agcagggcca gaaccaactg tataacgagc tcaacctggg acgcagggaa 1140
gagtatgacg ttttggacaa gcgcagagga cgggaccctg agatgggtgg caaaccaaga 1200
cgaaaaaacc cccaggaggg tctctataat gagctgcaga aggataagat ggctgaagcc 1260
tattctgaaa taggcatgaa aggagagcgg agaaggggaa aagggcacga cggtttgtac 1320
cagggactca gcactgctac gaaggatact tatgacgctc tccacatgca agccctgcca 1380
cctagg 1386
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<210> 220
 <211> 462
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<220>
 <223> anti-CLL-1 CAR construct

<400> 220
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asp Lys Tyr Tyr Val Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Arg Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

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

Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly		
		115					120					125					
Gly	Gly	Gly	Ser	Glu	Ile	Val	Met	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser		
	130					135					140						
Val	Ser	Pro	Gly	Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser		
145					150					155					160		
Val	Ser	Ser	Leu	Leu	Thr	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro		
			165						170					175			
Arg	Leu	Leu	Ile	Phe	Gly	Ala	Ser	Thr	Arg	Ala	Thr	Gly	Ile	Pro	Ala		
			180					185					190				
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Gly	Phe	Thr	Leu	Thr	Ile	Ser		
		195					200					205					
Ser	Leu	Gln	Ser	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Asp		
	210					215					220						
Thr	Trp	Pro	Phe	Thr	Phe	Gly	Pro	Gly	Thr	Lys	Val	Asp	Phe	Lys	Arg		
225					230					235					240		
Ala	Ala	Ala	Ile	Glu	Val	Met	Tyr	Pro	Pro	Pro	Tyr	Leu	Asp	Asn	Glu		
			245						250					255			
Lys	Ser	Asn	Gly	Thr	Ile	Ile	His	Val	Lys	Gly	Lys	His	Leu	Cys	Pro		
		260					265						270				
Ser	Pro	Leu	Phe	Pro	Gly	Pro	Ser	Lys	Pro	Phe	Trp	Val	Leu	Val	Val		
		275					280					285					
Val	Gly	Gly	Val	Leu	Ala	Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe		
	290					295					300						
Ile	Ile	Phe	Trp	Val	Arg	Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp		
305					310					315					320		
Tyr	Met	Asn	Met	Thr	Pro	Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr		
				325					330					335			

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val
340 345 350

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
355 360 365

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
370 375 380

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
385 390 395 400

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
405 410 415

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
420 425 430

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
435 440 445

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
450 455 460

<210> 221
<211> 1533
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 221
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60
ccgcaggtgc agttggttga atcaggaggg ggtgtggtgc aaccggtcg gtcactgcgc 120
ctcagttgtg ctgcttccgg gtttactttc agctcatatg ggatgcactg ggtacggcag 180
gctccaggta aaggcttggga atgggtggcg gtgatcagct atgacggctc tgacaaatat 240

tatgtggact ccgtgaaagg cagattcacc atcagtcgag acaactcaaa gaatagactc	300
tacttgcaga tgaatagcct ccggggccgaa gatactgcag tctattattg cgcccgggag	360
cgctacagtg gaagagacta ttggggggcaa ggaactcttg tcacagtctc atctggcggc	420
ggcggcagcg gtggggggcgg atctggcggg ggcggcagcg aaatcgttat gactcagagt	480
cctgccacac tgagcgttag ccctggtgag agagcaacac ttagctgcag agctagtcag	540
agtgtttcca gtcttttgac atggtaccaa cagaagcccg gtcaagctcc acgactgctc	600
atcttcggtg catccacccg cgcaaccggg ataccgccc ggttttccgg ttctggaagt	660
ggcacaggat tcacgctcac catttcttct ctgcagtctg aagactttgc cgtgtattac	720
tgccagcagt acgatacctg gccctttacc tttggcccag gtactaaagt ggattttaaa	780
cgagctgctg cactttccaa tagtattatg tacttttcac attttgtgcc cgtgttcctg	840
cctgcgaagc ctacgacaac ccagcccct aggccgccc caccggcccc aactattgcc	900
tcccagccat tgtctctgag acccgaagct tgcagacctg ctgctggagg cgccgttcac	960
acccgaggat tggatttcgc atgtgacatt tacatctggg cccctttggc cggaacctgc	1020
ggtgtgctgc tgctgtcact cgtgattaca ctttactgca accaccgaaa cagatccaaa	1080
agaagccgcc tgctccatag cgattacatg aatatgactc cacgccgcc tggccccaca	1140
aggaaacact accagcctta cgcaccacct agagatttcg ctgcctatcg gagcagggcg	1200
aagttttcca gatctgcaga tgcaccagcg tatcagcagg gccagaacca actgtataac	1260
gagctcaacc tgggacgcag ggaagagtat gacgttttg acaagcgcag aggacgggac	1320
cctgagatgg gtggcaaacc aagacgaaaa aacccccagg agggctctta taatgagctg	1380
cagaaggata agatggctga agcctattct gaaataggca tgaaaggaga gcggagaagg	1440
ggaaaagggc acgacggttt gtaccaggga ctcagcactg ctacgaagga tacttatgac	1500
gctctccaca tgcaagccct gccacctagg taa	1533

<210> 222

<211> 510

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<223> anti-CLL-1 CAR construct

<400> 222

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val
 20 25 30

Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
 35 40 45

Thr Phe Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys
 50 55 60

Gly Leu Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asp Lys Tyr
 65 70 75 80

Tyr Val Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
 85 90 95

Lys Asn Arg Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
 100 105 110

Ala Val Tyr Tyr Cys Ala Arg Glu Arg Tyr Ser Gly Arg Asp Tyr Trp
 115 120 125

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
 130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Met Thr Gln Ser
 145 150 155 160

Pro Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
 165 170 175

Arg Ala Ser Gln Ser Val Ser Ser Leu Leu Thr Trp Tyr Gln Gln Lys
 180 185 190

Pro Gly Gln Ala Pro Arg Leu Leu Ile Phe Gly Ala Ser Thr Arg Ala

195					200					205					
Thr	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Gly	Phe
	210					215					220				
Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Ser	Glu	Asp	Phe	Ala	Val	Tyr	Tyr
	225					230					235				240
Cys	Gln	Gln	Tyr	Asp	Thr	Trp	Pro	Phe	Thr	Phe	Gly	Pro	Gly	Thr	Lys
				245					250					255	
Val	Asp	Phe	Lys	Arg	Ala	Ala	Ala	Leu	Ser	Asn	Ser	Ile	Met	Tyr	Phe
			260					265					270		
Ser	His	Phe	Val	Pro	Val	Phe	Leu	Pro	Ala	Lys	Pro	Thr	Thr	Thr	Pro
			275					280					285		
Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu
							295				300				
Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His
	305					310					315				320
Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu
				325					330					335	
Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr
			340					345					350		
Cys	Asn	His	Arg	Asn	Arg	Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp
			355				360					365			
Tyr	Met	Asn	Met	Thr	Pro	Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr
	370					375					380				
Gln	Pro	Tyr	Ala	Pro	Pro	Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser	Arg	Val
	385					390					395				400
Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn
				405					410					415	

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
420 425 430

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
435 440 445

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
450 455 460

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
465 470 475 480

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
485 490 495

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
500 505 510

<210> 223

<211> 1467

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> anti-CLL-1 CAR construct

<400> 223

caggtgcagt tggttgaatc aggaggggggt gtggtgcaac ccggtcggtc actgcgcctc 60

agttgtgctg cttccgggtt tacttttcagc tcatatggga tgcaactgggt acggcaggct 120

ccaggtaaag gcttggaatg ggtggcgggtg atcagctatg acggctctga caaatattat 180

gtggactccg tgaaaggcag attcaccatc agtcgagaca actcaaagaa tagactctac 240

ttgcagatga atagcctccg ggccgaagat actgcagtct attattgcgc ccgggagcgc 300

tacagtggaa gagactattg ggggcaagga actcttgtca cagtctcatc tggcggcggc 360

ggcagcgggtg ggggcggatc tggcgggggc ggcagcgaaa tcgttatgac tcagagtcct 420

gccacactga gcgttagccc tggtagagaga gcaacactta gctgcagagc tagtcagagt 480

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gtttccagtc ttttgacatg gtaccaacag aagcccggtc aagctccacg actgctcatc      540
ttcgggtgcat ccacccgcgc aaccgggata cccgcccggc tttccgggtc tggaagtggc      600
acaggattca cgctcaccat ttcttctctg cagtctgaag actttgccgt gtattactgc      660
cagcagtagc atacctggcc ctttaccttt ggcccaggta ctaaagtgga ttttaaacga      720
gctgctgcac tttccaatag tattatgtac ttttcacatt ttgtgcccgt gttcctgcct      780
gcgaagccta cgacaacccc agcccctagg ccgcccacac cggccccaac tattgcctcc      840
cagccattgt ctctgagacc cgaagcttgc agacctgctg ctggaggcgc cgttcacacc      900
cgaggattgg atttcgcatg tgacatttac atctggggccc ctttggccgg aacctgcggt      960
gtgctgctgc tgtcactcgt gattacactt tactgcaacc accgaaacag atccaaaaga     1020
agccgcctgc tccatagcga ttacatgaat atgactccac gccgccctgg cccacaagg      1080
aaacactacc agccttacgc accacctaga gatttcgctg cctatcggag caggggtgaag     1140
ttttccagat ctgcagatgc accagcgtat cagcagggcc agaaccaact gtataacgag     1200
ctcaacctgg gacgcaggga agagtatgac gttttggaca agcgagagg acgggaccct     1260
gagatgggtg gcaaaccaag acgaaaaaac ccccaggagg gtctctataa tgagctgcag     1320
aaggataaga tggctgaagc ctattctgaa ataggcatga aaggagagcg gagaagggga     1380
aaagggcacg acggtttgta ccagggactc agcactgcta cgaaggatac ttatgacgct     1440
ctccacatgc aagccctgcc acctagg                                     1467

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<210> 224
 <211> 489
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<220>
 <223> anti-CLL-1 CAR construct

<400> 224
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

31 Jul 2019
2017240667

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asp Lys Tyr Tyr Val Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Arg Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser
130 135 140

Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
145 150 155 160

Val Ser Ser Leu Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
165 170 175

Arg Leu Leu Ile Phe Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala
180 185 190

Arg Phe Ser Gly Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser
195 200 205

Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp
210 215 220

Thr Trp Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Phe Lys Arg
225 230 235 240

Ala	Ala	Ala	Leu	Ser	Asn	Ser	Ile	Met	Tyr	Phe	Ser	His	Phe	Val	Pro	245	250	255	
Val	Phe	Leu	Pro	Ala	Lys	Pro	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	260	265	270	
Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	275	280	285	
Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp	290	295	300	
Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	305	310	315	320
Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Asn	His	Arg	Asn	325	330	335	
Arg	Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	340	345	350	
Pro	Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	355	360	365	
Pro	Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser	Arg	Val	Lys	Phe	Ser	Arg	Ser	370	375	380	
Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	385	390	395	400
Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	405	410	415	
Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	420	425	430	
Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	435	440	445	
Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	450	455	460	

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
465 470 475 480

Leu His Met Gln Ala Leu Pro Pro Arg
485

<210> 225
<211> 1425
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 225
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60
ccggagattg tgatgaccca gtcccctgct accctgtccg tcagtccggg cgagagagcc 120
accttgatcat gccgggccag ccagtccgtc agcagtctcc tgacttggtg tcagcaaaaa 180
ccagggcagg caccgcggct tttgattttt ggtgcaagca cacgcgccac tggcattcca 240
gctaggtttt ctggaagtgg atctgggaca ggcttcactc tgacaatcag tagcctgcag 300
agtgaggact ttgctgttta ctactgtcaa cagtacgaca cctggccatt cacattcggg 360
cccggcacca aggtcgactt caagaggggc ggtggagggt cagggtgggtg cgggtcaggc 420
ggcgggtgggt ctcaggttca actggtggaa tcagggtggcg gcgttgtcca accggggcga 480
tcacttcgac tttcctgtgc tgcctcaggc tttacttttt catcctatgg gatgcactgg 540
gttcggcagg ctcccggaaa aggactcgag tgggttgtag tgatctctta cgatgggtca 600
gacaagtatt atgtggactc agtcaagggg agattcacia taagccgaga caactccaaa 660
aaccggcctt atctccagat gaacagcctt agagcggaag ataccgcggt atactactgt 720
gcccgcgaga ggtattccgg cagagactac tggggacagg gcacactggg caccgtgagt 780
tctgccgcag cgctcgataa cgaaaagagc aacggaacca ttatccacgt taagggcaag 840
cacctgtgcc ccagtcccct cttcccagga ccatctaaac ctttctgggt tctggtagta 900
gttggagggg tccttgcatg ttactccctt ttggtcaccg tcgccttcat tttttctgg 960

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gtgagatcca aaagaagccg cctgctccat agcgattaca tgaatatgac tccacgccgc      1020
cctggcccca caaggaaaca ctaccagcct tacgcaccac ctagagattt cgctgcctat      1080
cggagcaggg tgaagttttc cagatctgca gatgcaccag cgtatcagca gggccagaac      1140
caactgtata acgagctcaa cctgggacgc aggggaagagt atgacgtttt ggacaagcgc      1200
agaggacggg accctgagat ggggtggcaaa ccaagacgaa aaaaccccca ggagggtctc      1260
tataatgagc tgcagaagga taagatggct gaagcctatt ctgaaatagg catgaaagga      1320
gagcggagaa ggggaaaagg gcacgacggt ttgtaccagg gactcagcac tgctacgaag      1380
gatacttatg acgctctcca catgcaagcc ctgccaccta ggtaa                        1425

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<210> 226
 <211> 474
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<220>
 <223> anti-CLL-1 CAR construct

<400> 226
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu
 20 25 30

Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
 35 40 45

Ser Val Ser Ser Leu Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln Ala
 50 55 60

Pro Arg Leu Leu Ile Phe Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro
 65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile
 85 90 95

Ser Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
100 105 110

Asp Thr Trp Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Phe Lys
115 120 125

Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
145 150 155 160

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
165 170 175

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
180 185 190

Ala Val Ile Ser Tyr Asp Gly Ser Asp Lys Tyr Tyr Val Asp Ser Val
195 200 205

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Arg Leu Tyr
210 215 220

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
225 230 235 240

Ala Arg Glu Arg Tyr Ser Gly Arg Asp Tyr Trp Gly Gln Gly Thr Leu
245 250 255

Val Thr Val Ser Ser Ala Ala Ala Leu Asp Asn Glu Lys Ser Asn Gly
260 265 270

Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe
275 280 285

Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val
290 295 300

Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp

305		310		315		320
Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met						
		325		330		335
Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala						
		340		345		350
Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg						
		355		360		365
Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn						
		370		375		380
Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg						
		385		390		400
Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro						
		405		410		415
Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala						
		420		425		430
Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His						
		435		440		445
Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp						
		450		455		460
Ala Leu His Met Gln Ala Leu Pro Pro Arg						
		465		470		

<210> 227

<211> 1359

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> anti-CLL-1 CAR construct

<400> 227
gagattgtga tgaccagtc ccctgctacc ctgtccgtca gtccgggcga gagagccacc 60
ttgtcatgcc gggccagcca gtccgtcagc agtctcctga cttggtatca gcaaaaacca 120
gggcaggcac cgcggtttt gatttttgggt gcaagcacac gcgccactgg cattccagct 180
aggttttctg gaagtggatc tgggacaggc ttcactctga caatcagtag cctgcagagt 240
gaggactttg ctgtttacta ctgtcaacag tacgacacct ggccattcac attcgggccc 300
ggcaccaagg tcgacttcaa gaggggcggt ggaggttcag gtggtggcgg gtcaggcggc 360
ggtgggtctc aggttcaact ggtggaatca ggtggcggcg ttgtccaacc ggggcgatca 420
cttcgacttt cctgtgctgc ctgaggcttt actttttcat cctatgggat gcactgggtt 480
cggcaggctc ccggaaaagg actcgagtgg gttgcagtga tctcttacga tggctcagac 540
aagtattatg tggactcagt caaggggaga ttcacaataa gccgagacaa ctcaaaaac 600
cggctttatc tccagatgaa cagccttaga gcggaagata ccgcggtata ctactgtgcc 660
cgcgagaggt attccggcag agactactgg ggacagggca cactggtcac cgtgagttct 720
gccgcagcgc tcgataacga aaagagcaac ggaaccatta tccacgttaa gggcaagcac 780
ctgtgccccca gtcccctctt cccaggacca tctaaacctt tctgggttct ggtagtagtt 840
ggaggggtcc ttgcatgtta ctcccttttg gtcaccgtcg ctttcattat tttctgggtg 900
agatccaaaa gaagccgcct gctccatagc gattacatga atatgactcc acgccgcct 960
ggccccacaa ggaaacacta ccagccttac gcaccaccta gagatttcgc tgcctatcgg 1020
agcagggtga agttttccag atctgcagat gcaccagcgt atcagcaggg ccagaaccaa 1080
ctgtataacg agctcaacct gggacgcagg gaagagtatg acgttttgga caagcgaga 1140
ggacgggacc ctgagatggg tggcaaacca agacgaaaaa acccccagga gggctcttat 1200
aatgagctgc agaaggataa gatggctgaa gcctattctg aaataggcat gaaaggagag 1260
cggagaaggg gaaaagggca cgacggtttg taccagggac tcagcactgc tacgaaggat 1320
acttatgacg ctctccacat gcaagccctg ccacctagg 1359

<210> 228
<211> 453
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<223> anti-CLL-1 CAR construct

<400> 228

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Leu
 20 25 30

Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

Phe Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
 65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp Thr Trp Pro Phe
 85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Phe Lys Arg Gly Gly Gly Gly
 100 105 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val
 115 120 125

Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser
 130 135 140

Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Gly Met His Trp Val
 145 150 155 160

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Val Ile Ser Tyr
 165 170 175

Asp Gly Ser Asp Lys Tyr Tyr Val Asp Ser Val Lys Gly Arg Phe Thr
 180 185 190

31 Jul 2019
2017240667

Ile Ser Arg Asp Asn Ser Lys Asn Arg Leu Tyr Leu Gln Met Asn Ser
195 200 205

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Arg Tyr
210 215 220

Ser Gly Arg Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
225 230 235 240

Ala Ala Ala Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val
245 250 255

Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys
260 265 270

Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
275 280 285

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
290 295 300

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
305 310 315 320

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
325 330 335

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
340 345 350

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
355 360 365

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
370 375 380

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
385 390 395 400

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
405 410 415

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
420 425 430

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
435 440 445

Ala Leu Pro Pro Arg
450

<210> 229

<211> 1452

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> anti-CLL-1 CAR construct

<400> 229

atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc	60
ccggagatcg tcatgacaca gagtccagct accctgagcg tgtcccctgg agagagagcc	120
accctgtcct gtagggctag tcagagtgtg tccagcctcc tcacctggta tcaacagaag	180
cctgggtcaag ctccccggct gcttatcttc ggggccagca cgcgagccac aggcattccc	240
gccagattct ctggctctgg cagtggcacc gggttcactc tcacgatctc atccctgcag	300
tcagaggatt tcgctgtgta ttactgtcag cagtacgata catggccctt caccttcggc	360
ccgggcacaa aagtagattt caagcgcggc ggcgggggta gtggggggcgg gggatcagga	420
ggagggggct cccaagtaca gctggttgag agcggcggcg ggggtgggttca gcccgggcgc	480
agcctcaggc tgagttgcgc agcatcagga ttcacattca gttcttatgg aatgcattgg	540
gtcagacagg ctccccggaa gggccttgaa tgggtggcag tcattagcta cgacggaagc	600
gataagtact atgtggactc agttaaaggg agatttacta tcagccgcga caattccaaa	660
aacagattgt atttgcagat gaactccctc agggcggagg aactgtctgt atattactgc	720
gcacgagaga gatactccgg ccgagactat tggggccaag gaacattgggt aactgtgagc	780

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tccgccgcag ctattgaggt catgtacccc ccaccttatc tcgataatga gaagagtaat      840
gggactataa ttcacgtaaa gggcaaacac ctgtgccctt ccccgctgtt tccaggtcca      900
agtaagccgt tctgggtcct ggttgtggtg ggaggggtgc tggcctgcta ttctctgttg      960
gttaccgtgg cctttatcat tttctgggtg agatccaaaa gaagccgcct gctccatagc     1020
gattacatga atatgactcc acgccgccct ggccccacaa ggaaacacta ccagccttac     1080
gcaccaccta gagatttcgc tgcctatcgg agcaggggtga agttttccag atctgcagat     1140
gcaccagcgt atcagcaggg ccagaaccaa ctgtataacg agctcaacct gggacgcagg     1200
gaagagtatg acgttttggg caagcgcaga ggacggggacc ctgagatggg tggcaaacca     1260
agacgaaaaa acccccagga gggctctctat aatgagctgc agaaggataa gatggctgaa     1320
gcctattctg aaataggcat gaaaggagag cggagaaggg gaaaagggca cgacggtttg     1380
taccagggac tcagcactgc tacgaaggat acttatgacg ctctccacat gcaagccctg     1440
ccacctaggt aa                                                              1452

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<210> 230
 <211> 483
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<220>
 <223> anti-CLL-1 CAR construct

<400> 230
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu
 20 25 30

Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
 35 40 45

Ser Val Ser Ser Leu Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln Ala
 50 55 60

Pro 65	Arg	Leu	Leu	Ile	Phe 70	Gly	Ala	Ser	Thr	Arg 75	Ala	Thr	Gly	Ile	Pro 80
Ala	Arg	Phe	Ser	Gly 85	Ser	Gly	Ser	Gly	Thr 90	Gly	Phe	Thr	Leu	Thr 95	Ile
Ser	Ser	Leu	Gln 100	Ser	Glu	Asp	Phe	Ala 105	Val	Tyr	Tyr	Cys	Gln 110	Gln	Tyr
Asp	Thr	Trp 115	Pro	Phe	Thr	Phe	Gly 120	Pro	Gly	Thr	Lys	Val 125	Asp	Phe	Lys
Arg	Gly 130	Gly	Gly	Gly	Ser	Gly 135	Gly	Gly	Gly	Ser	Gly 140	Gly	Gly	Gly	Ser
Gln 145	Val	Gln	Leu	Val	Glu 150	Ser	Gly	Gly	Gly	Val 155	Val	Gln	Pro	Gly	Arg 160
Ser	Leu	Arg	Leu	Ser 165	Cys	Ala	Ala	Ser	Gly 170	Phe	Thr	Phe	Ser	Ser	Tyr
Gly	Met	His	Trp 180	Val	Arg	Gln	Ala	Pro 185	Gly	Lys	Gly	Leu	Glu	Trp	Val
Ala	Val	Ile 195	Ser	Tyr	Asp	Gly	Ser	Asp 200	Lys	Tyr	Tyr	Val 205	Asp	Ser	Val
Lys	Gly 210	Arg	Phe	Thr	Ile	Ser 215	Arg	Asp	Asn	Ser	Lys 220	Asn	Arg	Leu	Tyr
Leu 225	Gln	Met	Asn	Ser	Leu 230	Arg	Ala	Glu	Asp	Thr 235	Ala	Val	Tyr	Tyr	Cys
Ala	Arg	Glu	Arg	Tyr 245	Ser	Gly	Arg	Asp	Tyr 250	Trp	Gly	Gln	Gly	Thr 255	Leu
Val	Thr	Val	Ser 260	Ser	Ala	Ala	Ala	Ile 265	Glu	Val	Met	Tyr	Pro 270	Pro	Pro
Tyr	Leu	Asp	Asn	Glu	Lys	Ser	Asn	Gly	Thr	Ile	Ile	His	Val	Lys	Gly

		275					280					285			
Lys	His	Leu	Cys	Pro	Ser	Pro	Leu	Phe	Pro	Gly	Pro	Ser	Lys	Pro	Phe
	290					295					300				
Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	Cys	Tyr	Ser	Leu	Leu
305					310					315					320
Val	Thr	Val	Ala	Phe	Ile	Ile	Phe	Trp	Val	Arg	Ser	Lys	Arg	Ser	Arg
				325					330					335	
Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro	Arg	Arg	Pro	Gly	Pro
			340					345					350		
Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	Arg	Asp	Phe	Ala	Ala
		355					360					365			
Tyr	Arg	Ser	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr
	370					375					380				
Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg
385					390					395					400
Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met
				405					410					415	
Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu
			420					425					430		
Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys
		435					440					445			
Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu
	450					455					460				
Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu
465					470					475					480
Pro	Pro	Arg													

<210> 231
 <211> 1386
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
 <223> anti-CLL-1 CAR construct

<400> 231
 gagatcgtca tgacacagag tccagctacc ctgagcgtgt cccctggaga gagagccacc 60
 ctgtcctgta gggctagtca gagtgtgtcc agcctcctca cctggatatca acagaagcct 120
 ggtcaagctc cccggctgct tatcttcggg gccagcacgc gagccacagg catcccggcc 180
 agattctctg gctctggcag tggcaccggg ttactctca cgatctcatc cctgcagtca 240
 gaggatttcg ctgtgtatta ctgtcagcag tacgatacat ggcccttcac cttcgggccc 300
 ggcacaaaag tagatttcaa gcgcggcggc gggggtagtg ggggcggggg atcaggagga 360
 gggggctccc aagtacagct ggttgagagc ggcggcgggg tggttcagcc cgggcgcagc 420
 ctcaggctga gttgcgcagc atcaggattc acattcagtt cttatggaat gcattgggtc 480
 agacaggctc ccgggaaggg cttgaatgg gtggcagtca ttagctacga cggaagcgat 540
 aagtactatg tggactcagt taaagggaga ttactatca gccgcgacaa ttcaaaaaac 600
 agattgtatt tgcagatgaa ctccctcagg gcggaggaca ctgctgtata ttactgcgca 660
 cgagagagat actccggccg agactattgg ggccaaggaa cattggtaac tgtgagctcc 720
 gccgcagcta ttgaggtcat gtacccccca cttatctcg ataatgagaa gagtaatggg 780
 actataattc acgtaaaggg caaacacctg tgcccttccc cgctgtttcc aggtccaagt 840
 aagccgttct gggtcctggt tgtggtggga ggggtgctgg cctgctattc tctgttggtt 900
 accgtggcct ttatcatttt ctgggtgaga tccaaaagaa gccgcctgct ccatagcgat 960
 tacatgaata tgactccacg ccgccctggc cccacaagga aacactacca gccttacgca 1020
 ccacctagag atttcgctgc ctatcgagc aggggtgaagt tttccagatc tgcagatgca 1080
 ccagcgtatc agcagggcc aaccaactg tataacgagc tcaacctggg acgcagggaa 1140
 gagtatgacg ttttggacaa gcgcagagga cgggaccctg agatgggtgg caaaccaaga 1200

cgaaaaaacc cccaggaggg tctctataat gagctgcaga aggataagat ggctgaagcc 1260
tattctgaaa taggcatgaa aggagagcgg agaaggggaa aagggcacga cggtttgtac 1320
cagggactca gcactgctac gaaggatact tatgacgctc tccacatgca agccctgcca 1380
cctagg 1386

<210> 232
<211> 462
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 232
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Leu
20 25 30

Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Phe Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp Thr Trp Pro Phe
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Phe Lys Arg Gly Gly Gly Gly
100 105 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val
115 120 125

Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser	130	135	140
Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Gly	Met	His	Trp	Val	145	150	155
Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Val	Ile	Ser	Tyr	165	170	175
Asp	Gly	Ser	Asp	Lys	Tyr	Tyr	Val	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	180	185	190
Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Arg	Leu	Tyr	Leu	Gln	Met	Asn	Ser	195	200	205
Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Glu	Arg	Tyr	210	215	220
Ser	Gly	Arg	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	225	230	235
Ala	Ala	Ala	Ile	Glu	Val	Met	Tyr	Pro	Pro	Pro	Tyr	Leu	Asp	Asn	Glu	245	250	255
Lys	Ser	Asn	Gly	Thr	Ile	Ile	His	Val	Lys	Gly	Lys	His	Leu	Cys	Pro	260	265	270
Ser	Pro	Leu	Phe	Pro	Gly	Pro	Ser	Lys	Pro	Phe	Trp	Val	Leu	Val	Val	275	280	285
Val	Gly	Gly	Val	Leu	Ala	Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	290	295	300
Ile	Ile	Phe	Trp	Val	Arg	Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	305	310	315
Tyr	Met	Asn	Met	Thr	Pro	Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	325	330	335
Gln	Pro	Tyr	Ala	Pro	Pro	Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser	Arg	Val	340	345	350

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
355 360 365

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
370 375 380

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
385 390 395 400

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
405 410 415

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
420 425 430

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
435 440 445

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
450 455 460

<210> 233

<211> 1533

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>

<223> anti-CLL-1 CAR construct

<400> 233

atggcactcc ccgtaactgc tctgctgctg ccgttgcat tgctcctgca cgccgcacgc 60

ccggaaatag tgatgactca gtccccggcc accctcagcg tgtcccccg ggagcgagcg 120

accctgtcat gcagggttc ccagagtgtc agctccctgc tacttggtg taagcaaaag 180

ccggggcagg ctccccgcct cctcatcttc ggggcatcaa ctagggccac cggcattcct 240

gcaagatttt ccgggtctgg cagcggcacc ggcttcaccc ttaccattag ctctctgcag 300

tctgaggact tcgccgttta ctattgtcag cagtatgata cttggccctt taccttcggt 360


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ccccggaacta aggtggactt caagcgcggg gggggtggat ctggaggtgg tggctccggg      420
ggcgggtggaa gccaggtcca gttggttgag agcggcggcg gagtggtgca gcccgggagg      480
tccttgcggc tgagctgtgc agcctccggt tttacttttt ctagctatgg aatgcattgg      540
gtaagacagg ctcccggaaa aggcctcgag tgggtggcgg tcattagcta tgatggatct      600
gataaatact atgtggactc agttaagggg cgcttcacaa tctcaagaga caatagcaaa      660
aatagactgt acctgcagat gaatagtctg cgcgccgagg aactgcccgt gtactactgc      720
gcccgcgaga gatacagcgg acgggattac tggggccagg gtaccctcgt aacggtgtcc      780
tccgctgccg cccttagcaa cagcattatg tacttttctc atttcgtgcc agtctttctc      840
ccagcaaagc ccaccactac cccggccccc aggccgccta ctcctgcccc cactatcgcg      900
tctcagcctc tctccttgcg gcccgaggcc tgccggccag ccgcaggggg cgccgtacat      960
actcgggggtt tggatttcgc ttgcgacata tatatttggg cccccctcgc cggcacatgt    1020
ggagtgcctgc tcctgagtct cgttataacc ctctattgca accatagaaa cagatccaaa    1080
agaagccgcc tgctccatag cgattacatg aatatgactc cacgccgccc tggccccaca    1140
aggaaacact accagcctta cgcaccacct agagatttcg ctgcctatcg gagcaggggtg    1200
aagttttcca gatctgcaga tgcaccagcg tatcagcagg gccagaacca actgtataac    1260
gagctcaacc tgggacgcag ggaagagtat gacgttttgg acaagcgagc aggacggggac    1320
cctgagatgg gtggcaaacc aagacgaaaa aacccccagg agggctctta taatgagctg    1380
cagaaggata agatggctga agcctattct gaaataggca tgaaaggaga gcggagaagg    1440
ggaaaagggc acgacggttt gtaccaggga ctcagcactg ctacgaagga tacttatgac    1500
gctctccaca tgcaagccct gccacctagg taa                                  1533

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<210> 234

<211> 510

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<223> anti-CLL-1 CAR construct

31 Jul 2019 2017240667

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<400> 234
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1          5          10          15

His Ala Ala Arg Pro Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu
          20          25          30

Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
          35          40          45

Ser Val Ser Ser Leu Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln Ala
          50          55          60

Pro Arg Leu Leu Ile Phe Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro
65          70          75          80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile
          85          90          95

Ser Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
          100          105          110

Asp Thr Trp Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Phe Lys
          115          120          125

Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
          130          135          140

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
145          150          155          160

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
          165          170          175

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          180          185          190

Ala Val Ile Ser Tyr Asp Gly Ser Asp Lys Tyr Tyr Val Asp Ser Val
          195          200          205

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Arg Leu Tyr

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2017240667 31 Jul 2019

210	215	220
Leu Gln Met Asn Ser	Leu Arg Ala Glu Asp	Thr Ala Val Tyr Tyr Cys
225	230	235
Ala Arg Glu Arg Tyr	Ser Gly Arg Asp Tyr	Trp Gly Gln Gly Thr Leu
	245	250
Val Thr Val Ser Ser	Ala Ala Ala Leu Ser	Asn Ser Ile Met Tyr Phe
	260	265
Ser His Phe Val Pro	Val Phe Leu Pro Ala	Lys Pro Thr Thr Thr Pro
	275	280
Ala Pro Arg Pro Pro	Thr Pro Ala Pro Thr	Ile Ala Ser Gln Pro Leu
	290	295
Ser Leu Arg Pro Glu	Ala Cys Arg Pro Ala	Ala Gly Gly Ala Val His
305	310	315
Thr Arg Gly Leu Asp	Phe Ala Cys Asp Ile	Tyr Ile Trp Ala Pro Leu
	325	330
Ala Gly Thr Cys Gly	Val Leu Leu Leu Ser	Leu Val Ile Thr Leu Tyr
	340	345
Cys Asn His Arg Asn	Arg Ser Lys Arg Ser	Arg Leu Leu His Ser Asp
	355	360
Tyr Met Asn Met Thr	Pro Arg Arg Pro Gly	Pro Thr Arg Lys His Tyr
	370	375
Gln Pro Tyr Ala Pro	Pro Arg Asp Phe Ala	Ala Tyr Arg Ser Arg Val
385	390	395
Lys Phe Ser Arg Ser	Ala Asp Ala Pro Ala	Tyr Gln Gln Gly Gln Asn
	405	410
Gln Leu Tyr Asn Glu	Leu Asn Leu Gly Arg	Arg Glu Glu Tyr Asp Val
	420	425
		430

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
435 440 445

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
450 455 460

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
465 470 475 480

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
485 490 495

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
500 505 510

<210> 235

<211> 1467

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>

<223> anti-CLL-1 CAR construct

<400> 235

gaaatagtga tgactcagtc cccggccacc ctcagcgtgt cccccgggga gcgagcgacc	60
ctgtcatgca gggcttccca gagtgtcagc tccctgctca cttggtatca gcaaaagccg	120
gggcaggctc cccgcctcct catcttcggg gcatcaacta gggccaccgg cattcctgca	180
agattttccg ggtctggcag cggcaccggc ttcaccctta ccattagctc tctgcagtct	240
gaggacttcg ccgtttacta ttgtcagcag tatgatactt ggccctttac cttcggtccc	300
ggaactaagg tggacttcaa gcgcgggggg ggtggatctg gaggtggtgg ctccgggggc	360
ggtggaagcc aggtccagtt ggttgagagc ggccggcgag tggcgcagcc cgggaggtcc	420
ttgcggctga gctgtgcagc ctccggtttt actttttcta gctatggaat gcattgggta	480
agacaggctc ccgaaaagg cctcgagtgg gtggcggtca ttagctatga tggatctgat	540
aaatactatg tggactcagt taaggggcgc ttcacaatct caagagacaa tagcaaaaat	600

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agactgtacc tgcagatgaa tagtctgcgc gccgaggaca ctgccgtgta ctactgcgcc      660
cgcgagagat acagcggacg ggattactgg ggccagggta ccctcgtaac ggtgtcctcc      720
gctgccgccc ttagcaacag cattatgtac ttttctcatt tcgtgccagt ctttctccca      780
gcaaagccca ccactacccc ggccccaggg ccgcctactc ctgccccac tatcgcgtct      840
cagcctctct ctttgcggcc cgaggcctgc cggccagccg cagggggcgc cgtacatact      900
cgggggtttgg atttcgcttg cgacatatat atttgggccc ccctcgccgg cacatgtgga      960
gtgctgctcc tgagtctcgt tataaccctc tattgcaacc atagaaacag atccaaaaga     1020
agccgcctgc tccatagcga ttacatgaat atgactccac gccgccctgg cccacaagg     1080
aaacactacc agccttacgc accacctaga gatttcgctg cctatcggag caggggtgaag     1140
ttttccagat ctgcagatgc accagcgtat cagcagggcc agaaccaact gtataacgag     1200
ctcaacctgg gacgcaggga agagtatgac gttttggaca agcgcagagg acgggaccct     1260
gagatgggtg gcaaaccaag acgaaaaaac ccccaggagg gtctctataa tgagctgcag     1320
aaggataaga tggctgaagc ctattctgaa ataggcatga aaggagagcg gagaagggga     1380
aaagggcacg acggtttgta ccagggactc agcactgcta cgaaggatac ttatgacgct     1440
ctccacatgc aagccctgcc acctagg                                     1467

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<210> 236
 <211> 489
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<220>
 <223> anti-CLL-1 CAR construct

<400> 236
 Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Leu
 20 25 30

Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

31 Jul 2019
2017240667

Phe	Gly	Ala	Ser	Thr	Arg	Ala	Thr	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly	
50						55					60					
Ser	Gly	Ser	Gly	Thr	Gly	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Ser	
65					70					75					80	
Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Asp	Thr	Trp	Pro	Phe	
				85					90					95		
Thr	Phe	Gly	Pro	Gly	Thr	Lys	Val	Asp	Phe	Lys	Arg	Gly	Gly	Gly	Gly	
			100					105					110			
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	Val	
		115					120					125				
Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser	
	130					135					140					
Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Gly	Met	His	Trp	Val	
145					150					155					160	
Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Val	Ile	Ser	Tyr	
				165					170					175		
Asp	Gly	Ser	Asp	Lys	Tyr	Tyr	Val	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	
			180					185					190			
Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Arg	Leu	Tyr	Leu	Gln	Met	Asn	Ser	
		195					200					205				
Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Glu	Arg	Tyr	
	210					215					220					
Ser	Gly	Arg	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	
225					230					235					240	
Ala	Ala	Ala	Leu	Ser	Asn	Ser	Ile	Met	Tyr	Phe	Ser	His	Phe	Val	Pro	
				245					250					255		

Val	Phe	Leu	Pro	Ala	Lys	Pro	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	
			260					265					270			
Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	
		275					280					285				
Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp	
	290					295					300					
Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	
305					310					315					320	
Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Asn	His	Arg	Asn	
				325					330					335		
Arg	Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	
			340					345					350			
Pro	Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	
		355					360					365				
Pro	Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser	Arg	Val	Lys	Phe	Ser	Arg	Ser	
	370					375					380					
Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	
385					390					395					400	
Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	
				405					410					415		
Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	
			420					425					430			
Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	
		435					440					445				
Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	
	450					455					460					
Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	
465					470					475					480	

Leu His Met Gln Ala Leu Pro Pro Arg
485

<210> 237
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<223> scFv G4s linker

<400> 237
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 238
<211> 288
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> Description of Combined DNA/RNA Molecule: Synthetic polynucleotide

<220>
<223> CD8 extracellular

<400> 238
gctgcagcat tgagcaactc aataatgtat tttagtcact ttgtaccagt gttcttgccg 60
gctaagccta ctaccacacc cgctccacgg ccacctaccc cagctcctac catcgcttca 120
cagcctctgt ccctgcgccc agaggcttgc cgaccggccg cagggggcgc tgttcatacc 180
agaggactgg atttcgcctg cgatatctat atctgggcac ccctggccgg aacctgcggc 240
gtactcctgc tgtccctggt catcacgctc tattgtaatc acaggaac 288

<210> 239
<211> 96
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<223> Description of Combined DNA/RNA Molecule: Synthetic polypeptide

<220>

<223> CD8 extracellular

<400> 239

Ala Ala Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val Pro
1 5 10 15

Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro
20 25 30

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
35 40 45

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
50 55 60

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
65 70 75 80

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn
85 90 95

<210> 240

<211> 294

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> extracellular and intracellular domains

<400> 240

cttgataatg aaaagtcaaa cggaacaatc attcacgtga agggcaagca cctctgtccg 60

tcacccttgt tcctggtcc atccaagcca ttctgggtgt tggtcgtagt gggtggagtc 120

ctcgcttggt actctctgct cgtcaccgtg gcttttataa tcttctgggt tagatccaaa 180
 agaagccgcc tgctccatag cgattacatg aatatgactc cacgccgccc tggccccaca 240
 aggaaacact accagcctta cgcaccacct agagatttcg ctgcctatcg gagc 294

<210> 241
 <211> 98
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Synthetic
 polypeptide
 <220>
 <223> extracellular and intracellular domains

<400> 241
 Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys
 1 5 10 15

His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp
 20 25 30

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
 35 40 45

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu
 50 55 60

Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr
 65 70 75 80

Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr
 85 90 95

Arg Ser

<210> 242
 <211> 1482
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<223> 10E3_CHD_DNA

<400> 242

atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc	60
ccgcaggtga ccctcaaaga gtctggaccc gtgctcgtaa aacctacgga gaccctgaca	120
ctcacctgca cagtctccgg cttcagcctc atcaatgcca ggatgggagt ttcctggatc	180
aggcaaccgc ccggaaaggc cctggaatgg ctgcacata ttttcagtaa cgctgaaaaa	240
agctatcgga cttctctgaa aagtcggctc acgattagta aggacacatc caagagccaa	300
gtggtgctta cgatgactaa catggaccct gtggatactg caacctatta ctgtgctcga	360
atccctgggtt atggcggaag tggggactac cactactacg gtatggatgt ctggggccaa	420
gggaccacgg ttactgtttc aagcggaggg ggagggagtg ggggtggcgg atctggcggg	480
ggaggcagcg atatccagat gacgcagtcc cctagttcac tttccgcatc cctgggggat	540
cgggttacca ttacatgccg cgcgtcacag ggtatccgga atgatctggg atggtaccag	600
cagaagccgg gaaaggctcc taagcgcctc atctacgcca gctccaccct gcagagtgga	660
gtgccctccc ggttttcagg cagtggctcc ggtacggagt ttactcttac aattagcagc	720
ctgcagccag aagattttgc aacttactac tgtttgcagc ataataattt cccctggacc	780
tttggtcagg gcaccaaggt ggagatcaaa agagcagccg ccatcgaagt aatgtatccc	840
ccccgtacc ttgacaatga gaagtcaa at ggaaccatta tccatgttaa gggcaaacac	900
ctctgccctt ctccactgtt ccctggccct agtaagccgt tttgggtgct ggtggtagtc	960
ggtgggggtgc tggcttggtta ctctcttctc gtgaccgtcg cttttataat cttttgggtc	1020
agatccaaaa gaagccgcct gtcctatagc gattacatga atatgactcc acgccgcct	1080
ggccccacaa ggaaacacta ccagccttac gcaccaccta gagatttcgc tgcctatcgg	1140
agccgagtga aattttctag atcagctgat gctccgcct atcagcaggg acagaatcaa	1200
ctttacaatg agctgaacct gggtcgcaga gaagagtacg acgttttgga caaacgccgg	1260
ggccgagatc ctgagatggg ggggaagccg agaaggaaga atcctcaaga aggcctgtac	1320
aacgagcttc aaaaagacaa aatggctgag gcgtactctg agatcggcat gaagggcgag	1380

cggagacgag gcaaggggtca cgatggcttg tatcagggcc tgagtacagc cacaaaggac 1440
acctatgacg ccctccacat gcaggcactg cccccacgct ag 1482

<210> 243
<211> 493
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<223> 10E3_CHD_AA

<400> 243
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu
20 25 30

Val Lys Pro Thr Glu Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe
35 40 45

Ser Leu Ile Asn Ala Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro
50 55 60

Gly Lys Ala Leu Glu Trp Leu Ala His Ile Phe Ser Asn Ala Glu Lys
65 70 75 80

Ser Tyr Arg Thr Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr
85 90 95

Ser Lys Ser Gln Val Val Leu Thr Met Thr Asn Met Asp Pro Val Asp
100 105 110

Thr Ala Thr Tyr Tyr Cys Ala Arg Ile Pro Gly Tyr Gly Gly Asn Gly
115 120 125

Asp Tyr His Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val
130 135 140

Thr 145	Val	Ser	Ser	Gly	Gly 150	Gly	Gly	Ser	Gly	Gly 155	Gly	Gly	Ser	Gly	Gly 160
Gly	Gly	Ser	Asp	Ile 165	Gln	Met	Thr	Gln	Ser 170	Pro	Ser	Ser	Leu	Ser 175	Ala
Ser	Leu	Gly	Asp 180	Arg	Val	Thr	Ile	Thr 185	Cys	Arg	Ala	Ser	Gln 190	Gly	Ile
Arg	Asn	Asp 195	Leu	Gly	Trp	Tyr	Gln 200	Gln	Lys	Pro	Gly	Lys 205	Ala	Pro	Lys
Arg	Leu 210	Ile	Tyr	Ala	Ser	Ser 215	Thr	Leu	Gln	Ser	Gly 220	Val	Pro	Ser	Arg
Phe 225	Ser	Gly	Ser	Gly	Ser 230	Gly	Thr	Glu	Phe	Thr 235	Leu	Thr	Ile	Ser	Ser 240
Leu	Gln	Pro	Glu	Asp 245	Phe	Ala	Thr	Tyr	Tyr 250	Cys	Leu	Gln	His	Asn 255	Asn
Phe	Pro	Trp	Thr 260	Phe	Gly	Gln	Gly	Thr 265	Lys	Val	Glu	Ile	Lys 270	Arg	Ala
Ala	Ala	Ile 275	Glu	Val	Met	Tyr	Pro 280	Pro	Pro	Tyr	Leu	Asp 285	Asn	Glu	Lys
Ser 290	Asn	Gly	Thr	Ile	Ile	His 295	Val	Lys	Gly	Lys 300	His	Leu	Cys	Pro	Ser
Pro 305	Leu	Phe	Pro	Gly	Pro 310	Ser	Lys	Pro	Phe	Trp 315	Val	Leu	Val	Val	Val 320
Gly	Gly	Val	Leu	Ala 325	Cys	Tyr	Ser	Leu	Leu 330	Val	Thr	Val	Ala	Phe 335	Ile
Ile	Phe	Trp	Val 340	Arg	Ser	Lys	Arg	Ser 345	Arg	Leu	Leu	His	Ser 350	Asp	Tyr
Met	Asn	Met 355	Thr	Pro	Arg	Arg	Pro 360	Gly	Pro	Thr	Arg	Lys 365	His	Tyr	Gln

Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys
370 375 380

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
385 390 395 400

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
405 410 415

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
420 425 430

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
435 440 445

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
450 455 460

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
465 470 475 480

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 244
<211> 1455
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> 10E3_THD_DNA

<400> 244
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60
ccgcaagtta ctttgaagga gtctggacct gtactggtga agccaaccga gacactgaca 120
ctcacgtgta cagtgagtgg tttttccttg atcaacgcaa ggatgggCGT cagctggatc 180
aggcaacccc ctggcaaggc tctggaatgg ctgctcaca tattcagcaa tgccgaaaaa 240

agctaccgga caagcctgaa atcccgccctg actattttcca aggacacttc taagtctcag	300
gtggtgctga ccatgaccaa catggaccgc gtggacaccg ccacctatta ctgcgcaaga	360
atccctgggt atggtgggaa tgggtgactac cattattatg ggatggatgt gtgggggcaa	420
ggcacaaccg taacggtctc aagcgggtggg ggaggctcag ggggcggagg ctccggagggt	480
ggcgggtccg acattcagat gacccaaagc ccgtccagcc tgtccgccag cctgggagat	540
agagtgacaa tcacgtgtag agcttcccaa gggataagaa atgatctcgg gtggtatcag	600
cagaagcccg gcaaagcccc caaaaggctt atatatgcta gtagtacact gcagtctgga	660
gttccttccc gattttcagg tagcggctcc ggtacagagt tcaccctcac gataagctca	720
ctccagcctg aggatttcgc aacgtactac tgcctccagc acaacaattt tccctggact	780
ttcggccagg gcaccaaggt ggagatcaag agggccgctg cccttgataa tgaaaagtca	840
aacggaacaa tcattcacgt gaagggaag cacctctgtc cgtcaccctt gttccctggt	900
ccatccaagc cattctgggt gttggtcgta gtgggtggag tcctcgcttg ttactctctg	960
ctcgtcaccg tggcttttat aatcttctgg gttagatcca aaagaagccg cctgctccat	1020
agcgattaca tgaatatgac tccacgccgc cctggcccca caaggaaaca ctaccagcct	1080
tacgcaccac ctagagattt cgctgcctat cggagccgag tgaaattttc tagatcagct	1140
gatgctcccg cctatcagca gggacagaat caactttaca atgagctgaa cctgggtcgc	1200
agagaagagt acgacgtttt ggacaaacgc cggggccgag atcctgagat gggggggaag	1260
ccgagaagga agaatcctca agaaggcctg tacaacgagc ttcaaaaaga caaaatggct	1320
gaggcgact ctgagatcgg catgaagggc gagcggagac gaggcaaggg tcacgatggc	1380
ttgtatcagg gcctgagtac agccacaaag gacacctatg acgccctcca catgcaggca	1440
ctgccccac gctag	1455

<210> 245

<211> 484

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

2017240667 31 Jul 2019

<223> 10E3_THD_AA

<400> 245

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu
20 25 30

Val Lys Pro Thr Glu Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe
35 40 45

Ser Leu Ile Asn Ala Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro
50 55 60

Gly Lys Ala Leu Glu Trp Leu Ala His Ile Phe Ser Asn Ala Glu Lys
65 70 75 80

Ser Tyr Arg Thr Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr
85 90 95

Ser Lys Ser Gln Val Val Leu Thr Met Thr Asn Met Asp Pro Val Asp
100 105 110

Thr Ala Thr Tyr Tyr Cys Ala Arg Ile Pro Gly Tyr Gly Gly Asn Gly
115 120 125

Asp Tyr His Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val
130 135 140

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
145 150 155 160

Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
165 170 175

Ser Leu Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile
180 185 190

Arg Asn Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
195 200 205

31 Jul 2019
2017240667

Arg	Leu	Ile	Tyr	Ala	Ser	Ser	Thr	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	210	215	220
Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	225	230	235
Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Leu	Gln	His	Asn	Asn	245	250	255
Phe	Pro	Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Ala	260	265	270
Ala	Ala	Leu	Asp	Asn	Glu	Lys	Ser	Asn	Gly	Thr	Ile	Ile	His	Val	Lys	275	280	285
Gly	Lys	His	Leu	Cys	Pro	Ser	Pro	Leu	Phe	Pro	Gly	Pro	Ser	Lys	Pro	290	295	300
Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	Cys	Tyr	Ser	Leu	305	310	315
Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Phe	Trp	Val	Arg	Ser	Lys	Arg	Ser	325	330	335
Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro	Arg	Arg	Pro	Gly	340	345	350
Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	Arg	Asp	Phe	Ala	355	360	365
Ala	Tyr	Arg	Ser	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	370	375	380
Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	385	390	395
Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	405	410	415
Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn			

420

425

430

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
 435 440 445

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
 450 455 460

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
 465 470 475 480

Leu Pro Pro Arg

<210> 246

<211> 1464

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polynucleotide

<220>

<223> 8B5_CHD_DNA

<400> 246

atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc	60
ccgcagatcc agttggtgga atcagggggc ggtgtggtgc agccgggtag gagcctgaga	120
ctgtcatgcg tggcgtctgg cttcacattc aagaactacg gcatgcactg ggtgcgacag	180
gccccggaa agggtttggga gtgggtcgcc gtgatctggt acgacggatc taatgagtat	240
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ccatctctcc tgatttacgt tgccagcaga cgggcggctg gcattcccga caggttctct	660

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atgcaggcac tgccccacg ctag                                             1464

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<210> 247
 <211> 487
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<220>
 <223> 8B5_CHD_AA

<400> 247
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His Ala Ala Arg Pro Gln Ile Gln Leu Val Glu Ser Gly Gly Gly Val
 20 25 30

Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe
 35 40 45

Thr	Phe	Lys	Asn	Tyr	Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	
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Gly	Leu	Glu	Trp	Val	Ala	Val	Ile	Trp	Tyr	Asp	Gly	Ser	Asn	Glu	Tyr	
65					70					75					80	
Tyr	Gly	Asp	Pro	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	
				85					90					95		
Lys	Asn	Met	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Asp	Asp	Thr	
			100					105					110			
Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Ser	Gly	Ile	Ala	Val	Ala	Gly	Ala	Phe	
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Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	
	130					135					140					
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Ile	Val	Leu	
145					150					155					160	
Thr	Gln	Ser	Pro	Asp	Thr	Leu	Ser	Leu	Ser	Pro	Gly	Glu	Lys	Ala	Thr	
				165					170					175		
Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ser	Phe	Leu	Ala	Trp	
			180					185					190			
Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Ser	Leu	Leu	Ile	Tyr	Val	Ala	
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Ser	Arg	Arg	Ala	Ala	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	
	210					215					220					
Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu	Pro	Glu	Asp	Phe	
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Gly	Met	Phe	Tyr	Cys	Gln	His	Tyr	Gly	Arg	Thr	Pro	Phe	Thr	Phe	Gly	
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Pro	Gly	Thr	Lys	Val	Asp	Ile	Lys	Arg	Ala	Ala	Ala	Ile	Glu	Val	Met	
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31 Jul 2019
2017240667

Tyr	Pro	Pro	Pro	Tyr	Leu	Asp	Asn	Glu	Lys	Ser	Asn	Gly	Thr	Ile	Ile	
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His	Val	Lys	Gly	Lys	His	Leu	Cys	Pro	Ser	Pro	Leu	Phe	Pro	Gly	Pro	
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Ser	Lys	Pro	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	Cys	
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Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Phe	Trp	Val	Arg	Ser	
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Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro	Arg	
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Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	Arg	
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Asp	Phe	Ala	Ala	Tyr	Arg	Ser	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	
	370					375					380					
Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	
385					390					395					400	
Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	
				405					410					415		
Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	
			420					425					430			
Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	
		435					440				445					
Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	
	450					455					460					
Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	
465					470					475					480	

Met Gln Ala Leu Pro Pro Arg
485

<210> 248
<211> 1437
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> 8B5_THD_DNA

<400> 248
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ctctcttggtg tggcaagcgg atttaccttt aagaactatg gcatgcactg ggtgaggcag 180
gcccctggaa aaggactgga gtgggttgct gtgatctggt acgacgggtc caacgaatat 240
tatggcgatc ctgtgaaggg acggtttaca atctcacgcg ataactcaaa gaacatgctg 300
tacctgcaaa tgaactctct gcgcgctgat gacactgccg tgtattattg cgctcggagt 360
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tccggagggg gaggttctgg tggaggcggc tctggtgggg gaggcagcga gatcgttctg 480
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ggaatgtttt attgccagca ctacggaaga actccattca cttttggccc gggaacgaag 780
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<210> 249
 <211> 478
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<220>
 <223> 8B5_THD_AA

<400> 249
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His Ala Ala Arg Pro Gln Ile Gln Leu Val Glu Ser Gly Gly Gly Val
 20 25 30

Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe
 35 40 45

Thr Phe Lys Asn Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys
 50 55 60

Gly Leu Glu Trp Val Ala Val Ile Trp Tyr Asp Gly Ser Asn Glu Tyr
 65 70 75 80

Tyr Gly Asp Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
 85 90 95

Lys Asn Met Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr
 100 105 110

Ala Val Tyr Tyr Cys Ala Arg Ser Gly Ile Ala Val Ala Gly Ala Phe

	115		120		125														
Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly				
	130					135					140								
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Ile	Val	Leu				
145					150					155					160				
Thr	Gln	Ser	Pro	Asp	Thr	Leu	Ser	Leu	Ser	Pro	Gly	Glu	Lys	Ala	Thr				
				165					170					175					
Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ser	Phe	Leu	Ala	Trp				
			180					185					190						
Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Ser	Leu	Leu	Ile	Tyr	Val	Ala				
		195					200					205							
Ser	Arg	Arg	Ala	Ala	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser				
	210					215					220								
Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu	Pro	Glu	Asp	Phe				
225					230					235					240				
Gly	Met	Phe	Tyr	Cys	Gln	His	Tyr	Gly	Arg	Thr	Pro	Phe	Thr	Phe	Gly				
				245					250						255				
Pro	Gly	Thr	Lys	Val	Asp	Ile	Lys	Arg	Ala	Ala	Ala	Leu	Asp	Asn	Glu				
			260					265					270						
Lys	Ser	Asn	Gly	Thr	Ile	Ile	His	Val	Lys	Gly	Lys	His	Leu	Cys	Pro				
		275					280					285							
Ser	Pro	Leu	Phe	Pro	Gly	Pro	Ser	Lys	Pro	Phe	Trp	Val	Leu	Val	Val				
	290					295					300								
Val	Gly	Gly	Val	Leu	Ala	Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe				
305					310					315					320				
Ile	Ile	Phe	Trp	Val	Arg	Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp				
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31 Jul 2019 2017240667

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
340 345 350

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val
355 360 365

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
370 375 380

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
385 390 400

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
405 410 415

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
420 425 430

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
435 440 445

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
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Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
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<210> 250
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<212> PRT
<213> Homo sapiens

<400> 250
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<210> 251
<211> 112
<212> PRT
<213> Homo sapiens

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

<210> 252

<211> 6762

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 252

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ggccatcgcc ctgatagacg gtttttcgcc ctttgacgtt ggagtccacg ttctttaata	300
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<211> 7

<212> PRT

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<220>

<223> Description of Artificial Sequence: Synthetic
VH CDR1

<400> 253
Gly Phe Thr Phe Ser Ser Tyr
1 5

<210> 254
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR1

<400> 254
Gly Phe Thr Phe Ser Ser Tyr
1 5

<210> 255
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR1

<400> 255
Gly Tyr Thr Phe Thr Ser Tyr
1 5

<210> 256
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR1

<400> 256
Gly Gly Ser Ile Ser Ser Ser Ser Tyr
1 5

<210> 257
<211> 7
<212> PRT
<213> Artificial Sequence

31 Jul 2019

2017240667

<220>

<223> Description of Artificial Sequence: Synthetic
VH CDR1

<400> 257

Gly Phe Thr Phe Ser Ser Tyr
1 5

<210> 258

<211> 7

<212> PRT

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VH CDR1

<400> 258

Gly Phe Thr Phe Ser Ser Tyr
1 5

<210> 259

<211> 7

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<223> Description of Artificial Sequence: Synthetic
VH CDR1

<400> 259

Gly Gly Thr Phe Ser Ser Tyr
1 5

<210> 260

<211> 7

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
VH CDR1

<400> 260

Gly Phe Thr Phe Ser Ser Tyr
1 5

<210> 261

<211> 17

<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
VH CDR2

<400> 261

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

Gly

<210> 262

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
VH CDR2

<400> 262

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

Gly

<210> 263

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
VH CDR2

<400> 263

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

Gly

<210> 264

<211> 16

<212> PRT
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 <223> Description of Artificial Sequence: Synthetic
 VH CDR2
 <400> 264
 Ser Ile Ser Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Lys Ser
 1 5 10 15

<210> 265
 <211> 17
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Synthetic
 VH CDR2
 <400> 265
 Thr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys
 1 5 10 15

Gly

<210> 266
 <211> 17
 <212> PRT
 <213> Artificial Sequence
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 VH CDR2
 <400> 266
 Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
 1 5 10 15

Gly

<210> 267
 <211> 17
 <212> PRT
 <213> Artificial Sequence
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<223> Description of Artificial Sequence: Synthetic
VH CDR2

<400> 267

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

Gly

<210> 268

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
VH CDR2

<400> 268

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

Gly

<210> 269

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
VH CDR3

<400> 269

Ala	Arg	Ala	Glu	Met	Gly	Ala	Val	Phe	Asp	Ile
1				5					10	

<210> 270

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
VH CDR3

<400> 270

31 Jul 2019
2017240667

Ala Arg Asp Gly Thr Tyr Leu Gly Gly Leu Trp Tyr Phe Asp Leu
1 5 10 15

<210> 271
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3

<400> 271
Ala Arg Glu Ser Trp Pro Met Asp Val
1 5

<210> 272
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3

<400> 272
Ala Arg Gly Arg Gly Tyr Ala Thr Ser Leu Ala Phe Asp Ile
1 5 10

<210> 273
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3

<400> 273
Ala Arg Gly Ser Gln Glu His Leu Ile Phe Asp Tyr
1 5 10

<210> 274
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3

<400> 274

Ala Arg Thr Asp Phe Trp Ser Gly Ser Pro Pro Gly Leu Asp Tyr
1 5 10 15

<210> 275

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
VH CDR3

<400> 275

Ala Arg Thr Pro Glu Tyr Ser Ser Ser Ile Trp His Tyr Tyr Tyr Gly
1 5 10 15

Met Asp Val

<210> 276

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
VH CDR3

<400> 276

Val Lys Gly Pro Leu Gln Glu Pro Pro Tyr Asp Tyr Gly Met Asp Val
1 5 10 15

<210> 277

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
VL CDR3

<400> 277

Gln Gln Arg Ile Ser Trp Pro Phe Thr Phe
1 5 10

<210> 278

<211> 10

<212> PRT
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<220>
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 VL CDR3

<400> 278
 Met Gln Gly Leu Gly Leu Pro Leu Thr Phe
 1 5 10

<210> 279
 <211> 9
 <212> PRT
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<220>
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 VL CDR3

<400> 279
 Gln Gln Tyr Ala Ala Tyr Pro Thr Phe
 1 5

<210> 280
 <211> 10
 <212> PRT
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<220>
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 VL CDR3

<400> 280
 Gln Gln Arg His Val Trp Pro Pro Thr Phe
 1 5 10

<210> 281
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 <212> PRT
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<220>
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 VL CDR3

<400> 281
 Gln Gln Arg Phe Tyr Tyr Pro Trp Thr Phe
 1 5 10

31 Jul 2019
2017240667

<210> 282
<211> 10
<212> PRT
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<220>
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VL CDR3

<400> 282
Gln Gln Ile Tyr Thr Phe Pro Phe Thr Phe
1 5 10

<210> 283
<211> 10
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR3

<400> 283
Gln Gln Phe Ala His Thr Pro Phe Thr Phe
1 5 10

<210> 284
<211> 10
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR3

<400> 284
Gln Gln His His Val Trp Pro Leu Thr Phe
1 5 10