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(57) Abrégé :

The invention provides antibodies, antigen binding fragments thereof, chimeric antigen receptors (CARs), and engineered T cell receptors, polynucleotides encoding the same, and in vitro cells comprising the same. The polynucleotides, polypeptides, and in vitro cells described herein can be used in an engineered CAR T cell therapy for the treatment of a patient suffering from a cancer. In one embodiment, the polynucleotides, polypeptides. and in vitro cells described herein can be used for the treatment of multiple myeloma

# BCMA BINDING MOLECULES AND METHODS OF USE THEREOF

## CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. Provisional Patent Application No. 62/317,334, 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 June 11, 2019, is named K-1030_02US_SL.txt and is 396,355 bytes in size.

## FIELD OF THE INVENTION

[0003] This invention relates to chimeric antigen receptors (CARs) and engineered T cell receptors (TCRs) comprising an antigen binding molecule which binds to B-cell maturation antigen (BCMA), polynucleotides encoding the same, and methods of treating a cancer or other disease or disorder in a patient using the same.

## BACKGROUND OF THE INVENTION

[0004] 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.

[0005] Human 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.

[0006] Current therapies for hematologic malignancies have shown varying levels of effectiveness with undesired side effects. Therefore, a need exists to identify novel and improved therapies for treating BCMA related diseases and disorders.

## SUMMARY OF THE INVENTION

[0007] The present invention is directed to an isolated polynucleotide encoding a chimeric antigen receptor (CAR) or T cell receptor (TCR) comprising a binding molecule that specifically binds to B-cell maturation antigen (BCMA), wherein the binding molecule comprises: (a) a heavy chain variable region (VH) complementarity determining region (CDR) 1 comprising, consisting of, or consisting essentially of the amino acid sequence $GX_2X_3X_4X_5X_6X_7SY$ (SEQ ID NO: 145) wherein: $X_2$ is not present or G; $X_3$ is not present or S; $X_4$ is F, G, I, or Y; $X_5$ is S or T; $X_6$ is F or S; and $X_7$ is S or T; and/or (b) a VH CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1IX_3X_4X_5X_6X_7X_8X_9X_{10}YX_{12}X_{13}X_{14}X_{15}X_{16}X_{17}$ (SEQ ID NO: 146), wherein: $X_1$ is A, G, I, S, T, or V; $X_3$ is I, N, or S; $X_4$ is G, P, S, or Y; $X_5$ is D, G, I, or S; $X_6$ is F, G, or S; $X_7$ is not present or G or S; $X_8$ is N, S, or T; $X_9$ is A, I, K, or T; $X_{10}$ is N, S, or Y; $X_{12}$ is A or N; $X_{13}$ is D, P, or Q; $X_{14}$ is K or S; $X_{15}$ is F, L, or V; $X_{16}$ is K or Q; and $X_{17}$ is G or S; and/or (c) a VH CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}DX_{19}$ (SEQ ID NO: 147), wherein: $X_1$ is A or V; $X_2$ is K or R; $X_3$ is not present or D, G, or T; $X_4$ is not present or A, D, G, P, R, or S; $X_5$ is not present or E, F, G, L, Q, or T; $X_6$ is not present or E, M, Q, W, or Y; $X_7$ is not present or A, E, L, or S; $X_8$ is not present or G, P, S, or T; $X_9$ is not present or G, P, or S; $X_{10}$ is not present or I, L, P, or Y; $X_{11}$ is not present or W; $X_{12}$ is not present or H; $X_{13}$ is not present or E or Y; $X_{14}$ is not present or D, G, H, P, S, W, or Y; $X_{15}$ is A, G, L, W, or Y; $X_{16}$ is not present or A, G, I, P, or V; $X_{17}$ is F, L, or M; and $X_{19}$ is I, L, V, or Y; and/or (d) a light chain variable region (VL) CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2SQX_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}LX_{17}$ (SEQ ID NO: 148), wherein $X_1$ is K or R; $X_2$ is A or S; $X_5$ is G or S; $X_6$ is I, L, or V; $X_7$ is L or S; $X_8$ is not present or H or Y; $X_9$ is not present or S; $X_{10}$ is not present or N or S; $X_{11}$ is not present or G or N; $X_{12}$ is not present or N; $X_{13}$ is not present or K or Y; $X_{14}$ is N, R, or S; $X_{15}$ is N, W, or Y; and $X_{17}$ is A or D; (e) a VL CDR2 comprising, consisting of, or consisting essentially of the amino acid

sequence $X_1X_2SX_4X_5X_6X_7$ (SEQ ID NO: 149), wherein $X_1$ is D, G, L, S, or W; $X_2$ is A or G; $X_4$ is N, S, or T; $X_5$ is L or R; $X_6$ is A, E, or Q; and $X_7$ is S or T; and/or (f) a VL CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1QX_3X_4X_5X_6PX_8T$ (SEQ ID NO: 150), wherein $X_1$ is M or Q; $X_3$ is F, G, H, I, R, or Y; $X_4$ is A, F, H, I, L, or Y; $X_5$ is A, G, H, S, T, V, or Y; $X_6$ is F, L, T, W, or Y; and $X_8$ is not present or F, L, P, or W.

[0008] In another embodiment, the invention is directed to an isolated polynucleotide encoding an antibody or an antigen binding molecule thereof that specifically binds to BCMA, wherein the antibody or the antigen binding molecule thereof comprises: (a) a heavy chain variable region (VH) complementarity determining region (CDR) 1 comprising, consisting of, or consisting essentially of the amino acid sequence $GX_2X_3X_4X_5X_6X_7SY$ (SEQ ID NO: 145), wherein: $X_2$ is not present or G; $X_3$ is not present or S; $X_4$ is F, G, I, or Y; $X_5$ is S or T; $X_6$ is F or S; and $X_7$ is S or T; and/or (b) a VH CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1IX_3X_4X_5X_6X_7X_8X_9X_{10}YX_{12}X_{13}X_{14}X_{15}X_{16}X_{17}$ (SEQ ID NO: 146), wherein: $X_1$ is A, G, I, S, T, or V; $X_3$ is I, N, or S; $X_4$ is G, P, S, or Y; $X_5$ is D, G, I, or S; $X_6$ is F, G, or S; $X_7$ is not present or G or S; $X_8$ is N, S, or T; $X_9$ is A, I, K, or T; $X_{10}$ is N, S, or Y; $X_{12}$ is A or N; $X_{13}$ is D, P, or Q; $X_{14}$ is K or S; $X_{15}$ is F, L, or V; $X_{16}$ is K or Q; and $X_{17}$ is G or S; and/or (c) a VH CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}DX_{19}$ (SEQ ID NO: 147), wherein: $X_1$ is A or V; $X_2$ is K or R; $X_3$ is not present or D, G, or T; $X_4$ is not present or A, D, G, P, R, or S; $X_5$ is not present or E, F, G, L, Q, or T; $X_6$ is not present or E, M, Q, W, or Y; $X_7$ is not present or A, E, L, or S; $X_8$ is not present or G, P, S, or T; $X_9$ is not present or G, P, or S; $X_{10}$ is not present or I, L, P, or Y; $X_{11}$ is not present or W; $X_{12}$ is not present or H; $X_{13}$ is not present or E or Y; $X_{14}$ is not present or D, G, H, P, S, W, or Y; $X_{15}$ is A, G, L, W, or Y; $X_{16}$ is not present or A, G, I, P, or V; $X_{17}$ is F, L, or M; and $X_{19}$ is I, L, V, or Y; and/or (d) a light chain variable region (VL) CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2SQX_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}LX_{17}$ (SEQ ID NO: 148), wherein $X_1$ is K or R; $X_2$ is A or S; $X_5$ is G or S; $X_6$ is I, L, or V; $X_7$ is L or S; $X_8$ is not present or H or Y; $X_9$ is not present or S; $X_{10}$ is not present or N or S; $X_{11}$ is not present or G or N; $X_{12}$ is not present or N; $X_{13}$ is not present or K or Y; $X_{14}$ is N, R, or S; $X_{15}$ is N, W, or Y; and $X_{17}$ is A or D; (e) a VL CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2SX_4X_5X_6X_7$ (SEQ ID NO: 149), wherein $X_1$ is D, G, L, S, or W; $X_2$ is A or G;

$X_4$ is N, S, or T; $X_5$ is L or R; $X_6$ is A, E, or Q; and $X_7$ is S or T; and/or (f) a VL CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1QX_3X_4X_5X_6PX_8T$ (SEQ ID NO: 150), wherein $X_1$ is M or Q; $X_3$ is F, G, H, I, R, or Y; $X_4$ is A, F, H, I, L, or Y; $X_5$ is A, G, H, S, T, V, or Y; $X_6$ is F, L, T, W, or Y; and $X_8$ is not present or F, L, P, or W.

[0009] In some embodiments, the VH CDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 9-16. In some embodiments, the VH CDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 25-32. In some embodiments, the VL CDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 81-88. In some embodiments, the VL CDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 97-104. In some embodiments, the VL CDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 113-120.

[0010] In some embodiments, the binding molecule comprises: (a) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 9; a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 25; a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 41; a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 81; a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 97; and a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 113; (b) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 10; a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 26; a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 42; a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 82; a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 98; and a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 114; (c) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 11; a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 27; a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 43; a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 83; a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 99; and a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 115; (d) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 12; a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 28; a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 44; a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 84; a VL CDR2 region comprising the

amino acid sequence of SEQ ID NO: 100; and a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 116; (e) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 13; a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 29; a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 45; a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 85; a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 101; and a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 117; (f) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 14; a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 30; a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 46; a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 86; a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 102; and a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 118; (g) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 15; a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 31; a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 47; a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 87; a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 103; and a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 119; or (h) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 16; a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 32; a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 48; a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 88; a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 104; and a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 120.

[0011] In some embodiments, the binding molecule is single chained. In some embodiments, the binding molecule comprises an scFv.

[0012] In some embodiments, the CAR comprises a transmembrane domain. In some embodiments, the transmembrane domain is a transmembrane domain of CD28, 4-1BB/CD137, CD8 (e.g., CD8 alpha, CD4, CD19, CD3 epsilon, CD45, CD5, CD9, CD16, CD22, CD33, CD37, CD64, CD80, CD86, CD134, CD137, CD154, an alpha chain of a T cell receptor, a beta chain of a T cell receptor, a zeta chain of a T cell receptor, or any combination thereof. In some embodiments, the CAR comprises a hinge region between the transmembrane domain and the binding molecule. In some embodiments, the hinge region is of IgG1, IgG2, IgG3, IgG4, IgA, IgD, IgE, IgM, CD28, or CD8 alpha. In some embodiments, the CAR or TCR comprises a costimulatory region. In some embodiments, the costimulatory

region is a signaling region of CD28, OX-40, 4-1BB/CD137, CD2, CD7, CD27, CD30, CD40, programmed death-1 (PD-1), inducible T cell costimulator (ICOS), lymphocyte function-associated antigen-1 (LFA-1 (CDl la/CD18), CD3 gamma, CD3 delta, CD3 epsilon, CD247, CD276 (B7-H3), LIGHT (tumor necrosis factor superfamily member 14; TNFSF14), NKG2C, Ig alpha (CD79a), DAP-10, Fc gamma receptor, MHC class I molecule, TNF receptor proteins, Immunoglobulin-like proteins, cytokine receptors, integrins, signaling lymphocytic activation molecules (SLAM proteins), activating NK cell receptors, BTLA, a Toll ligand receptor, ICAM-1, B7-H3, CDS, ICAM-1, GITR, BAFFR, LIGHT, HVEM (LIGHTR), KIRDS2, SLAMF7, NKp80 (KLRF1), NKp44, NKp30, NKp46, CD19, CD4, CD8alpha, CD8beta, IL2R beta, IL2R gamma, IL7R alpha, ITGA4, VLA1, CD49a, ITGA4, IA4, CD49D, ITGA6, VLA-6, CD49f, ITGAD, CDl ld, ITGAE, CD103, ITGAL, CDl la, LFA-1, ITGAM, CDl lb, ITGAX, CDl lc, ITGBl, CD29, ITGB2, CD18, LFA-1, ITGB7, NKG2D, TNFR2, TRANCE/RANKL, DNAM1 (CD226), SLAMF4 (CD244, 2B4), CD84, CD96 (Tactile), CEACAM1, CRT AM, Ly9 (CD229), CD160 (BY55), PSGL1, CD100 (SEMA4D), CD69, SLAMF6 (NTB-A, Lyl08), SLAM (SLAMF1, CD150, IPO-3), BLAME (SLAMF8), SELPLG (CD162), LTBR, LAT, GADS, SLP-76, PAG/Cbp, CD19a, a ligand that specifically binds with CD83, or any combination thereof. In some embodiments, the CAR or TCR comprises an activation domain. In some embodiments, the activation domain is a CD3 zeta domain.

[0013] In other embodiments, the invention is directed to a vector comprising the polynucleotide or a polypeptide encoded by the polynucleotide.

[0014] In certain embodiments, the invention is directed to a cell comprising the polynucleotide, the vector, the polypeptide, or any combination thereof. In other embodiments, the invention is directed to a cell, e.g., an immune cell, e.g., a tumor-infiltrating lymphocyte (TIL), autologous T cell, engineered autologous T cell (eACT), an allogeneic T cell, or any combination thereof.

[0015] In other embodiments, the 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 the polynucleotide, the vector, the polypeptide, or any combination thereof. Other aspects of the invention include a method of treating a cancer in a subject in need thereof comprising administering to the subject the polynucleotide, the vector, the polypeptide, the cell, or the composition. The cancer treatable by the method can be a hematologic cancer.

## BRIEF DESCRIPTION OF THE FIGURES

[0016] FIG.1A-1F show CLUTSTAL W (1.83) multiple sequence alignments of eight example anti-BCMA binding molecules disclosed herein. FIG. 1A 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. FIG. 1B is a table providing the SEQ ID NO for each VH, CDR, and FR sequence illustrated in FIG. 1A. FIG. 1C shows a sequence alignment of example anti-BCMA binding molecules comprising a VH domain, with alternate CDRs and FRs shown. FIG. 1D is a table providing the SEQ ID NO for each VH, CDR, and FR sequence illustrated in FIG. 1C. FIG. 1E shows a sequence alignment of example anti-BCMA binding molecules comprising a VL domain. CDRs and FRs are shown, as determined by Chothia. FIG. 1F is a table providing the SEQ ID NO for each VH, CDR, and FR sequence illustrated in FIG. 1E.

[0017] FIGs. 2A-2F show BCMA expression in various cells. FIG. 2A shows multiple myeloma cell expression of BCMA, CD138, CS-1, CD38, and CD19. Box-plot analysis shows the distribution of gene expression levels in the various multiple myeloma cell lines tested (FIG. 2A). FIGs. 2B-2D show BCMA expression in EoL1 (FIG. 2B), MM1S (FIG. 2C), and NCI-H929 (FIG. 2D) cancer cell lines as measured by flow cytometric analysis of BCMA cell surface expression on the respective cell lines. FIG. 2E shows the expression of BCMA, CS-1, CLL-1, DLL3, CD70, and FLT3 in alternatively activated macrophages; CD14-positive, CD16-negative cells; CD38-negative naïve B cells; CD4-positive, alpha-beta T cells; central memory CD4-positive cells; central memory CD8-positve cells; class switched memory B cells; cytotoxic CD56-dim natural killer cell; effector memory CD4-positive cells; effector memory CD8-positive cells; inflammatory macrophages; macrophages; mature neutrophils; memory B cells; monocytes; myeloid cells; and regulatory T cells. FIG. 2F shows the expression of BCMA, CD138, CS-1, CD38, and CD19 in the same cell types as in Fig. 2E. Gene expression is shown as fragments per kilobase of exon per million reads mapped (FPKM) (FIG. 2A, FIG. 2E, and FIG. 2F).

[0018] FIG. 3A and FIG. 3B show CAR expression in lentivirus transduced primary human T cells from a first healthy donor (FIG. 3A) and a second healthy donor (FIG. 3B).

[0019] FIGs 4A-4F shows IFNγ, TNFα, 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. 4A and 4B show the IFNγ (pg/ml; y-axis) production in lentivirus transduced CAR T cells from a first donor (FIG. 4A)

and a second donor (FIG. 4B). FIGs. 4C and 4D show the TNFα (pg/ml; y-axis) production in lentivirus transduced CAR T cells from a first donor (FIG. 4C) and a second donor (FIG. 4D). FIGs. 4E and 4F show the IL-2 production (pg/ml; y-axis) in lentivirus transduced CAR T cells from a first donor (FIG. 4E) and a second donor (FIG. 4F).

[0020] FIGs. 5A-5F 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. 5A and 5B), NCI-H929 (FIGs. 5C and 5D), or MM1S (FIGs. 5E and 5F) target cells for 16 hours, 40 hours, 64 hours, 88 hours, or 112 hours. FIGs. 5A and 5B show the average cytolytic activity of transduced CAR T cells from a first donor (FIG. 5A) and a second donor (FIG. 5B) co-cultured with EoL1 target cells for 16 hours, 40 hours, 64 hours, 88 hours, or 112 hours. FIGs. 5C and 5D show the average cytolytic activity of transduced CAR T cells from a first donor (FIG. 5C) and a second donor (FIG. 5D) co-cultured with NCI-H929 target cells for 16 hours, 40 hours, 64 hours, 88 hours, or 112 hours. FIGs. 5E and 5F show the average cytolytic activity of transduced CAR T cells from a first donor (FIG. 5E) and a second donor (FIG. 5F) co-cultured with MM1S target cells for 16 hours, 40 hours, 64 hours, 88 hours, or 112 hours.

[0021] FIGs. 6A and 6B show proliferation of CFSE-labeled lentivirus transduced CAR T cells from a first healthy donor (FIG. 6A) and a second healthy donor (FIG. 6B) following 5 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.

[0022] In the Figure descriptions below, underlined sequences denote CDR regions calculated using Chothia.

[0023] FIG. 7A shows Clone FS-26528 HC DNA sequence (SEQ ID NO: 271)

[0024] FIG. 7B shows Clone FS-26528 HC AA sequence (SEQ ID NO: 272)

[0025] FIG. 7C shows HC CDR sequences for clone FS-26528.

[0026] FIG. 7D shows Clone FS-26528 LC DNA sequence (SEQ ID NO: 276).

[0027] FIG. 7E shows Clone FS-26528 LC AA sequence (SEQ ID NO: 277).

[0028] FIG. 7F shows LC CDR sequences for clone FS-26528.

[0029] FIG. 7G shows Clone FS-26528 CAR DNA HxL sequences (SEQ ID NO: 281)

[0030] FIG. 7H shows Clone FS-26528 CAR HxL AA sequences (SEQ ID NO: 282)

[0031] FIG. 7I shows Clone FS-26528 CAR DNA LxH sequences (SEQ ID NO: 283).

[0032] FIG. 7J shows Clone FS-26528 CAR LxH sequences (SEQ ID NO: 284).

[0033] FIG. 8A shows Clone PC-26534 HC DNA sequence (SEQ ID NO: 285).

[0034] FIG. 8B shows Clone PC-26534 HC sequence (SEQ ID NO: 286).

[0035] FIG. 8C shows HC CDR sequences for clone FS-26528.

[0036] FIG. 8D shows Clone PC-26534 LC DNA sequences (SEQ ID NO: 290).

[0037] FIG. 8E shows the Clone PC-26534 LC sequence (SEQ ID NO: 291).

[0038] FIG. 8F shows LC CDR sequences for Clone PC-26534.

[0039] FIG. 8G shows the Clone PC-26534 CAR DNA HxL sequence (SEQ ID NO: 295).

[0040] FIG. 8H shows the Clone PC-26534 CAR HxL AA sequence (SEQ ID NO: 296)

[0041] FIG. 8I shows the Clone PC-26534 CAR DNA LxH sequence (SEQ ID NO: 297).

[0042] FIG. 8J shows Clone PC-26534 CAR LxH sequence (SEQ ID NO: 298).

[0043] FIG. 9A shows Clone AJ-26545 HC DNA sequence (SEQ ID NO: 299).

[0044] FIG. 9B shows Clone AJ-26545 variable HC sequence (SEQ ID NO: 300).

[0045] FIG. 9C shows HC CDR sequences for Clone AJ-26545.

[0046] FIG. 9D shows Clone AJ-26545 variable LC DNA sequence (SEQ ID NO: 304).

[0047] FIG. 9E shows Clone AJ-26545 variable LC AA sequence (SEQ ID NO: 305)

[0048] FIG. 9F shows Clone AJ-26545 LC CDR sequences.

[0049] FIG. 9G shows Clone AJ-26545 CAR DNA HxL sequence (SEQ ID NO: 309).

[0050] FIG. 9H shows Clone AJ-26545 CAR HxL AA sequence (SEQ ID NO: 310)

[0051] FIG. 9I shows Clone AJ-26545 CAR DNA LxH sequence (SEQ ID NO: 311)

[0052] FIG. 9J shows Clone AJ-26545 CAR LxH sequence (SEQ ID NO: 312).

[0053] FIG. 10A shows Clone AJ-26554 HC DNA sequence (SEQ ID NO: 313)

[0054] FIG. 10B shows Clone AJ-26554 HC AA sequence (SEQ ID NO: 314).

[0055] FIG. 10C shows Clone AJ-26554 HC CDR sequences

[0056] FIG. 10D shows Clone AJ-26554 LC DNA sequence (SEQ ID NO: 318).

[0057] FIG. 10E shows Clone AJ-26554 LC AA sequence (SEQ ID NO: 319).

[0058] FIG. 10F shows Clone AJ-26554 LC CDR sequences.

[0059] FIG. 10G shows Clone AJ-26554 CAR DNA HxL chain sequences (SEQ ID NO: 323).

[0060] FIG. 10H shows Clone AJ-26554 CAR HxL chain AA sequences (SEQ ID NO: 324).

[0061] FIG. 10I shows Clone AJ-26554 CAR DNA LxH chain sequences (SEQ ID NO: 325).

[0062] FIG. 10J shows Clone AJ-26554 CAR LxH AA sequences (SEQ ID NO: 326).

[0063] FIG. 11A shows Clone NM-26562 HC DNA sequence (SEQ ID NO: 327).

[0064] FIG. 11B shows Clone NM-26562 HC AA sequence (SEQ ID NO: 328).

[0065] FIG. 11C shows Clone NM-26562 HC CDR sequences.

[0066] FIG. 11D shows Clone NM-26562 LC DNA sequence (SEQ ID NO: 332).

[0067] FIG. 11E shows Clone NM-26562 LC AA sequence (SEQ ID NO: 333).

[0068] FIG. 11F shows the Clone NM-26562 LC CDR sequences.

[0069] FIG. 11G shows the Clone NM-26562 CAR DNA HxL sequences (SEQ ID NO: 337)

[0070] Figure 11H shows Clone NM-26562 CAR HxL AA sequences (SEQ ID NO: 338).

[0071] FIG. 11I shows Clone NM-26562 CAR DNA LxH sequences (SEQ ID NO: 339).

[0072] FIG. 11J shows Clone NM-26562 CAR LxH AA sequences (SEQ ID NO: 340).

[0073] FIG. 12A shows Clone TS-26564 HC DNA sequence (SEQ ID NO: 341).

[0074] FIG. 12B shows Clone TS-26564 HC AA sequence (SEQ ID NO: 342).

[0075] FIG. 12C shows the Clone TS-26564 HC CDR sequences.

[0076] FIG. 12D shows the Clone TS-26564 LC DNA sequence (SEQ ID NO: 346).

[0077] FIG. 12E shows the Clone TS-26564 LC AA sequence (SEQ ID NO: 347).

[0078] FIG. 12F shows the Clone TS-26564 LC CDR sequences.

[0079] FIG. 12G shows the Clone TS-26564 CAR DNA HxL sequences (SEQ ID NO: 351).

[0080] FIG. 12H shows the Clone TS-26564 CAR HxL chain AA sequences (SEQ ID NO: 352).

[0081] FIG. 12I shows the Clone TS-26564 CAR DNA LxH sequences (SEQ ID NO: 353)

[0082] FIG. 12J shows the Clone TS-26564 CAR LxH AA sequences (SEQ ID NO: 354)

[0083] FIG. 13A shows the Clone RY-26568 HC DNA sequence (SEQ ID NO: 355)

[0084] FIG. 13B shows the Clone RY-26568 HC AA sequence (SEQ ID NO: 356).

[0085] FIG. 13C shows the Clone RY-26568 HC CDR sequences.

[0086] FIG. 13D shows the Clone RY-26568 LC DNA sequence (SEQ ID NO: 360).

[0087] FIG. 13E shows the Clone RY-26568 LC AA sequence (SEQ ID NO: 361).

[0088] FIG. 13F shows the Clone RY-26568 LC CDR AA sequences.

[0089] FIG. 13G shows the Clone RY-26568 CAR DNA HxL sequences (SEQ ID NO: 365)

[0090] FIG. 13H shows the Clone RY-26568 CAR HxL AA sequences (SEQ ID NO: 366).

[0091] FIG. 13I shows the Clone RY-26568 CAR DNA LxH sequences (SEQ ID NO: 367).

[0092] FIG. 13J shows the Clone RY-26568 CAR LxH AA sequences (SEQ ID NO: 368).

[0093] FIG. 14A shows the Clone PP-26575 HC DNA sequence (SEQ ID NO: 369).

[0094] FIG. 14B shows the Clone PP-26575 HC AA sequence (SEQ ID NO: 370).

[0095] FIG. 14C shows the Clone PP-26575 HC CDR AA sequences.

[0096] FIG. 14D shows the Clone PP-26575 LC DNA sequence (SEQ ID NO: 374).

[0097] FIG. 14E shows the Clone PP-26575 LC AA sequence (SEQ ID NO: 375).

[0098] FIG. 14F shows the Clone PP-26575 LC CDR AA sequences.

[0099] FIG. 14G shows the Clone PP-26575 CAR DNA HxL sequences (SEQ ID NO: 379).

[0100] FIG. 14H shows Clone PP-26575 CAR HxL AA sequences (SEQ ID NO: 380).

[0101] FIG. 14I shows Clone PP-26575 CAR DNA LxH sequence (SEQ ID NO: 381).

[0102] FIG. 14J shows the Clone PP-26575 CAR LxH AA sequence (SEQ ID NO: 382).

[0103] FIG. 15A shows the Clone RD-26576 HC DNA sequence (SEQ ID NO: 383)

[0104] FIG. 15B shows Clone RD-26576 HC AA sequence (SEQ ID NO: 384).

[0105] FIG. 15C shows the Clone RD-26576 HC CDR sequences.

[0106] FIG. 15D shows the Clone RD-26576 LC DNA sequence (SEQ ID NO: 388)

[0107] FIG. 15E shows the Clone RD-26576 LC AA sequence (SEQ ID NO: 389).

[0108] FIG. 15F shows the Clone RD-26576 LC CDR sequences.

[0109] FIG. 15G shoes the Clone RD-26576 CAR DNA HxL sequences (SEQ ID NO: 393).

[0110] FIG. 15H shows the Clone RD-26576 CAR HxL chain AA sequences (SEQ ID NO: 394).

[0111] FIG. 15I shows the Clone RD-26576 CAR DNA LxH sequences (SEQ ID NO: 395).

[0112] FIG. 15J shows the Clone RD-26576 CAR LxH AA sequences (SEQ ID NO: 396).

[0113] FIG. 16A shows the Clone RD-26578 HC DNA sequences (SEQ ID NO: 397).

[0114] FIG. 16B shows the Clone RD-26578 HC AA sequence (SEQ ID NO: 398).

[0115] FIG. 16C shows the Clone RD-26578 HC CDR AA sequences.

[0116] FIG. 16D shows the Clone RD-26578 LC DNA sequence (SEQ ID NO: 402).

[0117] FIG. 16E shows the Clone RD-26578 LC AA sequence (SEQ ID NO: 403)

[0118] FIG. 16F shows the Clone RD-26578 LC CDR sequences.

[0119] FIG. 16G shows the Clone RD-26578 CAR DNA HxL chain sequence (SEQ ID NO: 407).

[0120] FIG. 16H shows the Clone RD-26578 CAR HxL AA sequence (SEQ ID NO: 408).

[0121] FIG. 16I shows the Clone RD-26578 CAR DNA LxH sequences (SEQ ID NO: 409).

[0122] FIG. 16J shows the Clone RD-26578 CAR LxH AA sequence (SEQ ID NO: 410).

[0123] FIG. 17 shows the outcome of an in vivo study examining the efficacy of clone RD-21530 in a subcutaneous RPMI-8226 mouse model. Cohorts of 10 mice each were tested for the CAR (dashed lines) and mock transduced (bolded lines) T cells.

[0124] FIG. 18A and FIG. 18B show the outcome of an in vitro cytotoxicity assay using the optimized BCMA scFv variants cocultured with NCI-H929 and MM.1S cells, respectively. CAR T cells using these optimized scFvs were incubated overnight with luciferase labeled target cells in 3:1 and 1:1 effector to target cell ratios.

## DETAILED DESCRIPTION OF THE INVENTION

[0125] The present invention relates to antibodies, antigen binding molecules thereof, chimeric antigen receptors (CARs), and engineered T cell receptors, which bind BCMA, polynucleotides encoding the same, and in vitro cells comprising the same. The polynucleotides, polypeptides, and in vitro cells described herein can be used in an engineered CAR T cell therapy, *e.g.*, an autologous cell therapy (eACT™), for the treatment of a patient suffering from a cancer. In particular, the polynucleotides, polypeptides, and in vitro cells described herein can be used for the treatment of multiple myeloma.

*Definitions*

[0126] In order that the present disclosure may be more readily understood, certain terms are first defined. As used in this application, except as otherwise expressly provided herein, each of the following terms shall have the meaning set forth below. Additional definitions are set forth throughout the application.

[0127] 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).

[0128] 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.

[0129] 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, the Concise Dictionary of Biomedicine and Molecular Biology, Juo, Pei-Show, 2nd ed., 2002, CRC Press; The Dictionary of Cell and Molecular Biology, 3rd ed., 1999, Academic Press; and the Oxford Dictionary Of Biochemistry And Molecular Biology, Revised, 2000, Oxford University Press, provide one of skill with a general dictionary of many of the terms used in this disclosure.

[0130] Units, prefixes, and symbols are denoted in their Système International de Unites (SI) accepted form. Numeric ranges are inclusive of the numbers defining the range. The headings provided herein are not limitations of the various aspects of the disclosure, which can be had by reference to the specification as a whole. Accordingly, the terms defined immediately below are more fully defined by reference to the specification in its entirety.

[0131] "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. 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, 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 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.

[0132] The term "antibody" (Ab) includes, without limitation, a glycoprotein immunoglobulin which binds specifically to an antigen. In general, and antibody can comprise 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 chain constant region is 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, FR4. The 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.

[0133] Antibodies can include, for example, monoclonal antibodies, recombinantly produced antibodies, monospecific antibodies, multispecific antibodies (including bispecific antibodies), human 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, affybodies, 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.

[0134] An immunoglobulin may derive from any of the commonly known isotypes, including but not limited to IgA, secretory IgA, IgG 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 molecule of any of the aforementioned immunoglobulins, and includes a monovalent and a divalent fragment or portion, and a single chain Ab.

[0135] 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. In further embodiments, the antigen binding molecule is an antibody of fragment thereof, 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.

[0136] As used herein, the terms "variable region" or "variable domain" are 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).

[0137] The terms "VL" and "VL domain" are used interchangeably to refer to the light chain variable region of an antibody or an antigen-binding fragment thereof.

[0138] The terms "VH" and "VH domain" are used interchangeably to refer to the heavy chain variable region of an antibody or an antigen-binding fragment thereof.

[0139] 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.

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 |

[0140] 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.

[0141] 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-HI 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.

[0142] 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.

[0143] 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.*, $IgG_1$, $IgG_2$, $IgG_3$ and $IgG_4$.

[0144] 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.

[0145] "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.

[0146] 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 fragment thereof can be replaced with an amino acid residue with a similar side chain.

[0147] 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.

[0148] 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).

[0149] 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.

[0150] In another embodiment, specific embodiment, molecules that specifically bind to an antigen bind with a dissociation constant ($K_d$) of about 1 x $10^{-7}$ M. In some embodiments, the antigen binding molecule specifically binds an antigen with "high affinity" when the $K_d$ is about 1 x $10^{-9}$ M to about 5 x $10^{-9}$ M. In some embodiments, the antigen binding molecule specifically binds an antigen with "very high affinity" when the $K_d$ is 1 x $10^{-10}$ M to about 5 x $10^{-10}$ 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 x $10^{-5}$. In other embodiments, the antigen binding molecule binds human BCMA with a $K_d$ of between about 1 x $10^{-7}$ M and about 1 x $10^{-13}$ M. In yet another embodiment, the antigen binding molecule binds human BCMA with a $K_d$ of about 1 x $10^{-10}$ M to about 5 x $10^{-10}$ M.

[0151] In another specific embodiment, molecules that specifically bind to an antigen do not cross react with other proteins under similar binding conditions. In another specific embodiment, molecules that specifically bind to an antigen do not cross react with other non-BCMA proteins. In a specific embodiment, provided herein is an antibody or fragment thereof that binds to BCMA with higher affinity than to another unrelated antigen. In certain embodiments, provided herein is an antibody or fragment thereof that binds to BCMA (*e.g.*, human BCMA) with a 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or higher affinity than to another, unrelated antigen as measured by, *e.g.*, a radioimmunoassay, surface plasmon resonance, or kinetic exclusion assay. In a specific embodiment, the extent of binding of an anti-BCMA antibody or antigen-binding fragment thereof described herein to an unrelated, non-BCMA protein is less than 10%, 15%, or 20% of the binding of the antibody to BCMA protein as measured by, *e.g.*, a radioimmunoassay.

[0152] In a specific embodiment, provided herein is an antibody or fragment thereof that binds to human BCMA with higher affinity than to another species of BCMA. In certain embodiments, provided herein is an antibody or fragment thereof that binds to human BCMA with a 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70% or higher affinity than to another species of BCMA as measured by, *e.g.*, a radioimmunoassay, surface plasmon resonance, or kinetic exclusion assay. In a specific embodiment, an antibody or fragment thereof described herein, which binds to human BCMA, will bind to another

species of BCMA protein with less than 10%, 15%, or 20% of the binding of the antibody or fragment thereof to the human BCMA protein as measured by, *e.g.*, a radioimmunoassay, surface plasmon resonance, or kinetic exclusion assay.

[0153] 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 BCMA.

[0154] 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.

[0155] 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 (FIG. 2A and FIG. 2C). The amino acid sequence of human BCMA (hBCMA) is provided in NCBI Accession Q02223.2 (GI:313104029) (SEQ ID NO: 163). 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).

[0156] 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.

[0157] 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.

[0158] 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.

[0159] 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 refractor 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.

[0160] 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.

[0161] 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).

[0162] "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 1α (MIP-1α, MIP-1a), MIP-1β (MIP-1b), gamma-induced protein 10 (IP-10), and thymus and activation regulated chemokine (TARC or CCL17).

[0163] 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.

[0164] 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 ((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 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 interaction. In mammals, immature B-cells are formed in the bone marrow, where its name is derived from.

[0165] 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 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.

[0166] An "immune response" refers to the action of a cell of the immune system (for 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, or, in cases of autoimmunity or pathological inflammation, normal human cells or tissues.

[0167] 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.

[0168] 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.

[0169] 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, *e.g.*, CD28, 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 malignances, 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.

[0170] 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.

[0171] 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.

[0172] 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 must contain 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.

[0173] In some aspects, the polypeptides and/or proteins have deletions from, additions to, and/or substitutions of one or more amino acid of antigen-binding protein, and in some embodiments preferably no more than 8 amino acid substitutions therein. Useful polypeptide fragments may include immunologically functional fragments of antigen binding molecules, including not limited to one or more CDR regions, variable domains of a heavy and/or light chain, a portion of other portions of an antibody chain, and the like. Additionally, polypeptide fragments of activating and/or costimulatory molecules and the like are within the scope of the invention.

[0174] "Activation" or "Stimulation" as used herein, refers to a primary response induced by binding of an activating molecule with its cognate ligand, wherein the binding mediates a signal transduction event. An "activating molecule" or "stimulating molecule" refers to a molecule on a T cell, *e.g.*, the TCR/CD3 complex that specifically binds with a cognate stimulatory ligand present on an antigen present cell. Suitable activating molecules are described herein.

[0175] A "stimulatory ligand" is a ligand that when present on an antigen presenting cell (*e.g.*, an aAPC, 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 MHC Class I molecule loaded

with a peptide, an anti-CD3 antibody, a superagonist anti-CD28 antibody, and a superagonist anti-CD2 antibody.

[0176] 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.

[0177] A "costimulatory ligand" as used herein, includes a molecule on an antigen 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 complex (MHC) molecule loaded with peptide. A co-stimulatory ligand can include, but is not limited to, CD7, B7-1 (CD80), B7-2 (CD86), programmed death (PD) L1, PD-L2, 4-1BB ligand, OX40 ligand, inducible costimulatory ligand (ICOS-L), intercellular adhesion molecule (ICAM), CD30 ligand, CD40, CD70, CD83, human leukocyte antigen G (HLA-G), MHC class I chain-related protein A (MICA), MHC class I chain-related protein B (MICB), herpes virus entry mediator (HVEM), lymphotoxin beta receptor, 3/TR6, immunoglobulin-like transcript (ILT) 3, ILT4, an agonist or antibody that binds Toll ligand receptor and a ligand that specifically binds with B7-H3. 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, CD27, CD28, 4-1BB, OX40, CD30, CD40, PD-1, ICOS, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, tumor necrosis factor superfamily member 14 (TNFSF14 or LIGHT), natural killer cell receptor C (NKG2C), B7-H3, and a ligand that specifically binds with CD83.

[0178] 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, CD28, CD28T, OX40, 4-1BB/CD137, CD2, CD3 (alpha, beta, delta, epsilon, gamma, zeta), CD4, CD5, CD7, CD9, CD16, CD22, CD27, CD30, CD 33, CD37, CD40, CD 45, CD64, CD80, CD86, CD134, CD137, CD154, PD-1, ICOS, lymphocyte function-associated antigen-1 (LFA-1 (CDl la/CD18), CD247, CD276 (B7-H3), LIGHT (tumor necrosis factor superfamily member 14; TNFSF14), NKG2C, Ig alpha (CD79a), DAP-10, Fc

gamma receptor, MHC class I molecule, TNF, TNFr, integrin, signaling lymphocytic activation molecule, BTLA, Toll ligand receptor, ICAM-1, B7-H3, CDS, ICAM-1, GITR, BAFFR, LIGHT, HVEM (LIGHTR), KIRDS2, SLAMF7, NKp80 (KLRF1), NKp44, NKp30, NKp46, CD19, CD4, CD8alpha, CD8beta, IL2R beta, IL2R gamma, IL7R alpha, ITGA4, VLA1, CD49a, ITGA4, IA4, CD49D, ITGA6, VLA-6, CD49f, ITGAD, CDl-ld, ITGAE, CD103, ITGAL, CDl-la, LFA-1, ITGAM, CDl-lb, ITGAX, CDl-lc, ITGBl, CD29, ITGB2, CD18, LFA-1, ITGB7, NKG2D, TNFR2, TRANCE/RANKL, DNAM1 (CD226), SLAMF4 (CD244, 2B4), CD84, CD96 (Tactile), CEACAM1, CRT AM, Ly9 (CD229), CD160 (BY55), PSGL1, CD100 (SEMA4D), CD69, SLAMF6 (NTB-A, Lyl08), SLAM (SLAMF1, CD150, IPO-3), BLAME (SLAMF8), SELPLG (CD162), LTBR, LAT, GADS, SLP-76, PAG/Cbp, CD19a, CD83 ligand, or fragments or combinations thereof.

[0179] 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.

[0180] "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.

[0181] 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.

[0182] The use of the alternative (*e.g.*, "or") should be understood to mean either one, both, or any combination thereof of the alternatives. As used herein, the indefinite articles "a" or "an" should be understood to refer to "one or more" of any recited or enumerated component.

[0183] The terms "about" or "comprising essentially of" refer 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 1 or more than 1 standard deviation per the practice in the art. Alternatively, "about" or "comprising essentially of" can mean a range of up to 10% (*i.e.*, ±10%). For example, about 3mg can include any number between 2.7 mg and 3.3 mg (for 10%). 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 application and claims, 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.

[0184] As described herein, any concentration range, percentage range, ratio range or integer range is to be understood to include 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.

[0185] Various aspects of the invention are described in further detail in the following subsections.

### *II. Binding Molecules and Polynucleotides Encoding the Same*

[0186] The present invention is directed to a polynucleotide encoding an anti-BCMA antibody or antigen binding molecule thereof which cross competes with one or more antibodies described herein (i.e., one or more described in Figure 1) or an antibody or antigen binding molecule thereof encoded by the polynucleotide. In one embodiment, the invention is directed to a polynucleotide encoding an anti-BCMA antibody or antigen binding molecule thereof which binds to the same epitope as one or more antibodies described in Figure 1 or an antibody or antigen binding molecule thereof encoded by the polynucleotide. In some embodiments, the polynucleotide encodes an antibody or antigen binding molecule thereof

that specifically binds to BCMA, wherein the antibody or binding molecule comprises a heavy chain VH comprising: (a) a VH CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence $GX_2X_3X_4X_5X_6X_7SY$ (SEQ ID NO: 145), wherein: $X_2$ is not present or G; $X_3$ is not present or S; $X_4$ is F, G, I, or Y; $X_5$ is S or T; $X_6$ is F or S; and $X_7$ is S or T; and/or (b) a VH CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1IX_3X_4X_5X_6X_7X_8X_9X_{10}YX_{12}X_{13}X_{14}X_{15}X_{16}X_{17}$ (SEQ ID NO: 146), wherein: $X_1$ is A, G, I, S, T, or V; $X_3$ is I, N, or S; $X_4$ is G, P, S, or Y; $X_5$ is D, G, I, or S; $X_6$ is F, G, or S; $X_7$ is not present or G or S; $X_8$ is N, S, or T; $X_9$ is A, I, K, or T; $X_{10}$ is N, S, or Y; $X_{12}$ is A or N; $X_{13}$ is D, P, or Q; $X_{14}$ is K or S; $X_{15}$ is F, L, or V; $X_{16}$ is K or Q; and $X_{17}$ is G or S; and/or (c) a VH CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}DX_{19}$ (SEQ ID NO: 147), wherein: $X_1$ is A or V; $X_2$ is K or R; $X_3$ is not present or D, G, or T; $X_4$ is not present or A, D, G, P, R, or S; $X_5$ is not present or E, F, G, L, Q, or T; $X_6$ is not present or E, M, Q, W, or Y; $X_7$ is not present or A, E, L, or S; $X_8$ is not present or G, P, S, or T; $X_9$ is not present or G, P, or S; $X_{10}$ is not present or I, L, P, or Y; $X_{11}$ is not present or W; $X_{12}$ is not present or H; $X_{13}$ is not present or E or Y; $X_{14}$ is not present or D, G, H, P, S, W, or Y; $X_{15}$ is A, G, L, W, or Y; $X_{16}$ is not present or A, G, I, P, or V; $X_{17}$ is F, L, or M; and $X_{19}$ is I, L, V, or Y.

[0187] In one particular embodiment, the polynucleotide encodes an antibody or antigen binding molecule that specifically binds to BCMA, wherein the antibody or antigen binding molecule comprises a VH comprising: (a) a VH CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2X_3X_4X_5X_6SYX_9X_{10}X_{11}$ (SEQ ID NO: 263), wherein: $X_1$ is not present or G; $X_2$ is not present or S $X_3$ is F, G, I, or Y; $X_4$ is S or T; $X_5$ is F or S; $X_6$ is S or T; $X_9$ is A, G, S, or Y; $X_{10}$ is I, M, or W; and $X_{11}$ is G, H, N, or S; and/or (b) a VH CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1IX_3X_4X_5X_6X_7X_8X_9X_{10}YX_{12}X_{13}X_{14}X_{15}X_{16}X_{17}$ (SEQ ID NO: 146), wherein: $X_1$ is A, G, I, S, T, or V; $X_3$ is I, N, or S; $X_4$ is G, P, S, or Y; $X_5$ is D, G, I, or S; $X_6$ is F, G, or S; $X_7$ is G or S; $X_8$ is not present or N, S, or T; $X_9$ is A, I, K, or T; $X_{10}$ is N, S, or Y; $X_{12}$ is A or N; $X_{13}$ is D, P, or Q; $X_{14}$ is K or S; $X_{15}$ is F, L, or V; $X_{16}$ is K or Q; and $X_{17}$ is G or S; and/or (c) a VH CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}X_{18}X_{19}DX_{21}$ (SEQ ID NO: 264), wherein: $X_1$ is A or V; $X_2$ is K or R; $X_3$ is not present or D, G, or T; $X_4$ is not present or D, G, or P; $X_5$ is not present or F, L, or T; $X_6$ is not present or P, Q, R, W, or Y; $X_7$ is not present or E, G, L, or S; $X_8$ is not present or A, G, P, S, or Y; $X_9$ is not present or A, E, G, P,

Q, or S; $X_{10}$ is not present or E, L, M, PS, T, or Y; $X_{11}$ is not present or D, G, H, P, S or W; $X_{12}$ is not present or A, G, I, L, or Y; $X_{13}$ is not present or A, G, I, V, or W; $X_{14}$ is not present or H; $X_{15}$ is not present or Y; $X_{16}$ is not present or Y; $X_{17}$ is not present or W or Y; $X_{18}$ is not present or P or G; $X_{19}$ is F, L, or M; and $X_{21}$ is I, L, V, or Y.

[0188] In another embodiment, the polynucleotide encodes an antibody or antigen binding molecule that specifically binds to BCMA, wherein the antibody or antigen binding molecule comprises a VL comprising: (a) a VL CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2SQX_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}LX_{17}$ (SEQ ID NO: 148), wherein $X_1$ is K or R; $X_2$ is A or S; $X_5$ is G or S; $X_6$ is I, L, or V; $X_7$ is L or S; $X_8$ is not present or H or Y; $X_9$ is not present or S; $X_{10}$ is not present or N or S; $X_{11}$ is not present or G or N; $X_{12}$ is not present or N; $X_{13}$ is not present or K or Y; $X_{14}$ is N, R, or S; $X_{15}$ is N, W, or Y; and $X_{17}$ is A or D; and/or (b) a VL CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2SX_4X_5X_6X_7$ (SEQ ID NO: 149), wherein $X_1$ is D, G, L, S, or W; $X_2$ is A or G; $X_4$ is N, S, or T; $X_5$ is L or R; $X_6$ is A, E, or Q; and $X_7$ is S or T; and/or (c) a VL CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1QX_3X_4X_5X_6PX_8T$ (SEQ ID NO: 150), wherein $X_1$ is M or Q; $X_3$ is F, G, H, I, R, or Y; $X_4$ is A, F, H, I, L, or Y; $X_5$ is A, G, H, S, T, V, or Y; $X_6$ is F, L, T, W, or Y; and $X_8$ is not present or F, L, P, or W.

[0189] In one particular embodiment, the polynucleotide encodes an antibody or antigen binding molecule that specifically binds to BCMA, wherein the antibody or antigen binding molecule comprises a VH comprising: (a) a VH CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence $GX_2X_3X_4X_5X_6X_7SY$ (SEQ ID NO: 145), wherein: $X_2$ is not present or G; $X_3$ is not present or S; $X_4$ is F, G, I, or Y; $X_5$ is S or T; $X_6$ is F or S; and $X_7$ is S or T; and/or (b) a VH CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1IX_3X_4X_5X_6X_7X_8X_9X_{10}YX_{12}X_{13}X_{14}X_{15}X_{16}X_{17}$ (SEQ ID NO: 146), wherein: $X_1$ is A, G, I, S, T, or V; $X_3$ is I, N, or S; $X_4$ is G, P, S, or Y; $X_5$ is D, G, I, or S; $X_6$ is F, G, or S; $X_7$ is not present or G or S; $X_8$ is N, S, or T; $X_9$ is A, I, K, or T; $X_{10}$ is N, S, or Y; $X_{12}$ is A or N; $X_{13}$ is D, P, or Q; $X_{14}$ is K or S; $X_{15}$ is F, L, or V; $X_{16}$ is K or Q; and $X_{17}$ is G or S; and/or (c) a VH CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}DX_{19}$ (SEQ ID NO: 147), wherein: $X_1$ is A or V; $X_2$ is K or R; $X_3$ is not present or D, G, or T; $X_4$ is not present or A, D, G, P, R, or S; $X_5$ is not present or E, F, G, L, Q, or T; $X_6$ is not present or E, M, Q, W, or Y; $X_7$ is not present

or A, E, L, or S; $X_8$ is not present or G, P, S, or T; $X_9$ is not present or G, P, or S; $X_{10}$ is not present or I, L, P, or Y; $X_{11}$ is not present or W; $X_{12}$ is not present or H; $X_{13}$ is not present or E or Y; $X_{14}$ is not present or D, G, H, P, S, W, or Y; $X_{15}$ is A, G, L, W, or Y; $X_{16}$ is not present or A, G, I, P, or V; $X_{17}$ is F, L, or M; and $X_{19}$ is I, L, V, or Y; and/or (d) a VL CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2SQX_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}LX_{17}$ (SEQ ID NO: 148), wherein $X_1$ is K or R; $X_2$ is A or S; $X_5$ is G or S; $X_6$ is I, L, or V; $X_7$ is L or S; $X_8$ is not present or H or Y; $X_9$ is not present or S; $X_{10}$ is not present or N or S; $X_{11}$ is not present or G or N; $X_{12}$ is not present or N; $X_{13}$ is not present or K or Y; $X_{14}$ is N, R, or S; $X_{15}$ is N, W, or Y; and $X_{17}$ is A or D; and/or (e) a VL CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2SX_4X_5X_6X_7$ (SEQ ID NO: 149), wherein $X_1$ is D, G, L, S, or W; $X_2$ is A or G; $X_4$ is N, S, or T; $X_5$ is L or R; $X_6$ is A, E, or Q; and $X_7$ is S or T; and/or (f) a VL CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1QX_3X_4X_5X_6PX_8T$ (SEQ ID NO: 150), wherein $X_1$ is M or Q; $X_3$ is F, G, H, I, R, or Y; $X_4$ is A, F, H, I, L, or Y; $X_5$ is A, G, H, S, T, V, or Y; $X_6$ is F, L, T, W, or Y; and $X_8$ is not present or F, L, P, or W.

[0190] In one particular embodiment, the polynucleotide encodes an antibody or antigen binding molecule that specifically binds to BCMA, wherein the antibody or antigen binding molecule comprises a VH comprising: (a) a VH CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2X_3X_4X_5X_6SYX_9X_{10}X_{11}$ (SEQ ID NO: 263), wherein: $X_1$ is not present or G; $X_2$ is not present or S $X_3$ is F, G, I, or Y; $X_4$ is S or T; $X_5$ is F or S; $X_6$ is S or T; $X_9$ is A, G, S, or Y; $X_{10}$ is I, M, or W; and $X_{11}$ is G, H, N, or S; and/or (b) a VH CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1IX_3X_4X_5X_6X_7X_8X_9X_{10}YX_{12}X_{13}X_{14}X_{15}X_{16}X_{17}$ (SEQ ID NO: 146), wherein: $X_1$ is A, G, I, S, T, or V; $X_3$ is I, N, or S; $X_4$ is G, P, S, or Y; $X_5$ is D, G, I, or S; $X_6$ is F, G, or S; $X_7$ is G or S; $X_8$ is not present or N, S, or T; $X_9$ is A, I, K, or T; $X_{10}$ is N, S, or Y; $X_{12}$ is A or N; $X_{13}$ is D, P, or Q; $X_{14}$ is K or S; $X_{15}$ is F, L, or V; $X_{16}$ is K or Q; and $X_{17}$ is G or S; and/or (c) a VH CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}X_{18}X_{19}DX_{21}$ (SEQ ID NO: 264), wherein: $X_1$ is A or V; $X_2$ is K or R; $X_3$ is not present or D, G, or T; $X_4$ is not present or D, G, or P; $X_5$ is not present or F, L, or T; $X_6$ is not present or P, Q, R, W, or Y; $X_7$ is not present or E, G, L, or S; $X_8$ is not present or A, G, P, S, or Y; $X_9$ is not present or A, E, G, P, Q, or S; $X_{10}$ is not present or E, L, M, PS, T, or Y; $X_{11}$ is not present or D, G, H, P, S or W; $X_{12}$ is not present or A, G, I, L, or Y; $X_{13}$ is not present or A, G, I, V, or W; $X_{14}$ is not present

or H; $X_{15}$ is not present or Y; $X_{16}$ is not present or Y; $X_{17}$ is not present or W or Y; $X_{18}$ is not present or P or G; $X_{19}$ is F, L, or M; and $X_{21}$ is I, L, V, or Y; and/or (d) a VL CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2SQX_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}LX_{17}$ (SEQ ID NO: 148), wherein $X_1$ is K or R; $X_2$ is A or S; $X_5$ is G or S; $X_6$ is I, L, or V; $X_7$ is L or S; $X_8$ is not present or H or Y; $X_9$ is not present or S; $X_{10}$ is not present or N or S; $X_{11}$ is not present or G or N; $X_{12}$ is not present or N; $X_{13}$ is not present or K or Y; $X_{14}$ is N, R, or S; $X_{15}$ is N, W, or Y; and $X_{17}$ is A or D; and/or (e) a VL CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2SX_4X_5X_6X_7$ (SEQ ID NO: 149), wherein $X_1$ is D, G, L, S, or W; $X_2$ is A or G; $X_4$ is N, S, or T; $X_5$ is L or R; $X_6$ is A, E, or Q; and $X_7$ is S or T; and/or (f) a VL CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1QX_3X_4X_5X_6PX_8T$ (SEQ ID NO: 150), wherein $X_1$ is M or Q; $X_3$ is F, G, H, I, R, or Y; $X_4$ is A, F, H, I, L, or Y; $X_5$ is A, G, H, S, T, V, or Y; $X_6$ is F, L, T, W, or Y; and $X_8$ is not present or F, L, P, or W.

[0191] In another embodiment, the polynucleotide encodes an antibody or antigen binding molecule that specifically binds to BCMA, wherein the antibody or antigen binding molecule comprises a VH and a VL, wherein: (i) the VH comprises: (a) a VH CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence $GX_2X_3X_4X_5X_6X_7SY$ (SEQ ID NO: 145), wherein: $X_2$ is not present or G; $X_3$ is not present or S; $X_4$ is F, G, I, or Y; $X_5$ is S or T; $X_6$ is F or S; and $X_7$ is S or T; and/or (b) a VH CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1IX_3X_4X_5X_6X_7X_8X_9X_{10}YX_{12}X_{13}X_{14}X_{15}X_{16}X_{17}$ (SEQ ID NO: 146), wherein: $X_1$ is A, G, I, S, T, or V; $X_3$ is I, N, or S; $X_4$ is G, P, S, or Y; $X_5$ is D, G, I, or S; $X_6$ is F, G, or S; $X_7$ is not present or G or S; $X_8$ is N, S, or T; $X_9$ is A, I, K, or T; $X_{10}$ is N, S, or Y; $X_{12}$ is A or N; $X_{13}$ is D, P, or Q; $X_{14}$ is K or S; $X_{15}$ is F, L, or V; $X_{16}$ is K or Q; and $X_{17}$ is G or S; and/or (c) a VH CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}DX_{19}$ (SEQ ID NO: 147), wherein: $X_1$ is A or V; $X_2$ is K or R; $X_3$ is not present or D, G, or T; $X_4$ is not present or A, D, G, P, R, or S; $X_5$ is not present or E, F, G, L, Q, or T; $X_6$ is not present or E, M, Q, W, or Y; $X_7$ is not present or A, E, L, or S; $X_8$ is not present or G, P, S, or T; $X_9$ is not present or G, P, or S; $X_{10}$ is not present or I, L, P, or Y; $X_{11}$ is not present or W; $X_{12}$ is not present or H; $X_{13}$ is not present or E or Y; $X_{14}$ is not present or D, G, H, P, S, W, or Y; $X_{15}$ is A, G, L, W, or Y; $X_{16}$ is not present or A, G, I, P, or V; $X_{17}$ is F, L, or M; and $X_{19}$ is I, L, V, or Y; and (ii) the VL comprises: (a) a VL CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence

$X_1X_2SQX_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}LX_{17}$ (SEQ ID NO: 148), wherein $X_1$ is K or R; $X_2$ is A or S; $X_5$ is G or S; $X_6$ is I, L, or V; $X_7$ is L or S; $X_8$ is not present or H or Y; $X_9$ is not present or S; $X_{10}$ is not present or N or S; $X_{11}$ is not present or G or N; $X_{12}$ is not present or N; $X_{13}$ is not present or K or Y; $X_{14}$ is N, R, or S; $X_{15}$ is N, W, or Y; and $X_{17}$ is A or D; and/or (b) a VL CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2SX_4X_5X_6X_7$ (SEQ ID NO: 149), wherein $X_1$ is D, G, L, S, or W; $X_2$ is A or G; $X_4$ is N, S, or T; $X_5$ is L or R; $X_6$ is A, E, or Q; and $X_7$ is S or T; and/or (c) a VL CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1QX_3X_4X_5X_6PX_8T$ (SEQ ID NO: 150), wherein $X_1$ is M or Q; $X_3$ is F, G, H, I, R, or Y; $X_4$ is A, F, H, I, L, or Y; $X_5$ is A, G, H, S, T, V, or Y; $X_6$ is F, L, T, W, or Y; and $X_8$ is not present or F, L, P, or W.

[0192] In another embodiment, the polynucleotide encodes an antibody or antigen binding molecule that specifically binds to BCMA, wherein the antibody or antigen binding molecule comprises a VH and a VL, wherein: (i) the VH comprises: (a) a VH CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2X_3X_4X_5X_6SYX_9X_{10}X_{11}$ (SEQ ID NO: 263), wherein: $X_1$ is not present or G; $X_2$ is not present or S $X_3$ is F, G, I, or Y; $X_4$ is S or T; $X_5$ is F or S; $X_6$ is S or T; $X_9$ is A, G, S, or Y; $X_{10}$ is I, M, or W; and $X_{11}$ is G, H, N, or S; and/or (b) a VH CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1IX_3X_4X_5X_6X_7X_8X_9X_{10}YX_{12}X_{13}X_{14}X_{15}X_{16}X_{17}$ (SEQ ID NO: 146), wherein: $X_1$ is A, G, I, S, T, or V; $X_3$ is I, N, or S; $X_4$ is G, P, S, or Y; $X_5$ is D, G, I, or S; $X_6$ is F, G, or S; $X_7$ is G or S; $X_8$ is not present or N, S, or T; $X_9$ is A, I, K, or T; $X_{10}$ is N, S, or Y; $X_{12}$ is A or N; $X_{13}$ is D, P, or Q; $X_{14}$ is K or S; $X_{15}$ is F, L, or V; $X_{16}$ is K or Q; and $X_{17}$ is G or S; and/or (c) a VH CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}X_{18}X_{19}DX_{21}$ (SEQ ID NO: 264), wherein: $X_1$ is A or V; $X_2$ is K or R; $X_3$ is not present or D, G, or T; $X_4$ is not present or D, G, or P; $X_5$ is not present or F, L, or T; $X_6$ is not present or P, Q, R, W, or Y; $X_7$ is not present or E, G, L, or S; $X_8$ is not present or A, G, P, S, or Y; $X_9$ is not present or A, E, G, P, Q, or S; $X_{10}$ is not present or E, L, M, P, S, T, or Y; $X_{11}$ is not present or D, G, H, P, S or W; $X_{12}$ is not present or A, G, I, L, or Y; $X_{13}$ is not present or A, G, I, V, or W; $X_{14}$ is not present or H; $X_{15}$ is not present or Y; $X_{16}$ is not present or Y; $X_{17}$ is not present or W or Y; $X_{18}$ is not present or P or G; $X_{19}$ is F, L, or M; and $X_{21}$ is I, L, V, or Y; and (ii) the VL comprises: (a) a VL CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2SQX_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}LX_{17}$ (SEQ ID NO: 148), wherein $X_1$ is K or R; $X_2$

is A or S; $X_5$ is G or S; $X_6$ is I, L, or V; $X_7$ is L or S; $X_8$ is not present or H or Y; $X_9$ is not present or S; $X_{10}$ is not present or N or S; $X_{11}$ is not present or G or N; $X_{12}$ is not present or N; $X_{13}$ is not present or K or Y; $X_{14}$ is N, R, or S; $X_{15}$ is N, W, or Y; and $X_{17}$ is A or D; and/or (b) a VL CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2SX_4X_5X_6X_7$ (SEQ ID NO: 149), wherein $X_1$ is D, G, L, S, or W; $X_2$ is A or G; $X_4$ is N, S, or T; $X_5$ is L or R; $X_6$ is A, E, or Q; and $X_7$ is S or T; and/or (c) a VL CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1QX_3X_4X_5X_6PX_8T$ (SEQ ID NO: 150), wherein $X_1$ is M or Q; $X_3$ is F, G, H, I, R, or Y; $X_4$ is A, F, H, I, L, or Y; $X_5$ is A, G, H, S, T, V, or Y; $X_6$ is F, L, T, W, or Y; and $X_8$ is not present or F, L, P, or W.

[0193] In one embodiment, the antibody or antigen binding molecule, which specifically binds to BCMA (*e.g.*, hBCMA), comprises a VH CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence $GX_2X_3X_4X_5X_6X_7SY$ (SEQ ID NO: 145), wherein: $X_2$ is not present or G; $X_3$ is not present or S; $X_4$ is F, G, I, or Y; $X_5$ is S or T; $X_6$ is F or S; and $X_7$ is S or T.

[0194] In one embodiment, the antibody or antigen binding molecule, which specifically binds to BCMA (*e.g.*, hBCMA), comprises a VH CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence $GX_2TFSSY$ (SEQ ID NO: 151), wherein: $X_2$ is F or G.

[0195] In one embodiment, the antibody or antigen binding molecule, which specifically binds to BCMA (*e.g.*, hBCMA), comprises a VH CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence $GX_2X_3X_4X_5X_6SSY$ (SEQ ID NO: 152), wherein: $X_2$ is not present or G; $X_3$ is not present or S; $X_4$ is F, G, or I; $X_5$ is S or T; and $X_6$ is F or S.

[0196] In one embodiment, the antibody or antigen binding molecule, which specifically binds to BCMA (*e.g.*, hBCMA), comprises a VH CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2X_3X_4X_5X_6SYX_9X_{10}X_{11}$ (SEQ ID NO: 263), wherein: $X_1$ is not present or G; $X_2$ is not present or S $X_3$ is F, G, I, or Y; $X_4$ is S or T; $X_5$ is F or S; $X_6$ is S or T; $X_9$ is A, G, S, or Y; $X_{10}$ is I, M, or W; and $X_{11}$ is G, H, N, or S.

[0197] In one embodiment, the antibody or antigen binding molecule, which specifically binds to BCMA (*e.g.*, hBCMA), comprises a VH CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1TFX_4SYX_7X_8X_9$ (SEQ ID NO:

265), wherein: $X_1$ is F, G, or Y; $X_4$ is S or T; $X_7$ is A, G, S, or Y; $X_8$ is I or M; and $X_9$ is H, N, or S.

[0198] In one embodiment, the antibody or antigen binding molecule, which specifically binds to BCMA (*e.g.*, hBCMA), comprises a VH CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence FTFSSYX$_7$MX$_9$ (SEQ ID NO: 266), wherein: $X_7$ is A, G, or S; and $X_9$ is H, N, or S.

[0199] In one embodiment, the antibody or antigen binding molecule, which specifically binds to BCMA (*e.g.*, hBCMA), comprises a VH CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1IX_3X_4X_5X_6X_7X_8X_9X_{10}YX_{12}X_{13}X_{14}X_{15}X_{16}X_{17}$ (SEQ ID NO: 146), wherein: $X_1$ is A, G, I, S, T, or V; $X_3$ is I, N, or S; $X_4$ is G, P, S, or Y; $X_5$ is D, G, I, or S; $X_6$ is F, G, or S; $X_7$ is G or S; $X_8$ is not present or N, S, or T; $X_9$ is A, I, K, or T; $X_{10}$ is N, S, or Y; $X_{12}$ is A or N; $X_{13}$ is D, P, or Q; $X_{14}$ is K or S; $X_{15}$ is F, L, or V; $X_{16}$ is K or Q; and $X_{17}$ is G or S.

[0200] In one embodiment, the antibody or antigen binding molecule, which specifically binds to BCMA (*e.g.*, hBCMA), comprises a VH CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1IX_3X_4X_5X_6X_7X_8X_9X_{10}YAX_{13}X_{14}X_{15}X_{16}G$ (SEQ ID NO: 153), wherein: $X_1$ is A, G, I, T, or V; $X_3$ is I, N, or S; $X_4$ is G, P, S, or Y; $X_5$ is D, G, I, or S; $X_6$ is F, G, or S; $X_7$ is G or S; $X_8$ is N, S, or T; $X_9$ is A, I, K, or T; $X_{10}$ is N, S, or Y; $X_{13}$ is D or Q; $X_{14}$ is K or S; $X_{15}$ is F or V; and $X_{16}$ is K or Q.

[0201] In one embodiment, the antibody or antigen binding molecule, which specifically binds to BCMA (*e.g.*, hBCMA), comprises a VH CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1ISX_4X_5X_6X_7X_8X_9YYADSVKG$ (SEQ ID NO: 154), wherein: $X_1$ is A, T, or V; $X_4$ is G, S, or Y; $X_5$ is D or S; $X_6$ is G or S; $X_7$ is G or S; $X_8$ is N, S, or T; and $X_9$ is I, K, or T.

[0202] In one embodiment, the antibody or antigen binding molecule, which specifically binds to BCMA (*e.g.*, hBCMA), comprises a VH CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1IX_3PX_5X_6GX_8X_9X_{10}YAQKFQG$ (SEQ ID NO: 155), wherein: $X_1$ is G or I; $X_3$ is I or N; $X_5$ is G or I; $X_6$ is F or G; $X_8$ is S or T; $X_9$ is A or T; and $X_{10}$ is N or S.

[0203] In one embodiment, the antibody or antigen binding molecule, which specifically binds to BCMA (*e.g.*, hBCMA), comprises three VH CDRs and three VL CDRs, wherein the VH CDR3 comprising, consisting of, or consisting essentially of the amino acid

sequence $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}DX_{19}$ (SEQ ID NO: 147) and wherein: $X_1$ is A or V; $X_2$ is K or R; $X_3$ is not present or D, G, or T; $X_4$ is not present or A, D, G, P, R, or S; $X_5$ is not present or E, F, G, L, Q, or T; $X_6$ is not present or E, M, Q, W, or Y; $X_7$ is not present or A, E, L, or S; $X_8$ is not present or G, P, S, or T; $X_9$ is not present or G, P, or S; $X_{10}$ is not present or I, L, P, or Y; $X_{11}$ is not present or W; $X_{12}$ is not present or H; $X_{13}$ is not present or E or Y; $X_{14}$ is not present or D, G, H, P, S, W, or Y; $X_{15}$ is A, G, L, W, or Y; $X_{16}$ is not present or A, G, I, P, or V; $X_{17}$ is F, L, or M; and $X_{19}$ is I, L, V, or Y.

[0204] In one embodiment, the antibody or antigen binding molecule, which specifically binds to BCMA (*e.g.*, hBCMA), comprises three VH CDRs and three VL CDRs, wherein the VH CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence $ARX_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}DX_{19}$ (SEQ ID NO: 156) and wherein: $X_3$ is not present or D, G, or T; $X_4$ is not present or A, D, G, P, R, or S; $X_5$ is not present or E, F, G, Q, or T; $X_6$ is not present or E, M, W, or Y; $X_7$ is not present or A, L, or S; $X_8$ is not present or G, S, or T; $X_9$ is not present or G or S; $X_{10}$ is not present or I, L, or P; $X_{11}$ is not present or W; $X_{12}$ is not present or H; $X_{13}$ is not present or E or Y; $X_{14}$ is not present or G, H, P, S, W, or Y; $X_{15}$ is A, G, L, W, or Y; $X_{16}$ is not present or A, G, I, P, or V; $X_{17}$ is F, L, or M; and $X_{19}$ is I, L, V, or Y.

[0205] In one embodiment, the antibody or antigen binding molecule, which specifically binds to BCMA (*e.g.*, hBCMA), comprises three VH CDRs and three VL CDRs, wherein the VH CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}X_{18}X_{19}DX_{21}$ (SEQ ID NO: 264) and wherein: $X_1$ is A or V; $X_2$ is K or R; $X_3$ is not present or D, G, or T; $X_4$ is not present or D, G, or P; $X_5$ is not present or F, L, or T; $X_6$ is not present or P, Q, R, W, or Y; $X_7$ is not present or E, G, L, or S; $X_8$ is not present or A, G, P, S, or Y; $X_9$ is A, E, G, P, Q, or S; $X_{10}$ is E, L, M, P, S, T, or Y; $X_{11}$ is not present or D, G, H, P, S or W; $X_{12}$ is not present or A, G, I, L, or Y; $X_{13}$ is not present or A, G, I, V, or W; $X_{14}$ is not present or H; $X_{15}$ is not present or Y; $X_{16}$ is not present or Y; $X_{17}$ is not present or W or Y; $X_{18}$ is not present or P or G; $X_{19}$ is F, L, or M; and $X_{21}$ is I, L, V, or Y.

[0206] In one embodiment, the antibody or antigen binding molecule, which specifically binds to BCMA (*e.g.*, hBCMA), comprises three VH CDRs and three VL CDRs, wherein the VH CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence $ARX_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}X_{18}X_{19}DX_{21}$ (SEQ ID NO: 267), wherein: $X_3$ is not present or D or T; $X_4$ is not present or D or G; $X_5$ is not present or F or T;

$X_6$ is not present or P, R, W, or Y; $X_7$ is not present or E, G, L, or S; $X_8$ is not present or A, G, S, or Y; $X_9$ is A, E, G, Q, or S; $X_{10}$ is E, L, M, P, S, or T; $X_{11}$ is not present or G, H, P, S or W; $X_{12}$ is not present or A, G, I, L, or Y; $X_{13}$ is not present or A, I, V, or W; $X_{14}$ is not present or H; $X_{15}$ is not present or Y; $X_{16}$ is not present or Y; $X_{17}$ is not present or W or Y; $X_{18}$ is not present or P or G; $X_{19}$ is F, L, or M; and $X_{21}$ is I, L, V, or Y.

[0207] In some embodiments, the polynucleotide encodes an antibody or antigen binding molecule that specifically binds to BCMA, wherein the antibody or antigen binding molecule comprises one, two, or all three of any of the VH CDRs listed above or described in FIG. 1A or FIG. 1B. In some embodiments, the antibody or antigen binding molecule comprises the VH framework regions (FRs) described herein. In specific embodiments, the antibody or antigen binding molecule comprises the VH FRs of an antibody set forth in FIG. 1A or FIG. 1B (*e.g.*, one, two, three, or four of the FRs in one sequence of FIG. 1A).

[0208] In one embodiment, the antibody or antigen binding molecule, which specifically binds to BCMA (*e.g.*, hBCMA), comprises a VL CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2SQX_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}LX_{17}$ (SEQ ID NO: 148), wherein: $X_1$ is K or R; $X_2$ is A or S; $X_5$ is G or S; $X_6$ is I, L, or V; $X_7$ is L or S; $X_8$ is not present or H or Y; $X_9$ is not present or S; $X_{10}$ is not present or N or S; $X_{11}$ is not present or G or N; $X_{12}$ is not present or N; $X_{13}$ is not present or K or Y; $X_{14}$ is N, R, or S; $X_{15}$ is N, W, or Y; and $X_{17}$ is A or D.

[0209] In one embodiment, the antibody or antigen binding molecule, which specifically binds to BCMA (*e.g.*, hBCMA), comprises a VL CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence $RASQX_5X_6SX_8X_9LA$ (SEQ ID NO: 157), wherein: $X_5$ is G or S; $X_6$ is I or V; $X_8$ is R or S; and $X_9$ is N, W, or Y.

[0210] In one embodiment, the antibody or antigen binding molecule, which specifically binds to BCMA (*e.g.*, hBCMA), comprises a VL CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1SSQSX_6LX_8SX_{10}X_{11}X_{12}X_{13}NYLX_{17}$ (SEQ ID NO: 158), wherein: $X_1$ is K or R; $X_6$ is L or V; $X_8$ is H or Y; $X_{10}$ is N or S; $X_{11}$ is G or N; $X_{12}$ is not present or N; $X_{13}$ is K or Y; and $X_{17}$ is A or D.

[0211] In one embodiment, the antibody or antigen binding molecule, which specifically binds to BCMA (*e.g.*, hBCMA), comprises a VL CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2SX_4X_5X_6X_7$ (SEQ ID NO: 149),

wherein: $X_1$ is D, G, L, S, or W; $X_2$ is A or G; $X_4$ is N, S, or T; $X_5$ is L or R; $X_6$ is A, E, or Q; and $X_7$ is S or T.

[0212] In one embodiment, the antibody or antigen binding molecule, which specifically binds to BCMA (*e.g.*, hBCMA), comprises a VL CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1ASX_4RAT$ (SEQ ID NO: 159), wherein: $X_1$ is D, G, or S; and $X_4$ is N or T.

[0213] In one embodiment, the antibody or antigen binding molecule, which specifically binds to BCMA (*e.g.*, hBCMA), comprises a VL CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1ASX_4X_5X_6X_7$ (SEQ ID NO: 160), wherein: $X_1$ is D, G, or S; $X_4$ is N, S, or T; $X_5$ is L or R; $X_6$ is A or Q; and $X_7$ is S or T.

[0214] In one embodiment, the antibody or antigen binding molecule, which specifically binds to BCMA (*e.g.*, hBCMA), comprises a VL CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2SX_4RX_6S$ (SEQ ID NO: 161), wherein $X_1$ is L or W; $X_2$ is A or G; $X_4$ is N or T; and $X_6$ is A or E.

[0215] In one embodiment, the antibody or antigen binding molecule, which specifically binds to BCMA (*e.g.*, hBCMA), comprises a VL CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1QX_3X_4X_5X_6PX_8T$ (SEQ ID NO: 150), wherein: $X_1$ is M or Q; $X_3$ is F, G, H, I, R, or Y; $X_4$ is A, F, H, I, L, or Y; $X_5$ is A, G, H, S, T, V, or Y; $X_6$ is F, L, T, W, or Y; and $X_8$ is not present or F, L, P, or W.

[0216] In one embodiment, the antibody or antigen binding molecule, which specifically binds to BCMA (*e.g.*, hBCMA), comprises a VL CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence $QQX_3X_4X_5X_6PX_8T$ (SEQ ID NO: 162), wherein: $X_3$ is H, I, R, or Y; $X_4$ is A, F, H, I, or Y; $X_5$ is A, S, T, V, or Y; $X_6$ is F, W, or Y; and $X_8$ is not present or F, L, P, or W.

[0217] In some embodiments, the polynucleotide encodes an antibody or antigen binding molecule that specifically binds to BCMA, wherein the antibody or antigen binding molecule comprises one, two, or all three of any of the VL CDRs listed above or described in FIG. 2. In some embodiments, the antibody or antigen binding molecule comprises the VL framework regions (FRs) described herein. In specific embodiments, the antibody or antigen binding molecule comprises the VL FRs of an antibody set forth in FIG. 4 (*e.g.*, one, two, three, or four of the FRs in one row of FIG. 4).

[0218] In some embodiments, the polynucleotide encodes an antibody or antigen binding molecule that specifically binds to BCMA, wherein the antibody or antigen binding

molecule comprises a VH CDR1, wherein the VH CDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 9-16. In other embodiments, the antibody or antigen binding molecule comprises a VH CDR1, wherein the VH CDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 215-222. In some embodiments, the antibody or antigen binding molecule comprises a VH CDR2, wherein the VH CDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 25-32. In some embodiments, the antibody or antigen binding molecule comprises a VH CDR2, wherein the VH CDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 231-238. In some embodiments, the antibody or antigen binding molecule comprises a VH CDR3, wherein the VH CDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 41-48. In some embodiments, the antibody or antigen binding molecule comprises a VH CDR3, wherein the VH CDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 247-254.

[0219] In some embodiments, the polynucleotide encodes an antibody or antigen binding molecule that specifically binds to BCMA, wherein the antibody or antigen binding molecule comprises a VH CDR1, a VH CDR2, and VH CDR3, wherein the VH CDR1, VH CDR2, and VH CDR3 comprise the amino acid sequence of the VH CDR1, VH CDR2, and VH CDR3 of an antibody in FIG. 1A or FIG. 1B, respectively.

[0220] In some embodiments, the polynucleotide encodes an antibody or antigen binding molecule that specifically binds to BCMA, wherein the antibody or antigen binding molecule comprises a VL CDR1, wherein the VL CDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 81-88. In some embodiments, the antibody or antigen binding molecule comprises a VL CDR2, wherein the VL CDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 97-104. In some embodiments, the antibody or antigen binding molecule comprises a VL CDR3, wherein the VL CDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 113-120.

[0221] In some embodiments, the polynucleotide encodes an antibody or antigen binding molecule that specifically binds to BCMA, wherein the antibody or antigen binding molecule comprises a VL CDR1, a VL CDR2, and VL CDR3, wherein the VL CDR1, VL CDR2, and VL CDR3 comprise the amino acid sequence of the VL CDR1, VL CDR2, and VL CDR3 of an antibody in FIG. 1C, respectively.

[0222] In some embodiments, the polynucleotide encodes an antibody or antigen binding molecule that specifically binds to BCMA, wherein the antibody or antigen binding molecule comprises a VH framework region 1 (FR1), wherein the VH FR1 comprises an amino acid sequence 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 an amino acid sequence selected from SEQ ID NOs: 1-8 and 207-214. In some embodiments, the antibody or antigen binding molecule comprises a VH FR2, wherein the VH FR2 comprises an amino acid sequence 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 an amino acid sequence selected from SEQ ID NOs: 17-24 and 223-23. In some embodiments, the antibody or antigen binding molecule comprises a VH FR3, wherein the VH FR3 comprises an amino acid sequence 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 an amino acid sequence selected from SEQ ID NOs: 33-40 and 239-246. In some embodiments, the antibody or antigen binding molecule comprises a VH FR4, wherein the VH FR4 comprises an amino acid sequence 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 an amino acid sequence selected from SEQ ID NOs: 49-56 and 255-262.

[0223] In some embodiments, the antibody or antigen binding molecule or a fragment thereof comprises a VL FR1, wherein the VL FR1 comprises an amino acid sequence 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 an amino acid sequence selected from SEQ ID NOs: 73-80. In some embodiments, the antibody or antigen binding molecule or a fragment thereof comprises a VL FR2, wherein the VL FR2 comprises an amino acid sequence 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 an amino acid sequence selected from SEQ ID NOs: 89-96. In some embodiments, the antibody or antigen binding molecule or a fragment thereof comprises a VL FR3, wherein the VL FR3 comprises an amino acid sequence 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 an amino acid sequence selected from SEQ ID NOs: 105-112. In some embodiments, the antibody or antigen binding molecule or a fragment thereof comprises a VL FR4, wherein the VL FR4 comprises an amino acid sequence 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 an amino acid sequence selected from SEQ ID NOs: 121-128.

[0224] In some embodiments, the polynucleotide encodes an antibody or antigen binding molecule that specifically binds to BCMA, wherein the antibody or antigen binding molecule comprises any one, two, and/or three VH CDR sequences disclosed herein. In certain embodiments, the antibody or antigen binding molecule comprises a VH CDR1, a VH CDR2, and a VH CDR3 having the amino acid sequence of any VH CDR1, VH CDR2, and VH CDR3 disclosed herein, respectively. In some embodiments, the antibody or antigen binding molecule comprises any one, two, and/or three VL CDR sequences disclosed herein. In certain embodiments, the antibody or antigen binding molecule comprises a VL CDR1, a VL CDR2, and a VL CDR3 having the amino acid sequence of any VL CDR1, VL CDR2, and VL CDR3 disclosed herein, respectively.

[0225] In one embodiment, the antibody or antigen binding molecule comprises: (a) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 9; (b) a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 25; (c) a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 41; (d) a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 81; (e) a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 97; and (f) a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 113.

[0226] In one embodiment, the antibody or antigen binding molecule comprises: (a) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 10; (b) a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 26; (c) a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 42; (d) a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 82; (e) a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 98; and (f) a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 114.

[0227] In one embodiment, the antibody or antigen binding molecule comprises:(a) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 11; (b) a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 27; (c) a VH CDR3 region

comprising the amino acid sequence of SEQ ID NO: 43; (d) a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 83; (e) a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 99; and (f) a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 115.

[0228] In one embodiment, the antibody or antigen binding molecule comprises: (a) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 12; (b) a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 28; (c) a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 44; (d) a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 84; (e) a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 100; and (f) a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 116.

[0229] In one embodiment, the antibody or antigen binding molecule comprises: (a) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 13; (b) a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 29; (c) a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 45; (d) a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 85; (e) a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 101; and (f) a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 117.

[0230] In one embodiment, the antibody or antigen binding molecule comprises: (a) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 14; (b) a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 30; (c) a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 46; (d) a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 86; (e) a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 102; and (f) a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 118.

[0231] In one embodiment, the antibody or antigen binding molecule comprises: (a) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 15; (b) a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 31; (c) a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 47; (d) a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 87; (e) a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 103; and (f) a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 119.

[0232] In one embodiment, the antibody or antigen binding molecule comprises: (a) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 16; (b) a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 32; (c) a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 48; (d) a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 88; (e) a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 104; and (f) a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 120.

[0233] In one embodiment, the antibody or antigen binding molecule comprises: (a) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 215; (b) a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 231; (c) a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 247; (d) a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 81; (e) a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 97; and (f) a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 113.

[0234] In one embodiment, the antibody or antigen binding molecule comprises: (a) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 216; (b) a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 232; (c) a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 248; (d) a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 82; (e) a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 98; and (f) a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 114.

[0235] In one embodiment, the antibody or antigen binding molecule comprises: (a) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 217; (b) a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 233; (c) a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 249; (d) a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 83; (e) a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 99; and (f) a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 115.

[0236] In one embodiment, the antibody or antigen binding molecule comprises: (a) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO:218; (b) a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 234; (c) a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 250; (d) a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 84; (e) a VL CDR2 region comprising the amino

acid sequence of SEQ ID NO: 100; and (f) a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 116.

[0237] In one embodiment, the antibody or antigen binding molecule comprises: (a) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 219; (b) a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 235; (c) a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 251; (d) a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 85; (e) a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 101; and (f) a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 117.

[0238] In one embodiment, the antibody or antigen binding molecule comprises: (a) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 220; (b) a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 236; (c) a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 252; (d) a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 86; (e) a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 102; and (f) a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 118.

[0239] In one embodiment, the antibody or antigen binding molecule comprises: (a) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 221; (b) a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 237; (c) a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 253; (d) a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 87; (e) a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 103; and (f) a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 119.

[0240] In one embodiment, the antibody or antigen binding molecule comprises: (a) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 222; (b) a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 238; (c) a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 254; (d) a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 88; (e) a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 104; and (f) a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 120.

[0241] In some embodiments, the antibody or antigen binding molecule comprises a heavy chain variable region sequence comprising an amino acid sequence of FIG. 1A or FIG. 1B. In some embodiments, the antibody or antigen binding molecule comprises a heavy chain

variable region sequence comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 65-72. In some embodiments, the antibody or antigen binding molecule comprises a light chain variable region sequence comprising an amino acid sequence selected from FIG. 1C. In some embodiments, the antibody or antigen binding molecule comprises a light chain variable region sequence comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 137-144.

[0242] In some embodiments, the antibody or antigen binding molecule comprises (a) a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 65; and (b) a light chain variable region comprising the amino acid sequence of SEQ ID NO 137.

[0243] In some embodiments, the antibody or antigen binding molecule comprises (a) a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 66; and (b) a light chain variable region comprising the amino acid sequence of SEQ ID NO: 138.

[0244] In some embodiments, the antibody or antigen binding molecule comprises (a) a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 67; and (b) a light chain variable region comprising the amino acid sequence of SEQ ID NO: 139.

[0245] In some embodiments, the antibody or antigen binding molecule comprises (a) a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 68; and (b) a light chain variable region comprising the amino acid sequence of SEQ ID NO: 140.

[0246] In some embodiments, the antibody or antigen binding molecule comprises (a) a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 69; and (b) a light chain variable region comprising the amino acid sequence of SEQ ID NO: 141.

[0247] In some embodiments, the antibody or antigen binding molecule comprises (a) a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 70; and (b) a light chain variable region comprising the amino acid sequence of SEQ ID NO: 142.

[0248] In some embodiments, the antibody or antigen binding molecule comprises (a) a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 71; and (b) a light chain variable region comprising the amino acid sequence of SEQ ID NO: 143.

[0249] In some embodiments, the antibody or antigen binding molecule comprises (a) a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 72; and (b) a light chain variable region comprising the amino acid sequence of SEQ ID NO: 144.

[0250] 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 form the group consisting of SEQ ID NOs: 57-64. 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 form the group consisting of SEQ ID NOs: 129-136.

[0251] The antibody or antigen binding molecule encoded by the polypeptide of the present invention can be single chained or double chained. In some embodiments, the antibody or antigen binding molecule comprises 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 antibody or antigen binding molecule comprises an scFv.

[0252] In certain embodiments, the antibody or 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 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 GSTSGSGKPGSGEGSTKG (SEQ ID NO: 174) or a poly-Gly linker such as the amino acid sequence GGGGSGGGGSGGGGS (SEQ ID NO: 268). Or GGGGSGGGGSGGGGSGGGGS (SEQ ID NO: 411). In one embodiment, the linker is a Whitlow linker. In certain embodiments, the antibody or antigen 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: 174.

[0253] In some embodiments, the antibody or antigen binding molecules of the present invention specifically bind BCMA (*e.g.*, hBCMA). In certain embodiments, an anti-BCMA antibody or antigen binding molecule of the present invention binds human BCMA with a $K_D$ of less than 1 x $10^{-6}$ M, less than 1 x $10^{-7}$ M, less than 1 x $10^{-8}$ M, or less than 1 x $10^{-9}$ M. In one particular embodiment, the anti-BCMA antibody or antigen binding molecules binds human BCMA with a $K_D$ of less than 1 x $10^{-7}$ M. In another embodiment, the anti-BCMA antibody or antigen binding molecules binds human BCMA with a $K_D$ of less than 1 x $10^{-8}$ M. In some embodiments, the anti-BCMA antibody or antigen binding molecules binds human BCMA with a $K_D$ of about 1 x $10^{-7}$ M, about 2 x $10^{-7}$ M, about 3 x $10^{-7}$ M, about 4 x $10^{-7}$ M, about 5 x $10^{-7}$ M, about 6 x $10^{-7}$ M, about 7 x $10^{-7}$ M, about 8 x $10^{-7}$ M, about 9 x $10^{-7}$ M, about 1 x $10^{-8}$ M, about 2 x $10^{-8}$ M, about 3 x $10^{-8}$ M, about 4 x $10^{-8}$ M, about 5 x $10^{-8}$ M, about 6 x $10^{-8}$ M, about 7 x $10^{-8}$ M, about 8 x $10^{-8}$ M, about 9 x $10^{-8}$ M, about 1 x $10^{-9}$ M, about 2 x $10^{-9}$ M, about 3 x $10^{-9}$ M, about 4 x $10^{-9}$ M, about 5 x $10^{-9}$ M, about 6 x $10^{-9}$ M, about 7 x $10^{-9}$ M, about 8 x $10^{-9}$ M, about 9 x $10^{-9}$ M, about 1 x $10^{-10}$ M, or about 5 x $10^{-10}$ 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, 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.

[0254] In other embodiments, the anti-BCMA antibody or antigen binding molecule binds human BCMA-Fc with a $K_D$ of less than 1 x $10^{-9}$ M, less than 3 x $10^{-9}$ M, less than 5 x $10^{-9}$ M, less than 1 x $10^{-10}$ M, less than 3 x $10^{-10}$ M, or less than 5 x $10^{-10}$ M. In other embodiments, the anti-BCMA antibody or antigen binding molecules binds cyno BCMA-Fc with a $K_D$ of less than 1 x $10^{-5}$ M, less than 1 x $10^{-6}$ M, less than 1 x $10^{-7}$ M, less than 1 x $10^{-8}$ M, less than 1 x $10^{-9}$ M, or less than 1 x $10^{-10}$ M.

[0255] In some embodiments, the anti-BCMA antibody or antigen binding molecule binds human BCMA with an association rate ($k_{on}$) of less than 1 x $10^{-4}$ $M^{-1}$ $s^{-1}$, less than 2 x $10^{-4}$ $M^{-1}$ $s^{-1}$, less than 3 x $10^{-4}$ $M^{-1}$ $s^{-1}$, less than 4 x $10^{-4}$ $M^{-1}$ $s^{-1}$, less than 5 x $10^{-4}$ $M^{-1}$ $s^{-1}$, less than 6 x $10^{-4}$ $M^{-1}$ $s^{-1}$, less than 7 x $10^{-4}$ $M^{-1}$ $s^{-1}$, less than 8 x $10^{-4}$ $M^{-1}$ $s^{-1}$, less than 9 x $10^{-4}$ $M^{-1}$ $s^{-1}$, less than 1 x $10^{-5}$ $M^{-1}$ $s^{-1}$, less than 2 x $10^{-5}$ $M^{-1}$ $s^{-1}$, less than 3 x $10^{-5}$ $M^{-1}$ $s^{-1}$, less than 4 x $10^{-5}$ $M^{-1}$ $s^{-1}$, less than 5 x $10^{-5}$ $M^{-1}$ $s^{-1}$, less than 6 x $10^{-5}$ $M^{-1}$ $s^{-1}$, less than 7 x $10^{-5}$ $M^{-1}$ $s^{-1}$, less than 8 x $10^{-5}$ $M^{-1}$ $s^{-1}$, less than 9 x $10^{-5}$ $M^{-1}$ $s^{-1}$, less than 1 x $10^{-6}$ $M^{-1}$ $s^{-1}$, less than 2 x $10^{-6}$ $M^{-1}$ $s^{-1}$, less than 3 x $10^{-6}$ $M^{-1}$ $s^{-1}$, less than 4 x $10^{-6}$ $M^{-1}$ $s^{-1}$, less than 5 x $10^{-6}$ $M^{-1}$ $s^{-1}$, less than

6 x $10^{-6}$ $M^{-1}$ $s^{-1}$, less than 7 x $10^{-6}$ $M^{-1}$ $s^{-1}$, less than 8 x $10^{-6}$ $M^{-1}$ $s^{-1}$, less than 9 x $10^{-6}$ $M^{-1}$ $s^{-1}$, or less than 1 x $10^{-7}$ $M^{-1}$ $s^{-1}$. 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.

[0256] In some embodiments, the anti-BCMA antibody or antigen binding molecule binds human BCMA with an dissociation rate ($k_{off}$) of less than 1 x $10^{-2}$ $s^{-1}$, less than 2 x $10^{-2}$ $s^{-1}$, less than 3 x $10^{-2}$ $s^{-1}$, less than 4 x $10^{-2}$ $s^{-1}$, less than 5 x $10^{-2}$ $s^{-1}$, less than 6 x $10^{-2}$ $s^{-1}$, less than 7 x $10^{-2}$ $s^{-1}$, less than 8 x $10^{-2}$ $s^{-1}$, less than 9 x $10^{-2}$ $s^{-1}$, less than 1 x $10^{-3}$ $s^{-1}$, less than 2 x $10^{-3}$ $s^{-1}$, less than 3 x $10^{-3}$ $s^{-1}$, less than 4 x $10^{-3}$ $s^{-1}$, less than 5 x $10^{-3}$ $s^{-1}$, less than 6 x $10^{-3}$ $s^{-1}$, less than 7 x $10^{-3}$ $s^{-1}$, less than 8 x $10^{-3}$ $s^{-1}$, less than 9 x $10^{-3}$ $s^{-1}$, less than 1 x $10^{-4}$ $s^{-1}$, less than 2 x $10^{-4}$ $s^{-1}$, less than 3 x $10^{-4}$ $s^{-1}$, less than 4 x $10^{-4}$ $s^{-1}$, less than 5 x $10^{-4}$ $s^{-1}$, less than 6 x $10^{-4}$ $s^{-1}$, less than 7 x $10^{-4}$ $s^{-1}$, less than 8 x $10^{-4}$ $s^{-1}$, less than 9 x $10^{-4}$ $s^{-1}$, less than 1 x $10^{-4}$ $s^{-1}$, or less than 5 x $10^{-4}$ $s^{-1}$. 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.

[0257] In some embodiments, the polynucleotide of the present invention encodes an antibody or antigen binding molecule that specifically binds to BCMA, wherein the antibody or antigen binding molecule cross competes with a reference antibody disclosed herein. In certain embodiments, the antibody or antigen binding molecule cross competes with a reference antibody comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-56, 65-128, and 137-144. In some embodiments, the antibody or antigen binding molecule cross competes with a reference antibody comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 65-72 and 137-144. In certain embodiments, the antibody or antigen binding molecule cross competes with a reference antibody, wherein the reference antibody comprises a VH CDR1 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 9-16. In certain embodiments, the antibody or antigen binding molecule cross competes with a reference antibody, wherein the reference antibody comprises a VH CDR2 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 25-32. In certain embodiments, the antibody or antigen binding molecule cross competes with a reference antibody, wherein the reference antibody comprises a VH CDR3 comprising an amino acid sequence selected from the group

consisting of SEQ ID NOs: 41-48. In some embodiments, the antibody or antigen binding molecule cross competes with a reference antibody, wherein the reference antibody comprises a VL CDR1 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 89-96. In certain embodiments, the antibody or antigen binding molecule cross competes with a reference antibody, wherein the reference antibody comprises a VL CDR2 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 105-112. In certain embodiments, the antibody or antigen binding molecule cross competes with a reference antibody, wherein the reference antibody comprises a VL CDR3 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 121-128. In one embodiment, the antibody or antigen binding molecule cross competes with a reference antibody, wherein the reference antibody comprises a VH comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 65-72. In another embodiment, the antibody or antigen binding molecule cross competes with a reference antibody, wherein the reference antibody comprises a VL comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 137-144.

[0258] In some embodiments, the polynucleotide of the present invention encodes an antibody or antigen binding molecule that specifically binds to BCMA, wherein the antibody or antigen binding molecule binds the same or an overlapping epitope as a reference antibody disclosed herein (*e.g.*, Figure 1). In certain embodiments, the antibody or antigen binding molecule binds the same or an overlapping epitope as a reference antibody comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-56, 65-128, and 137-144. In some embodiments, the antibody or antigen binding molecule binds the same or an overlapping epitope as a reference antibody comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 65-72 and 137-144.

### *III Polynucleotides Encoding Chimeric Antigen Receptors and T Cell Receptors*

[0259] The present invention is also directed to polynucleotides encoding chimeric antigen receptors (CARs) or T cell receptors (TCRs) comprising an antigen binding molecule that specifically binds to BCMA described in Section II, and engineered T cells comprising an antigen binding molecule that specifically binds to BCMA described in Section II. In some embodiments, an anti-BCMA CAR or TCR encoded by the polynucleotide of the present invention comprises an antigen binding molecule that specifically binds to BCMA. In some embodiments, the anti-BCMA CAR or TCR encoded by the polynucleotide further comprises

a costimulatory domain. In some embodiments, the costimulatory domain in the anti-BCMA CAR or TCR encoded by the polynucleotide comprises an extracellular domain (i.e., a hinge region), a transmembrane domain, and/or an intracellular (signaling) domain. In some embodiments, the anti-BCMA CAR or TCR encoded by the polynucleotide further comprises a CD3 zeta activating domain. In one particular embodiment, the anti-BCMA CAR or TCR encoded by the polynucleotide comprises an antigen binding molecule that specifically binds BCMA (*e.g.*, hBCMA), a costimulatory domain comprising an extracellular domain, a transmembrane domain, and an intracellular domain, and a CD3 zeta activating domain.

[0260] In some embodiments, the polynucleotide of the present invention encodes a TCR, wherein the TCR comprises an antigen binding molecule that specifically binds to BCMA, and wherein the TCR further comprises a fourth complementarity determining region (CDR4). In certain embodiments, the polynucleotide encodes a TCR, wherein the TCR comprises an antigen binding molecule that specifically binds to BCMA, and 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.

### *III.A. Costimulatory Domain*

[0261] In some embodiments, the polynucleotide of the present invention encodes a CAR, wherein the CAR comprises an antigen binding molecule that specifically binds to BCMA (one or more antigen binding molecules in Section II), and wherein the CAR further comprises a costimulatory domain. In some embodiments, the costimulatory domain is positioned between the antigen binding molecule and an activating domain. In certain embodiments, the costimulatory domain can comprise an extracellular domain, a transmembrane domain, and an intracellular signaling domain.

[0262] ***Extracellular Domain***: In one embodiment, the extracellular domain comprises a hinge region (e.g., a spacer region). In another embodiment, the extracellular domain is from or derived from (e.g., comprises) CD28, CD28T, OX40, 4-1BB/CD137, CD2, CD3 (alpha, beta, delta, epsilon, gamma, zeta), CD4, CD5, CD7, CD8, CD9, CD16, CD22, CD27, CD30, CD 33, CD37, CD40, CD 45, CD64, CD80, CD86, CD134, CD137, CD154, programmed death-1 (PD-1), ICOS, April, BAFF, lymphocyte function-associated antigen-1 (LFA-1 (CDl la/CD18), CD247, CD276 (B7-H3), LIGHT (tumor necrosis factor superfamily member 14; TNFSF14), NKG2C, Ig alpha (CD79a), DAP-10, Fc gamma receptor, MHC class I molecule, TNFr, integrin, signaling lymphocytic activation molecule, BTLA, Toll ligand receptor, ICAM-1, B7-H3, CDS, ICAM-1, GITR, BAFFR, LIGHT, HVEM (LIGHTR), KIRDS2, SLAMF7, NKp80 (KLRF1), NKp44, NKp30, NKp46, CD19, CD4, CD8alpha, CD8beta, IL2R beta, IL2R gamma, IL7R alpha, ITGA4, VLA1, CD49a, ITGA4, IA4, CD49D, ITGA6, VLA-6, CD49f, ITGAD, CDl-ld, ITGAE, CD103, ITGAL, CDl-la, LFA-1, ITGAM, CDl-lb, ITGAX, CDl-lc, ITGBl, CD29, ITGB2, CD18, LFA-1, ITGB7, NKG2D, TNFR2, TRANCE/RANKL, DNAM1 (CD226), SLAMF4 (CD244, 2B4), CD84, CD96 (Tactile), CEACAM1, CRT AM, Ly9 (CD229), CD160 (BY55), PSGL1, CD100 (SEMA4D), CD69, SLAMF6 (NTB-A, Lyl08), SLAM (SLAMF1, CD150, IPO-3), BLAME (SLAMF8), SELPLG (CD162), LTBR, LAT, GADS, SLP-76, PAG/Cbp, CD19a, CD83 ligand, or fragments or combinations thereof. The extracellular domain can be derived either from a natural or from a synthetic source.

[0263] In some embodiments, the extracellular domain in the costimulatory domain is positioned between the antigen binding molecule and the transmembrane domain. In certain embodiments, the extracellular domain in the costimulatory domain is from or derived from an immunoglobulin. In some embodiments, the extracellular domain in the costimulatory domain is selected from the hinge regions of IgG1, IgG2, IgG3, IgG4, IgA, IgD, IgE, and

IgM, or a fragment thereof. In other embodiments, the extracellular domain in the costimulatory domain is from or derived from the hinge region of CD8 alpha. In one particular embodiment, the extracellular domain in the costimulatory domain is from or derived from the hinge region of CD28. In certain embodiments, the extracellular domain in the costimulatory domain comprises a fragment of the hinge region of CD8 alpha or a fragment of the hinge region of CD28, wherein the fragment is anything less than the whole hinge region. In some embodiments, the fragment of the CD8 alpha hinge region or the fragment of the CD28 hinge region comprises an amino acid sequence that excludes at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, or at least 20 amino acids at the N-terminus or C-Terminus, or both, of the CD8 alpha hinge region of the CD28 hinge region.

[0264] In certain embodiments, the extracellular domain in the costimulatory domain 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 LDNEKSNGTIIHVKGKHLCPSPLFPGPSKP (SEQ ID NO: 167) or a fragment thereof. In some embodiments, the extracellular domain in the costimulatory domain comprises the amino acid sequence of SEQ ID NO: 167 or a fragment thereof.

[0265] In certain embodiments, the extracellular domain in the costimulatory domain is encoded by a nucleotide sequence 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 nucleotide sequence CTTGATAATGAAAAGTCAAACGGAACAATCATT CACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAG CCA (SEQ ID NO: 166) or a fragment thereof. In some embodiments, the extracellular domain in the costimulatory domain is encoded by a nucleotide sequence that comprises the nucleotide sequence of SEQ ID NO: 166 or a fragment thereof.

[0266] In some embodiments, the CD28T domain is derived from a human CD28 hinge region. In other embodiments, the CD28T domain is derived from a rodent, murine, or primate (*e.g.*, non-human primate) CD28 hinge region. In some embodiments, the CD28T domain is derived from a chimeric CD28 hinge region.

[0267] In some embodiments, the extracellular domain comprises some or all of a member of the immunoglobulin family such as IgG1, IgG2, IgG3, IgG4, IgA, IgD, IgE, IgM, or fragment thereof.

[0268] ***Transmembrane Domain:*** The costimulatory domain for the CAR or TCR of the invention can further comprise a transmembrane domain. The transmembrane domain can be designed to be fused to the extracellular domain in the costimulatory domain. It can similarly be fused to the intracellular domain in the costimulatory domain. 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 may 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. In some embodiments, the transmembrane domain is derived from CD28, OX-40, 4-1BB/CD137, CD2, CD3 (alpha, beta, delta, epsilon, zeta), CD4, CD5, CD7, CD8, CD9, CD16, CD22, CD27, CD30, CD 33, CD37, CD40, CD 45, CD64, CD80, CD86, CD134, CD137, CD154, programmed death-1 (PD-1), ICOS, lymphocyte function-associated antigen-1 (LFA-1 (CDl la/CD18), CD3 gamma, CD247, CD276 (B7-H3), LIGHT (tumor necrosis factor superfamily member 14; TNFSF14), NKG2C, Ig alpha (CD79a), DAP-10, Fc gamma receptor, MHC class I molecule, TNFr, integrin, signaling lymphocytic activation molecule, BTLA, Toll ligand receptor, ICAM-1, B7-H3, CDS, ICAM-1, GITR, BAFFR, LIGHT, HVEM (LIGHTR), KIRDS2, SLAMF7, NKp80 (KLRF1), NKp44, NKp30, NKp46, CD19, CD4, CD8alpha, CD8beta, IL2R beta, IL2R gamma, IL7R alpha, ITGA4, VLA1, CD49a, ITGA4, IA4, CD49D, ITGA6, VLA-6, CD49f, ITGAD, CDl-ld, ITGAE, CD103, ITGAL, CDl-la, LFA-1, ITGAM, CDl-lb, ITGAX, CDl-lc, ITGBl, CD29, ITGB2, CD18, LFA-1, ITGB7, NKG2D, TNFR2, TRANCE/RANKL, DNAM1 (CD226), SLAMF4 (CD244, 2B4), CD84, CD96 (Tactile), CEACAM1, CRT AM, Ly9 (CD229), CD160 (BY55), PSGL1, CD100 (SEMA4D), CD69, SLAMF6 (NTB-A, Lyl08), SLAM (SLAMF1, CD150, IPO-3), BLAME (SLAMF8), SELPLG (CD162), LTBR, LAT, GADS, SLP-76, PAG/Cbp, CD19a, CD83 ligand, or a fragment thereof.

[0269] Optionally, a short oligo or polypeptide linker, preferably between 2 and 10 amino acids in length may form the linkage between the transmembrane domain and the

cytoplasmic signaling domain of the CAR. A glycine-serine doublet provides a particularly suitable linker.

[0270] In one embodiment, the transmembrane domain in the CAR of the invention comprises the CD8 transmembrane domain. In one embodiment, the CD8 transmembrane domain comprises the transmembrane portion of the nucleic acid sequence of GCTGCAGCATTGAGCAACTCAATAATGTATTTTAGTCACTTTGTACCAGTGTTCT TGCCGGCTAAGCCTACTACCACACCCGCTCCACGGCCACCTACCCCAGCTCCTA CCATCGCTTCACAGCCTCTGTCCCTGCGCCCAGAGGCTTGCCGACCGGCCGCAG GGGGCGCTGTTCATACCAGAGGACTGGATTTCGCCTGCGATATCTATATCTGGG CACCCCTGGCCGGAACCTGCGGCGTACTCCTGCTGTCCCTGGTCATCACGCTCT ATTGTAATCACAGGAAC (SEQ ID NO: 269). In one embodiment, the CD8 transmembrane domain comprises the nucleic acid sequence that encodes the transmembrane amino acid sequence contained within AAALSNSIMYFSHFVPVFLPAKPTTTPAPRPPTPAPTIASQP LSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCNHRN (SEQ ID NO: 270).

[0271] In another embodiment, the transmembrane domain in the costimulating domain is a CD28 transmembrane domain. In some embodiments, the transmembrane domain 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 FWVLVVVGGVLACYSLLVTVAFIIFWV (SEQ ID NO: 169). In some embodiments, the transmembrane domain comprises the amino acid sequence of SEQ ID NO: 169.

[0272] In some embodiments, the transmembrane domain is encoded by a nucleotide sequence 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 nucleotide sequence TTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCA CCGTGGCTTTTATAATCTTCTGGGTT (SEQ ID NO: 168). In some embodiments, the transmembrane domain is encoded by a nucleotide sequence that comprises the nucleotide sequence of SEQ ID NO: 168.

[0273] ***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 cytokines.

[0274] In certain embodiments, suitable intracellular signaling domain include (*i.e.*, comprise), but are not limited to CD28, CD28T, OX-40, 4-1BB/CD137, CD2, CD7, CD27, CD30, CD40, programmed death-1 (PD-1), inducible T cell costimulator (ICOS), lymphocyte function-associated antigen-1 (LFA-1, CDl-la/CD18), CD3 gamma, CD3 delta, CD3 epsilon, CD247, CD276 (B7-H3), LIGHT, (TNFSF14), NKG2C, Ig alpha (CD79a), DAP-10, Fc gamma receptor, MHC class 1 molecule, TNF receptor proteins, an Immunoglobulin protein, cytokine receptor, integrins, Signaling Lymphocytic Activation Molecules (SLAM proteins), activating NK cell receptors, BTLA, a Toll ligand receptor, ICAM-1, B7-H3, CDS, ICAM-1, GITR, BAFFR, LIGHT, HVEM (LIGHTR), KIRDS2, SLAMF7, NKp80 (KLRF1), NKp44, NKp30, NKp46, CD19, CD4, CD8alpha, CD8beta, IL-2R beta, IL-2R gamma, IL-7R alpha, ITGA4, VLA1, CD49a, ITGA4, IA4, CD49D, ITGA6, VLA-6, CD49f, ITGAD, CDl ld, ITGAE, CD103, ITGAL, CDl la, LFA-1, ITGAM, CDl lb, ITGAX, CDl lc, ITGBl, CD29, ITGB2, CD18, LFA-1, ITGB7, NKG2D, TNFR2, TRANCE/RANKL, DNAM1 (CD226), SLAMF4 (CD244, 2B4), CD84, CD96 (Tactile), CEACAM1, CRT AM, Ly9 (CD229), CD160 (BY55), PSGL1, CD100 (SEMA4D), CD69, SLAMF6 (NTB-A, Lyl08), SLAM (SLAMF1, CD150, IPO-3), BLAME (SLAMF8), SELPLG (CD162), LTBR, LAT, GADS, SLP-76, PAG/Cbp, CD19a, a ligand that specifically binds with CD83, or any combination thereof.

[0275] An example of a nucleotide sequence encoding the intracellular signaling domain is set forth in SEQ ID NO. 170:

AGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTC
CACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACC
TAGAGATTTCGCTGCCTATCGGAGC

[0276] 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: 170.

[0277] An example of an intracellular signaling domain is set forth in SEQ ID NO. 171:

RSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRS.

[0278] 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: 171.

[0279] The intracellular signaling sequences within the CAR of the invention can be linked to each other or to an activating domain in a random or specified order. Optionally, a short oligo- or polypeptide linker, preferably between 2 and 10 amino acids in length may form the linkage. A glycine-serine doublet provides a particularly suitable linker.

[0280] It will further be appreciated that where desired, the costimulatory regions described herein can be expressed in a separate chain from the antigen binding molecule (*e.g.*, scFv) and activating domains, in so-called "trans" configuration.

### *III.B Activating Domain*

[0281] In some embodiments, intracellular domains for use in the engineered T cell of the invention include cytoplasmic sequences of the T cell receptor (TCR) and co-receptors that act in concert to initiate signal transduction following antigen/receptor engagement, as well as any derivative or variant of these sequences and any synthetic sequence that has the same functional capability. 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 activating domain is CD3, e.g., CD3 zeta, the nucleotide sequence of which is set forth in SEQ ID NO. 172:

AGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCC
AGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATG
ACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACC
AAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGA
TAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAG
AAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTACG
AAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG.

[0282] 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: 172.

[0283] The corresponding amino acid of intracellular CD3 zeta is set forth in SEQ ID NO. 173:

RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPR
RKNPQEGLYNELQK
DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR.

[0284] 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 SEQ ID NO: 173.

[0285] Additionally, in certain 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 a CD3 zeta variant as set forth in SEQ ID NO: 412:

RVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRR
KNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTY
DALHMQALPPR

### *III.C. Leader Peptide*

[0286] In some embodiments, the polynucleotide of the present invention encodes a CAR or a TCR, wherein the CAR or the TCR comprises an antigen binding molecule that specifically binds to BCMA, and wherein the CAR or the TCR 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: 165). In some embodiments, the signal peptide comprises the amino acid sequence of SEQ ID NO: 165. In some embodiments, the

leader peptide is encoded by 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 SEQ ID NO: 164.

[0287] In some embodiments, the polynucleotide of the present invention encodes a CAR, wherein the CAR comprises a leader peptide (P), an antigen binding molecule (B), a hinge domain (H), a transmembrane domain (T), a costimulatory region (C), and an activation domain (A), wherein the CAR is configured according to the following: P-B-H-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-H-T-C-A or P-VL-VH-H-T-C-A. In some embodiments, the VH and the VL are connected by a linker (L), wherein the anti-BCMA CAR is configured according to the following, from N-terminus to C-terminus: P-VH-L-VL-H-T-C-A or P-VH-L-VL-H-T-C-A.

[0288] 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.

Table 2. Example CAR Sequences

| Anti-BCMA CAR | Nucleotide Sequence | SEQ ID NO: | Amino Acid Sequence | SEQ ID NO: |
|---|---|---|---|---|
| FS-21495CAR HxL | ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTG<br>CTCCTGCACGCCGCACGCCCGGAGGTGCAGCTGTTGGAGTCT<br>GGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCC<br>TGTGCAGCCTCTGGATTCACCTTTAGCAGCTATGCCATGAGC<br>TGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCA<br>GCTATTAGTGGTAGTGGTGGTAGCACATACTACGCAGACTCC<br>GTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAAC<br>ACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACG<br>GCGGTGTACTACTGCGCAAGAGCCGAGATGGGAGCCGTATTC<br>GACATATGGGGTCAGGGTACAATGGTCACCGTCTCCTCAGGG<br>TCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGT<br>ACAAAGGGGGAAATTGTGTTGACACAGTCTCCAGCCACCCTG<br>TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCC<br>AGTCAGAGTGTTAGCAGGTACTTAGCCTGGTACCAACAGAAA<br>CCTGGCCAGGCTCCCAGGCTCCTCATCTATGATGCATCCAAC<br>AGGGCCACTGGCATCCCAGCCAGGTTCAGTGGCAGTGGGTCT<br>GGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAA<br>GATTTTGCAGTTTATTACTGTCAGCAGAGAATCTCCTGGCCT | 175 | MALPVTALLLPLALLLHAA<br>RPEVQLLESGGGLVQPGGS<br>LRLSCAASGFTFSSYAMSW<br>VRQAPGKGLEWVSAISGSG<br>GSTYYADSVKGRFTISRDN<br>SKNTLYLQMNSLRAEDTAV<br>YYCARAEMGAVFDIWGQGT<br>MVTVSSGSTSGSGKPGSGE<br>GSTKGEIVLTQSPATLSLS<br>PGERATLSCRASQSVSRYL<br>AWYQQKPGQAPRLLIYDAS<br>NRATGIPARFSGSGSGTDF<br>TLTISSLEPEDFAVYYCQQ<br>RISWPFTFGGGTKVEIKRA<br>AALDNEKSNGTIIHVKGKH<br>LCPSPLFPGPSKPFWVLVV<br>VGGVLACYSLLVTVAFIIF<br>WVRSKRSRLLHSDYMNMTP | 176 |

| | | | | |
|---|---|---|---|---|
| | TTCACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGGCC<br>GCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTCAC<br>GTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGT<br>CCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTC<br>CTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATC<br>TTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGAT<br>TACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAA<br>CACTACCAGCCTTACGCACCACCTAGAGATTTCGCTGCCTAT<br>CGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCG<br>TATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTG<br>GGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGA<br>CGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCC<br>CAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCT<br>GAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGG<br>GGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCT<br>ACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCA<br>CCTAGGTAA | | RRPGPTRKHYQPYAPPRDF<br>AAYRSRVKFSRSADAPAYQ<br>QGQNQLYNELNLGRREEYD<br>VLDKRRGRDPEMGGKPRRK<br>NPQEGLYNELQKDKMAEAY<br>SEIGMKGERRRGKGHDGLY<br>QGLSTATKDTYDALHMQAL<br>PPR | |
| FS-21495CARLxH | ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTG<br>CTCCTGCACGCCGCACGCCCGGAAATTGTGTTGACACAGTCT<br>CCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTC<br>TCCTGCAGGGCCAGTCAGAGTGTTAGCAGGTACTTAGCCTGG<br>TACCAACAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT<br>GATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTCAGT<br>GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGC<br>CTAGAGCCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGA<br>ATCTCCTGGCCTTTCACTTTTGGCGGAGGGACCAAGGTTGAG<br>ATCAAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGT<br>GGCGAAGGTAGTACAAAGGGGGAGGTGCAGCTGTTGGAGTCT<br>GGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCC<br>TGTGCAGCCTCTGGATTCACCTTTAGCAGCTATGCCATGAGC<br>TGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCA<br>GCTATTAGTGGTAGTGGTGGTAGCACATACTACGCAGACTCC<br>GTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAAC<br>ACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACG<br>GCGGTGTACTACTGCGCAAGAGCCGAGATGGGAGCCGTATTC<br>GACATATGGGGTCAGGGTACAATGGTCACCGTCTCCTCAGCC<br>GCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTCAC<br>GTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGT<br>CCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTC<br>CTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATC<br>TTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGAT<br>TACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAA<br>CACTACCAGCCTTACGCACCACCTAGAGATTTCGCTGCCTAT<br>CGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCG<br>TATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTG<br>GGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGA<br>CGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCC<br>CAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCT<br>GAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGG<br>GGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCT<br>ACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCA<br>CCTAGGTAA | 177 | MALPVTALLLPLALLLHAA<br>RPEIVLTQSPATLSLSPGE<br>RATLSCRASQSVSRYLAWY<br>QQKPGQAPRLLIYDASNRA<br>TGIPARFSGSGSGTDFTLT<br>ISSLEPEDFAVYYCQQRIS<br>WPFTFGGGTKVEIKRGSTS<br>GSGKPGSGEGSTKGEVQLL<br>ESGGGLVQPGGSLRLSCAA<br>SGFTFSSYAMSWVRQAPGK<br>GLEWVSAISGSGGSTYYAD<br>SVKGRFTISRDNSKNTLYL<br>QMNSLRAEDTAVYYCARAE<br>MGAVFDIWGQGTMVTVSSA<br>AALDNEKSNGTIIHVKGKH<br>LCPSPLFPGPSKPFWVLVV<br>VGGVLACYSLLVTVAFIIF<br>WVRSKRSRLLHSDYMNMTP<br>RRPGPTRKHYQPYAPPRDF<br>AAYRSRVKFSRSADAPAYQ<br>QGQNQLYNELNLGRREEYD<br>VLDKRRGRDPEMGGKPRRK<br>NPQEGLYNELQKDKMAEAY<br>SEIGMKGERRRGKGHDGLY<br>QGLSTATKDTYDALHMQAL<br>PPR | 178 |
| PC-21497CARHxL | ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTG<br>CTCCTGCACGCCGCACGCCCGCAGGTGCAGCTGGTGGAGTCT<br>GGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC<br>TGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCAC<br>TGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCA<br>GTTATATCGTATGATGGAAGTAATAAATACTATGCAGACTCC | 179 | MALPVTALLLPLALLLHAA<br>RPQVQLVESGGGVVQPGRS<br>LRLSCAASGFTFSSYGMHW<br>VRQAPGKGLEWVAVISYDG<br>SNKYYADSVKGRFTISRDN<br>SKNTLYLQMNSLRAEDTAV | 180 |

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| | GTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAAC<br>ACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACG<br>GCGGTGTACTACTGCGCCAGAGACGGTACTTATCTAGGTGGT<br>CTCTGGTACTTCGACTTATGGGGGAGAGGTACCTTGGTCACC<br>GTCTCCTCAGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGT<br>GGCGAAGGTAGTACAAAGGGGGATATTGTGATGACTCAGTCT<br>CCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCATC<br>TCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATAC<br>AACTATTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCA<br>CAGCTCCTGATCTATTTGGGTTCTAATCGGGCCTCCGGGGTC<br>CCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACA<br>CTGAAAATCAGCAGAGTGGAGGCTGAGGATGTTGGGGTTTAT<br>TACTGCATGCAGGGACTCGGCCTCCCTCTCACTTTTGGCGGA<br>GGGACCAAGGTTGAGATCAAACGGGCCGCTGCCCTTGATAAT<br>GAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCAC<br>CTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCATTC<br>TGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCT<br>CTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCC<br>AAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACT<br>CCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTAC<br>GCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAG<br>TTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCCAG<br>AACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAG<br>TATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATG<br>GGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTAT<br>AATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAA<br>ATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGAC<br>GGTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTAT<br>GACGCTCTCCACATGCAAGCCCTGCCACCTAGGTAA | | YYCARDGTYLGGLWYFDLW<br>GRGTLVTVSSGSTSGSGKP<br>GSGEGSTKGDIVMTQSPLS<br>LPVTPGEPASISCRSSQSL<br>LHSNGYNYLDWYLQKPGQS<br>PQLLIYLGSNRASGVPDRF<br>SGSGSGTDFTLKISRVEAE<br>DVGVYYCMQGLGLPLTFGG<br>GTKVEIKRAAALDNEKSNG<br>TIIHVKGKHLCPSPLFPGP<br>SKPFWVLVVVGGVLACYSL<br>LVTVAFIIFWVRSKRSRLL<br>HSDYMNMTPRRPGPTRKHY<br>QPYAPPRDFAAYRSRVKFS<br>RSADAPAYQQGQNQLYNEL<br>NLGRREEYDVLDKRRGRDP<br>EMGGKPRRKNPQEGLYNEL<br>QKDKMAEAYSEIGMKGERR<br>RGKGHDGLYQGLSTATKDT<br>YDALHMQALPPR | |
| PC-<br>21497CAR<br>HxL | ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTG<br>CTCCTGCACGCCGCACGCCCGGATATTGTGATGACTCAGTCT<br>CCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCATC<br>TCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATAC<br>AACTATTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCA<br>CAGCTCCTGATCTATTTGGGTTCTAATCGGGCCTCCGGGGTC<br>CCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACA<br>CTGAAAATCAGCAGAGTGGAGGCTGAGGATGTTGGGGTTTAT<br>TACTGCATGCAGGGACTCGGCCTCCCTCTCACTTTTGGCGGA<br>GGGACCAAGGTTGAGATCAAACGGGGGTCTACATCCGGCTCC<br>GGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGCAGGTG<br>CAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGG<br>TCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGT<br>AGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG<br>CTGGAGTGGGTGGCAGTTATATCGTATGATGGAAGTAATAAA<br>TACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGA<br>GACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTG<br>AGAGCCGAGGACACGGCGGTGTACTACTGCGCCAGAGACGGT<br>ACTTATCTAGGTGGTCTCTGGTACTTCGACTTATGGGGGAGA<br>GGTACCTTGGTCACCGTCTCCTCAGCCGCTGCCCTTGATAAT<br>GAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCAC<br>CTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCATTC<br>TGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCT<br>CTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCC<br>AAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACT<br>CCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTAC<br>GCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAG<br>TTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCCAG<br>AACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAG<br>TATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATG | 181 | MALPVTALLLPLALLLHAA<br>RPDIVMTQSPLSLPVTPGE<br>PASISCRSSQSLLHSNGYN<br>YLDWYLQKPGQSPQLLIYL<br>GSNRASGVPDRFSGSGSGT<br>DFTLKISRVEAEDVGVYYC<br>MQGLGLPLTFGGGTKVEIK<br>RGSTSGSGKPGSGEGSTKG<br>QVQLVESGGGVVQPGRSLR<br>LSCAASGFTFSSYGMHWVR<br>QAPGKGLEWVAVISYDGSN<br>KYYADSVKGRFTISRDNSK<br>NTLYLQMNSLRAEDTAVYY<br>CARDGTYLGGLWYFDLWGR<br>GTLVTVSSAAALDNEKSNG<br>TIIHVKGKHLCPSPLFPGP<br>SKPFWVLVVVGGVLACYSL<br>LVTVAFIIFWVRSKRSRLL<br>HSDYMNMTPRRPGPTRKHY<br>QPYAPPRDFAAYRSRVKFS<br>RSADAPAYQQGQNQLYNEL<br>NLGRREEYDVLDKRRGRDP<br>EMGGKPRRKNPQEGLYNEL<br>QKDKMAEAYSEIGMKGERR<br>RGKGHDGLYQGLSTATKDT<br>YDALHMQALPPR | 182 |

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| | GGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTAT<br>AATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAA<br>ATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGAC<br>GGTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTAT<br>GACGCTCTCCACATGCAAGCCCTGCCACCTAGGTAA | | | |
| AJ-<br>21508CAR<br>HxL | ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTG<br>CTCCTGCACGCCGCACGCCCGCAGGTGCAGCTGGTGCAGTCT<br>GGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCC<br>TGCAAGGCATCTGGATACACCTTCACCAGCTACTATATGCAC<br>TGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGA<br>ATAATCAACCCTGGTGGTGGTAGCACAAGCTACGCACAGAAG<br>TTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGC<br>ACAGTCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACG<br>GCGGTGTACTACTGCGCCAGAGAGAGTTGGCCAATGGACGTA<br>TGGGGCCAGGGAACAACTGTCACCGTCTCCTCAGGGTCTACA<br>TCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAG<br>GGGGAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTG<br>TCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAG<br>AGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGC<br>CAGGCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCC<br>ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACA<br>GAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTT<br>GCAGTTTATTACTGTCAGCAGTACGCCGCCTACCCTACTTTT<br>GGCGGAGGGACCAAGGTTGAGATCAAACGGGCCGCTGCCCTT<br>GATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGC<br>AAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAG<br>CCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGT<br>TACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTT<br>AGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAAT<br>ATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAG<br>CCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGG<br>GTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAG<br>GGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGG<br>GAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCT<br>GAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGT<br>CTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTAT<br>TCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGG<br>CACGACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGAT<br>ACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGGTAA | 183 | MALPVTALLLPLALLLHAA<br>RPQVQLVQSGAEVKKPGAS<br>VKVSCKASGYTFTSYYMHW<br>VRQAPGQGLEWMGIINPGG<br>GSTSYAQKFQGRVTMTRDT<br>STSTVYMELSSLRSEDTAV<br>YYCARESWPMDVWGQGTTV<br>TVSSGSTSGSGKPGSGEGS<br>TKGEIVMTQSPATLSVSPG<br>ERATLSCRASQSVSSNLAW<br>YQQKPGQAPRLLIYGASTR<br>ATGIPARFSGSGSGTEFTL<br>TISSLQSEDFAVYYCQQYA<br>AYPTFGGGTKVEIKRAAAL<br>DNEKSNGTIIHVKGKHLCP<br>SPLFPGPSKPFWVLVVVGG<br>VLACYSLLVTVAFIIFWVR<br>SKRSRLLHSDYMNMTPRRP<br>GPTRKHYQPYAPPRDFAAY<br>RSRVKFSRSADAPAYQQGQ<br>NQLYNELNLGRREEYDVLD<br>KRRGRDPEMGGKPRRKNPQ<br>EGLYNELQKDKMAEAYSEI<br>GMKGERRRGKGHDGLYQGL<br>STATKDTYDALHMQALPPR | 184 |
| AJ-<br>21508CAR<br>LxH | ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTG<br>CTCCTGCACGCCGCACGCCCGGAAATAGTGATGACGCAGTCT<br>CCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTC<br>TCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGG<br>TACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT<br>GGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGT<br>GGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGC<br>CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTAC<br>GCCGCCTACCCTACTTTTGGCGGAGGGACCAAGGTTGAGATC<br>AAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGC<br>GAAGGTAGTACAAAGGGGCAGGTGCAGCTGGTGCAGTCTGGG<br>GCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGC<br>AAGGCATCTGGATACACCTTCACCAGCTACTATATGCACTGG<br>GTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAATA<br>ATCAACCCTGGTGGTGGTAGCACAAGCTACGCACAGAAGTTC<br>CAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACA<br>GTCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCG<br>GTGTACTACTGCGCCAGAGAGAGTTGGCCAATGGACGTATGG<br>GGCCAGGGAACAACTGTCACCGTCTCCTCAGCCGCTGCCCTT | 185 | MALPVTALLLPLALLLHAA<br>RPEIVMTQSPATLSVSPGE<br>RATLSCRASQSVSSNLAWY<br>QQKPGQAPRLLIYGASTRA<br>TGIPARFSGSGSGTEFTLT<br>ISSLQSEDFAVYYCQQYAA<br>YPTFGGGTKVEIKRGSTSG<br>SGKPGSGEGSTKGQVQLVQ<br>SGAEVKKPGASVKVSCKAS<br>GYTFTSYYMHWVRQAPGQG<br>LEWMGIINPGGGSTSYAQK<br>FQGRVTMTRDTSTSTVYME<br>LSSLRSEDTAVYYCARESW<br>PMDVWGQGTTVTVSSAAAL<br>DNEKSNGTIIHVKGKHLCP<br>SPLFPGPSKPFWVLVVVGG<br>VLACYSLLVTVAFIIFWVR<br>SKRSRLLHSDYMNMTPRRP<br>GPTRKHYQPYAPPRDFAAY | 186 |

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| | GATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGC<br>AAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAG<br>CCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGT<br>TACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTT<br>AGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAAT<br>ATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAG<br>CCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGG<br>GTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAG<br>GGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGG<br>GAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCT<br>GAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGT<br>CTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTAT<br>TCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGG<br>CACGACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGAT<br>ACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGGTAA | | RSRVKFSRSADAPAYQQGQ<br>NQLYNELNLGRREEYDVLD<br>KRRGRDPEMGGKPRRKNPQ<br>EGLYNELQKDKMAEAYSEI<br>GMKGERRRGKGHDGLYQGL<br>STATKDTYDALHMQALPPR | |
| NM-21517CARHxL | ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTG<br>CTCCTGCACGCCGCACGCCCGCAGCTGCAGCTGCAGGAGTCG<br>GGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC<br>TGCACTGTCTCTGGTGGCTCCATCAGCAGTAGTAGTTACTAC<br>TGGGGCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGG<br>ATTGGGAGTATCTCCTATAGTGGGAGCACCTACTACAACCCG<br>TCCCTCAAGAGTCGAGTCACCATATCCGTAGACACGTCCAAG<br>AACCAGTTCTCCCTGAAGCTGAGTTCTGTGACCGCCGCAGAC<br>ACGGCGGTGTACTACTGCGCCAGAGGCAGGGGATATGCAACC<br>AGCTTAGCCTTCGATATCTGGGGTCAGGGTACAATGGTCACC<br>GTCTCCTCAGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGT<br>GGCGAAGGTAGTACAAAGGGGGAAATTGTGTTGACACAGTCT<br>CCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTC<br>TCCTGCAGGGCCAGTCAGAGTGTTAGCAGCTACTTAGCCTGG<br>TACCAACAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT<br>GATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTCAGT<br>GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGC<br>CTAGAGCCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGA<br>CACGTCTGGCCTCCTACTTTTGGCGGAGGGACCAAGGTTGAG<br>ATCAAACGGGCCGCTGCCCTTGATAATGAAAAGTCAAACGGA<br>ACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCC<br>TTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTA<br>GTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTG<br>GCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTG<br>CTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGC<br>CCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGAT<br>TTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCA<br>GATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAAC<br>GAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGAC<br>AAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGA<br>CGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAG<br>GATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGA<br>GAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGA<br>CTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATG<br>CAAGCCCTGCCACCTAGGTAA | 187 | MALPVTALLLPLALLLHAA<br>RPQLQLQESGPGLVKPSET<br>LSLTCTVSGGSISSSSYYW<br>GWIRQPPGKGLEWIGSISY<br>SGSTYYNPSLKSRVTISVD<br>TSKNQFSLKLSSVTAADTA<br>VYYCARGRGYATSLAFDIW<br>GQGTMVTVSSGSTSGSGKP<br>GSGEGSTKGEIVLTQSPAT<br>LSLSPGERATLSCRASQSV<br>SSYLAWYQQKPGQAPRLLI<br>YDASNRATGIPARFSGSGS<br>GTDFTLTISSLEPEDFAVY<br>YCQQRHVWPPTFGGGTKVE<br>IKRAAALDNEKSNGTIIHV<br>KGKHLCPSPLFPGPSKPFW<br>VLVVVGGVLACYSLLVTVA<br>FIIFWVRSKRSRLLHSDYM<br>NMTPRRPGPTRKHYQPYAP<br>PRDFAAYRSRVKFSRSADA<br>PAYQQGQNQLYNELNLGRR<br>EEYDVLDKRRGRDPEMGGK<br>PRRKNPQEGLYNELQKDKM<br>AEAYSEIGMKGERRRGKGH<br>DGLYQGLSTATKDTYDALH<br>MQALPPR | 188 |
| NM-21517CARLxH | ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTG<br>CTCCTGCACGCCGCACGCCCGGAAATTGTGTTGACACAGTCT<br>CCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTC<br>TCCTGCAGGGCCAGTCAGAGTGTTAGCAGCTACTTAGCCTGG<br>TACCAACAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT<br>GATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTCAGT<br>GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGC<br>CTAGAGCCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGA | 189 | MALPVTALLLPLALLLHAA<br>RPEIVLTQSPATLSLSPGE<br>RATLSCRASQSVSSYLAWY<br>QQKPGQAPRLLIYDASNRA<br>TGIPARFSGSGSGTDFTLT<br>ISSLEPEDFAVYYCQQRHV<br>WPPTFGGGTKVEIKRGSTS<br>GSGKPGSGEGSTKGQLQLQ | 190 |

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| | CACGTCTGGCCTCCTACTTTTGGCGGAGGGACCAAGGTTGAG<br>ATCAAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGT<br>GGCGAAGGTAGTACAAAGGGGCAGCTGCAGCTGCAGGAGTCG<br>GGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC<br>TGCACTGTCTCTGGTGGCTCCATCAGCAGTAGTAGTTACTAC<br>TGGGGCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGG<br>ATTGGGAGTATCTCCTATAGTGGGAGCACCTACTACAACCCG<br>TCCCTCAAGAGTCGAGTCACCATATCCGTAGACACGTCCAAG<br>AACCAGTTCTCCCTGAAGCTGAGTTCTGTGACCGCCGCAGAC<br>ACGGCGGTGTACTACTGCGCCAGAGGCAGGGGATATGCAACC<br>AGCTTAGCCTTCGATATCTGGGGTCAGGGTACAATGGTCACC<br>GTCTCCTCAGCCGCTGCCCTTGATAATGAAAAGTCAAACGGA<br>ACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCC<br>TTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTA<br>GTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTG<br>GCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTG<br>CTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGC<br>CCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGAT<br>TTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCA<br>GATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAAC<br>GAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGAC<br>AAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGA<br>CGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAG<br>GATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGA<br>GAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGA<br>CTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATG<br>CAAGCCCTGCCACCTAGGTAA | | ESGPGLVKPSETLSLTCTV<br>SGGSISSSSYYWGWIRQPP<br>GKGLEWIGSISYSGSTYYN<br>PSLKSRVTISVDTSKNQFS<br>LKLSSVTAADTAVYYCARG<br>RGYATSLAFDIWGQGTMVT<br>VSSAAALDNEKSNGTIIHV<br>KGKHLCPSPLFPGPSKPFW<br>VLVVVGGVLACYSLLVTVA<br>FIIFWVRSKRSRLLHSDYM<br>NMTPRRPGPTRKHYQPYAP<br>PRDFAAYRSRVKFSRSADA<br>PAYQQGQNQLYNELNLGRR<br>EEYDVLDKRRGRDPEMGGK<br>PRRKNPQEGLYNELQKDKM<br>AEAYSEIGMKGERRRGKGH<br>DGLYQGLSTATKDTYDALH<br>MQALPPR | |
| TS-21522CARHxL | ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTG<br>CTCCTGCACGCCGCACGCCCGGAGGTGCAGCTGGTGGAGTCT<br>GGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCC<br>TGTGCAGCCTCTGGATTCACCTTCAGTAGCTATAGCATGAAC<br>TGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTTCA<br>ACCATTAGTAGTAGTAGTAGTACCATATACTACGCAGACTCT<br>GTGAAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAAC<br>TCACTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACG<br>GCGGTGTACTACTGCGCCAGAGGTTCTCAGGAGCACCTGATT<br>TTCGATTATTGGGGACAGGGTACATTGGTCACCGTCTCCTCA<br>GGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGT<br>AGTACAAAGGGGGAAATTGTGTTGACACAGTCTCCAGCCACC<br>CTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG<br>GCCAGTCAGAGTGTTAGCAGGTACTTAGCCTGGTACCAACAG<br>AAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGATGCATCC<br>AACAGGGCCACTGGCATCCCAGCCAGGTTCAGTGGCAGTGGG<br>TCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCT<br>GAAGATTTTGCAGTTTATTACTGTCAGCAGAGATTCTACTAC<br>CCTTGGACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGG<br>GCCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATT<br>CACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCT<br>GGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGA<br>GTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATA<br>ATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGC<br>GATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGG<br>AAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCTGCC<br>TATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCA<br>GCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAAC<br>CTGGGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGA<br>GGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAAC<br>CCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATG<br>GCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAGA | 191 | MALPVTALLLPLALLLHAA<br>RPEVQLVESGGGLVQPGGS<br>LRLSCAASGFTFSSYSMNW<br>VRQAPGKGLEWVSTISSSS<br>STIYYADSVKGRFTISRDN<br>AKNSLYLQMNSLRAEDTAV<br>YYCARGSQEHLIFDYWGQG<br>TLVTVSSGSTSGSGKPGSG<br>EGSTKGEIVLTQSPATLSL<br>SPGERATLSCRASQSVSRY<br>LAWYQQKPGQAPRLLIYDA<br>SNRATGIPARFSGSGSGTD<br>FTLTISSLEPEDFAVYYCQ<br>QRFYYPWTFGGGTKVEIKR<br>AAALDNEKSNGTIIHVKGK<br>HLCPSPLFPGPSKPFWVLV<br>VVGGVLACYSLLVTVAFII<br>FWVRSKRSRLLHSDYMNMT<br>PRRPGPTRKHYQPYAPPRD<br>FAAYRSRVKFSRSADAPAY<br>QQGQNQLYNELNLGRREEY<br>DVLDKRRGRDPEMGGKPRR<br>KNPQEGLYNELQKDKMAEA<br>YSEIGMKGERRRGKGHDGL<br>YQGLSTATKDTYDALHMQA<br>LPPR | 192 |

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| | AGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACT<br>GCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTG<br>CCACCTAGGTAA | | | |
| TS-<br>21522CAR<br>LxH | ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTG<br>CTCCTGCACGCCGCACGCCCGGAAATTGTGTTGACACAGTCT<br>CCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTC<br>TCCTGCAGGGCCAGTCAGAGTGTTAGCAGGTACTTAGCCTGG<br>TACCAACAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT<br>GATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTCAGT<br>GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGC<br>CTAGAGCCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGA<br>TTCTACTACCCTTGGACTTTTGGCGGAGGGACCAAGGTTGAG<br>ATCAAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGT<br>GGCGAAGGTAGTACAAAGGGGGAGGTGCAGCTGGTGGAGTCT<br>GGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCC<br>TGTGCAGCCTCTGGATTCACCTTCAGTAGCTATAGCATGAAC<br>TGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTTCA<br>ACCATTAGTAGTAGTAGTAGTACCATATACTACGCAGACTCT<br>GTGAAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAAC<br>TCACTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACG<br>GCGGTGTACTACTGCGCCAGAGGTTCTCAGGAGCACCTGATT<br>TTCGATTATTGGGGACAGGGTACATTGGTCACCGTCTCCTCA<br>GCCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATT<br>CACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCT<br>GGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGA<br>GTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATA<br>ATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGC<br>GATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGG<br>AAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCTGCC<br>TATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCA<br>GCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAAC<br>CTGGGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGA<br>GGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAAC<br>CCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATG<br>GCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAGA<br>AGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACT<br>GCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTG<br>CCACCTAGGTAA | 193 | MALPVTALLLPLALLLHAA<br>RPEIVLTQSPATLSLSPGE<br>RATLSCRASQSVSRYLAWY<br>QQKPGQAPRLLIYDASNRA<br>TGIPARFSGSGSGTDFTLT<br>ISSLEPEDFAVYYCQQRFY<br>YPWTFGGGTKVEIKRGSTS<br>GSGKPGSGEGSTKGEVQLV<br>ESGGGLVQPGGSLRLSCAA<br>SGFTFSSYSMNWVRQAPGK<br>GLEWVSTISSSSSTIYYAD<br>SVKGRFTISRDNAKNSLYL<br>QMNSLRAEDTAVYYCARGS<br>QEHLIFDYWGQGTLVTVSS<br>AAALDNEKSNGTIIHVKGK<br>HLCPSPLFPGPSKPFWVLV<br>VVGGVLACYSLLVTVAFII<br>FWVRSKRSRLLHSDYMNMT<br>PRRPGPTRKHYQPYAPPRD<br>FAAYRSRVKFSRSADAPAY<br>QQGQNQLYNELNLGRREEY<br>DVLDKRRGRDPEMGGKPRR<br>KNPQEGLYNELQKDKMAEA<br>YSEIGMKGERRRGKGHDGL<br>YQGLSTATKDTYDALHMQA<br>LPPR | 194 |
| RY-<br>21527CAR<br>HxL | ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTG<br>CTCCTGCACGCCGCACGCCCGCAGGTGCAGCTGGTGGAGTCT<br>GGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC<br>TGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCAC<br>TGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCA<br>GTTATATCGTATGATGGAAGTAATAAATACTATGCAGACTCC<br>GTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAAC<br>ACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACG<br>GCGGTGTACTACTGCGCCAGAACTGACTTCTGGAGCGGATCC<br>CCTCCAGGCTTAGATTACTGGGGACAGGGTACATTGGTCACC<br>GTCTCCTCAGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGT<br>GGCGAAGGTAGTACAAAGGGGGACATCCAGTTGACCCAGTCT<br>CCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATC<br>ACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGG<br>TATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTAT<br>GGTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGC<br>GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGC<br>CTGCAGCCTGAAGATTTTGCAACTTATTACTGTCAGCAGATA<br>TACACCTTCCCTTTCACTTTTGGCGGAGGGACCAAGGTTGAG<br>ATCAAACGGGCCGCTGCCCTTGATAATGAAAAGTCAAACGGA | 195 | MALPVTALLLPLALLLHAA<br>RPQVQLVESGGGVVQPGRS<br>LRLSCAASGFTFSSYGMHW<br>VRQAPGKGLEWVAVISYDG<br>SNKYYADSVKGRFTISRDN<br>SKNTLYLQMNSLRAEDTAV<br>YYCARTDFWSGSPPGLDYW<br>GQGTLVTVSSGSTSGSGKP<br>GSGEGSTKGDIQLTQSPSS<br>VSASVGDRVTITCRASQGI<br>SSWLAWYQQKPGKAPKLLI<br>YGASSLQSGVPSRFSGSGS<br>GTDFTLTISSLQPEDFATY<br>YCQQIYTFPFTFGGGTKVE<br>IKRAAALDNEKSNGTIIHV<br>KGKHLCPSPLFPGPSKPFW<br>VLVVVGGVLACYSLLVTVA<br>FIIFWVRSKRSRLLHSDYM<br>NMTPRRPGPTRKHYQPYAP<br>PRDFAAYRSRVKFSRSADA | 196 |

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| | ACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCC<br>TTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTA<br>GTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTG<br>GCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTG<br>CTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGC<br>CCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGAT<br>TTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCA<br>GATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAAC<br>GAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGAC<br>AAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGA<br>CGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAG<br>GATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGA<br>GAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGA<br>CTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATG<br>CAAGCCCTGCCACCTAGGTAA | | PAYQQGQNQLYNELNLGRR<br>EEYDVLDKRRGRDPEMGGK<br>PRRKNPQEGLYNELQKDKM<br>AEAYSEIGMKGERRRGKGH<br>DGLYQGLSTATKDTYDALH<br>MQALPPR | |
| RY-21527CARLxH | ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTG<br>CTCCTGCACGCCGCACGCCCGGACATCCAGTTGACCCAGTCT<br>CCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATC<br>ACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGG<br>TATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTAT<br>GGTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGC<br>GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGC<br>CTGCAGCCTGAAGATTTTGCAACTTATTACTGTCAGCAGATA<br>TACACCTTCCCTTTCACTTTTGGCGGAGGGACCAAGGTTGAG<br>ATCAAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGT<br>GGCGAAGGTAGTACAAAGGGGCAGGTGCAGCTGGTGGAGTCT<br>GGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC<br>TGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCAC<br>TGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCA<br>GTTATATCGTATGATGGAAGTAATAAATACTATGCAGACTCC<br>GTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAAC<br>ACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACG<br>GCGGTGTACTACTGCGCCAGAACTGACTTCTGGAGCGGATCC<br>CCTCCAGGCTTAGATTACTGGGGACAGGGTACATTGGTCACC<br>GTCTCCTCAGCCGCTGCCCTTGATAATGAAAAGTCAAACGGA<br>ACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCC<br>TTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTA<br>GTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTG<br>GCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTG<br>CTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGC<br>CCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGAT<br>TTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCA<br>GATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAAC<br>GAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGAC<br>AAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGA<br>CGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAG<br>GATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGA<br>GAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGA<br>CTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATG<br>CAAGCCCTGCCACCTAGGTAA | 197 | MALPVTALLLPLALLLHAA<br>RPDIQLTQSPSSVSASVGD<br>RVTITCRASQGISSWLAWY<br>QQKPGKAPKLLIYGASSLQ<br>SGVPSRFSGSGSGTDFTLT<br>ISSLQPEDFATYYCQQIYT<br>FPFTFGGGTKVEIKRGSTS<br>GSGKPGSGEGSTKGQVQLV<br>ESGGGVVQPGRSLRLSCAA<br>SGFTFSSYGMHWVRQAPGK<br>GLEWVAVISYDGSNKYYAD<br>SVKGRFTISRDNSKNTLYL<br>QMNSLRAEDTAVYYCARTD<br>FWSGSPPGLDYWGQGTLVT<br>VSSAAALDNEKSNGTIIHV<br>KGKHLCPSPLFPGPSKPFW<br>VLVVVGGVLACYSLLVTVA<br>FIIFWVRSKRSRLLHSDYM<br>NMTPRRPGPTRKHYQPYAP<br>PRDFAAYRSRVKFSRSADA<br>PAYQQGQNQLYNELNLGRR<br>EEYDVLDKRRGRDPEMGGK<br>PRRKNPQEGLYNELQKDKM<br>AEAYSEIGMKGERRRGKGH<br>DGLYQGLSTATKDTYDALH<br>MQALPPR | 198 |
| PP-21528CARHxL | ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTG<br>CTCCTGCACGCCGCACGCCCGCAGGTGCAGCTGGTGCAGTCT<br>GGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCC<br>TGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGC<br>TGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGA<br>GGGATCATCCCTATCTTTGGTACAGCAAACTACGCACAGAAG<br>TTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGC<br>ACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACG | 199 | MALPVTALLLPLALLLHAA<br>RPQVQLVQSGAEVKKPGSS<br>VKVSCKASGGTFSSYAISW<br>VRQAPGQGLEWMGGIIPIF<br>GTANYAQKFQGRVTITADE<br>STSTAYMELSSLRSEDTAV<br>YYCARTPEYSSSIWHYYYG<br>MDVWGQGTTVTVSSGSTSG | 200 |

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| | GCGGTGTACTACTGCGCCAGAACTCCTGAATACTCCTCCAGC<br>ATATGGCACTATTACTACGGCATGGACGTATGGGGCCAGGGA<br>ACAACTGTCACCGTCTCCTCAGGGTCTACATCCGGCTCCGGG<br>AAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGACATCGTG<br>ATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAG<br>AGGGCCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTATAC<br>AGCTCCAACAATAAGAACTACTTAGCTTGGTACCAGCAGAAA<br>CCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACC<br>CGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCT<br>GGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAA<br>GATGTGGCAGTTTATTACTGTCAGCAGTTCGCCCACACTCCT<br>TTCACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGGCC<br>GCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTCAC<br>GTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGT<br>CCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTC<br>CTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATC<br>TTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGAT<br>TACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAA<br>CACTACCAGCCTTACGCACCACCTAGAGATTTCGCTGCCTAT<br>CGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCG<br>TATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTG<br>GGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGA<br>CGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCC<br>CAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCT<br>GAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGG<br>GGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCT<br>ACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCA<br>CCTAGGTAA | | SGKPGSGEGSTKGDIVMTQ<br>SPDSLAVSLGERATINCKS<br>SQSVLYSSNNKNYLAWYQQ<br>KPGQPPKLLIYWASTRESG<br>VPDRFSGSGSGTDFTLTIS<br>SLQAEDVAVYYCQQFAHTP<br>FTFGGGTKVEIKRAAALDN<br>EKSNGTIIHVKGKHLCPSP<br>LFPGPSKPFWVLVVVGGVL<br>ACYSLLVTVAFIIFWVRSK<br>RSRLLHSDYMNMTPRRPGP<br>TRKHYQPYAPPRDFAAYRS<br>RVKFSRSADAPAYQQGQNQ<br>LYNELNLGRREEYDVLDKR<br>RGRDPEMGGKPRRKNPQEG<br>LYNELQKDKMAEAYSEIGM<br>KGERRRGKGHDGLYQGLST<br>ATKDTYDALHMQALPPR | |
| PP-<br>21528CAR<br>LxH | ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTG<br>CTCCTGCACGCCGCACGCCCGGACATCGTGATGACCCAGTCT<br>CCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATC<br>AACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAAT<br>AAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCT<br>CCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG<br>GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC<br>ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTT<br>TATTACTGTCAGCAGTTCGCCCACACTCCTTTCACTTTTGGC<br>GGAGGGACCAAGGTTGAGATCAAACGGGGGTCTACATCCGGC<br>TCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGCAG<br>GTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGG<br>TCCTCGGTGAAGGTCTCCTGCAAGGCTTCTGGAGGCACCTTC<br>AGCAGCTATGCTATCAGCTGGGTGCGACAGGCCCCTGGACAA<br>GGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACA<br>GCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACC<br>GCGGACGAATCCACGAGCACAGCCTACATGGAGCTGAGCAGC<br>CTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGAACT<br>CCTGAATACTCCTCCAGCATATGGCACTATTACTACGGCATG<br>GACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCAGCC<br>GCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTCAC<br>GTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGT<br>CCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTC<br>CTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATC<br>TTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGAT<br>TACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAA<br>CACTACCAGCCTTACGCACCACCTAGAGATTTCGCTGCCTAT<br>CGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCG<br>TATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTG<br>GGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGA<br>CGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCC | 201 | MALPVTALLLPLALLLHAA<br>RPDIVMTQSPDSLAVSLGE<br>RATINCKSSQSVLYSSNNK<br>NYLAWYQQKPGQPPKLLIY<br>WASTRESGVPDRFSGSGSG<br>TDFTLTISSLQAEDVAVYY<br>CQQFAHTPFTFGGGTKVEI<br>KRGSTSGSGKPGSGEGSTK<br>GQVQLVQSGAEVKKPGSSV<br>KVSCKASGGTFSSYAISWV<br>RQAPGQGLEWMGGIIPIFG<br>TANYAQKFQGRVTITADES<br>TSTAYMELSSLRSEDTAVY<br>YCARTPEYSSSIWHYYYGM<br>DVWGQGTTVTVSSAAALDN<br>EKSNGTIIHVKGKHLCPSP<br>LFPGPSKPFWVLVVVGGVL<br>ACYSLLVTVAFIIFWVRSK<br>RSRLLHSDYMNMTPRRPGP<br>TRKHYQPYAPPRDFAAYRS<br>RVKFSRSADAPAYQQGQNQ<br>LYNELNLGRREEYDVLDKR<br>RGRDPEMGGKPRRKNPQEG<br>LYNELQKDKMAEAYSEIGM<br>KGERRRGKGHDGLYQGLST<br>ATKDTYDALHMQALPPR | 202 |

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| | CAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCT<br>GAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGG<br>GGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCT<br>ACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCA<br>CCTAGGTAA | | | |
| RD-<br>21530CAR<br>HxL | ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTG<br>CTCCTGCACGCCGCACGCCCGCAGGTGCAGCTGGTGGAGTCT<br>GGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC<br>TGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCAC<br>TGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCA<br>GTTATATCGTATGATGGAAGTAATAAATACTATGCAGACTCC<br>GTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAAC<br>ACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACG<br>GCGGTGTACTACTGCGTCAAGGGGCCGTTGCAGGAGCCGCCA<br>TACGATTATGGAATGGACGTATGGGGCCAGGGAACAACTGTC<br>ACCGTCTCCTCAGGGTCTACATCCGGCTCCGGGAAGCCCGGA<br>AGTGGCGAAGGTAGTACAAAGGGGGAAATAGTGATGACGCAG<br>TCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACC<br>CTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCC<br>TGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATC<br>TATAGCGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTC<br>AGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGC<br>AGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAG<br>CACCACGTCTGGCCTCTCACTTTTGGCGGAGGGACCAAGGTT<br>GAGATCAAACGGGCCGCTGCCCTTGATAATGAAAAGTCAAAC<br>GGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCA<br>CCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTC<br>GTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACC<br>GTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGC<br>CTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCT<br>GGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGA<br>GATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCT<br>GCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTAT<br>AACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTG<br>GACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCA<br>AGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAG<br>AAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAA<br>GGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAG<br>GGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCAC<br>ATGCAAGCCCTGCCACCTAGGTAA | 203 | MALPVTALLLPLALLLHAA<br>RPQVQLVESGGGVVQPGRS<br>LRLSCAASGFTFSSYGMHW<br>VRQAPGKGLEWVAVISYDG<br>SNKYYADSVKGRFTISRDN<br>SKNTLYLQMNSLRAEDTAV<br>YYCVKGPLQEPPYDYGMDV<br>WGQGTTVTVSSGSTSGSGK<br>PGSGEGSTKGEIVMTQSPA<br>TLSVSPGERATLSCRASQS<br>VSSNLAWYQQKPGQAPRLL<br>IYSASTRATGIPARFSGSG<br>SGTEFTLTISSLQSEDFAV<br>YYCQQHHVWPLTFGGGTKV<br>EIKRAAALDNEKSNGTIIH<br>VKGKHLCPSPLFPGPSKPF<br>WVLVVVGGVLACYSLLVTV<br>AFIIFWVRSKRSRLLHSDY<br>MNMTPRRPGPTRKHYQPYA<br>PPRDFAAYRSRVKFSRSAD<br>APAYQQGQNQLYNELNLGR<br>REEYDVLDKRRGRDPEMGG<br>KPRRKNPQEGLYNELQKDK<br>MAEAYSEIGMKGERRRGKG<br>HDGLYQGLSTATKDTYDAL<br>HMQALPPR | 204 |
| RD-<br>21530CAR<br>LxH | ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTG<br>CTCCTGCACGCCGCACGCCCGGAAATAGTGATGACGCAGTCT<br>CCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTC<br>TCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGG<br>TACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT<br>AGCGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGT<br>GGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGC<br>CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGCAC<br>CACGTCTGGCCTCTCACTTTTGGCGGAGGGACCAAGGTTGAG<br>ATCAAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGT<br>GGCGAAGGTAGTACAAAGGGGCAGGTGCAGCTGGTGGAGTCT<br>GGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC<br>TGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCAC<br>TGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCA<br>GTTATATCGTATGATGGAAGTAATAAATACTATGCAGACTCC<br>GTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAAC<br>ACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACG<br>GCGGTGTACTACTGCGTCAAGGGGCCGTTGCAGGAGCCGCCA | 205 | MALPVTALLLPLALLLHAA<br>RPEIVMTQSPATLSVSPGE<br>RATLSCRASQSVSSNLAWY<br>QQKPGQAPRLLIYSASTRA<br>TGIPARFSGSGSGTEFTLT<br>ISSLQSEDFAVYYCQQHHV<br>WPLTFGGGTKVEIKRGSTS<br>GSGKPGSGEGSTKGQVQLV<br>ESGGGVVQPGRSLRLSCAA<br>SGFTFSSYGMHWVRQAPGK<br>GLEWVAVISYDGSNKYYAD<br>SVKGRFTISRDNSKNTLYL<br>QMNSLRAEDTAVYYCVKGP<br>LQEPPYDYGMDVWGQGTTV<br>TVSSAAALDNEKSNGTIIH<br>VKGKHLCPSPLFPGPSKPF<br>WVLVVVGGVLACYSLLVTV<br>AFIIFWVRSKRSRLLHSDY | 206 |

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|---|---|---|---|---|
| | TACGATTATGGAATGGACGTATGGGGCCAGGGAACAACTGTC<br>ACCGTCTCCTCAGCCGCTGCCCTTGATAATGAAAAGTCAAAC<br>GGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCA<br>CCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTC<br>GTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACC<br>GTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGC<br>CTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCT<br>GGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGA<br>GATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCT<br>GCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTAT<br>AACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTG<br>GACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCA<br>AGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAG<br>AAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAA<br>GGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAG<br>GGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCAC<br>ATGCAAGCCCTGCCACCTAGGTAA | | MNMTPRRPGPTRKHYQPYA<br>PPRDFAAYRSRVKFSRSAD<br>APAYQQGQNQLYNELNLGR<br>REEYDVLDKRRGRDPEMGG<br>KPRRKNPQEGLYNELQKDK<br>MAEAYSEIGMKGERRRGKG<br>HDGLYQGLSTATKDTYDAL<br>HMQALPPR | |

[0289] 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: 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, and 206. In certain embodiments, the CAR comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, and 206. In one embodiment, the CAR comprises the amino acid sequence of SEQ ID NO: 176. In another embodiment, the CAR comprises the amino acid sequence of SEQ ID NO: 178. In another embodiment, the CAR comprises the amino acid sequence of SEQ ID NO: 180. In another embodiment, the CAR comprises the amino acid sequence of SEQ ID NO: 182. In another embodiment, the CAR comprises the amino acid sequence of SEQ ID NO: 184. In another embodiment, the CAR comprises the amino acid sequence of SEQ ID NO: 186. In another embodiment, the CAR comprises the amino acid sequence of SEQ ID NO: 188. In another embodiment, the CAR comprises the amino acid sequence of SEQ ID NO: 190. In another embodiment, the CAR comprises the amino acid sequence of SEQ ID NO: 192. In another embodiment, the CAR comprises the amino acid sequence of SEQ ID NO: 194. In another embodiment, the CAR comprises the amino acid sequence of SEQ ID NO: 196. In another embodiment, the CAR comprises the amino acid sequence of SEQ ID NO: 198. In another embodiment, the CAR comprises the amino acid sequence of SEQ ID NO: 200. In another embodiment, the CAR comprises the amino acid sequence of SEQ ID NO: 202. In another

embodiment, the CAR comprises the amino acid sequence of SEQ ID NO: 204. In another embodiment, the CAR comprises the amino acid sequence of SEQ ID NO: 206.

[0290] 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: 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205. In certain embodiments, the polynucleotide comprises a nucleotide sequence selected from the group consisting of SEQ ID NOs: 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205. In one embodiment, the polynucleotide comprises the nucleotide sequence of SEQ ID NO: 175. In another embodiment, the polynucleotide comprises the nucleotide sequence of SEQ ID NO: 177. In another embodiment, the polynucleotide comprises the nucleotide sequence of SEQ ID NO: 179. In another embodiment, the polynucleotide comprises the nucleotide sequence of SEQ ID NO: 181. In another embodiment, the polynucleotide comprises the nucleotide sequence of SEQ ID NO: 183. In another embodiment, the polynucleotide comprises the nucleotide sequence of SEQ ID NO: 185. In another embodiment, the polynucleotide comprises the nucleotide sequence of SEQ ID NO: 187. In another embodiment, the polynucleotide comprises the nucleotide sequence of SEQ ID NO: 189. In another embodiment, the polynucleotide comprises the nucleotide sequence of SEQ ID NO: 191. In another embodiment, the polynucleotide comprises the nucleotide sequence of SEQ ID NO: 193. In another embodiment, the polynucleotide comprises the nucleotide sequence of SEQ ID NO: 195. In another embodiment, the polynucleotide comprises the nucleotide sequence of SEQ ID NO: 197. In another embodiment, the polynucleotide comprises the nucleotide sequence of SEQ ID NO: 199. In another embodiment, the polynucleotide comprises the nucleotide sequence of SEQ ID NO: 201. In another embodiment, the polynucleotide comprises the nucleotide sequence of SEQ ID NO: 203. In another embodiment, the polynucleotide comprises the nucleotide sequence of SEQ ID NO: 205.

[0291] In further embodiments, the invention relates to Clone FS-26528 HC DNA (SEQ ID NO: 271) as follows:

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGT
CCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACGACTATGCC

ATGGCATGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAG
CTATTAGTGATGCAGGTGACAGAACATACTACGCAGACTCCGTGAGGGG
CCGGTTCACCATCTCCAGAGACAATTCCAAGAACACACTGTATCTGCAA
ATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCAAGA
GCCGAGATGGGAGCCGTATTCGACATATGGGGTCAGGGTACAATGGTCA
CCGTCTCCTCA

[0292] In further embodiments, the invention relates to the Clone FS-26528 HC amino acid sequence (SEQ ID NO: 272):

EVQLLESGGG LVQPGGSLRL SCAASGFTFD DYAMAWVRQA
PGKGLEWVSA ISDAGDRTYY ADSVRGRFTI SRDNSKNTLY LQMNSLRAED
TAVYYCARAE MGAVFDIWGQ GTMVTVSS

[0293] In further embodiments, the invention relates to HC CDR1 thereof: SCAASGFTFDDYAMA (SEQ ID NO: 273). In further embodiments, the invention relates to HC CDR2 thereof: AISDAGDRTYYADSVRG (SEQ ID NO: 274). In further embodiments, the invention relates to HC CDR3 thereof: ARAEMGAVFDI (SEQ ID NO: 275) [HC CDR3]

[0294] In further embodiments, the invention relates to Clone FS-26528 LC DNA (SEQ ID NO: 276):

GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGA
AAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGGTACTTA
GCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATG
ATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTCAGTGGCAGTGG
GTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGAT
TTTGCAGTTTATTACTGTCAGCAGAGAATCTCCTGGCCTTTCACTTTTGGC
GGAGGGACCAAGGTTGAGATCAAACGG

[0295] In further embodiments, the invention relates to Clone FS-26528 LC AA sequence (SEQ ID NO: 277):

EIVLTQSPAT LSLSPGERAT LSCRASQSVS RYLAWYQQKP GQAPRLLIYD
ASNRATGIPA RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ RISWPFTFGG
GTKVEIKR.

[0296] In further embodiments, the invention relates to LC CDR1 thereof: RASQSVSRYLA (SEQ ID NO: 278). In further embodiments, the invention relates to LC

CDR2 thereof: DASNRAT (SEQ ID NO: 279). In further embodiments, the invention relates to the LC CDR3 thereof: QQRISWPFT (SEQ ID NO: 280).

[0297] In further embodiments, the invention relates to Clone FS-26528 CAR DNA HxL (SEQ ID NO: 281):

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCA
CGCCGCACGCCCGGAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTA
CAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTT
TGACGACTATGCCATGGCATGGGTCCGCCAGGCTCCAGGGAAGGGGCTG
GAGTGGGTCTCAGCTATTAGTGATGCAGGTGACAGAACATACTACGCAG
ACTCCGTGAGGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACAC
ACTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTAC
TACTGCGCAAGAGCCGAGATGGGAGCCGTATTCGACATATGGGGTCAGG
GTACAATGGTCACCGTCTCCTCAGGGTCTACATCCGGCTCCGGGAAGCCC
GGAAGTGGCGAAGGTAGTACAAAGGGGGAAATTGTGTTGACACAGTCTC
CAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG
GCCAGTCAGAGTGTTAGCAGGTACTTAGCCTGGTACCAACAGAAACCTG
GCCAGGCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGG
CATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTC
ACCATCAGCAGCCTAGAGCCTGAAGATTTTGCAGTTTATTACTGTCAGCA
GAGAATCTCCTGGCCTTTCACTTTTGGCGGAGGGACCAAGGTTGAGATC
AAACGGGCCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTC
ACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCC
AAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTC
TCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAA
GCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGC
CCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCTG
CCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTA
TCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGG
GAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATG
GGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAG
CTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAG
GAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCA

GCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCC
ACCTAGG

[0298] In further embodiments, the invention relates to Clone FS-26528 CAR HxL AA sequence (SEQ ID NO: 282):

MALPVTALLL PLALLLHAAR PEVQLLESGG GLVQPGGSLR LSCAASGFTF DDYAMAWVRQ APGKGLEWVS AISDAGDRTY YADSVRGRFT ISRDNSKNTL YLQMNSLRAE DTAVYYCARA EMGAVFDIWG QGTMVTVSSG STSGSGKPGS GEGSTKGEIV LTQSPATLSL SPGERATLSC RASQSVSRYL AWYQQKPGQA PRLLIYDASN RATGIPARFS GSGSGTDFTL TISSLEPEDF AVYYCQQRIS WPFTFGGGTK VEIKRAAALD NEKSNGTIIH VKGKHLCPSP LFPGPSKPFW VLVVVGGVLA CYSLLVTVAF IIFWVRSKRS RLLHSDYMNM TPRRPGPTRK HYQPYAPPRD FAAYRSRVKF SRSADAPAYQ QGQNQLYNEL NLGRREEYDV LDKRRGRDPE MGGKPRRKNP QEGLYNELQK DKMAEAYSEI GMKGERRRGK GHDGLYQGLS TATKDTYDAL HMQALPPR

[0299] In further embodiments, the invention relates to Clone FS-26528 CAR DNA LxH (SEQ ID NO: 283):

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCA
CGCCGCACGCCCGGAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTT
TGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGT
TAGCAGGTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGG
CTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTT
CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTA
GAGCCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGAATCTCCTGGCC
TTTCACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGGGGTCTACA
TCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGAG
GTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCC
TGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACGACTATGCCATG
GCATGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTA
TTAGTGATGCAGGTGACAGAACATACTACGCAGACTCCGTGAGGGGCCG
GTTCACCATCTCCAGAGACAATTCCAAGAACACACTGTATCTGCAAATG
AACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCAAGAGCC
GAGATGGGAGCCGTATTCGACATATGGGGTCAGGGTACAATGGTCACCG

TCTCCTCAGCCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATT
CACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATC
CAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACT
CTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGA
AGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGG
CCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCT
GCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGT
ATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAG
GGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGAT
GGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGA
GCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAA
GGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTC
AGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGC
CACCTAGG

[0300] In further embodiments, the invention relates to the Clone FS-26528 CAR LxH AA sequence (SEQ ID NO: 284):

MALPVTALLL PLALLLHAAR PEIVLTQSPA TLSLSPGERA TLSCRASQSV SRYLAWYQQK PGQAPRLLIY DASNRATGIP ARFSGSGSGT DFTLTISSLE PEDFAVYYCQ QRISWPFTFG GGTKVEIKRG STSGSGKPGS GEGSTKGEVQ LLESGGGLVQ PGGSLRLSCA ASGFTFDDYA MAWVRQAPGK GLEWVSAISD AGDRTYYADS VRGRFTISRD NSKNTLYLQM NSLRAEDTAV YYCARAEMGA VFDIWGQGTM VTVSSAAALD NEKSNGTIIH VKGKHLCPSP LFPGPSKPFW VLVVVGGVLA CYSLLVTVAF IIFWVRSKRS RLLHSDYMNM TPRRPGPTRK HYQPYAPPRD FAAYRSRVKF SRSADAPAYQ QGQNQLYNEL NLGRREEYDV LDKRRGRDPE MGGKPRRKNP QEGLYNELQK DKMAEAYSEI GMKGERRRGK GHDGLYQGLS TATKDTYDAL HMQALPPR

[0301] In further embodiments, the invention relates to Clone PC-26534 HC DNA (SEQ ID NO: 285) as follows:

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGT
CCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTGAGCATGGC
ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAG
CTATATCTTATGATGGAAGGAATAAACACTATGCAGACTCCGTGAAGGG

CCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAA
ATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCCAGAG
ACGGTACTTATCTAGGTGGTCTCTGGTACTTCGACTTATGGGGGAGAGGT
ACCTTGGTCACCGTCTCCTCA

[0302] In further embodiments, the invention relates to Clone PC-26534 HC (SEQ ID NO: 286):

QVQLVESGGG VVQPGRSLRL SCAASGFTFS EHGMHWVRQA
PGKGLEWVAA ISYDGRNKHY ADSVKGRFTI SRDNSKNTLY
LQMNSLRAED TAVYYCARDG TYLGGLWYFD LWGRGTLVTV SS.

[0303] In further embodiments, the invention relates to HC CDR1 thereof: FTFSEHGMH (SEQ ID NO: 287). In further embodiments, the invention relates to HC CDR2 thereof: AISYDGRNKHYADSVKG (SEQ ID NO: 288). In further embodiments, the invention relates to HC CDR3 thereof: ARDGTYLGGLWYFDL (SEQ ID NO: 289).

[0304] In further embodiments, the invention relates to Clone PC-26534 LC DNA (SEQ ID NO: 290) as follows:

GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGA
GCCGGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATG
GATACAACTATTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACA
GCTCCTGATCTATTTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGGT
TCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGT
GGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAGGGACTCGGCCTC
CCTCTCACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGG

[0305] In further embodiments, the invention relates to Clone PC-26534 LC AA sequence (SEQ ID NO: 291):

DIVMTQSPLS LPVTPGEPAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ
LLIYLGSNRA SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQGLGLP
LTFGGGTKVE IKR.

[0306] In further embodiments, the invention relates to LC CDR1 AA sequence thereof: RSSQSLLHSNGYNYLD (SEQ ID NO: 292). In further embodiments, the invention relates to LC CDR2 thereof: LGSNRAS (SEQ ID NO: 293). In further embodiments, the invention relates to LC CDR3 thereof: MQGLGLPLT (SEQ ID NO: 294).

[0307] In further embodiments, the invention relates to Clone PC-26534 CAR DNA HxL (SEQ ID NO: 295) as follows:

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCA
CGCCGCACGCCCGCAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTC
CAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTT
CAGTGAGCATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTG
GAGTGGGTGGCAGCTATATCTTATGATGGAAGGAATAAACACTATGCAG
ACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACAC
GCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTAC
TACTGCGCCAGAGACGGTACTTATCTAGGTGGTCTCTGGTACTTCGACTT
ATGGGGGAGAGGTACCTTGGTCACCGTCTCCTCAGGGTCTACATCCGGCT
CCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGATATTGTGA
TGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCC
ATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACAACTA
TTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCT
ATTTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTCAGTGGCAGT
GGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGGCTGAGG
ATGTTGGGGTTTATTACTGCATGCAGGGACTCGGCCTCCCTCTCACTTTT
GGCGGAGGGACCAAGGTTGAGATCAAACGGGCCGCTGCCCTTGATAATG
AAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCC
GTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAG
TGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAA
TCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATG
AATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTT
ACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCC
AGATCTGCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATA
ACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGACAAGCG
CAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCC
CCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCC
TATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCAC
GACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATGACG
CTCTCCACATGCAAGCCCTGCCACCTAGG

[0308] In further embodiments, the invention relates to Clone PC-26534 CAR HxL AA sequence (SEQ ID NO: 296):

MALPVTALLL PLALLLHAAR PQVQLVESGG GVVQPGRSLR LSCAASGFTF SEHGMHWVRQ APGKGLEWVA AISYDGRNKH YADSVKGRFT ISRDNSKNTL YLQMNSLRAE DTAVYYCARD GTYLGGLWYF DLWGRGTLVT VSSGSTSGSG KPGSGEGSTK GDIVMTQSPL SLPVTPGEPA SISCRSSQSL LHSNGYNYLD WYLQKPGQSP QLLIYLGSNR ASGVPDRFSG SGSGTDFTLK ISRVEAEDVG VYYCMQGLGL PLTFGGGTKV EIKRAAALDN EKSNGTIIHV KGKHLCPSPL FPGPSKPFWV LVVVGGVLAC YSLLVTVAFI IFWVRSKRSR LLHSDYMNMT PRRPGPTRKH YQPYAPPRDF AAYRSRVKFS RSADAPAYQQ GQNQLYNELN LGRREEYDVL DKRRGRDPEM GGKPRRKNPQ EGLYNELQKD KMAEAYSEIG MKGERRRGKG HDGLYQGLST ATKDTYDALH MQALPPR

[0309] In further embodiments, the invention relates to Clone PC-26534 CAR DNA LxH (SEQ ID NO: 297):

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCA
CGCCGCACGCCCGGATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCG
TCACCCCTGGAGAGCCGGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTC
CTGCATAGTAATGGATACAACTATTTGGATTGGTACCTGCAGAAGCCAG
GGCAGTCTCCACAGCTCCTGATCTATTTGGGTTCTAATCGGGCCTCCGGG
GTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGA
AAATCAGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCA
GGGACTCGGCCTCCCTCTCACTTTTGGCGGAGGGACCAAGGTTGAGATC
AAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGT
AGTACAAAGGGGCAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTC
CAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTT
CAGTGAGCATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTG
GAGTGGGTGGCAGCTATATCTTATGATGGAAGGAATAAACACTATGCAG
ACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACAC
GCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTAC
TACTGCGCCAGAGACGGTACTTATCTAGGTGGTCTCTGGTACTTCGACTT
ATGGGGGAGAGGTACCTTGGTCACCGTCTCCTCAGCCGCTGCCCTTGATA
ATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTG
TCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGT
AGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTAT

AATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTAC
ATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGC
CTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTT
TCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGT
ATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGACAA
GCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAA
CCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAA
GCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGG
CACGACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATG
ACGCTCTCCACATGCAAGCCCTGCCACCTAGG

[0310] In further embodiments, the invention relates to Clone PC-26534 CAR LxH chain sequences (SEQ ID NO: 298):

MALPVTALLL PLALLLHAAR PDIVMTQSPL SLPVTPGEPA SISCRSSQSL LHSNGYNYLD WYLQKPGQSP QLLIYLGSNR ASGVPDRFSG SGSGTDFTLK ISRVEAEDVG VYYCMQGLGL PLTFGGGTKV EIKRGSTSGS GKPGSGEGST KGQVQLVESG GGVVQPGRSL RLSCAASGFT FSEHGMHWVR QAPGKGLEWV AAISYDGRNK HYADSVKGRF TISRDNSKNT LYLQMNSLRA EDTAVYYCAR DGTYLGGLWY FDLWGRGTLV TVSSAAALDN EKSNGTIIHV KGKHLCPSPL FPGPSKPFWV LVVVGGVLAC YSLLVTVAFI IFWVRSKRSR LLHSDYMNMT PRRPGPTRKH YQPYAPPRDF AAYRSRVKFS RSADAPAYQQ GQNQLYNELN LGRREEYDVL DKRRGRDPEM GGKPRRKNPQ EGLYNELQKD KMAEAYSEIG MKGERRRGKG HDGLYQGLST ATKDTYDALH MQALPPR

[0311] In further embodiments, the invention relates to Clone AJ-26545 HC DNA (SEQ ID NO: 299):

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCT
CAGTGAAGGTTTCCTGCAGGGCATCTGGATACACCTTCATGGAGCACTAT
ATGCACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAG
TAATCGGGCCTAGTGGTGGTAAGACAAGCTACGCACAGAAGTTCCAGGG
CAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAG
CTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGAG
AGAATTGGCCAATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTC
CTCA

[0312] In further embodiments, the invention relates to Clone AJ-26545 HC AA sequence (SEQ ID NO: 300):

QVQLVQSGAE VKKPGASVKV SCRASGYTFM EHYMHWVRQA PGQGLEWMGV IGPSGGKTSY AQKFQGRVTM TRDTSTSTVY MELSSLRSED TAVYYCARES WPMDVWGQGT TVTVSS.

[0313] In further embodiments, the invention relates to HC CDR1 thereof: YTFMEHYMH (SEQ ID NO: 301). In further embodiments, the invention relates to HC CDR2 thereof: VIGPSGGKTSYAQKFQG (SEQ ID NO: 302). In further embodiments, the invention relates to HC CDR3 thereof: ARESWPMDV (SEQ ID NO: 303).

[0314] In further embodiments, the invention relates to Clone AJ-26545 LC DNA (SEQ ID NO: 304):

GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGG AAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTT AGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT GGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGTGGCAGTG GGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGA TTTTGCAGTTTATTACTGTCAGCAGTACGCCGCCTACCCTACTTTTGGCG GAGGGACCAAGGTTGAGATCAAACGG

[0315] In further embodiments, the invention relates to Clone AJ-26545 LC AA sequence (SEQ ID NO: 305):

EIVMTQSPAT LSVSPGERAT LSCRASQSVS SNLAWYQQKP GQAPRLLIYG ASTRATGIPA RFSGSGSGTE FTLTISSLQS EDFAVYYCQQ YAAYPTFGGG TKVEIKR.

[0316] In further embodiments, the invention relates to LC CDR1 thereof: RASQSVSSNLA (SEQ ID NO: 306). In further embodiments, the invention relates to LC CDR2 thereof: GASTRAT (SEQ ID NO: 307). In further embodiments, the invention relates to the LC CDR3 thereof: QQYAAYPT (SEQ ID NO: 308).

[0317] In further embodiments, the invention relates to Clone AJ-26545 CAR DNA HxL (SEQ ID NO: 309):

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCA CGCCGCACGCCCGCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAG AAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAGGGCATCTGGATACACCT TCATGGAGCACTATATGCACTGGGTGCGACAGGCCCCTGGACAAGGGCT

TGAGTGGATGGGAGTAATCGGGCCTAGTGGTGGTAAGACAAGCTACGCA
CAGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCA
CAGTCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTA
CTACTGCGCCAGAGAGAATTGGCCAATGGACGTATGGGGCCAGGGAACA
ACTGTCACCGTCTCCTCAGGGTCTACATCCGGCTCCGGGAAGCCCGGAA
GTGGCGAAGGTAGTACAAAGGGGGAAATAGTGATGACGCAGTCTCCAG
CCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCC
AGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCC
AGGCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGTATC
CCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCA
TCAGCAGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTAC
GCCGCCTACCCTACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGG
CCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGAA
GGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCAT
TCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTC
GTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCT
GCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACA
AGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCTGCCTATC
GGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCA
GGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGA
GTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGC
AAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAG
AAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAG
CGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACT
GCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTA
GG

[0318] In further embodiments, the invention relates to Clone AJ-26545 CAR HxL AA sequence (SEQ ID NO: 310):

MALPVTALLL PLALLLHAAR PQVQLVQSGA EVKKPGASVK
VSCRASGYTF MEHYMHWVRQ APGQGLEWMG VIGPSGGKTS
YAQKFQGRVT MTRDTSTSTV YMELSSLRSE DTAVYYCARE
SWPMDVWGQG TTVTVSSGST SGSGKPGSGE GSTKGEIVMT QSPATLSVSP
GERATLSCRA SQSVSSNLAW YQQKPGQAPR LLIYGASTRA TGIPARFSGS

GSGTEFTLTI SSLQSEDFAV YYCQQYAAYP TFGGGTKVEI KRAAALDNEK
SNGTIIHVKG KHLCPSPLFP GPSKPFWVLV VVGGVLACYS LLVTVAFIIF
WVRSKRSRLL HSDYMNMTPR RPGPTRKHYQ PYAPPRDFAA
YRSRVKFSRS ADAPAYQQGQ NQLYNELNLG RREEYDVLDK
RRGRDPEMGG KPRRKNPQEG LYNELQKDKM AEAYSEIGMK
GERRRGKGHD GLYQGLSTAT KDTYDALHMQ ALPPR

[0319] In further embodiments, the invention relates to Clone AJ-26545 CAR DNA LxH (SEQ ID NO: 311):

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCA
CGCCGCACGCCCGGAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT
GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTG
TTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAG
GCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGT
TCAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCT
GCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACGCCGCCTACC
CTACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGGGGTCTACATC
CGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGCAGGT
GCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTG
AAGGTTTCCTGCAGGGCATCTGGATACACCTTCATGGAGCACTATATGCA
CTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAGTAATC
GGGCCTAGTGGTGGTAAGACAAGCTACGCACAGAAGTTCCAGGGCAGA
GTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGA
GCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGAGAGAA
TTGGCCAATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA
GCCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGA
AGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCA
TTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTC
GTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCT
GCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACA
AGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCTGCCTATC
GGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCA
GGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGA
GTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGC

AAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAG
AAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAG
CGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACT
GCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTA
GG

[0320] In further embodiments, the invention relates to Clone AJ-26545 CAR LxH AA sequence (SEQ ID NO: 312):

MALPVTALLL PLALLLHAAR PEIVMTQSPA TLSVSPGERA TLSCRASQSV
SSNLAWYQQK PGQAPRLLIY GASTRATGIP ARFSGSGSGT EFTLTISSLQ
SEDFAVYYCQ QYAAYPTFGG GTKVEIKRGS TSGSGKPGSG EGSTKGQVQL
VQSGAEVKKP GASVKVSCRA SGYTFMEHYM HWVRQAPGQG
LEWMGVIGPS GGKTSYAQKF QGRVTMTRDT STSTVYMELS
SLRSEDTAVY YCARESWPMD VWGQGTTVTV SSAAALDNEK
SNGTIIHVKG KHLCPSPLFP GPSKPFWVLV VVGGVLACYS LLVTVAFIIF
WVRSKRSRLL HSDYMNMTPR RPGPTRKHYQ PYAPPRDFAA
YRSRVKFSRS ADAPAYQQGQ NQLYNELNLG RREEYDVLDK
RRGRDPEMGG KPRRKNPQEG LYNELQKDKM AEAYSEIGMK
GERRRGKGHD GLYQGLSTAT KDTYDALHMQ ALPPR

[0321] In further embodiments, the invention relates to Clone AJ-26554 HC DNA (SEQ ID NO: 313):

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCT
CAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACGGAGCACTA
TATGCACTGGGTGCGACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGA
GTAATCGGGCCTAGTGGTGGTAAGACAAGCTACGCACAGAAGTTCCAGG
GCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGA
GCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGA
GAGAGTTGGCCAATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCT
CCTCA

[0322] In further embodiments, the invention relates to Clone AJ-26554 HC (SEQ ID NO: 314): QVQLVQSGAE VKKPGASVKV SCKASGYTFT EHYMHWVRQA PGQRLEWMGV IGPSGGKTSY AQKFQGRVTM TRDTSTSTVY MELSSLRSED TAVYYCARES WPMDVWGQGT TVTVSS

[0323] In further embodiments, the invention relates to HC CDR1 thereof: YTFTEHYMH (SEQ ID NO: 315). In further embodiments, the invention relates to HC CDR2 thereof: VIGPSGGKTSYAQKFQG (SEQ ID NO: 316). In further embodiments, the invention relates to HC CDR3 thereof: ARESWPMDV (SEQ ID NO: 317).

[0324] In further embodiments, the invention relates to Clone AJ-26554 LC DNA (SEQ ID NO: 318):

GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGG
AAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTT
AGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT
GGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGTGGCAGTG
GGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGA
TTTTGCAGTTTATTACTGTCAGCAGTACGCCGCCTACCCTACTTTTGGCG
GAGGGACCAAGGTTGAGATCAAACGG

[0325] In further embodiments, the invention relates to Clone AJ-26554 LC AA sequence (SEQ ID NO: 319): EIVMTQSPAT LSVSPGERAT LSCRASQSVS SNLAWYQQKP GQAPRLLIYG ASTRATGIPA RFSGSGSGTE FTLTISSLQS EDFAVYYCQQ YAAYPTFGGG TKVEIKR.

[0326] In further embodiments, the invention relates to the LC CDR1 thereof: RASQSVSSNLA (SEQ ID NO: 320). In further embodiments, the invention relates to the LC CDR2 thereof: GASTRAT (SEQ ID NO: 321). In further embodiments, the invention relates to LC CDR3 thereof: QQYAAYPT (SEQ ID NO: 322).

[0327] In further embodiments, the invention relates to Clone AJ-26554 CAR DNA HxL (SEQ ID NO: 323):

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCA
CGCCGCACGCCCGCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAG
AAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCT
TCACGGAGCACTATATGCACTGGGTGCGACAGGCCCCTGGACAAAGGCT
TGAGTGGATGGGAGTAATCGGGCCTAGTGGTGGTAAGACAAGCTACGCA
CAGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCA
CAGTCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTA
CTACTGCGCCAGAGAGAGTTGGCCAATGGACGTATGGGGCCAGGGAACA
ACTGTCACCGTCTCCTCAGGGTCTACATCCGGCTCCGGGAAGCCCGGAA
GTGGCGAAGGTAGTACAAAGGGGGAAATAGTGATGACGCAGTCTCCAG

CCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCC
AGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCC
AGGCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGTATC
CCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCA
TCAGCAGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTAC
GCCGCCTACCCTACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGG
CCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGAA
GGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCAT
TCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTC
GTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCT
GCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACA
AGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCTGCCTATC
GGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCA
GGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGA
GTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGC
AAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAG
AAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAG
CGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACT
GCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTA
GG

[0328] In further embodiments, the invention relates to Clone AJ-26554 CAR HxL AA sequence (SEQ ID NO: 324):

MALPVTALLL PLALLLHAAR PQVQLVQSGA EVKKPGASVK
VSCKASGYTF TEHYMHWVRQ APGQRLEWMG VIGPSGGKTS
YAQKFQGRVT MTRDTSTSTV YMELSSLRSE DTAVYYCARE
SWPMDVWGQG TTVTVSSGST SGSGKPGSGE GSTKGEIVMT QSPATLSVSP
GERATLSCRA SQSVSSNLAW YQQKPGQAPR LLIYGASTRA TGIPARFSGS
GSGTEFTLTI SSLQSEDFAV YYCQQYAAYP TFGGGTKVEI KRAAALDNEK
SNGTIIHVKG KHLCPSPLFP GPSKPFWVLV VVGGVLACYS LLVTVAFIIF
WVRSKRSRLL HSDYMNMTPR RPGPTRKHYQ PYAPPRDFAA
YRSRVKFSRS ADAPAYQQGQ NQLYNELNLG RREEYDVLDK
RRGRDPEMGG KPRRKNPQEG LYNELQKDKM AEAYSEIGMK
GERRRGKGHD GLYQGLSTAT KDTYDALHMQ ALPPR.

[0329] In further embodiments, the invention relates to Clone AJ-26554 CAR DNA LxH (SEQ ID NO: 325):

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCA
CGCCGCACGCCCGGAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT
GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTG
TTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAG
GCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGT
TCAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCT
GCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACGCCGCCTACC
CTACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGGGGTCTACATC
CGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGCAGGT
GCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTG
AAGGTTTCCTGCAAGGCATCTGGATACACCTTCACGGAGCACTATATGC
ACTGGGTGCGACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGAGTAAT
CGGGCCTAGTGGTGGTAAGACAAGCTACGCACAGAAGTTCCAGGGCAGA
GTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGA
GCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGAGAGAG
TTGGCCAATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA
GCCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGA
AGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCA
TTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTC
GTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCT
GCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACA
AGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCTGCCTATC
GGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCA
GGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGA
GTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGC
AAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAG
AAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAG
CGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACT
GCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTA
GG

[0330]

[0331] In further embodiments, the invention relates to Clone AJ-26554 CAR LxH AA sequence (SEQ ID NO: 326):

MALPVTALLL PLALLLHAAR PEIVMTQSPA TLSVSPGERA TLSCRASQSV SSNLAWYQQK PGQAPRLLIY GASTRATGIP ARFSGSGSGT EFTLTISSLQ SEDFAVYYCQ QYAAYPTFGG GTKVEIKRGS TSGSGKPGSG EGSTKGQVQL VQSGAEVKKP GASVKVSCKA SGYTFTEHYM HWVRQAPGQR LEWMGVIGPS GGKTSYAQKF QGRVTMTRDT STSTVYMELS SLRSEDTAVY YCARESWPMD VWGQGTTVTV SSAAALDNEK SNGTIIHVKG KHLCPSPLFP GPSKPFWVLV VVGGVLACYS LLVTVAFIIF WVRSKRSRLL HSDYMNMTPR RPGPTRKHYQ PYAPPRDFAA YRSRVKFSRS ADAPAYQQGQ NQLYNELNLG RREEYDVLDK RRGRDPEMGG KPRRKNPQEG LYNELQKDKM AEAYSEIGMK GERRRGKGHD GLYQGLSTAT KDTYDALHMQ ALPPR

[0332] In further embodiments, the invention relates to Clone NM-26562 HC DNA (SEQ ID NO: 327):

CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGA CCCTGTCCCTCACCTGTACTGTCTCTGGTGGCTCCATCGGGAGTGGTGGT AGTTACTGGAGCTGGATCCGCCAGCACCCAGGGAAGGGCCTGGAGTGGA TTGGGTTGATCTATTACGATGGGAGCACCTACTACAACCCGTCCCTCAAG AGTCGAGTTACCATATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGA AGCTGAGTTCTGTGACCGCCGCAGACACGGCGGTGTACTACTGCGCCAG AGGCAGGGGATATGAGACTTCTTTAGCCTTCGATATCTGGGGTCAGGGT ACAATGGTCACCGTCTCCTCA

[0333] In further embodiments, the invention relates to Clone NM-26562 HC AA sequence (SEQ ID NO: 328): QVQLQESGPG LVKPSQTLSL TCTVSGGSIG SGGSYWSWIR QHPGKGLEWI GLIYYDGSTY YNPSLKSRVT ISVDTSKNQF SLKLSSVTAA DTAVYYCARG RGYETSLAFD IWGQGTMVTV SS.

[0334] In further embodiments, the invention relates to HC CDR1 thereof: GSIGSGGSYWS (SEQ ID NO: 329). In further embodiments, the invention relates to HC CDR2 thereof: LIYYDGSTYYNPSLKS (SEQ ID NO: 330). In further embodiments, the invention relates to HC CDR3 thereof: ARGRGYETSLAFDI (SEQ ID NO: 331).

[0335] In further embodiments, the invention relates to Clone NM-26562 LC DNA (SEQ ID NO: 332):

GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGA
AAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCTACTTA
GCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATG
ATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTCAGTGGCAGTGG
GTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGAT
TTTGCAGTTTATTACTGTCAGCAGAGACACGTCTGGCCTCCTACTTTTGG
CGGAGGGACCAAGGTTGAGATCAAACGG

[0336] In further embodiments, the invention relates to Clone NM-26562 LC AA sequence (SEQ ID NO: 333):

EIVLTQSPAT LSLSPGERAT LSCRASQSVS SYLAWYQQKP GQAPRLLIYD ASNRATGIPA RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ RHVWPPTFGG GTKVEIKR

[0337] In further embodiments, the invention relates to LC CDR1 AA sequence thereof: RASQSVSSYLA (SEQ ID NO: 334) In further embodiments, the invention relates to LC CDR2 AA sequence thereof: DASNRAT (SEQ ID NO: 335). In further embodiments, the invention relates to LC CDR3 AA sequence thereof: QQRHVWPPT (SEQ ID NO: 336) (LC CDR3).

[0338] In further embodiments, the invention relates to Clone NM-26562 CAR DNA HxL (SEQ ID NO: 337):

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCA
CGCCGCACGCCCGCAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTG
AAGCCTTCACAGACCCTGTCCCTCACCTGTACTGTCTCTGGTGGCTCCAT
CGGGAGTGGTGGTAGTTACTGGAGCTGGATCCGCCAGCACCCAGGGAAG
GGCCTGGAGTGGATTGGGTTGATCTATTACGATGGGAGCACCTACTACA
ACCCGTCCCTCAAGAGTCGAGTTACCATATCAGTAGACACGTCTAAGAA
CCAGTTCTCCCTGAAGCTGAGTTCTGTGACCGCCGCAGACACGGCGGTGT
ACTACTGCGCCAGAGGCAGGGGATATGAGACTTCTTTAGCCTTCGATATC
TGGGGTCAGGGTACAATGGTCACCGTCTCCTCAGGGTCTACATCCGGCTC
CGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGAAATTGTGTT
GACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACC
CTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCTACTTAGCCTGGTACCA
ACAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGATGCATCCAAC
AGGGCCACTGGCATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAG

ACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGATTTTGCAGTTTAT
TACTGTCAGCAGAGACACGTCTGGCCTCCTACTTTTGGCGGAGGGACCA
AGGTTGAGATCAAACGGGCCGCTGCCCTTGATAATGAAAAGTCAAACGG
AACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCC
CTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTC
GCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGA
TCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCAC
GCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAG
AGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATG
CACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCT
GGGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGA
CCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCT
CTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATA
GGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTAC
CAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGC
AAGCCCTGCCACCTAGG.

[0339] In further embodiments, the invention relates to Clone NM-26562 CAR HxL (SEQ ID NO: 338):

MALPVTALLL PLALLLHAAR PQVQLQESGP GLVKPSQTLS LTCTVSGGSI GSGGSYWSWI RQHPGKGLEW IGLIYYDGST YYNPSLKSRV TISVDTSKNQ FSLKLSSVTA ADTAVYYCAR GRGYETSLAF DIWGQGTMVT VSSGSTSGSG KPGSGEGSTK GEIVLTQSPA TLSLSPGERA TLSCRASQSV SSYLAWYQQK PGQAPRLLIY DASNRATGIP ARFSGSGSGT DFTLTISSLE PEDFAVYYCQ QRHVWPPTFG GGTKVEIKRA AALDNEKSNG TIIHVKGKHL CPSPLFPGPS KPFWVLVVVG GVLACYSLLV TVAFIIFWVR SKRSRLLHSD YMNMTPRRPG PTRKHYQPYA PPRDFAAYRS RVKFSRSADA PAYQQGQNQL YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR.

[0340]

[0341] In further embodiments, the invention relates to Clone NM-26562 CAR DNA LxH (SEQ ID NO: 339):

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCA
CGCCGCACGCCCGGAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTT
TGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGT
TAGCAGCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGG
CTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTT
CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTA
GAGCCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGACACGTCTGGCC
TCCTACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGGGGTCTACA
TCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGCAG
GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGACCC
TGTCCCTCACCTGTACTGTCTCTGGTGGCTCCATCGGGAGTGGTGGTAGT
TACTGGAGCTGGATCCGCCAGCACCCAGGGAAGGGCCTGGAGTGGATTG
GGTTGATCTATTACGATGGGAGCACCTACTACAACCCGTCCCTCAAGAGT
CGAGTTACCATATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAAGCT
GAGTTCTGTGACCGCCGCAGACACGGCGGTGTACTACTGCGCCAGAGGC
AGGGGATATGAGACTTCTTTAGCCTTCGATATCTGGGGTCAGGGTACAAT
GGTCACCGTCTCCTCAGCCGCTGCCCTTGATAATGAAAAGTCAAACGGA
ACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCC
TGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCG
CTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGAT
CCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACG
CCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGA
GATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGC
ACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTG
GGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGAC
CCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCT
ATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGG
CATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCA
GGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAA
GCCCTGCCACCTAGG

[0342] In further embodiments, the invention relates to Clone NM-26562 CAR LxH (SEQ ID NO: 340):

MALPVTALLL PLALLLHAAR PEIVLTQSPA TLSLSPGERA TLSCRASQSV SSYLAWYQQK PGQAPRLLIY DASNRATGIP ARFSGSGSGT DFTLTISSLE PEDFAVYYCQ QRHVWPPTFG GGTKVEIKRG STSGSGKPGS GEGSTKGQVQ LQESGPGLVK PSQTLSLTCT VSGGSIGSGG SYWSWIRQHP GKGLEWIGLI YYDGSTYYNP SLKSRVTISV DTSKNQFSLK LSSVTAADTA VYYCARGRGY ETSLAFDIWG QGTMVTVSSA AALDNEKSNG TIIHVKGKHL CPSPLFPGPS KPFWVLVVVG GVLACYSLLV TVAFIIFWVR SKRSRLLHSD YMNMTPRRPG PTRKHYQPYA PPRDFAAYRS RVKFSRSADA PAYQQGQNQL YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR

[0343] In further embodiments, the invention relates to Clone TS-26564 HC DNA sequence (SEQ ID NO: 341):

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGT CCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATAGC ATGAACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTTCAA CCATTAGTAGTAGTAGTAGTATCATATACTACGCAGACTCTGTGAAGGG CCGATTCACCATCTCCAGAGACAATGCCAAGAACTCACTGTATCTGCAA ATGAACAGCCTGAGAGCTGAGGACACGGCGGTGTACTACTGCGCCAGAG GTTCTCAGGAGCACCTGATTTTCGATTATTGGGGACAGGGTACATTGGTC ACCGTCTCCTCA

[0344] In further embodiments, the invention relates to Clone TS-26564 HC AA sequence (SEQ ID NO: 342): EVQLVESGGG LVQPGGSLRL SCAASGFTFS SYSMNWVRQA PGKGLEWVST ISSSSSIIYY ADSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARGS QEHLIFDYWG QGTLVTVSS

[0345] In further embodiments, the invention relates to HC CDR1 AA sequence thereof: FTFSSYSMN (SEQ ID NO: 343). In further embodiments, the invention relates to HC CDR2 AA sequence thereof: TISSSSSIIYYADSVKG (SEQ ID NO: 344). In further embodiments, the invention relates to HC CDR3 AA sequence thereof: ARGSQEHLIFDY (SEQ ID NO: 345).

[0346] In further embodiments, the invention relates to Clone TS-26564 LC DNA (SEQ ID NO: 346):

GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGA
AAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGGTACTTA
GCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATG
ATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTCAGTGGCAGTGG
GTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGAT
TTTGCAGTTTATTACTGTCAGCAGAGATTCTACTACCCTTGGACTTTTGGC
GGAGGGACCAAGGTTGAGATCAAACGG

[0347] In further embodiments, the invention relates to Clone TS-26564 LC AA sequence (SEQ ID NO: 347):

EIVLTQSPAT LSLSPGERAT LSCRASQSVS RYLAWYQQKP GQAPRLLIYD ASNRATGIPA RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ RFYYPWTFGG GTKVEIKR.

[0348] In further embodiments, the invention relates to LC CDR1 AA sequence thereof: RASQSVSRYLA (SEQ ID NO: 348). In further embodiments, the invention relates to LC CDR2 AA sequence thereof: DASNRAT (SEQ ID NO: 349). In further embodiments, the invention relates to LC CDR3 AA sequence thereof: QQRFYYPWT (SEQ ID NO: 350).

[0349] In further embodiments, the invention relates to Clone TS-26564 CAR DNA HxL (SEQ ID NO: 351):

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCA
CGCCGCACGCCCGGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTA
CAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTT
CAGTAGCTATAGCATGAACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTG
GAGTGGGTTTCAACCATTAGTAGTAGTAGTAGTATCATATACTACGCAG
ACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACTC
ACTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCGGTGTAC
TACTGCGCCAGAGGTTCTCAGGAGCACCTGATTTTCGATTATTGGGGACA
GGGTACATTGGTCACCGTCTCCTCAGGGTCTACATCCGGCTCCGGGAAGC
CCGGAAGTGGCGAAGGTAGTACAAAGGGGGAAATTGTGTTGACACAGTC
TCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCA
GGGCCAGTCAGAGTGTTAGCAGGTACTTAGCCTGGTACCAACAGAAACC
TGGCCAGGCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTG
GCATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCT
CACCATCAGCAGCCTAGAGCCTGAAGATTTTGCAGTTTATTACTGTCAGC

AGAGATTCTACTACCCTTGGACTTTTGGCGGAGGGACCAAGGTTGAGAT
CAAACGGGCCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATT
CACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATC
CAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACT
CTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGA
AGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGG
CCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCT
GCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGT
ATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAG
GGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGAT
GGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGA
GCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAA
GGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTC
AGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGC
CACCTAGG

[0350] In further embodiments, the invention relates to Clone TS-26564 CAR HxL AA sequence (SEQ ID NO: 352):

MALPVTALLL PLALLLHAAR PEVQLVESGG GLVQPGGSLR LSCAASGFTF SSYSMNWVRQ APGKGLEWVS TISSSSSIIY YADSVKGRFT ISRDNAKNSL YLQMNSLRAE DTAVYYCARG SQEHLIFDYW GQGTLVTVSS GSTSGSGKPG SGEGSTKGEI VLTQSPATLS LSPGERATLS CRASQSVSRY LAWYQQKPGQ APRLLIYDAS NRATGIPARF SGSGSGTDFT LTISSLEPED FAVYYCQQRF YYPWTFGGGT KVEIKRAAAL DNEKSNGTII HVKGKHLCPS PLFPGPSKPF WVLVVVGGVL ACYSLLVTVA FIIFWVRSKR SRLLHSDYMN MTPRRPGPTR KHYQPYAPPR DFAAYRSRVK FSRSADAPAY QQGQNQLYNE LNLGRREEYD VLDKRRGRDP EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRG KGHDGLYQGL STATKDTYDA LHMQALPPR

[0351] In further embodiments, the invention relates to Clone TS-26564 CAR DNA LxH (SEQ ID NO: 353):

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCA
CGCCGCACGCCCGGAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTT
TGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGT

TAGCAGGTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGG
CTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTT
CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTA
GAGCCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGATTCTACTACCC
TTGGACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGGGGTCTACA
TCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGAG
GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCC
TGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATAGCATG
AACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTTCAACCA
TTAGTAGTAGTAGTAGTATCATATACTACGCAGACTCTGTGAAGGGCCG
ATTCACCATCTCCAGAGACAATGCCAAGAACTCACTGTATCTGCAAATG
AACAGCCTGAGAGCTGAGGACACGGCGGTGTACTACTGCGCCAGAGGTT
CTCAGGAGCACCTGATTTTCGATTATTGGGGACAGGGTACATTGGTCACC
GTCTCCTCAGCCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCA
TTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCA
TCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTA
CTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAA
GAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCT
GGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCG
CTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGC
GTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGC
AGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAG
ATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATG
AGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAA
AGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACT
CAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTG
CCACCTAGG

[0352] In further embodiments, the invention relates to Clone TS-26564 CAR LxH AA sequence (SEQ ID NO: 354):

MALPVTALLL PLALLLHAAR PEIVLTQSPA TLSLSPGERA TLSCRASQSV SRYLAWYQQK PGQAPRLLIY DASNRATGIP ARFSGSGSGT DFTLTISSLE PEDFAVYYCQ QRFYYPWTFG GGTKVEIKRG STSGSGKPGS GEGSTKGEVQ LVESGGGLVQ PGGSLRLSCA ASGFTFSSYS MNWVRQAPGK GLEWVSTISS

SSSIIYYADS VKGRFTISRD NAKNSLYLQM NSLRAEDTAV YYCARGSQEH LIFDYWGQGT LVTVSSAAAL DNEKSNGTII HVKGKHLCPS PLFPGPSKPF WVLVVVGGVL ACYSLLVTVA FIIFWVRSKR SRLLHSDYMN MTPRRPGPTR KHYQPYAPPR DFAAYRSRVK FSRSADAPAY QQGQNQLYNE LNLGRREEYD VLDKRRGRDP EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRG KGHDGLYQGL STATKDTYDA LHMQALPPR

[0353] In further embodiments, the invention relates to Clone RY-26568 HC DNA (SEQ ID NO: 355):

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGT
CCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCGGGAGCTATGGC
ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAG
TTATACATTATGATGGAAGTGTTGAATACTATGCAGACTCCGTGAAGGG
CCGATTCACCATCTCCAGAGACAATTCCAAGGACACGCTGTATCTGCAA
ATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCCAGAA
CTGACTTCTGGAGCGGATCCCCTCCAAGCTTAGATTACTGGGGACAGGG
TACATTGGTCACCGTCTCCTCA

[0354] In further embodiments, the invention relates to Clone RY-26568 HC AA sequence (SEQ ID NO: 356): QVQLVESGGG VVQPGRSLRL SCAASGFTFG SYGMHWVRQA PGKGLEWVAV IHYDGSVEYY ADSVKGRFTI SRDNSKDTLY LQMNSLRAED TAVYYCARTD FWSGSPPSLD YWGQGTLVTV SS

[0355] In further embodiments, the invention relates to HC CDR1 thereof: FTFGSYGMH (SEQ ID NO: 357). In further embodiments, the invention relates to HC CDR2 thereof: VIHYDGSVEYYADSVKG (SEQ ID NO: 358). In further embodiments, the invention relates to HC CDR3 thereof: ARTDFWSGSPPSLDY (SEQ ID NO: 359).

[0356] In further embodiments, the invention relates to Clone RY-26568 LC DNA (SEQ ID NO: 360):

GACATCCAGTTGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGA
CAGAGTCACCATCACTTGTCGGGCGAGTCGGGGTATTAGCAGCTGGTTA
GCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATG
GTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGG
ATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATT

TTGCAACTTATTACTGTCAGCAGATATACACCTTCCCTTTCACTTTTGGCG
GAGGGACCAAGGTTGAGATCAAACGG

[0357] In further embodiments, the invention relates to Clone RY-26568 LC AA sequence (SEQ ID NO: 361):

DIQLTQSPSS VSASVGDRVT ITCRASRGIS SWLAWYQQKP GKAPKLLIYG ASSLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ IYTFPFTFGG GTKVEIKR.

[0358] In further embodiments, the invention relates to LC CDR1 AA sequence thereof: RASRGISSWLA (SEQ ID NO: 362). In further embodiments, the invention relates to LC CDR2 AA sequence thereof: GASSLQS (SEQ ID NO: 363). In further embodiments, the invention relates to LC CDR3 AA sequence thereof: QQIYTFPFT (SEQ ID NO: 364) (LC CDR3).

[0359] In further embodiments, the invention relates to Clone RY-26568 CAR DNA HxL (SEQ ID NO: 365):

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCA
CGCCGCACGCCCGCAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTC
CAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTT
CGGGAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTG
GAGTGGGTGGCAGTTATACATTATGATGGAAGTGTTGAATACTATGCAG
ACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGGACAC
GCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTAC
TACTGCGCCAGAACTGACTTCTGGAGCGGATCCCCTCCAAGCTTAGATTA
CTGGGGACAGGGTACATTGGTCACCGTCTCCTCAGGGTCTACATCCGGCT
CCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGACATCCAGT
TGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACC
ATCACTTGTCGGGCGAGTCGGGGTATTAGCAGCTGGTTAGCCTGGTATCA
GCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGGTGCATCCAGT
TTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAG
ATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTAT
TACTGTCAGCAGATATACACCTTCCCTTTCACTTTTGGCGGAGGGACCAA
GGTTGAGATCAAACGGGCCGCTGCCCTTGATAATGAAAAGTCAAACGGA
ACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCC
TGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCG

CTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGAT
CCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACG
CCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGA
GATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGC
ACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTG
GGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGAC
CCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCT
ATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGG
CATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCA
GGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAA
GCCCTGCCACCTAGG

[0360] In further embodiments, the invention relates to Clone RY-26568 CAR HxL AA sequence (SEQ ID NO: 366):

MALPVTALLL PLALLLHAAR PQVQLVESGG GVVQPGRSLR LSCAASGFTF GSYGMHWVRQ APGKGLEWVA VIHYDGSVEY YADSVKGRFT ISRDNSKDTL YLQMNSLRAE DTAVYYCART DFWSGSPPSL DYWGQGTLVT VSSGSTSGSG KPGSGEGSTK GDIQLTQSPS SVSASVGDRV TITCRASRGI SSWLAWYQQK PGKAPKLLIY GASSLQSGVP SRFSGSGSGT DFTLTISSLQ PEDFATYYCQ QIYTFPFTFG GGTKVEIKRA AALDNEKSNG TIIHVKGKHL CPSPLFPGPS KPFWVLVVVG GVLACYSLLV TVAFIIFWVR SKRSRLLHSD YMNMTPRRPG PTRKHYQPYA PPRDFAAYRS RVKFSRSADA PAYQQGQNQL YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR

[0361] In further embodiments, the invention relates to Clone RY-26568 CAR DNA LxH (SEQ ID NO: 367):

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCA
CGCCGCACGCCCGGACATCCAGTTGACCCAGTCTCCATCTTCCGTGTCTG
CATCTGTAGGAGACAGAGTCACCATCACTTGTCGGGCGAGTCGGGGTAT
TAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAG
CTCCTGATCTATGGTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT
CAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG
CAGCCTGAAGATTTTGCAACTTATTACTGTCAGCAGATATACACCTTCCC

TTTCACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGGGGTCTACA
TCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGCAG
GTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC
TGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCGGGAGCTATGGCATG
CACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTA
TACATTATGATGGAAGTGTTGAATACTATGCAGACTCCGTGAAGGGCCG
ATTCACCATCTCCAGAGACAATTCCAAGGACACGCTGTATCTGCAAATG
AACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCCAGAACTG
ACTTCTGGAGCGGATCCCCTCCAAGCTTAGATTACTGGGGACAGGGTAC
ATTGGTCACCGTCTCCTCAGCCGCTGCCCTTGATAATGAAAAGTCAAACG
GAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTC
CCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCT
CGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAG
ATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCA
CGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTA
GAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGAT
GCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACC
TGGGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGG
ACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTC
TCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAAT
AGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTA
CCAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATG
CAAGCCCTGCCACCTAGG

[0362] In further embodiments, the invention relates to Clone RY-26568 CAR LxH AA sequence (SEQ ID NO: 368):

MALPVTALLL PLALLLHAAR PDIQLTQSPS SVSASVGDRV TITCRASRGI SSWLAWYQQK PGKAPKLLIY GASSLQSGVP SRFSGSGSGT DFTLTISSLQ PEDFATYYCQ QIYTFPFTFG GGTKVEIKRG STSGSGKPGS GEGSTKGQVQ LVESGGGVVQ PGRSLRLSCA ASGFTFGSYG MHWVRQAPGK GLEWVAVIHY DGSVEYYADS VKGRFTISRD NSKDTLYLQM NSLRAEDTAV YYCARTDFWS GSPPSLDYWG QGTLVTVSSA AALDNEKSNG TIIHVKGKHL CPSPLFPGPS KPFWVLVVVG GVLACYSLLV TVAFIIFWVR SKRSRLLHSD YMNMTPRRPG PTRKHYQPYA PPRDFAAYRS

RVKFSRSADA PAYQQGQNQL YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR

[0363] In further embodiments, the invention relates to Clone PP-26575 HC DNA (SEQ ID NO: 369):

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCT
CGGTGAAGGTCTCCTGCAAGGCTTCTGGAGGCACCCTCAGCAGCCTGGC
TATCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGA
GGGGTCATCCCTATCTTGGGTCGGGCAAACTACGCACAGAAGTTCCAGG
GCAGAGTCACGATTACCGCGGACGAGTCCACGAGCACAGCCTACATGGA
GCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGA
ACTCCTGAATACTCCTCCAGCATATGGCACTATTACTACGGCATGGACGT
ATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA

[0364] In further embodiments, the invention relates to Clone PP-26575 HC AA sequence (SEQ ID NO: 370):

QVQLVQSGAE VKKPGSSVKV SCKASGGTLS SLAISWVRQA PGQGLEWMGG VIPILGRANY AQKFQGRVTI TADESTSTAY MELSSLRSED TAVYYCARTP EYSSSIWHYY YGMDVWGQGT TVTVSS.

[0365] In further embodiments, the invention relates to HC CDR1 AA sequence thereof: GTLSSLAIS (SEQ ID NO: 371). In further embodiments, the invention relates to HC CDR2 AA sequence thereof: GVIPILGRANYAQKFQG (SEQ ID NO: 372). In further embodiments, the invention relates to HC CDR3 thereof: ARTPEYSSSIWHYYYGMDV (SEQ ID NO: 373).

[0366] In further embodiments, the invention relates to Clone PP-26575 LC DNA (SEQ ID NO: 374):

GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGA
GAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCC
AACAATAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGCCTC
CTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC
CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCA
GCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTTCGCCCAC
ACTCCTTTCACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGG

[0367] In further embodiments, the invention relates to Clone PP-26575 LC AA sequence (SEQ ID NO: 375):

DIVMTQSPDS LAVSLGERAT INCKSSQSVL YSSNNKNYLA WYQQKPGQPP KLLIYWASTR ESGVPDRFSG SGSGTDFTLT ISSLQAEDVA VYYCQQFAHT PFTFGGGTKV EIKR.

[0368] In further embodiments, the invention relates to LC CDR 1 AA sequence thereof: KSSQSVLYSSNNKNYLA (SEQ ID NO: 376). In further embodiments, the invention relates to LC CDR2 AA sequence thereof: WASTRES (SEQ ID NO: 377). In further embodiments, the invention relates to LC CDR3 AA sequence thereof: QQFAHTPFT (SEQ ID NO: 378).

[0369] In further embodiments, the invention relates to Clone PP-26575 CAR DNA HxL (SEQ ID NO: 379):

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCA
CGCCGCACGCCCGCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAG
AAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCTTCTGGAGGCACCC
TCAGCAGCCTGGCTATCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCT
TGAGTGGATGGGAGGGGTCATCCCTATCTTGGGTCGGGCAAACTACGCA
CAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAGTCCACGAGCA
CAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTA
CTACTGCGCCAGAACTCCTGAATACTCCTCCAGCATATGGCACTATTACT
ACGGCATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCAGG
GTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAG
GGGGACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGG
CGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGC
TCCAACAATAAGAACTACTTAGCTTGGTACCAGCAGAAACCAGGACAGC
CTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCT
GACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCA
GCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTTCGCC
CACACTCCTTTCACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGG
CCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGAA
GGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCAT
TCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTC
GTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCT

GCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACA
AGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCTGCCTATC
GGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCA
GGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGA
GTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGC
AAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAG
AAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAG
CGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACT
GCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTA
GG

[0370] In further embodiments, the invention relates to Clone PP-26575 CAR HxL AA sequence (SEQ ID NO: 380):

MALPVTALLL PLALLLHAAR PQVQLVQSGA EVKKPGSSVK VSCKASGGTL SSLAISWVRQ APGQGLEWMG GVIPILGRAN YAQKFQGRVT ITADESTSTA YMELSSLRSE DTAVYYCART PEYSSSIWHY YYGMDVWGQG TTVTVSSGST SGSGKPGSGE GSTKGDIVMT QSPDSLAVSL GERATINCKS SQSVLYSSNN KNYLAWYQQK PGQPPKLLIY WASTRESGVP DRFSGSGSGT DFTLTISSLQ AEDVAVYYCQ QFAHTPFTFG GGTKVEIKRA AALDNEKSNG TIIHVKGKHL CPSPLFPGPS KPFWVLVVVG GVLACYSLLV TVAFIIFWVR SKRSRLLHSD YMNMTPRRPG PTRKHYQPYA PPRDFAAYRS RVKFSRSADA PAYQQGQNQL YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR

[0371] In further embodiments, the invention relates to Clone PP-26575 CAR DNA LxH (SEQ ID NO: 381):

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCA
CGCCGCACGCCCGGACATCGTGATGACCCAGTCTCCAGACTCCCTGGCT
GTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTG
TTTTATACAGCTCCAACAATAAGAACTACTTAGCTTGGTACCAGCAGAA
ACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAAT
CCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCAC
TCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTC
AGCAGTTCGCCCACACTCCTTTCACTTTTGGCGGAGGGACCAAGGTTGAG

ATCAAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAG
GTAGTACAAAGGGGCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAA
GAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCTTCTGGAGGCACC
CTCAGCAGCCTGGCTATCAGCTGGGTGCGACAGGCCCCTGGACAAGGGC
TTGAGTGGATGGGAGGGGTCATCCCTATCTTGGGTCGGGCAAACTACGC
ACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAGTCCACGAGC
ACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGT
ACTACTGCGCCAGAACTCCTGAATACTCCTCCAGCATATGGCACTATTAC
TACGGCATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCAG
CCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGAA
GGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCAT
TCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTC
GTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCT
GCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACA
AGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCTGCCTATC
GGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCA
GGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGA
GTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGC
AAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAG
AAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAG
CGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACT
GCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTA
GG

[0372] In further embodiments, the invention relates to Clone PP-26575 CAR LxH AA sequence (SEQ ID NO: 382):

MALPVTALLL PLALLLHAAR PDIVMTQSPD SLAVSLGERA TINCKSSQSV
LYSSNNKNYL AWYQQKPGQP PKLLIYWAST RESGVPDRFS GSGSGTDFTL
TISSLQAEDV AVYYCQQFAH TPFTFGGGTK VEIKRGSTSG SGKPGSGEGS
TKGQVQLVQS GAEVKKPGSS VKVSCKASGG TLSSLAISWV
RQAPGQGLEW MGGVIPILGR ANYAQKFQGR VTITADESTS TAYMELSSLR
SEDTAVYYCA RTPEYSSSIW HYYYGMDVWG QGTTVTVSSA
AALDNEKSNG TIIHVKGKHL CPSPLFPGPS KPFWVLVVVG GVLACYSLLV
TVAFIIFWVR SKRSRLLHSD YMNMTPRRPG PTRKHYQPYA PPRDFAAYRS

RVKFSRSADA PAYQQGQNQL YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR

[0373] In further embodiments, the invention relates to Clone RD-26576 HC DNA (SEQ ID NO: 383):

CAGGTGCGGCTGGTGGAGTCTGGGGGGGGCGTGGTCCAGCCTGGGAGGT
CCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAG
TTATAGGGTATGATGGACAGGAGAAATACTATGCAGACTCCGTGAAGGG
CCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAA
ATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAAGG
GGCCGTTGCAGGAGCCGCCATACGCTTTTGGGATGGACGTATGGGGCCA
GGGAACAACTGTCACCGTCTCCTCA

[0374] In further embodiments, the invention relates to Clone RD-26576 HC AA sequence (SEQ ID NO: 384):

QVRLVESGGG VVQPGRSLRL SCAASGFTFS SYGIHWVRQA PGKGLEWVAV IGYDGQEKYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKGP LQEPPYAFGM DVWGQGTTVT VSS.

[0375] In further embodiments, the invention relates to HC CDR1 AA sequence thereof: FTFSSYGIH (SEQ ID NO: 385). In further embodiments, the invention relates to HC CDR2 AA sequence thereof: VIGYDGQEKYYADSVKG (SEQ ID NO: 386). In further embodiments, the invention relates to the HC CDR3 AA sequence thereof: VKGPLQEPPYAFGMDV (SEQ ID NO: 387).

[0376] In further embodiments, the invention relates to Clone RD-26576 LC DNA (SEQ ID NO: 388):

GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGG
AAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTT
AGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT
AGCGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGTGGCAGTG
GGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGA
TTTTGCAGTTTATTACTGTCAGCAGCACCACGTCTGGCCTCTCACTTTTGG
CGGAGGGACCAAGGTTGAGATCAAACGG

[0377] In further embodiments, the invention relates to Clone RD-26576 LC AA sequence (SEQ ID NO: 389):

EIVMTQSPAT LSVSPGERAT LSCRASQSVS SNLAWYQQKP GQAPRLLIYS ASTRATGIPA RFSGSGSGTE FTLTISSLQS EDFAVYYCQQ HHVWPLTFGG GTKVEIKR.

[0378] In further embodiments, the invention relates to LC CDR1 AA sequence thereof: RASQSVSSNLA (SEQ ID NO: 390). In further embodiments, the invention relates to LC CDR2 AA sequence thereof: SASTRAT (SEQ ID NO: 391). In further embodiments, the invention relates to LC CDR3 AA sequence thereof: QQHHVWPLT (SEQ ID NO: 392).

[0379] In further embodiments, the invention relates to Clone RD-26576 CAR DNA HxL (SEQ ID NO: 393):

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCA
CGCCGCACGCCCGCAGGTGCGGCTGGTGGAGTCTGGGGGGGGCGTGGTC
CAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTT
CAGTAGCTATGGCATACACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTG
GAGTGGGTGGCAGTTATAGGGTATGATGGACAGGAGAAATACTATGCAG
ACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACAC
GCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTAC
TACTGCGTCAAGGGGCCGTTGCAGGAGCCGCCATACGCTTTTGGGATGG
ACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCAGGGTCTACATC
CGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGAAAT
AGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGA
GCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCT
GGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATAGCGC
ATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGGTCT
GGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC
AGTTTATTACTGTCAGCAGCACCACGTCTGGCCTCTCACTTTTGGCGGAG
GGACCAAGGTTGAGATCAAACGGGCCGCTGCCCTTGATAATGAAAAGTC
AAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCC
TTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGG
AGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTG
GGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATG
ACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCAC

CACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCT
GCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGC
TCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGG
ACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGA
GGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCT
GAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGG
TTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCC
ACATGCAAGCCCTGCCACCTAGG

[0380] In further embodiments, the invention relates to Clone RD-26576 CAR HxL AA sequence (SEQ ID NO: 394);

MALPVTALLL PLALLLHAAR PQVRLVESGG GVVQPGRSLR LSCAASGFTF
SSYGIHWVRQ APGKGLEWVA VIGYDGQEKY YADSVKGRFT
ISRDNSKNTL YLQMNSLRAE DTAVYYCVKG PLQEPPYAFG
MDVWGQGTTV TVSSGSTSGS GKPGSGEGST KGEIVMTQSP ATLSVSPGER
ATLSCRASQS VSSNLAWYQQ KPGQAPRLLI YSASTRATGI PARFSGSGSG
TEFTLTISSL QSEDFAVYYC QQHHVWPLTF GGGTKVEIKR AAALDNEKSN
GTIIHVKGKH LCPSPLFPGP SKPFWVLVVV GGVLACYSLL VTVAFIIFWV
RSKRSRLLHS DYMNMTPRRP GPTRKHYQPY APPRDFAAYR SRVKFSRSAD
APAYQQGQNQ LYNELNLGRR EEYDVLDKRR GRDPEMGGKP
RRKNPQEGLY NELQKDKMAE AYSEIGMKGE RRRGKGHDGL
YQGLSTATKD TYDALHMQAL PPR.

[0381] In further embodiments, the invention relates to Clone RD-26576 CAR DNA LxH (SEQ ID NO: 395):

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCA
CGCCGCACGCCCGGAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT
GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTG
TTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAG
GCTCCTCATCTATAGCGCATCCACCAGGGCCACTGGTATCCCAGCCAGGT
TCAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCT
GCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGCACCACGTCTGGC
CTCTCACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGGGGTCTAC
ATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGCA
GGTGCGGCTGGTGGAGTCTGGGGGGGGCGTGGTCCAGCCTGGGAGGTCC

CTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCAT
ACACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTT
ATAGGGTATGATGGACAGGAGAAATACTATGCAGACTCCGTGAAGGGCC
GATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAAT
GAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAAGGG
GCCGTTGCAGGAGCCGCCATACGCTTTTGGGATGGACGTATGGGGCCAG
GGAACAACTGTCACCGTCTCCTCAGCCGCTGCCCTTGATAATGAAAAGTC
AAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCC
TTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGG
AGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTG
GGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATG
ACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCAC
CACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCT
GCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGC
TCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGG
ACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGA
GGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCT
GAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGG
TTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCC
ACATGCAAGCCCTGCCACCTAGG

[0382] In further embodiments, the invention relates to Clone RD-26576 CAR LxH AA sequence (SEQ ID NO: 396):

MALPVTALLL PLALLLHAAR PEIVMTQSPA TLSVSPGERA TLSCRASQSV SSNLAWYQQK PGQAPRLLIY SASTRATGIP ARFSGSGSGT EFTLTISSLQ SEDFAVYYCQ QHHVWPLTFG GGTKVEIKRG STSGSGKPGS GEGSTKGQVR LVESGGGVVQ PGRSLRLSCA ASGFTFSSYG IHWVRQAPGK GLEWVAVIGY DGQEKYYADS VKGRFTISRD NSKNTLYLQM NSLRAEDTAV YYCVKGPLQE PPYAFGMDVW GQGTTVTVSS AAALDNEKSN GTIIHVKGKH LCPSPLFPGP SKPFWVLVVV GGVLACYSLL VTVAFIIFWV RSKRSRLLHS DYMNMTPRRP GPTRKHYQPY APPRDFAAYR SRVKFSRSAD APAYQQGQNQ LYNELNLGRR EEYDVLDKRR GRDPEMGGKP RRKNPQEGLY NELQKDKMAE AYSEIGMKGE RRRGKGHDGL YQGLSTATKD TYDALHMQAL PPR.

[0383] In further embodiments, the invention relates to Clone RD-26578 HC DNA (SEQ ID NO: 397):

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGT
CCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCCGTGGC
ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAG
TTATAGGGTATGATGGACAGGAGAAATACTATGCAGACTCCGTGAAGGG
CCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAA
ATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAAGG
GGCCGTTGCAGGAGCCGCCATACGATTATGGAATGGACGTATGGGGCCA
GGGAACAACTGTCACCGTCTCCTCA

[0384] In further embodiments, the invention relates to Clone RD-26578 HC AA sequence (SEQ ID NO: 398):

QVQLVESGGG VVQPGRSLRL SCAASGFTFS SRGMHWVRQA
PGKGLEWVAV IGYDGQEKYY ADSVKGRFTI SRDNSKNTLY
LQMNSLRAED TAVYYCVKGP LQEPPYDYGM DVWGQGTTVT VSS.

[0385] In further embodiments, the invention relates to HC CDR1 AA sequence thereof: FTFSSRGMH (SEQ ID NO: 399). In further embodiments, the invention relates to HC CDR2 AA sequence thereof: VIGYDGQEKYYADSVKG (SEQ ID NO: 400). In further embodiments, the invention relates to HC CDR3 thereof: VKGPLQEPPYDYGMDV (SEQ ID NO: 401).

[0386] In further embodiments, the invention relates to Clone RD-26578 LC DNA (SEQ ID NO: 402):

GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGG
AAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTT
AGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT
AGCGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGTGGCAGTG
GGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGA
TTTTGCAGTTTATTACTGTCAGCAGCACCACGTCTGGCCTCTCACTTTTGG
CGGAGGGACCAAGGTTGAGATCAAACGG

[0387] In further embodiments, the invention relates to Clone RD-26578 LC AA sequence (SEQ ID NO: 403):

EIVMTQSPAT LSVSPGERAT LSCRASQSVS SNLAWYQQKP GQAPRLLIYS ASTRATGIPA RFSGSGSGTE FTLTISSLQS EDFAVYYCQQ HHVWPLTFGG GTKVEIKR.

[0388] In further embodiments, the invention relates to LC CDR1 AA sequence: RASQSVSSNLA (SEQ ID NO: 404). In further embodiments, the invention relates to LC CDR2 AA sequence thereof: SASTRAT (SEQ ID NO: 405). In further embodiments, the invention relates to LC CDR3 AA sequence thereof: QQHHVWPLT (SEQ ID NO: 406).

[0389] In further embodiments, the invention relates to Clone RD-26578 CAR DNA HxL (SEQ ID NO: 407):

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCA
CGCCGCACGCCCGCAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTC
CAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTT
CAGTAGCCGTGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTG
GAGTGGGTGGCAGTTATAGGGTATGATGGACAGGAGAAATACTATGCAG
ACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACAC
GCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTAC
TACTGCGTCAAGGGGCCGTTGCAGGAGCCGCCATACGATTATGGAATGG
ACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCAGGGTCTACATC
CGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGAAAT
AGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGA
GCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCT
GGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATAGCGC
ATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGGTCT
GGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGC
AGTTTATTACTGTCAGCAGCACCACGTCTGGCCTCTCACTTTTGGCGGAG
GGACCAAGGTTGAGATCAAACGGGCCGCTGCCCTTGATAATGAAAAGTC
AAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCC
TTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGG
AGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTG
GGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATG
ACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCAC
CACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCT
GCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGC

TCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGG
ACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGA
GGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCT
GAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGG
TTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCC
ACATGCAAGCCCTGCCACCTAGG

[0390] In further embodiments, the invention relates to Clone RD-26578 CAR HxL AA sequence (SEQ ID NO: 408):

MALPVTALLL PLALLLHAAR PQVQLVESGG GVVQPGRSLR LSCAASGFTF
SSRGMHWVRQ APGKGLEWVA VIGYDGQEKY YADSVKGRFT
ISRDNSKNTL YLQMNSLRAE DTAVYYCVKG PLQEPPYDYG
MDVWGQGTTV TVSSGSTSGS GKPGSGEGST KGEIVMTQSP ATLSVSPGER
ATLSCRASQS VSSNLAWYQQ KPGQAPRLLI YSASTRATGI PARFSGSGSG
TEFTLTISSL QSEDFAVYYC QQHHVWPLTF GGGTKVEIKR AAALDNEKSN
GTIIHVKGKH LCPSPLFPGP SKPFWVLVVV GGVLACYSLL VTVAFIIFWV
RSKRSRLLHS DYMNMTPRRP GPTRKHYQPY APPRDFAAYR SRVKFSRSAD
APAYQQGQNQ LYNELNLGRR EEYDVLDKRR GRDPEMGGKP
RRKNPQEGLY NELQKDKMAE AYSEIGMKGE RRRGKGHDGL
YQGLSTATKD TYDALHMQAL PPR

[0391] In further embodiments, the invention relates to Clone RD-26578 CAR DNA LxH (SEQ ID NO: 409):

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCA
CGCCGCACGCCCGGAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCT
GTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTG
TTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAG
GCTCCTCATCTATAGCGCATCCACCAGGGCCACTGGTATCCCAGCCAGGT
TCAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCT
GCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGCACCACGTCTGGC
CTCTCACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGGGGTCTAC
ATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGCA
GGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCC
CTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCCGTGGCAT
GCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTT

ATAGGGTATGATGGACAGGAGAAATACTATGCAGACTCCGTGAAGGGCC
GATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAAT
GAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAAGGG
GCCGTTGCAGGAGCCGCCATACGATTATGGAATGGACGTATGGGGCCAG
GGAACAACTGTCACCGTCTCCTCAGCCGCTGCCCTTGATAATGAAAAGTC
AAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCC
TTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGG
AGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTG
GGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATG
ACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCAC
CACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCT
GCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGC
TCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGG
ACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGA
GGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCT
GAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGG
TTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCC
ACATGCAAGCCCTGCCACCTAGG

[0392] In further embodiments, the invention relates to Clone RD-26578 CAR LxH AA sequence (SEQ ID NO: 410):

MALPVTALLL PLALLLHAAR PEIVMTQSPA TLSVSPGERA TLSCRASQSV
SSNLAWYQQK PGQAPRLLIY SASTRATGIP ARFSGSGSGT EFTLTISSLQ
SEDFAVYYCQ QHHVWPLTFG GGTKVEIKRG STSGSGKPGS
GEGSTKGQVQ LVESGGGVVQ PGRSLRLSCA ASGFTFSSRG
MHWVRQAPGK GLEWVAVIGY DGQEKYYADS VKGRFTISRD
NSKNTLYLQM NSLRAEDTAV YYCVKGPLQE PPYDYGMDVW
GQGTTVTVSS AAALDNEKSN GTIIHVKGKH LCPSPLFPGP SKPFWVLVVV
GGVLACYSLL VTVAFIIFWV RSKRSRLLHS DYMNMTPRRP GPTRKHYQPY
APPRDFAAYR SRVKFSRSAD APAYQQGQNQ LYNELNLGRR
EEYDVLDKRR GRDPEMGGKP RRKNPQEGLY NELQKDKMAE
AYSEIGMKGE RRRGKGHDGL YQGLSTATKD TYDALHMQAL PPR.

[0393] It will be appreciated that the sequences recited herein can be useful by themselves, in combination with one or more sequences recited herein, and/or incorporated

into cells (such as CAR or TCR- based T cells) for use in immune- or other therapies. It will be further appreciated that these sequences can be used in accordance with the invention incorporated in vectors for transduction, transfection, and the like, into cells.

[0394] 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.

[0395] 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., WO2014/127261, WO2015/090229, US2014/0286987, US2015/0266973, US2016/0046700, U.S. Patent No. 8,486,693, US2014/0171649, and US2012/0130076, the contents of which are further incorporated by reference herein in their entirety.

### *IV. Vectors, Cells, and Pharmaceutical Compositions*

[0396] 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, as described herein. In other embodiments, the present invention is directed to a vector or a set of vectors comprising

a polynucleotide encoding an antibody or an antigen binding molecule thereof that specifically binds to BCMA, as disclosed herein.

[0397] Any vector known in the art can be suitable for the present invention. In some embodiments, the vector is a viral vector. In some embodiments, the vector is a retroviral vector (such as pMSVG1), 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 (such as pGAR), or any combination thereof.

[0398] The pGAR sequence is as follows:

[0399] CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGG
TTACGCGCAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTT
TCGCTTTCTTCCCTTCCTTTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGC
TCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTTAGTGCTTTACGGCACCT
CGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGGCCATCGC
CCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA
GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATT
CTTTTGATTTATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATG
AGCTGATTTAACAAAAATTTAACGCGAATTTTAACAAAATATTAACGCTTA
CAATTTGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCG
GTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGC
AAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTA
AAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGACCCGGGG
ATGGCGCGCCAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATG
GAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCC
AACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACG
CCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACT
GCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATT
GACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGAC
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CCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAG
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TCGACGCAGGACTCGGCTTGCTGAAGCGCGCACGGCAAGAGGCGAGGGG
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ACAACCATCCCTTCAGACAGGATCAGAAGAACTTAGATCATTATATAATA
CAGTAGCAACCCTCTATTGTGTGCATCAAAGGATAGAGATAAAAGACACC
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GGTGTTGTCGGGGAAGCTGACGTCCTTTTCATGGCTGCTCGCCTGTGTTGC
CACCTGGATTCTGCGCGGGACGTCCTTCTGCTACGTCCCTTCGGCCCTCAA
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AGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCC
TCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCA
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CGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCC
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TGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGT
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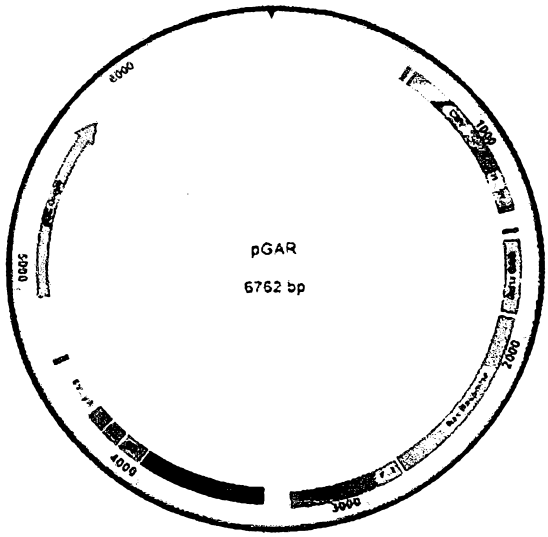
TTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCC
AGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACC
AGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATA
AGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAG
CATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAA
ATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCAC **(SEQ ID NO: 413)**

[0400] The pGAR vector map is set forth below:




[0401] Suitable additional exemplary 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.

[0402] In other aspects, provided herein are cells comprising a polynucleotide or a vector of the present invention. In some embodiments, the present invention is directed to cells, in vitro cells, comprising a polynucleotide encoding a CAR or a TCR, as described herein. In some embodiments, the present invention is directed to cells, *e.g.*, in vitro cells, comprising a polynucleotide encoding an antibody or an antigen binding molecule thereof that specifically binds to BCMA, as disclosed herein. In other embodiments, the present invention is directed to in vitro cells comprising a polypeptide encoded by a polynucleotide encoding a CAR or a TCR, as disclosed herein. In other embodiments, the present invention is directed to cells, in vitro cells, comprising a polypeptide encoded by a polynucleotide encoding an antibody or an antigen binding molecule thereof that specifically binds to BCMA, as disclosed herein.

[0403] 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 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.

[0404] The cell of the present invention can 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.

[0405] 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 $CD28^+$, $CD4^+$, $CD8^+$, $CD45RA^+$, 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 CD14, CD20, CD11b, CD16, HLA-DR, and CD8. In certain embodiments, flow cytometry and cell sorting are used to isolate cell populations of interest for use in the present invention.

[0406] 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 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.

[0407] 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 types of $CD8^+$ cells. In some embodiments, the expression of phenotypic markers of

central memory T cells includes CD45RO, CD62L, CCR7, CD28, CD3, and CD127 and are negative for granzyme B. In some embodiments, central memory T cells are $CD45RO^+$, $CD62L^+$, $CD8^+$ T cells. In some embodiments, effector T cells are negative for CD62L, CCR7, CD28, and CD127 and positive for granzyme B and perforin. In certain embodiments, $CD4^+$ T cells 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.

[0408] 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 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 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.

[0409] 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.

[0410] 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, wherein the CAR or the TCR comprises an antigen binding molecule that specifically binds to BCMA. In another embodiment, the composition comprises a CAR or a TCR encoded by a polynucleotide of the present invention, wherein the CAR or the TCR comprises an antigen binding molecule that specifically binds to BCMA. In another embodiment, the composition comprises a T cell comprising a polynucleotide encoding a CAR or a TCR, wherein the CAR or the TCR comprises an antigen binding molecule that specifically binds to BCMA. In another embodiment, the composition comprises an antibody or an antigen binding molecule thereof encoded by a polynucleotide of the present invention. In another embodiment, the composition comprises an in vitro cell comprising a polynucleotide encoding an antibody or an antigen binding molecule thereof encoded by a polynucleotide of the present invention.

[0411] In some embodiments, the composition includes more than one different antigen binding molecule to BMCA. In some embodiments, the composition included more than one antigen binding molecule to BCMA, wherein the antigen binding molecules to BCMA bind more than one epitope. In some embodiments, the antigen binding molecules will not compete with one another for binding to BCMA. In some embodiments, any of the antigen binding molecules provided herein are combined together in a pharmaceutical composition.

[0412] 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 desired antigen binding molecule to BCMA, 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 an antigen binding molecule to BCMA, 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.

### *V. Methods of the Invention*

[0413] 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, wherein the CAR or the TCR comprises an antigen binding molecule that specifically binds to BCMA, as disclosed herein. In some embodiments, the method comprises transducing a cell with a vector comprising the polynucleotide encoding a CAR or a TCR, wherein the CAR or the TCR comprises an antigen binding molecule that specifically binds to BCMA. In other embodiments, the method comprises transducing a cell with a polynucleotide encoding an antibody or an antigen binding molecule thereof that specifically binds to BCMA, as disclosed herein. In some embodiments, the method comprises transducing a cell with a vector comprising the polynucleotide encoding an antibody or an antigen binding molecule thereof that specifically binds to BCMA, as described herein. In some embodiments, the method further comprises isolating the cell.

[0414] 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 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, wherein the CAR or the TCR comprises an antigen binding molecule that specifically binds to BCMA, as 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, wherein the CAR or the TCR comprises an antigen binding molecule that specifically binds to BCMA, as disclosed herein. In another embodiment, the method comprises administering to a subject an effective amount of a cell comprising a CAR or a TCR encoded by a polynucleotide disclosed herein, wherein the CAR or the TCR comprises an antigen binding molecule that specifically binds to BCMA. In other embodiments, the method comprises administering to a subject an effective amount of a cell comprising a polynucleotide encoding an antibody or an antigen binding molecule thereof that specifically

binds to BCMA, as 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 an antibody or an antigen binding molecule thereof that specifically binds to BCMA, as disclosed herein. In another embodiment, the method comprises administering to a subject an effective amount of a cell comprising an antibody or antigen binding molecule thereof encoded by a polynucleotide disclosed herein, wherein the antibody or antigen binding molecule thereof specifically binds to BCMA.

[0415] 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 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. In some embodiments, the target cell is a tumor cell.

[0416] Another aspect of the present invention is directed to a method for treating or preventing a malignancy, said method comprising administering to a subject in need thereof an effective amount of at least one isolated antigen binding molecule described herein or at least one immune cell, wherein the immune cell comprises at least one CAR, TCR, and/or an isolated antigen binding molecule as described herein.

[0417] Another aspect of the present invention is directed to a method of treating a hyperproliferative disorder or an inflammatory disease in a subject in need thereof comprising administering to the subject a polynucleotide disclosed herein, a vector disclosed herein, a CAR or a TCR disclosed herein, a cell disclosed herein, or a composition disclosed herein. In some embodiments, the inflammatory disease is selected from the group consisting of rheumatoid arthritis, psoriasis, allergies, asthma, autoimmune diseases such as Crohn's, IBD, fibromyalga, mastocytosis, Celiac disease, and any combination thereof. Additionally, the present invention may be useful to treat diabetes, particularly Type 1 diabetes.

[0418] 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 disclosed herein, a vector disclosed herein, a CAR or a TCR disclosed herein, a cell disclosed herein, or a composition disclosed herein. In one embodiment, the method comprises administering a polynucleotide encoding a CAR or a TCR, wherein the CAR or the TCR comprises an antigen binding molecule that specifically binds to BCMA, as disclosed herein. In another embodiment, the method comprises administering a vector comprising a

polynucleotide encoding a CAR or a TCR, wherein the CAR or the TCR comprises an antigen binding molecule that specifically binds to BCMA, as disclosed herein. In another embodiment, the method comprises administering a CAR or a TCR encoded by a polynucleotide disclosed herein, wherein the CAR or the TCR comprises an antigen binding molecule that specifically binds to BCMA. In another embodiment, the method comprises administering a cell comprising the polynucleotide, or a vector comprising the polynucleotide, encoding a CAR or a TCR, wherein the CAR or the TCR comprises an antigen binding molecule that specifically binds to BCMA, as disclosed herein. In other embodiments, the method comprises administering a polynucleotide encoding an antibody or an antigen binding molecule thereof that specifically binds to BCMA, as disclosed herein. In another embodiment, the method comprises administering a vector comprising a polynucleotide encoding an antibody or an antigen binding molecule thereof that specifically binds to BCMA, as disclosed herein. In another embodiment, the method comprises administering an antibody or an antigen binding molecule thereof encoded by a polynucleotide disclosed herein, wherein the antibody or the antigen binding molecule thereof specifically binds to BCMA. In another embodiment, the method comprises administering a cell comprising the polynucleotide, or a vector comprising the polynucleotide, encoding an antibody or an antigen binding molecule thereof that specifically binds to BCMA, as disclosed herein.

[0419] In some embodiments, an antigen binding molecule to BCMA is administered alone. In certain embodiments, an antigen binding molecule to BCMA is administered as part of a CAR, TCR, or other immune cell. In such immune cells, the antigen binding molecule to BCMA can be under the control of the same promoter region, or a separate promoter. In certain embodiments, the genes encoding protein agents and/or an antigen binding molecule to BCMA can be in separate vectors.

[0420] 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 an anti-BCMA CAR of the present invention ("anti-BCMA CAR T cells"). In a particular embodiment, the anti-BCMA CAR T cells are administered to the patient. In some embodiments, the anti-BCMA CAR T cells treat a tumor

or a cancer in the patient. In one embodiment the anti-BCMA CAR T cells reduce the size of a tumor or a cancer.

[0421] 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.

[0422] 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 $10^9$ cells, at least about $10^{10}$ cells, or at least about $10^{11}$ cells. 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 anti-BCMA CAR T cells is about 2 X $10^6$ cells/kg, about 3 X $10^6$ cells/kg, about 4 X $10^6$ cells/kg, about 5 X $10^6$ cells/kg, about 6 X $10^6$ cells/kg, about 7 X $10^6$ cells/kg, about 8 X $10^6$ cells/kg, about 9 X $10^6$ cells/kg, about 1 X $10^7$ cells/kg, about 2 X $10^7$ cells/kg, about 3 X $10^7$ cells/kg, about 4 X $10^7$ cells/kg, about 5 X $10^7$ cells/kg, about 6 X $10^7$ cells/kg, about 7 X $10^7$ cells/kg, about 8 X $10^7$ cells/kg, or about 9 X $10^7$ cells/kg.

[0423] Another aspect of the present invention is directed to methods of diagnosis, detection, or validation. In some embodiments, the antigen binding molecule is used as a diagnostic or validation tool. In certain embodiments, the antigen binding molecules disclosed herein are used to assay the amount of BCMA present in a sample and/or subject. In some embodiments, the diagnostic antigen binding molecule is not neutralizing. In some embodiments, the antigen binding molecules disclosed herein are used or provided in an assay kit and/or method for the detection of BCMA in mammalian tissues or cells in order to screen/diagnose for a disease or disorder associated with changes in levels of BCMA. In some embodiments, the kit comprises an antigen binding molecule that binds BCMA, along with means for indicating the binding of the antigen binding molecule with BCMA, if present, and optionally BCMA protein levels. Various means for indicating the presence of an antigen binding molecule can be used. For example, fluorophores, other molecular probes, or enzymes can be linked to the antigen binding molecule and the presence of the antigen binding molecule can be observed in a variety of ways. As will be appreciated by one of skill in the art, the degree of antigen binding molecule binding can be used to determine how much BCMA is in a sample.

### *V.A. Cancer Treatment*

[0424] 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.

[0425] 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 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), chronic or acute leukemia, myeloid diseases including but not limited to acute myeloid leukemia (AML), chronic myeloid leukemia (CML), acute lymphoblastic leukemia (ALL) (including non T cell ALL), chronic lymphocytic leukemia (CLL), T-cell lymphoma, one or more of B-cell acute lymphoid leukemia ("BALL"), T-cell acute lymphoid leukemia ("TALL"), acute lymphoid leukemia (ALL), chronic myelogenous leukemia (CML), B cell prolymphocytic leukemia, blastic plasmacytoid dendritic cell neoplasm, Burkitt's lymphoma, diffuse large B cell lymphoma, follicular lymphoma, hairy cell leukemia, small cell- or a large cell-follicular lymphoma, malignant lymphoproliferative conditions, MALT lymphoma, mantle cell lymphoma, Marginal zone lymphoma, myelodysplasia and myelodysplastic syndrome (MDS), hemophagocytic syndrome (Macrophage Activating Syndrome (MAS), and hemophagocytic lymphohistocytosis (HLH)), chronic or acute granulomatous disease, large cell granuloma, leukocyte adhesion deficiency, plasmablastic lymphoma, plasmacytoid dendritic cell neoplasm, Waldenstrom macroglobulinemia, plasma cell proliferative disorders (e.g., asymptomatic myeloma (smoldering multiple myeloma or indolent myeloma), monoclonal gammapathy of undetermined significance (MGUS), plasmacytomas (e.g., plasma cell dyscrasia, solitary myeloma, solitary plasmacytoma, extramedullary plasmacytoma, and multiple plasmacytoma), systemic amyloid light chain amyloidosis, POEMS syndrome (Crow-Fukase

syndrome, Takatsuki disease, PEP syndrome), or combinations thereof. In one embodiment, the cancer is a myeloma. In one particular embodiment, the cancer is multiple myeloma.

[0426] 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/m$^2$/day and 2000 mg/m$^2$/day) and specified doses of fludarabine (between 20 mg/m$^2$/day and 900 mg/m$^2$/day). A preferred dose regimen involves treating a patient comprising administering daily to the patient about 500 mg/m$^2$/day of cyclophosphamide and about 60 mg/m$^2$/day of fludarabine for three days prior to administration of a therapeutically effective amount of engineered T cells to the patient.

[0427] 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.

[0428] 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 (CYTOXAN$^{TM}$); alkyl sulfonates such as busulfan, improsulfan and piposulfan; aziridines such as benzodopa, carboquone, meturedopa, and uredopa; ethylenimines and methylamelamines including altretamine, triethylenemelamine, trietylenephosphoramide, triethylenethiophosphaoramide and trimethylolomelamine resume; nitrogen mustards such as chlorambucil, chlornaphazine, cholophosphamide, estramustine, ifosfamide, mechlorethamine, mechlorethamine oxide hydrochloride, melphalan, novembichin, phenesterine, prednimustine, trofosfamide, uracil mustard; nitrosureas such as carmustine, chlorozotocin, fotemustine, lomustine, nimustine, ranimustine; antibiotics such as aclacinomysins, actinomycin, authramycin, azaserine, bleomycins, cactinomycin, calicheamicin, carabicin, carminomycin, carzinophilin, chromomycins, dactinomycin, daunorubicin, detorubicin, 6-diazo-5-oxo-L-norleucine, doxorubicin, epirubicin, esorubicin, idarubicin, marcellomycin, mitomycins, mycophenolic acid, nogalamycin, olivomycins, peplomycin, potfiromycin, puromycin, quelamycin,

rodorubicin, streptonigrin, streptozocin, tubercidin, ubenimex, zinostatin, zorubicin; anti-metabolites such as methotrexate and 5-fluorouracil (5-FU); folic acid analogues such as denopterin, methotrexate, pteropterin, trimetrexate; purine analogs such as fludarabine, 6-mercaptopurine, thiamiprine, thioguanine; pyrimidine analogs such as ancitabine, azacitidine, 6-azauridine, carmofur, cytarabine, dideoxyuridine, doxifluridine, enocitabine, floxuridine, 5-FU; androgens such as calusterone, dromostanolone propionate, epitiostanol, mepitiostane, testolactone; anti-adrenals such as aminoglutethimide, mitotane, trilostane; folic acid replenisher such as frolinic acid; aceglatone; aldophosphamide glycoside; aminolevulinic acid; amsacrine; bestrabucil; bisantrene; edatraxate; defofamine; demecolcine; diaziquone; elformithine; elliptinium acetate; etoglucid; gallium nitrate; hydroxyurea; lentinan; lonidamine; mitoguazone; mitoxantrone; mopidamol; nitracrine; pentostatin; phenamet; pirarubicin; podophyllinic acid; 2-ethylhydrazide; procarbazine; PSK®; razoxane; sizofiran; spirogermanium; tenuazonic acid; triaziquone; 2, 2',2''-trichlorotriethylamine; urethan; vindesine; dacarbazine; mannomustine; mitobronitol; mitolactol; pipobroman; gacytosine; arabinoside ("Ara-C"); cyclophosphamide; thiotepa; taxoids, e.g. paclitaxel (TAXOL™, Bristol-Myers Squibb) 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 (Cytoxan®), Doxorubicin (hydroxydoxorubicin), Vincristine (Oncovin®), and Prednisone.

[0429] 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 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 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.

[0430] 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®), pembrolizumab, pidilizumab (CureTech), and atezolizumab (Roche).

[0431] 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®), 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, 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).

[0432] In additional embodiments, the composition comprising CAR- and/or TCR-containing immune are administered with an anti-inflammatory agent. Anti-inflammatory 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 proporxyphene 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.

[0433] 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.

[0434] 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 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.

[0435] 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 application are expressly incorporated herein by reference.

## EXAMPLES

### EXAMPLE 1

[0436] BCMA expression was measured in various cell lines. BCMA was found to be expressed, with a fragments/kilobase of exon/million reads mapped (FPKM) greater than 35, in 99% of multiple myeloma tumor cell lines tested (FIG. 2A). BCMA expression was greater than that of CD70, CS-1, CLL-1, DLL-1 and FLT3 (FIG. 2A). To further characterize the expression of BCMA, EoL-1 (Sigma), NCI-H929 (Molecular Imaging), and MM1S (Molecular Imaging) cells were stained with an anti-BCMA antibody conjugated to PE (Biolegend, San Diego, CA) in stain buffer (BD Pharmingen, San Jose, CA) for 30 minutes at 4°C. Cells were then washed and resuspended in stain buffer with propidium iodide (BD Pharmingen) prior to data acquisition. Samples were then acquired by flow cytometry and data analyzed (FIGs. 2B-2C). BCMA expression was observed in the myeloma cell lines MM1S (FIG. 2C) and NCI-H929 (FIG. 2D), but not in the human eosinophil cell line EoL-1 (FIG. 2B). In addition, little to no BCMA expression was observed in normal immune cells (FIG. 2E).

### EXAMPLE 2

[0437] A third generation lentiviral transfer vector containing the BCMA CAR constructs was used along with the ViraPower™ Lentiviral Packaging Mix (Life Technologies, FIX™) to generate the lentiviral supernatants. Briefly, a transfection mix was generated by mixing 15μg of DNA and 22.5μl of polyethileneimine (Polysciences,

1mg/ml) in 600µl of OptiMEM media. The transfection mix was incubated for 5 minutes at room temperature. Simultaneously, 293T cells (ATCC) were trypsinized and counted. A total of 10 x $10^6$ total 293T cells were then plated in a T75 flask with the transfection mix. Following culture for three days, supernatants were collected and filtered through a 0.45µm filter and stored at -80°C.

[0438] Peripheral blood mononuclear cells (PBMCs) were isolated from two different healthy donor leukopaks (Hemacare) using ficoll-paque density centrifugation according to the manufacturer's instructions. PBMCs were stimulated using OKT3 (Muromonab-CD3, 50ng/ml, Miltenyi Biotec) in R10 media supplemented with IL-2 (300IU/ml, Proleukin®, Prometheus® Therapeutics and Diagnostics). Forty-eight hours post-stimulation, cells were transduced using lentivirus containing the different BCMA CAR constructs at a multiplicity of infection (MOI) of 10. Cells were maintained at 0.5 x $10^6$ - 2.0 x $10^6$ cells/ml prior to use in activity assays.

[0439] At day 12 post-stimulation, transduced T cells were stained with recombinant BCMA-Fc (R&D Systems) in stain buffer (BD Pharmingen) for 30 minutes at 4°C. Cells were then washed and stained with goat anti-human IgG Fc PE (Jackson ImmunoResearch, West Grove, PA) 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. All experiments were performed in two different donors. BCMA CAR expression was observed for each of the constructs in both Donor 1 (FIG. 3A) and Donor 2 (FIG. 3B) transduced cells.

[0440] Effector cells, *e.g.*, anti-BCMA CAR T cells, 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, NCI-H929 and MM1S. Sixteen hours post-co-culture, supernatants were analyzed by Luminex (EMD Millipore), according to the manufacturer's instructions, for production of the cytokines IFNγ (FIGs. 4A-4B), TNFα (FIG. 4C-4D), and IL-2 (FIG. 4E-4F). IFNγ (FIGs. 4A-4B), TNFα (FIG. 4C-4D), and IL-2 (FIG. 4E-4F) 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. 4A-4B); however, IFNγ (FIGs. 4A-4B), TNFα (FIG. 4C-4D), and IL-2 (FIG. 4E-4F) were only observed in the supernatant of EoL-1 target cell co-cultures above background for the IR negative control T cells (FIG. 4A).

[0441] 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. 5A-5B), NCI-H929 (FIGs. 5C-5D), or MM1S (FIGs. 5E-5F) 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. 5A-5B). 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.

[0442] 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. Data was analyzed and plotted as histogram using FlowJo™ (FIGs. 6A-6B). All experiments were performed in two different donors.

EXAMPLE 3

[0443] Antigens were biotinylated using the EZ-Link Sulfo-NHS-Biotinylation Kit from Pierce/ThermoFisher (Waltham, MA). Goat anti-human F(ab')2 kappa-FITC (LC-FITC), Extravidin-PE (EA-PE) and streptavidin-633 (SA-633) were obtained from Southern Biotech (Birmingham, AL), Sigma (St. Louis, MO) and Molecular Probes/Invitrogen (Waltham, MA), respectively. Streptavidin MicroBeads and MACS LC separation columns were purchased from Miltenyi Biotec (Gladbachn, Germany).

Naïve Discovery

[0444] Eight naïve human synthetic yeast libraries each of ~109 diversity were propagated as described herein (see WO2009036379, WO2010105256, and WO2012009568 to Xu *et al.*). For the first two rounds of selection, a magnetic bead sorting technique utilizing the Miltenyi MACs system was performed, as described (Siegel *et al.*, 2004). Briefly, yeast cells (~1010 cells/library) were incubated with 3 ml of 100 nM biotinylated monomeric antigen or 10 nM biotinylated Fc fusion antigen for 15 minutes at room temperature in FACS wash buffer (phosphate-buffered saline (PBS)/0.1% bovine serum albumin (BSA)). After washing once with 50 ml ice-cold wash buffer, the cell pellet was resuspended in 40 mL wash buffer, and Streptavidin MicroBeads (500 µl) were added to the yeast and incubated for 15 minutes at 4°C. Next, the yeast were pelleted, resuspended in 5 mL wash buffer, and loaded onto a Miltenyi LS column. After the 5 mL was loaded, the column was washed 3 times with 3 ml FACS wash buffer. The column was then removed from the magnetic field, and the yeast were eluted with 5 mL of growth media and

then grown overnight. The following rounds of sorting were performed using flow cytometry. Approximately 1×108 yeast were pelleted, washed three times with wash buffer, and incubated with decreasing concentrations of biotinylated monomeric or Fc fusion antigen (100 to 1 nM) under equilibrium conditions at room temperature. Yeast were then washed twice and stained with LC-FITC (diluted 1:100) and either SA-633 (diluted 1:500) or EA-PE (diluted 1:50) secondary reagents for 15 minutes at 4°C. After washing twice with ice-cold wash buffer, the cell pellets were resuspended in 0.4 mL wash buffer and transferred to strainer-capped sort tubes. Sorting was performed using a FACS ARIA sorter (BD Biosciences, San Jose, CA) and sort gates were assigned to select for specific binders relative to a background control. Subsequent rounds of selection were focused on reduction of non-specific reagent binders (utilizing soluble membrane proteins from CHO cell), as well as pressuring for affinity to BCMA. After the final round of sorting, yeast were plated and individual colonies were picked for characterization.

[0445] Affinity Maturation

[0446] Binding optimization of naïve clones was carried out using three maturation strategies: light chain diversification, diversification of VH CDRH1/CDRH2, and performing VHmut/VKmut selections.

[0447] Light Chain Diversification: Heavy chain plasmids were extracted and transformed into a light chain library with a diversity of 1 x $10^6$. Selections were performed as described above with one round of MACS sorting and two rounds of FACS sorting using 10 nM or 1 nM biotinylated antigen for respective rounds.

[0448] CDRH1 and CDRH2 Selection: A selected donor CDRH3 was recombined into a premade library with CDRH1 and CDRH2 variants of a diversity of 1 x $10^8$ and selections were performed as described above. Affinity pressures were applied by incubating the biotinylated antigen-antibody yeast complex with unbiotinylated antigen for varying amounts of time to select for the highest affinity antibodies.

[0449] VHmut/VKmut Selection: This round of affinity maturation included error prone PCR-based mutagenesis of the heavy chain and/or light chain. Selections were performed similar to previous cycles, but employing FACS sorting for all selection rounds. Antigen concentration was reduced and cold antigen competition times were increased to pressure further for optimal affinity.

Antibody Production and Purification

[0450] Yeast clones were grown to saturation and then induced for 48 h at 30°C with shaking. After induction, yeast cells were pelleted and the supernatants were harvested for purification. IgGs were purified using a Protein A column and eluted with acetic acid, pH 2.0. Fab fragments were generated by papain digestion and purified over KappaSelect™ (GE Healthcare LifeSciences, Pittsburg, PA).

ForteBio KD Measurements

[0451] ForteBio affinity measurements were performed generally as previously described (Estep *et al.*, 2013). Briefly, ForteBio affinity measurements were performed by loading IgGs on-line onto AHQ sensors. Sensors were equilibrated off-line in assay buffer for 30 minutes and then monitored on-line for 60 seconds for baseline establishment. Sensors with loaded IgGs were exposed to 100 nM antigen for 5 minutes, afterwards they were transferred to assay buffer for 5 minutes for off-rate measurement. Kinetics were analyzed using the 1:1 binding model.

MSD-SET KD Measurements

[0452] Equilibrium affinity measurements performed generally as previously described (Estep *et al.*, 2013). Briefly, solution equilibrium titrations (SET) were performed in PBS + 0.1% IgG-Free BSA (PBSF) with antigen (BCMA monomer) held constant at 10-100 pM and incubated with 3-to 5-fold serial dilutions of Fab or mAbs starting at 10pM-10nM (experimental condition is sample dependent). Antibodies (20 nM in PBS) were coated onto standard bind MSD-ECL plates overnight at 4°C or at room temperature for 30 minutes. Plates were then blocked by BSA for 30 minutes with shaking at 700 rpm, followed by three washes with wash buffer (PBSF + 0.05% Tween 20). SET samples were applied and incubated on the plates for 150 seconds with shaking at 700 rpm followed by one wash. Antigen captured on a plate was detected with 250ng/mL sulfotag™-labeled streptavidin in PBSF by incubation on the plate for 3 minutes. The plates were washed three times with wash buffer and then read on the MSD Sector Imager 2400™ instrument using 1x Read Buffer T with surfactant. The percent free antigen was plotted as a function of titrated antibody in Prism™ and fit to a quadratic equation to extract the KD. To improve throughput, liquid handling robots were used throughout MSD-SET experiments, including SET sample preparation.

Octet Red384 Epitope Binning/ligand blocking

[0453] Epitope binning/ligand blocking was performed using a standard sandwich format cross-blocking assay. Control anti-target IgG was loaded onto AHQ sensors and unoccupied Fc-binding sites on the sensor were blocked with an irrelevant human IgG1 antibody. The sensors were then exposed to 100 nM target antigen followed by a second anti-target antibody or ligand. Data was processed using ForteBio's Data Analysis Software 7.0. Additional binding by the second antibody or ligand after antigen association indicates an unoccupied epitope (non-competitor), while no binding indicates epitope blocking (competitor or ligand blocking).

Size Exclusion Chromatography

[0454] A TSKgel SuperSW mAb HTP column (22855) was used for fast SEC analysis of yeast produced mAbs at 0.4 mL/minute with a cycle time of 6 minutes/run. 200 mM Sodium Phosphate and 250 mM Sodium Chloride was used as the mobile phase.

Dynamic Scanning Fluorimetry

[0455] 10 uL of 20x Sypro Orange™ is added to 20 uL of 0.2-1mg/mL mAb or Fab solution. A RT-PCR instrument (BioRad CFX96 RT PCR) is used to ramp the sample plate temperature from 40° to 95° C at 0.5C increment, with 2 minutes to equilibrate at each temperature. The negative of first derivative for the raw data is used to extract Tm.

**Clone FS-26528 HC DNA (SEQ ID NO: 271)**

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCT
CCTGTGCAGCCTCTGGATTCACCTTTGACGACTATGCCATGGCATGGGTCCGCCAGGCTCC
AGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGATGCAGGTGACAGAACATACTACGCA
GACTCCGTGAGGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACACTGTATCTGC
AAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCAAGAGCCGAGATGGG
AGCCGTATTCGACATATGGGGTCAGGGTACAATGGTCACCGTCTCCTCA

**Clone FS-26528 HC (SEQ ID NO: 272). CDRs 1, 2, and 3 are underlined.**

EVQLLESGGGLVQPGGSLRLSCAASGFTFDDYAMAWVRQAPGKGLEWVSAISDAGDRTYY
ADSVRGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARAEMGAVFDIWGQGTMVTVSS

SCAASGFTFDDYAMA (SEQ ID NO: 273) [HC CDR1]

AISDAGDRTYYADSVRG (SEQ ID NO: 274) [HC CDR2]

ARAEMGAVFDI (SEQ ID NO: 275) [HC CDR3]

**Clone FS-26528 LC DNA (SEQ ID NO: 276)**

GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCC
TCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGGTACTTAGCCTGGTACCAACAGAAACCTGG
CCAGGCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGG
TTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAG
ATTTTGCAGTTTATTACTGTCAGCAGAGAATCTCCTGGCCTTTCACTTTTGGCGGAGGGAC
CAAGGTTGAGATCAAACGG

**Clone FS-26528 LC (SEQ ID NO: 277). CDRs 1, 2, and 3 are underlined.**

EIVLTQSPATLSLSPGERATLSCRASQSVSRYLAWYQQKPGQAPRLLIYDASNRATGIPAR
FSGSGSGTDFTLTISSLEPEDFAVYYCQQ RISWPFTFGGGTKVEIKR

RASQSVSRYLA (SEQ ID NO: 278) [LC CDR1]

DASNRAT (SEQ ID NO: 279) [LC CDR2]

QQRISWPFT (SEQ ID NO: 280) [LC CDR3]

**Clone FS-26528 CAR DNA HxL (SEQ ID NO: 281)**

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCC
CGGAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACT
CTCCTGTGCAGCCTCTGGATTCACCTTTGACGACTATGCCATGGCATGGGTCCGCCAGGCT
CCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGATGCAGGTGACAGAACATACTACG
CAGACTCCGTGAGGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACACTGTATCT
GCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCAAGAGCCGAGATG
GGAGCCGTATTCGACATATGGGGTCAGGGTACAATGGTCACCGTCTCCTCAGGGTCTACAT
CCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGAAATTGTGTTGACACA
GTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGT
CAGAGTGTTAGCAGGTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTCC
TCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTCAGTGGCAGTGGGTC
TGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGATTTTGCAGTTTATTAC
TGTCAGCAGAGAATCTCCTGGCCTTTCACTTTTGGCGGAGGGACCAAGGTTGAGATCAAAC
GGGCCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCA
CCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTG
GGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTA
GATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGG
CCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGC
AGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGT
ATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACG
GGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAG
CTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAGAA
GGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATGA
CGCTCTCCACATGCAAGCCCTGCCACCTAGG

**Clone FS-26528 CAR HxL (SEQ ID NO: 282)**

MALPVTALLLPLALLLHAARPEVQLLESGGGLVQPGGSLRLSCAASGFTFDDYAMAWVRQA
PGKGLEWVSAISDAGDRTYYADSVRGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARAEM
GAVFDIWGQGTMVTVSSGSTSGSGKPGSGEGSTKGEIVLTQSPATLSLSPGERATLSCRAS
QSVSRYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYY
CQQRISWPFTFGGGTKVEIKRAAALDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVV
GGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRS
RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE
LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

Clone FS-26528 CAR DNA LxH (SEQ ID NO: 283)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCC
CGGAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCAC
CCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGGTACTTAGCCTGGTACCAACAGAAACCT
GGCCAGGCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCA
GGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGA
AGATTTTGCAGTTTATTACTGTCAGCAGAGAATCTCCTGGCCTTTCACTTTTGGCGGAGGG
ACCAAGGTTGAGATCAAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAG
GTAGTACAAAGGGGGAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGG
GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGACGACTATGCCATGGCATGG
GTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGATGCAGGTGACA
GAACATACTACGCAGACTCCGTGAGGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAA
CACACTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCA
AGAGCCGAGATGGGAGCCGTATTCGACATATGGGGTCAGGGTACAATGGTCACCGTCTCCT
CAGCCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCA
CCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTG
GGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTA
GATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGG
CCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGC
AGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGT
ATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACG
GGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAG
CTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAGAA
GGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATGA
CGCTCTCCACATGCAAGCCCTGCCACCTAGG

Clone FS-26528 CAR LxH (SEQ ID NO: 284)

MALPVTALLLPLALLLHAARPEIVLTQSPATLSLSPGERATLSCRASQSVSRYLAWYQQKP
GQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRISWPFTFGGG
TKVEIKRGSTSGSGKPGSGEGSTKGEVQLLESGGGLVQPGGSLRLSCAASGFTFDDYAMAW
VRQAPGKGLEWVSAISDAGDRTYYADSVRGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCA
RAEMGAVFDIWGQGTMVTVSSAAALDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVV
GGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRS
RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNE
LQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

**Clone PC-26534 HC DNA (SEQ ID NO: 285)**
CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT
CCTGTGCAGCGTCTGGATTCACCTTCAGTGAGCATGGCATGCACTGGGTCCGCCAGGCTCC
AGGCAAGGGGCTGGAGTGGGTGGCAGCTATATCTTATGATGGAAGGAATAAACACTATGCA
GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCCAGAGACGGTACTTA
TCTAGGTGGTCTCTGGTACTTCGACTTATGGGGGAGAGGTACCTTGGTCACCGTCTCCTCA

**Clone PC-26534 HC (SEQ ID NO: 286). CDRs 1, 2, and 3 are underlined.**
QVQLVESGGGVVQPGRSLRLSCAASGFTFSEHGMHWVRQAPGKGLEWVAAISYDGRNKHY
ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGTYLGGLWYFDLWGRGTLVTVS
S

FTFSEHGMH (SEQ ID NO: 287) [HC CDR1]

AISYDGRNKHYADSVKG (SEQ ID NO: 288) [HC CDR2]

ARDGTYLGGLWYFDL (SEQ ID NO: 289) [HC CDR3]

**Clone PC-26534 LC DNA (SEQ ID NO: 290)**
GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCA
TCTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACAACTATTTGGATTGGTA
CCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGGGTTCTAATCGGGCCTCC
GGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCA
GAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAGGGACTCGGCCTCCCTCTCAC
TTTTGGCGGAGGGACCAAGGTTGAGATCAAACGG

**Clone PC-26534 LC (SEQ ID NO: 291). CDRs 1, 2, and 3 are underlined.**
DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGLGLPLTFGGGTKVEIKR

RSSQSLLHSNGYNYLD (SEQ ID NO: 292) [LC CDR1]

LGSNRAS (SEQ ID NO: 293) [LC CDR2]

MQGLGLPLT (SEQ ID NO: 294) [LC CDR3]

**Clone PC-26534 CAR DNA HxL (SEQ ID NO: 295)**
ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCC
CGCAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACT
CTCCTGTGCAGCGTCTGGATTCACCTTCAGTGAGCATGGCATGCACTGGGTCCGCCAGGCT
CCAGGCAAGGGGCTGGAGTGGGTGGCAGCTATATCTTATGATGGAAGGAATAAACACTATG
CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCT
GCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCCAGAGACGGTACT
TATCTAGGTGGTCTCTGGTACTTCGACTTATGGGGGAGAGGTACCTTGGTCACCGTCTCCT
CAGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGATAT
TGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCATCTCC

TGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACAACTATTTGGATTGGTACCTGC
AGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGGGTTCTAATCGGGCCTCCGGGGT
CCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTG
GAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAGGGACTCGGCCTCCCTCTCACTTTTG
GCGGAGGGACCAAGGTTGAGATCAAACGGGCCGCTGCCCTTGATAATGAAAAGTCAAACGG
AACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCC
AAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCA
CCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTA
CATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCA
CCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAG
CGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTA
TGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAA
AACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTG
AAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACT
CAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

**Clone PC-26534 CAR HxL (SEQ ID NO: 296)**

MALPVTALLLPLALLLHAARPQVQLVESGGGVVQPGRSLRLSCAASGFTFSEHGMHWVRQA
PGKGLEWVAAISYDGRNKHYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGT
YLGGLWYFDLWGRGTLVTVSSGSTSGSGKPGSGEGSTKGDIVMTQSPLSLPVTPGEPASIS
CRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRV
EAEDVGVYYCMQGLGLPLTFGGGTKVEIKRAAALDNEKSNGTIIHVKGKHLCPSPLFPGPS
KPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAP
PRDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRK
NPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

Clone PC-26534 CAR DNA LxH (SEQ ID NO: 297)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCC
CGGATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTC
CATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACAACTATTTGGATTGG
TACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGGGTTCTAATCGGGCCT
CCGGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAG
CAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAGGGACTCGGCCTCCCTCTC
ACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGGGGTCTACATCCGGCTCCGGGAAGC
CCGGAAGTGGCGAAGGTAGTACAAAGGGGCAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGT
GGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTGAG
CATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGCTATAT
CTTATGATGGAAGGAATAAACACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAG
AGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCG
GTGTACTACTGCGCCAGAGACGGTACTTATCTAGGTGGTCTCTGGTACTTCGACTTATGGG
GGAGAGGTACCTTGGTCACCGTCTCCTCAGCCGCTGCCCTTGATAATGAAAAGTCAAACGG
AACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCC
AAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCA
CCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTA
CATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCA
CCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAG
CGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTA
TGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAA
AACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTG
AAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACT
CAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

Clone PC-26534 CAR LxH (SEQ ID NO: 298)

MALPVTALLL PLALLLHAAR PDIVMTQSPL SLPVTPGEPA SISCRSSQSL
LHSNGYNYLD WYLQKPGQSP QLLIYLGSNR ASGVPDRFSG SGSGTDFTLK
ISRVEAEDVG VYYCMQGLGL PLTFGGGTKV EIKRGSTSGS GKPGSGEGST
KGQVQLVESG GGVVQPGRSL RLSCAASGFT FSEHGMHWVR QAPGKGLEWV
AAISYDGRNK HYADSVKGRF TISRDNSKNT LYLQMNSLRA EDTAVYYCAR
DGTYLGGLWY FDLWGRGTLV TVSSAAALDN EKSNGTIIHV KGKHLCPSPL
FPGPSKPFWV LVVVGGVLAC YSLLVTVAFI IFWVRSKRSR LLHSDYMNMT
PRRPGPTRKH YQPYAPPRDF AAYRSRVKFS RSADAPAYQQ GQNQLYNELN
LGRREEYDVL DKRRGRDPEM GGKPRRKNPQ EGLYNELQKD KMAEAYSEIG
MKGERRRGKG HDGLYQGLST ATKDTYDALH MQALPPR

**Clone AJ-26545 HC DNA (SEQ ID NO: 299)**

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTT
CCTGCAGGGCATCTGGATACACCTTCATGGAGCACTATATGCACTGGGTGCGACAGGCCCC
TGGACAAGGGCTTGAGTGGATGGGAGTAATCGGGCCTAGTGGTGGTAAGACAAGCTACGCA
CAGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGG
AGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGAGAGAATTGGCC
AATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA

**Clone AJ-26545 HC (SEQ ID NO: 300). CDRs 1, 2, and 3 are underlined.**

QVQLVQSGAEVKKPGASVKVSCRASGYTFMEHYMHWVRQAPGQGLEWMGVIGPSGGKTSY
AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARESWPMDVWGQGTTVTVSS

YTFMEHYMH (SEQ ID NO: 301) (HC CDR1)

VIGPSGGKTSYAQKFQG (SEQ ID NO: 302) (HC CDR2)

ARESWPMDV (SEQ ID NO: 303) (HC CDR3)

**Clone AJ-26545 LC DNA (SEQ ID NO: 304)**

GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCC
TCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGG
CCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGG
TTCAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAG
ATTTTGCAGTTTATTACTGTCAGCAGTACGCCGCCTACCCTACTTTTGGCGGAGGGACCAA
GGTTGAGATCAAACGG

**Clone AJ-26545 LC (SEQ ID NO: 305). CDRs 1, 2, and 3 are underlined.**

EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPAR
FSGSGSGTEFTLTISSLQSEDFAVYYCQQYAAYPTFGGGTKVEIKR

RASQSVSSNLA (SEQ ID NO: 306) (LC CDR1)

GASTRAT (SEQ ID NO: 307) (LC CDR2)

QQYAAYPT (SEQ ID NO: 308) (LC CDR3)

**Clone AJ-26545 CAR DNA HxL (SEQ ID NO: 309)**

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCC
CGCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGT
TTCCTGCAGGGCATCTGGATACACCTTCATGGAGCACTATATGCACTGGGTGCGACAGGCC
CCTGGACAAGGGCTTGAGTGGATGGGAGTAATCGGGCCTAGTGGTGGTAAGACAAGCTACG
CACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACAT
GGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGAGAGAATTGG
CCAATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCAGGGTCTACATCCGGCT
CCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGAAATAGTGATGACGCAGTCTCC
AGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGT
GTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCT
ATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGAC
AGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAG
CAGTACGCCGCCTACCCTACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGGCCGCTG
CCCTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCC
GTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTC
CTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAA
GAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAG
GAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAG
TTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGC
TCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGA
GATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAG
GATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAG
GGCACGACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCA
CATGCAAGCCCTGCCACCTAGG

**Clone AJ-26545 CAR HxL (SEQ ID NO: 310)**

MALPVTALLL PLALLLHAAR PQVQLVQSGA EVKKPGASVK VSCRASGYTF
MEHYMHWVRQ APGQGLEWMG VIGPSGGKTS YAQKFQGRVT MTRDTSTSTV
YMELSSLRSE DTAVYYCARE SWPMDVWGQG TTVTVSSGST SGSGKPGSGE
GSTKGEIVMT QSPATLSVSP GERATLSCRA SQSVSSNLAW YQQKPGQAPR
LLIYGASTRA TGIPARFSGS GSGTEFTLTI SSLQSEDFAV YYCQQYAAYP
TFGGGTKVEI KRAAALDNEK SNGTIIHVKG KHLCPSPLFP GPSKPFWVLV
VVGGVLACYS LLVTVAFIIF WVRSKRSRLL HSDYMNMTPR RPGPTRKHYQ
PYAPPRDFAA YRSRVKFSRS ADAPAYQQGQ NQLYNELNLG RREEYDVLDK
RRGRDPEMGG KPRRKNPQEG LYNELQKDKM AEAYSEIGMK GERRRGKGHD
GLYQGLSTAT KDTYDALHMQ ALPPR

Clone AJ-26545 CAR DNA LxH (SEQ ID NO: 311)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCC
CGGAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCAC
CCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCT
GGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCA
GGTTCAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGA
AGATTTTGCAGTTTATTACTGTCAGCAGTACGCCGCCTACCCTACTTTTGGCGGAGGGACC
AAGGTTGAGATCAAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTA
GTACAAAGGGGCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTTTCCTGCAGGGCATCTGGATACACCTTCATGGAGCACTATATGCACTGGGTG
CGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAGTAATCGGGCCTAGTGGTGGTAAGA
CAAGCTACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCAC
AGTCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGA
GAGAATTGGCCAATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCAGCCGCTG
CCCTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCC
GTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTC
CTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAA
GAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAG
GAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAG
TTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGC
TCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGA
GATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAG
GATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAG
GGCACGACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCA
CATGCAAGCCCTGCCACCTAGG

Clone AJ-26545 CAR LxH (SEQ ID NO: 312)

MALPVTALLL PLALLLHAAR PEIVMTQSPA TLSVSPGERA TLSCRASQSV
SSNLAWYQQK PGQAPRLLIY GASTRATGIP ARFSGSGSGT EFTLTISSLQ
SEDFAVYYCQ QYAAYPTFGG GTKVEIKRGS TSGSGKPGSG EGSTKGQVQL
VQSGAEVKKP GASVKVSCRA SGYTFMEHYM HWVRQAPGQG LEWMGVIGPS
GGKTSYAQKF QGRVTMTRDT STSTVYMELS SLRSEDTAVY YCARESWPMD
VWGQGTTVTV SSAAALDNEK SNGTIIHVKG KHLCPSPLFP GPSKPFWVLV
VVGGVLACYS LLVTVAFIIF WVRSKRSRLL HSDYMNMTPR RPGPTRKHYQ
PYAPPRDFAA YRSRVKFSRS ADAPAYQQGQ NQLYNELNLG RREEYDVLDK
RRGRDPEMGG KPRRKNPQEG LYNELQKDKM AEAYSEIGMK GERRRGKGHD
GLYQGLSTAT KDTYDALHMQ ALPPR

**Clone AJ-26554 HC DNA (SEQ ID NO: 313)**

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTT
CCTGCAAGGCATCTGGATACACCTTCACGGAGCACTATATGCACTGGGTGCGACAGGCCCC
TGGACAAAGGCTTGAGTGGATGGGAGTAATCGGGCCTAGTGGTGGTAAGACAAGCTACGCA
CAGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGG
AGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGAGAGAGTTGGCC
AATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA

**Clone AJ-26554 HC (SEQ ID NO: 314). CDRs 1, 2, and 3 are underlined.**

QVQLVQSGAE VKKPGASVKV SCKASGYTFT EHYMHWVRQA PGQRLEWMGV
IGPSGGKTSY AQKFQGRVTM TRDTSTSTVY MELSSLRSED TAVYYCARES
WPMDVWGQGT TVTVSS

YTFTEHYMH (SEQ ID NO: 315) (HC CDR1)

VIGPSGGKTSYAQKFQG (SEQ ID NO: 316) (HC CDR2)

ARESWPMDV (SEQ ID NO: 317) (HC CDR3)

**Clone AJ-26554 LC DNA (SEQ ID NO: 318)**

GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCC
TCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGG
CCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGG
TTCAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAG
ATTTTGCAGTTTATTACTGTCAGCAGTACGCCGCCTACCCTACTTTTGGCGGAGGGACCAA
GGTTGAGATCAAACGG

**Clone AJ-26554 LC (SEQ ID NO: 319). CDRs 1, 2, and 3 are underlined.**

EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA
RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYAAYPTFGGGTKVEIKR

RASQSVSSNLA (SEQ ID NO: 320) (LC CDR1)

GASTRAT (SEQ ID NO: 321) (LC CDR2)

QQYAAYPT (SEQ ID NO: 322) (LC CDR3)

Clone AJ-26554 CAR DNA HxL (SEQ ID NO: 323)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCC
CGCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGT
TTCCTGCAAGGCATCTGGATACACCTTCACGGAGCACTATATGCACTGGGTGCGACAGGCC
CCTGGACAAAGGCTTGAGTGGATGGGAGTAATCGGGCCTAGTGGTGGTAAGACAAGCTACG
CACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACAT
GGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGAGAGAGTTGG
CCAATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCAGGGTCTACATCCGGCT
CCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGAAATAGTGATGACGCAGTCTCC
AGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGT
GTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCT
ATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGAC
AGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAG
CAGTACGCCGCCTACCCTACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGGCCGCTG
CCCTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCC
GTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTC
CTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAA
GAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAG
GAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAG
TTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGC
TCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGA
GATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAG
GATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAG
GGCACGACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCA
CATGCAAGCCCTGCCACCTAGG

Clone AJ-26554 CAR HxL (SEQ ID NO: 324)

MALPVTALLL PLALLLHAAR PQVQLVQSGA EVKKPGASVK VSCKASGYTF
TEHYMHWVRQ APGQRLEWMG VIGPSGGKTS YAQKFQGRVT MTRDTSTSTV
YMELSSLRSE DTAVYYCARE SWPMDVWGQG TTVTVSSGST SGSGKPGSGE
GSTKGEIVMT QSPATLSVSP GERATLSCRA SQSVSSNLAW YQQKPGQAPR
LLIYGASTRA TGIPARFSGS GSGTEFTLTI SSLQSEDFAV YYCQQYAAYP
TFGGGTKVEI KRAAALDNEK SNGTIIHVKG KHLCPSPLFP GPSKPFWVLV
VVGGVLACYS LLVTVAFIIF WVRSKRSRLL HSDYMNMTPR RPGPTRKHYQ
PYAPPRDFAA YRSRVKFSRS ADAPAYQQGQ NQLYNELNLG RREEYDVLDK
RRGRDPEMGG KPRRKNPQEG LYNELQKDKM AEAYSEIGMK GERRRGKGHD
GLYQGLSTAT KDTYDALHMQ ALPPR

**Clone AJ-26554 CAR DNA LxH (SEQ ID NO: 325)**

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCC
CGGAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCAC
CCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCT
GGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCA
GGTTCAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGA
AGATTTTGCAGTTTATTACTGTCAGCAGTACGCCGCCTACCCTACTTTTGGCGGAGGGACC
AAGGTTGAGATCAAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTA
GTACAAAGGGGCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACGGAGCACTATATGCACTGGGTG
CGACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGAGTAATCGGGCCTAGTGGTGGTAAGA
CAAGCTACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCAC
AGTCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGA
GAGAGTTGGCCAATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCAGCCGCTG
CCCTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCC
GTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTC
CTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAA
GAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAG
GAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAG
TTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGC
TCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGA
GATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAG
GATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAG
GGCACGACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCA
CATGCAAGCCCTGCCACCTAGG

**Clone AJ-26554 CAR LxH (SEQ ID NO: 326)**

MALPVTALLL PLALLLHAAR PEIVMTQSPA TLSVSPGERA TLSCRASQSV
SSNLAWYQQK PGQAPRLLIY GASTRATGIP ARFSGSGSGT EFTLTISSLQ
SEDFAVYYCQ QYAAYPTFGG GTKVEIKRGS TSGSGKPGSG EGSTKGQVQL
VQSGAEVKKP GASVKVSCKA SGYTFTEHYM HWVRQAPGQR LEWMGVIGPS
GGKTSYAQKF QGRVTMTRDT STSTVYMELS SLRSEDTAVY YCARESWPMD
VWGQGTTVTV SSAAALDNEK SNGTIIHVKG KHLCPSPLFP GPSKPFWVLV
VVGGVLACYS LLVTVAFIIF WVRSKRSRLL HSDYMNMTPR RPGPTRKHYQ
PYAPPRDFAA YRSRVKFSRS ADAPAYQQGQ NQLYNELNLG RREEYDVLDK
RRGRDPEMGG KPRRKNPQEG LYNELQKDKM AEAYSEIGMK GERRRGKGHD
GLYQGLSTAT KDTYDALHMQ ALPPR

**Clone NM-26562 HC DNA (SEQ ID NO: 327)**

CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCA
CCTGTACTGTCTCTGGTGGCTCCATCGGGAGTGGTGGTAGTTACTGGAGCTGGATCCGCCA
GCACCCAGGGAAGGGCCTGGAGTGGATTGGGTTGATCTATTACGATGGGAGCACCTACTAC
AACCCGTCCCTCAAGAGTCGAGTTACCATATCAGTAGACACGTCTAAGAACCAGTTCTCCC
TGAAGCTGAGTTCTGTGACCGCCGCAGACACGGCGGTGTACTACTGCGCCAGAGGCAGGGG
ATATGAGACTTCTTTAGCCTTCGATATCTGGGGTCAGGGTACAATGGTCACCGTCTCCTCA

**Clone NM-26562 HC (SEQ ID NO: 328). CDRs 1, 2, and 3 are underlined.**

QVQLQESGPGLVKPSQTLSLTCTVSGGSIGSGGSYWSWIRQHPGKGLEWIGLIYYDGSTY
YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGRGYETSLAFDIWGQGTMVTVS
S

GSIGSGGSYWS (SEQ ID NO: 329) (HC CDR1)

LIYYDGSTYYNPSLKS (SEQ ID NO: 330) (HC CDR2)

ARGRGYETSLAFDI (SEQ ID NO: 331) (HC CDR3)

**Clone NM-26562 LC DNA (SEQ ID NO: 332)**

GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCC
TCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCTACTTAGCCTGGTACCAACAGAAACCTGG
CCAGGCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGG
TTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAG
ATTTTGCAGTTTATTACTGTCAGCAGAGACACGTCTGGCCTCCTACTTTTGGCGGAGGGAC
CAAGGTTGAGATCAAACGG

**Clone NM-26562 LC (SEQ ID NO: 333). CDRs 1, 2, and 3 are underlined.**

EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA
RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRHVWPPTFGGGTKVEIKR

RASQSVSSYLA (SEQ ID NO: 334) (LC CDR1)

DASNRAT (SEQ ID NO: 335) (LC CDR2)

QQRHVWPPT (SEQ ID NO: 336) (LC CDR3)

**Clone NM-26562 CAR DNA HxL (SEQ ID NO: 337)**

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCC
CGCAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCT
CACCTGTACTGTCTCTGGTGGCTCCATCGGGAGTGGTGGTAGTTACTGGAGCTGGATCCGC
CAGCACCCAGGGAAGGGCCTGGAGTGGATTGGGTTGATCTATTACGATGGGAGCACCTACT
ACAACCCGTCCCTCAAGAGTCGAGTTACCATATCAGTAGACACGTCTAAGAACCAGTTCTC
CCTGAAGCTGAGTTCTGTGACCGCCGCAGACACGGCGGTGTACTACTGCGCCAGAGGCAGG
GGATATGAGACTTCTTTAGCCTTCGATATCTGGGGTCAGGGTACAATGGTCACCGTCTCCT

CAGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGAAAT
TGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCC
TGCAGGGCCAGTCAGAGTGTTAGCAGCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGG
CTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTCAG
TGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGATTTT
GCAGTTTATTACTGTCAGCAGAGACACGTCTGGCCTCCTACTTTTGGCGGAGGGACCAAGG
TTGAGATCAAACGGGCCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTCACGT
GAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTG
TTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAA
TCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCC
ACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCT
GCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCC
AGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGACAA
GCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGT
CTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAG
GAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTACGAA
GGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

**Clone NM-26562 CAR HxL (SEQ ID NO: 338)**

MALPVTALLL PLALLLHAAR PQVQLQESGP GLVKPSQTLS LTCTVSGGSI
GSGGSYWSWI RQHPGKGLEW IGLIYYDGST YYNPSLKSRV TISVDTSKNQ
FSLKLSSVTA ADTAVYYCAR GRGYETSLAF DIWGQGTMVT VSSGSTSGSG
KPGSGEGSTK GEIVLTQSPA TLSLSPGERA TLSCRASQSV SSYLAWYQQK
PGQAPRLLIY DASNRATGIP ARFSGSGSGT DFTLTISSLE PEDFAVYYCQ
QRHVWPPTFG GGTKVEIKRA AALDNEKSNG TIIHVKGKHL CPSPLFPGPS
KPFWVLVVVG GVLACYSLLV TVAFIIFWVR SKRSRLLHSD YMNMTPRRPG
PTRKHYQPYA PPRDFAAYRS RVKFSRSADA PAYQQGQNQL YNELNLGRRE
EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA YSEIGMKGER
RRGKGHDGLY QGLSTATKDT YDALHMQALP PR

**Clone NM-26562 CAR DNA LxH (SEQ ID NO: 339)**

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCC
CGGAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCAC
CCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCTACTTAGCCTGGTACCAACAGAAACCT
GGCCAGGCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCA
GGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGA
AGATTTTGCAGTTTATTACTGTCAGCAGAGACACGTCTGGCCTCCTACTTTTGGCGGAGGG
ACCAAGGTTGAGATCAAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAG
GTAGTACAAAGGGGCAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACA
GACCCTGTCCCTCACCTGTACTGTCTCTGGTGGCTCCATCGGGAGTGGTGGTAGTTACTGG
AGCTGGATCCGCCAGCACCCAGGGAAGGGCCTGGAGTGGATTGGGTTGATCTATTACGATG
GGAGCACCTACTACAACCCGTCCCTCAAGAGTCGAGTTACCATATCAGTAGACACGTCTAA
GAACCAGTTCTCCCTGAAGCTGAGTTCTGTGACCGCCGCAGACACGGCGGTGTACTACTGC
GCCAGAGGCAGGGGATATGAGACTTCTTTAGCCTTCGATATCTGGGGTCAGGGTACAATGG
TCACCGTCTCCTCAGCCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTCACGT
GAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTG
TTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAA
TCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCC
ACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCT
GCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCC
AGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGACAA
GCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGT
CTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAG
GAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTACGAA
GGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

**Clone NM-26562 CAR LxH (SEQ ID NO: 340)**

MALPVTALLL PLALLLHAAR PEIVLTQSPA TLSLSPGERA TLSCRASQSV
SSYLAWYQQK PGQAPRLLIY DASNRATGIP ARFSGSGSGT DFTLTISSLE
PEDFAVYYCQ QRHVWPPTFG GGTKVEIKRG STSGSGKPGS GEGSTKGQVQ
LQESGPGLVK PSQTLSLTCT VSGGSIGSGG SYWSWIRQHP GKGLEWIGLI
YYDGSTYYNP SLKSRVTISV DTSKNQFSLK LSSVTAADTA VYYCARGRGY
ETSLAFDIWG QGTMVTVSSA AALDNEKSNG TIIHVKGKHL CPSPLFPGPS
KPFWVLVVVG GVLACYSLLV TVAFIIFWVR SKRSRLLHSD YMNMTPRRPG
PTRKHYQPYA PPRDFAAYRS RVKFSRSADA PAYQQGQNQL YNELNLGRRE
EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA YSEIGMKGER
RRGKGHDGLY QGLSTATKDT YDALHMQALP PR

**Clone TS-26564 HC DNA (SEQ ID NO: 341)**

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCT
CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCGCCAGGCTCC
AGGGAAGGGGCTGGAGTGGGTTTCAACCATTAGTAGTAGTAGTAGTATCATATACTACGCA
GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACTCACTGTATCTGC
AAATGAACAGCCTGAGAGCTGAGGACACGGCGGTGTACTACTGCGCCAGAGGTTCTCAGGA
GCACCTGATTTTCGATTATTGGGGACAGGGTACATTGGTCACCGTCTCCTCA

**Clone TS-26564 HC (SEQ ID NO: 342). CDRs 1, 2, and 3 are underlined.**

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSTISSSSSIIYY
ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGSQEHLIFDYWGQGTLVTVSS

FTFSSYSMN (SEQ ID NO: 343) (HC CDR1)

TISSSSSIIYYADSVKG (SEQ ID NO: 344) (HC CDR2)

ARGSQEHLIFDY (SEQ ID NO: 345) (HC CDR3)

**Clone TS-26564 LC DNA (SEQ ID NO: 346)**

GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCC
TCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGGTACTTAGCCTGGTACCAACAGAAACCTGG
CCAGGCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGG
TTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAG
ATTTTGCAGTTTATTACTGTCAGCAGAGATTCTACTACCCTTGGACTTTTGGCGGAGGGAC
CAAGGTTGAGATCAAACGG

**Clone TS-26564 LC (SEQ ID NO: 347). CDRs 1, 2, and 3 are underlined.**

EIVLTQSPATLSLSPGERATLSCRASQSVSRYLAWYQQKPGQAPRLLIYDASNRATGIPA
RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRFYYPWTFGGGTKVEIKR

RASQSVSRYLA (SEQ ID NO: 348) (LC CDR1)

DASNRAT (SEQ ID NO: 349) (LC CDR2)

QQRFYYPWT (SEQ ID NO: 350) (LC CDR3)

**Clone TS-26564 CAR DNA HxL (SEQ ID NO: 351)**

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCC
CGGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACT
CTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCGCCAGGCT
CCAGGGAAGGGGCTGGAGTGGGTTTCAACCATTAGTAGTAGTAGTAGTATCATATACTACG
CAGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACTCACTGTATCT
GCAAATGAACAGCCTGAGAGCTGAGGACACGGCGGTGTACTACTGCGCCAGAGGTTCTCAG
GAGCACCTGATTTTCGATTATTGGGGACAGGGTACATTGGTCACCGTCTCCTCAGGGTCTA
CATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGAAATTGTGTTGAC
ACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCC
AGTCAGAGTGTTAGCAGGTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGC
TCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTCAGTGGCAGTGG
GTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGATTTTGCAGTTTAT
TACTGTCAGCAGAGATTCTACTACCCTTGGACTTTTGGCGGAGGGACCAAGGTTGAGATCA
AACGGGCCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAA
GCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTA
GTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGG
TTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCC
TGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCTGCCTATCGG
AGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAAC
TGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGG
ACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAAT
GAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGA
GAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTA
TGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

**Clone TS-26564 CAR HxL (SEQ ID NO: 352)**

MALPVTALLL PLALLLHAAR PEVQLVESGG GLVQPGGSLR LSCAASGFTF
SSYSMNWVRQ APGKGLEWVS TISSSSSIIY YADSVKGRFT ISRDNAKNSL
YLQMNSLRAE DTAVYYCARG SQEHLIFDYW GQGTLVTVSS GSTSGSGKPG
SGEGSTKGEI VLTQSPATLS LSPGERATLS CRASQSVSRY LAWYQQKPGQ
APRLLIYDAS NRATGIPARF SGSGSGTDFT LTISSLEPED FAVYYCQQRF
YYPWTFGGGT KVEIKRAAAL DNEKSNGTII HVKGKHLCPS PLFPGPSKPF
WVLVVVGGVL ACYSLLVTVA FIIFWVRSKR SRLLHSDYMN MTPRRPGPTR
KHYQPYAPPR DFAAYRSRVK FSRSADAPAY QQGQNQLYNE LNLGRREEYD
VLDKRRGRDP EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRG
KGHDGLYQGL STATKDTYDA LHMQALPPR

Clone TS-26564 CAR DNA LxH (SEQ ID NO: 353)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCC
CGGAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCAC
CCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGGTACTTAGCCTGGTACCAACAGAAACCT
GGCCAGGCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCA
GGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGA
AGATTTTGCAGTTTATTACTGTCAGCAGAGATTCTACTACCCTTGGACTTTTGGCGGAGGG
ACCAAGGTTGAGATCAAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAG
GTAGTACAAAGGGGGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGG
GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGG
GTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTTCAACCATTAGTAGTAGTAGTAGTA
TCATATACTACGCAGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAA
CTCACTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCGGTGTACTACTGCGCC
AGAGGTTCTCAGGAGCACCTGATTTTCGATTATTGGGGACAGGGTACATTGGTCACCGTCT
CCTCAGCCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAA
GCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTA
GTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGG
TTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCC
TGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCTGCCTATCGG
AGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAAC
TGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGG
ACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAAT
GAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGA
GAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTA
TGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

Clone TS-26564 CAR LxH (SEQ ID NO: 354)

MALPVTALLL PLALLLHAAR PEIVLTQSPA TLSLSPGERA TLSCRASQSV
SRYLAWYQQK PGQAPRLLIY DASNRATGIP ARFSGSGSGT DFTLTISSLE
PEDFAVYYCQ QRFYYPWTFG GGTKVEIKRG STSGSGKPGS GEGSTKGEVQ
LVESGGGLVQ PGGSLRLSCA ASGFTFSSYS MNWVRQAPGK GLEWVSTISS
SSSIIYYADS VKGRFTISRD NAKNSLYLQM NSLRAEDTAV YYCARGSQEH
LIFDYWGQGT LVTVSSAAAL DNEKSNGTII HVKGKHLCPS PLFPGPSKPF
WVLVVVGGVL ACYSLLVTVA FIIFWVRSKR SRLLHSDYMN MTPRRPGPTR
KHYQPYAPPR DFAAYRSRVK FSRSADAPAY QQGQNQLYNE LNLGRREEYD
VLDKRRGRDP EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRG
KGHDGLYQGL STATKDTYDA LHMQALPPR

**Clone RY-26568 HC DNA (SEQ ID NO: 355)**

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT
CCTGTGCAGCGTCTGGATTCACCTTCGGGAGCTATGGCATGCACTGGGTCCGCCAGGCTCC
AGGCAAGGGGCTGGAGTGGGTGGCAGTTATACATTATGATGGAAGTGTTGAATACTATGCA
GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGGACACGCTGTATCTGC
AAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCCAGAACTGACTTCTG
GAGCGGATCCCCTCCAAGCTTAGATTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA

**Clone RY-26568 HC (SEQ ID NO: 356). CDRs 1, 2, and 3 are underlined.**

QVQLVESGGG VVQPGRSLRL SCAASGFTFG SYGMHWVRQA PGKGLEWVAV
IHYDGSVEYY ADSVKGRFTI SRDNSKDTLY LQMNSLRAED TAVYYCARTD
FWSGSPPSLD YWGQGTLVTV SS

FTFGSYGMH (SEQ ID NO: 357) (HC CDR1)

VIHYDGSVEYYADSVKG (SEQ ID NO: 358) (HC CDR2)

ARTDFWSGSPPSLDY (SEQ ID NO: 359) (HC CDR3)

**Clone RY-26568 LC DNA (SEQ ID NO: 360)**

GACATCCAGTTGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCA
TCACTTGTCGGGCGAGTCGGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGG
GAAAGCCCCTAAGCTCCTGATCTATGGTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGG
TTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAG
ATTTTGCAACTTATTACTGTCAGCAGATATACACCTTCCCTTTCACTTTTGGCGGAGGGAC
CAAGGTTGAGATCAAACGG

**Clone RY-26568 LC (SEQ ID NO: 361). CDRs 1, 2, and 3 are underlined.**

DIQLTQSPSSVSASVGDRVTITCRASRGISSWLAWYQQKPGKAPKLLIYGASSLQSGVPSR
FSGSGSGTDFTLTISSLQPEDFATYYCQQIYTFPFTFGGGTKVEIKR

RASRGISSWLA (SEQ ID NO: 362) (LC CDR1)

GASSLQS (SEQ ID NO: 363) (LC CDR2)

QQIYTFPFT (SEQ ID NO: 364) (LC CDR3)

**Clone RY-26568 CAR DNA HxL (SEQ ID NO: 365)**

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCC
CGCAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACT
CTCCTGTGCAGCGTCTGGATTCACCTTCGGGAGCTATGGCATGCACTGGGTCCGCCAGGCT
CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATACATTATGATGGAAGTGTTGAATACTATG
CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGGACACGCTGTATCT
GCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCCAGAACTGACTTC
TGGAGCGGATCCCCTCCAAGCTTAGATTACTGGGGACAGGGTACATTGGTCACCGTCTCCT
CAGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGACAT

CCAGTTGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT
TGTCGGGCGAGTCGGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAG
CCCCTAAGCTCCTGATCTATGGTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAG
CGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTT
GCAACTTATTACTGTCAGCAGATATACACCTTCCCTTTCACTTTTGGCGGAGGGACCAAGG
TTGAGATCAAACGGGCCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTCACGT
GAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTG
TTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAA
TCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCC
ACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCT
GCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCC
AGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGACAA
GCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGT
CTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAG
GAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTACGAA
GGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

**Clone RY-26568 CAR HxL (SEQ ID NO: 366)**

MALPVTALLL PLALLLHAAR PQVQLVESGG GVVQPGRSLR LSCAASGFTF
GSYGMHWVRQ APGKGLEWVA VIHYDGSVEY YADSVKGRFT ISRDNSKDTL
YLQMNSLRAE DTAVYYCART DFWSGSPPSL DYWGQGTLVT VSSGSTSGSG
KPGSGEGSTK GDIQLTQSPS SVSASVGDRV TITCRASRGI SSWLAWYQQK
PGKAPKLLIY GASSLQSGVP SRFSGSGSGT DFTLTISSLQ PEDFATYYCQ
QIYTFPFTFG GGTKVEIKRA AALDNEKSNG TIIHVKGKHL CPSPLFPGPS
KPFWVLVVVG GVLACYSLLV TVAFIIFWVR SKRSRLLHSD YMNMTPRRPG
PTRKHYQPYA PPRDFAAYRS RVKFSRSADA PAYQQGQNQL YNELNLGRRE
EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA YSEIGMKGER
RRGKGHDGLY QGLSTATKDT YDALHMQALP PR

**Clone RY-26568 CAR DNA LxH (SEQ ID NO: 367)**

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCC
CGGACATCCAGTTGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCAC
CATCACTTGTCGGGCGAGTCGGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGGTGCATCCAGTTTGCAAAGTGGGGTCCCATCAA
GGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGA
AGATTTTGCAACTTATTACTGTCAGCAGATATACACCTTCCCTTTCACTTTTGGCGGAGGG
ACCAAGGTTGAGATCAAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAG
GTAGTACAAAGGGGCAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAG
GTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCGGGAGCTATGGCATGCACTGG
GTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATACATTATGATGGAAGTG
TTGAATACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGGA
CACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCC
AGAACTGACTTCTGGAGCGGATCCCCTCCAAGCTTAGATTACTGGGGACAGGGTACATTGG
TCACCGTCTCCTCAGCCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTCACGT
GAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTG
TTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAA
TCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCC
ACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCT
GCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCC
AGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGACAA
GCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGT
CTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAG
GAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTACGAA
GGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

**Clone RY-26568 CAR LxH (SEQ ID NO: 368)**

MALPVTALLL PLALLLHAAR PDIQLTQSPS SVSASVGDRV TITCRASRGI
SSWLAWYQQK PGKAPKLLIY GASSLQSGVP SRFSGSGSGT DFTLTISSLQ
PEDFATYYCQ QIYTFPFTFG GGTKVEIKRG STSGSGKPGS GEGSTKGQVQ
LVESGGGVVQ PGRSLRLSCA ASGFTFGSYG MHWVRQAPGK GLEWVAVIHY
DGSVEYYADS VKGRFTISRD NSKDTLYLQM NSLRAEDTAV YYCARTDFWS
GSPPSLDYWG QGTLVTVSSA AALDNEKSNG TIIHVKGKHL CPSPLFPGPS
KPFWVLVVVG GVLACYSLLV TVAFIIFWVR SKRSRLLHSD YMNMTPRRPG
PTRKHYQPYA PPRDFAAYRS RVKFSRSADA PAYQQGQNQL YNELNLGRRE
EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA YSEIGMKGER
RRGKGHDGLY QGLSTATKDT YDALHMQALP PR

**Clone PP-26575 HC DNA (SEQ ID NO: 369)**

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT
CCTGCAAGGCTTCTGGAGGCACCCTCAGCAGCCTGGCTATCAGCTGGGTGCGACAGGCCCC
TGGACAAGGGCTTGAGTGGATGGGAGGGGTCATCCCTATCTTGGGTCGGGCAAACTACGCA
CAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAGTCCACGAGCACAGCCTACATGG
AGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGAACTCCTGAATA
CTCCTCCAGCATATGGCACTATTACTACGGCATGGACGTATGGGGCCAGGGAACAACTGTC
ACCGTCTCCTCA

**Clone PP-26575 HC (SEQ ID NO: 370). CDRs 1, 2, and 3 are underlined.**

QVQLVQSGAEVKKPGSSVKVSCKASGGTLSSLAISWVRQAPGQGLEWMGGVIPILGRANYA
QKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARTPEYSSSIWHYYYGMDVWGQGTTV
TVSS

GTLSSLAIS (SEQ ID NO: 371) (HC CDR1)

GVIPILGRANYAQKFQG (SEQ ID NO: 372) (HC CDR2)

ARTPEYSSSIWHYYYGMDV (SEQ ID NO: 373) (HC CDR3)

**Clone PP-26575 LC DNA (SEQ ID NO: 374)**

GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCA
TCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCTTG
GTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAA
TCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCA
GCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTTCGCCCACACTCCTTT
CACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGG

**Clone PP-26575 LC (SEQ ID NO: 375). CDRs 1, 2, and 3 are underlined.**

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR
ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQFAHTPFTFGGGTKVEIKR

KSSQSVLYSSNNKNYLA (SEQ ID NO: 376) (LC CDR1)

WASTRES (SEQ ID NO: 377) (LC CDR2)

QQFAHTPFT (SEQ ID NO: 378) (LC CDR3)

**Clone PP-26575 CAR DNA HxL (SEQ ID NO: 379)**

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCC
CGCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGT
CTCCTGCAAGGCTTCTGGAGGCACCCTCAGCAGCCTGGCTATCAGCTGGGTGCGACAGGCC
CCTGGACAAGGGCTTGAGTGGATGGGAGGGGTCATCCCTATCTTGGGTCGGGCAAACTACG
CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAGTCCACGAGCACAGCCTACAT
GGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGAACTCCTGAA
TACTCCTCCAGCATATGGCACTATTACTACGGCATGGACGTATGGGGCCAGGGAACAACTG

TCACCGTCTCCTCAGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTAC
AAAGGGGGACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGG
GCCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACT
TAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTAC
CCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTC
ACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTTCGCCCACA
CTCCTTTCACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGGCCGCTGCCCTTGATAA
TGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTG
TTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTT
ACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCT
GCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTAC
CAGCCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGAT
CTGCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGG
ACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGC
AAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGG
CTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGG
TTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCC
CTGCCACCTAGG

**Clone PP-26575 CAR HxL (SEQ ID NO: 380)**

MALPVTALLL PLALLLHAAR PQVQLVQSGA EVKKPGSSVK VSCKASGGTL
SSLAISWVRQ APGQGLEWMG GVIPILGRAN YAQKFQGRVT ITADESTSTA
YMELSSLRSE DTAVYYCART PEYSSSIWHY YYGMDVWGQG TTVTVSSGST
SGSGKPGSGE GSTKGDIVMT QSPDSLAVSL GERATINCKS SQSVLYSSNN
KNYLAWYQQK PGQPPKLLIY WASTRESGVP DRFSGSGSGT DFTLTISSLQ
AEDVAVYYCQ QFAHTPFTFG GGTKVEIKRA AALDNEKSNG TIIHVKGKHL
CPSPLFPGPS KPFWVLVVVG GVLACYSLLV TVAFIIFWVR SKRSRLLHSD
YMNMTPRRPG PTRKHYQPYA PPRDFAAYRS RVKFSRSADA PAYQQGQNQL
YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA
YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR

**Clone PP-26575 CAR DNA LxH (SEQ ID NO: 381)**

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCC
CGGACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCAC
CATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT
TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGG
AATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCAT
CAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTTCGCCCACACTCCT
TTCACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGGGGTCTACATCCGGCTCCGGGA
AGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGCAGGTGCAGCTGGTGCAGTCTGGGGCTGA
GGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCTTCTGGAGGCACCCTCAGC
AGCCTGGCTATCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAGGGG
TCATCCCTATCTTGGGTCGGGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTAC
CGCGGACGAGTCCACGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACG
GCGGTGTACTACTGCGCCAGAACTCCTGAATACTCCTCCAGCATATGGCACTATTACTACG
GCATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCAGCCGCTGCCCTTGATAA
TGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTG
TTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTT
ACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCT
GCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTAC
CAGCCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGAT
CTGCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGG
ACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGC
AAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGG
CTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGG
TTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCC
CTGCCACCTAGG

**Clone PP-26575 CAR LxH (SEQ ID NO: 382)**

MALPVTALLL PLALLLHAAR PDIVMTQSPD SLAVSLGERA TINCKSSQSV
LYSSNNKNYL AWYQQKPGQP PKLLIYWAST RESGVPDRFS GSGSGTDFTL
TISSLQAEDV AVYYCQQFAH TPFTFGGGTK VEIKRGSTSG SGKPGSGEGS
TKGQVQLVQS GAEVKKPGSS VKVSCKASGG TLSSLAISWV RQAPGQGLEW
MGGVIPILGR ANYAQKFQGR VTITADESTS TAYMELSSLR SEDTAVYYCA
RTPEYSSSIW HYYYGMDVWG QGTTVTVSSA AALDNEKSNG TIIHVKGKHL
CPSPLFPGPS KPFWVLVVVG GVLACYSLLV TVAFIIFWVR SKRSRLLHSD
YMNMTPRRPG PTRKHYQPYA PPRDFAAYRS RVKFSRSADA PAYQQGQNQL
YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA
YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR

**Clone RD-26576 HC DNA (SEQ ID NO: 383)**

CAGGTGCGGCTGGTGGAGTCTGGGGGGGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT
CCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATACACTGGGTCCGCCAGGCTCC
AGGCAAGGGGCTGGAGTGGGTGGCAGTTATAGGGTATGATGGACAGGAGAAATACTATGCA
GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAAGGGGCCGTTGCA
GGAGCCGCCATACGCTTTTGGGATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCC
TCA

**Clone RD-26576 HC (SEQ ID NO: 384). CDRs 1, 2, and 3 are underlined.**

QVRLVESGGGVVQPGRSLRLSCAASGFTFSSYGIHWVRQAPGKGLEWVAVIGYDGQEKYYA
DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVKGPLQEPPYAFGMDVWGQGTTVTVS
S

FTFSSYGIH (SEQ ID NO: 385) (HC CDR1)

VIGYDGQEKYYADSVKG (SEQ ID NO: 386) (HC CDR2)

VKGPLQEPPYAFGMDV (SEQ ID NO: 387) (HC CDR3)

**Clone RD-26576 LC DNA (SEQ ID NO: 388)**

GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCC
TCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGG
CCAGGCTCCCAGGCTCCTCATCTATAGCGCATCCACCAGGGCCACTGGTATCCCAGCCAGG
TTCAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAG
ATTTTGCAGTTTATTACTGTCAGCAGCACCACGTCTGGCCTCTCACTTTTGGCGGAGGGAC
CAAGGTTGAGATCAAACGG

**Clone RD-26576 LC (SEQ ID NO: 389). CDRs 1, 2, and 3 are underlined.**

EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYSASTRATGIPA
RFSGSGSGTEFTLTISSLQSEDFAVYYCQQHHVWPLTFGGGTKVEIKR

RASQSVSSNLA (SEQ ID NO: 390) (LC CDR1)

SASTRAT (SEQ ID NO: 391) (LC CDR2)

QQHHVWPLT (SEQ ID NO: 392) (LC CDR3)

**Clone RD-26576 CAR DNA HxL (SEQ ID NO: 393)**

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCC
CGCAGGTGCGGCTGGTGGAGTCTGGGGGGGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACT
CTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATACACTGGGTCCGCCAGGCT
CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATAGGGTATGATGGACAGGAGAAATACTATG
CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCT
GCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAAGGGGCCGTTG
CAGGAGCCGCCATACGCTTTTGGGATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCT

CCTCAGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGA
AATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTC
TCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCC
AGGCTCCCAGGCTCCTCATCTATAGCGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTT
CAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGAT
TTTGCAGTTTATTACTGTCAGCAGCACCACGTCTGGCCTCTCACTTTTGGCGGAGGGACCA
AGGTTGAGATCAAACGGGCCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTCA
CGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGG
GTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTA
TAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGAC
TCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTC
GCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGG
GCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGA
CAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAG
GGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGA
AAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTAC
GAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

**Clone RD-26576 CAR HxL (SEQ ID NO: 394)**

MALPVTALLL PLALLLHAAR PQVRLVESGG GVVQPGRSLR LSCAASGFTF
SSYGIHWVRQ APGKGLEWVA VIGYDGQEKY YADSVKGRFT ISRDNSKNTL
YLQMNSLRAE DTAVYYCVKG PLQEPPYAFG MDVWGQGTTV TVSSGSTSGS
GKPGSGEGST KGEIVMTQSP ATLSVSPGER ATLSCRASQS VSSNLAWYQQ
KPGQAPRLLI YSASTRATGI PARFSGSGSG TEFTLTISSL QSEDFAVYYC
QQHHVWPLTF GGGTKVEIKR AAALDNEKSN GTIIHVKGKH LCPSPLFPGP
SKPFWVLVVV GGVLACYSLL VTVAFIIFWV RSKRSRLLHS DYMNMTPRRP
GPTRKHYQPY APPRDFAAYR SRVKFSRSAD APAYQQGQNQ LYNELNLGRR
EEYDVLDKRR GRDPEMGGKP RRKNPQEGLY NELQKDKMAE AYSEIGMKGE
RRRGKGHDGL YQGLSTATKD TYDALHMQAL PPR

Clone RD-26576 CAR DNA LxH (SEQ ID NO: 395)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCC
CGGAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCAC
CCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCT
GGCCAGGCTCCCAGGCTCCTCATCTATAGCGCATCCACCAGGGCCACTGGTATCCCAGCCA
GGTTCAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGA
AGATTTTGCAGTTTATTACTGTCAGCAGCACCACGTCTGGCCTCTCACTTTTGGCGGAGGG
ACCAAGGTTGAGATCAAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAG
GTAGTACAAAGGGGCAGGTGCGGCTGGTGGAGTCTGGGGGGGGCGTGGTCCAGCCTGGGAG
GTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATACACTGG
GTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATAGGGTATGATGGACAGG
AGAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAA
CACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTC
AAGGGGCCGTTGCAGGAGCCGCCATACGCTTTTGGGATGGACGTATGGGGCCAGGGAACAA
CTGTCACCGTCTCCTCAGCCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTCA
CGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGG
GTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTA
TAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGAC
TCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTC
GCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGG
GCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGA
CAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAG
GGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGA
AAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTAC
GAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

Clone RD-26576 CAR LxH (SEQ ID NO: 396)

MALPVTALLL PLALLLHAAR PEIVMTQSPA TLSVSPGERA TLSCRASQSV
SSNLAWYQQK PGQAPRLLIY SASTRATGIP ARFSGSGSGT EFTLTISSLQ
SEDFAVYYCQ QHHVWPLTFG GGTKVEIKRG STSGSGKPGS GEGSTKGQVR
LVESGGGVVQ PGRSLRLSCA ASGFTFSSYG IHWVRQAPGK GLEWVAVIGY
DGQEKYYADS VKGRFTISRD NSKNTLYLQM NSLRAEDTAV YYCVKGPLQE
PPYAFGMDVW GQGTTVTVSS AAALDNEKSN GTIIHVKGKH LCPSPLFPGP
SKPFWVLVVV GGVLACYSLL VTVAFIIFWV RSKRSRLLHS DYMNMTPRRP
GPTRKHYQPY APPRDFAAYR SRVKFSRSAD APAYQQGQNQ LYNELNLGRR
EEYDVLDKRR GRDPEMGGKP RRKNPQEGLY NELQKDKMAE AYSEIGMKGE
RRRGKGHDGL YQGLSTATKD TYDALHMQAL PPR

**Clone RD-26578 HC DNA (SEQ ID NO: 397)**

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT
CCTGTGCAGCGTCTGGATTCACCTTCAGTAGCCGTGGCATGCACTGGGTCCGCCAGGCTCC
AGGCAAGGGGCTGGAGTGGGTGGCAGTTATAGGGTATGATGGACAGGAGAAATACTATGCA
GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAAGGGGCCGTTGCA
GGAGCCGCCATACGATTATGGAATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCC
TCA

**Clone RD-26578 HC (SEQ ID NO: 398) CDRs 1, 2, and 3 are underlined.**

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSRGMHWVRQAPGKGLEWVAVIGYDGQEKYYA
DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVKGPLQEPPYDYGMDVWGQGTTVTVS
S

FTFSSRGMH (SEQ ID NO: 399) (HC CDR1)

VIGYDGQEKYYADSVKG (SEQ ID NO: 400) (HC CDR2)

VKGPLQEPPYDYGMDV (SEQ ID NO: 401) (HC CDR3)

**Clone RD-26578 LC DNA (SEQ ID NO: 402)**

GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCC
TCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGG
CCAGGCTCCCAGGCTCCTCATCTATAGCGCATCCACCAGGGCCACTGGTATCCCAGCCAGG
TTCAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAG
ATTTTGCAGTTTATTACTGTCAGCAGCACCACGTCTGGCCTCTCACTTTTGGCGGAGGGAC
CAAGGTTGAGATCAAACGG

**Clone RD-26578 LC (SEQ ID NO: 403). CDRs 1, 2, and 3 are underlined.**

EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYS
ASTRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQHHVWPLTFGGGTKVEIKR

RASQSVSSNLA (SEQ ID NO: 404) (LC CDR1)

SASTRAT (SEQ ID NO: 405) (LC CDR2)

QQHHVWPLT (SEQ ID NO: 406) (LC CDR3)

**Clone RD-26578 CAR DNA HxL (SEQ ID NO: 407)**

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCC
CGCAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACT
CTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCCGTGGCATGCACTGGGTCCGCCAGGCT
CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATAGGGTATGATGGACAGGAGAAATACTATG
CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCT
GCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAAGGGGCCGTTG
CAGGAGCCGCCATACGATTATGGAATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCT
CCTCAGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGA
AATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTC
TCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCC
AGGCTCCCAGGCTCCTCATCTATAGCGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTT
CAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGAT
TTTGCAGTTTATTACTGTCAGCAGCACCACGTCTGGCCTCTCACTTTTGGCGGAGGGACCA
AGGTTGAGATCAAACGGGCCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTCA
CGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGG
GTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTA
TAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGAC
TCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTC
GCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGG
GCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGA
CAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAG
GGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGA
AAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTAC
GAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

**Clone RD-26578 CAR HxL (SEQ ID NO: 408)**

MALPVTALLL PLALLLHAAR PQVQLVESGG GVVQPGRSLR LSCAASGFTF
SSRGMHWVRQ APGKGLEWVA VIGYDGQEKY YADSVKGRFT ISRDNSKNTL
YLQMNSLRAE DTAVYYCVKG PLQEPPYDYG MDVWGQGTTV TVSSGSTSGS
GKPGSGEGST KGEIVMTQSP ATLSVSPGER ATLSCRASQS VSSNLAWYQQ
KPGQAPRLLI YSASTRATGI PARFSGSGSG TEFTLTISSL QSEDFAVYYC
QQHHVWPLTF GGGTKVEIKR AAALDNEKSN GTIIHVKGKH LCPSPLFPGP
SKPFWVLVVV GGVLACYSLL VTVAFIIFWV RSKRSRLLHS DYMNMTPRRP
GPTRKHYQPY APPRDFAAYR SRVKFSRSAD APAYQQGQNQ LYNELNLGRR
EEYDVLDKRR GRDPEMGGKP RRKNPQEGLY NELQKDKMAE AYSEIGMKGE
RRRGKGHDGL YQGLSTATKD TYDALHMQAL PPR

Clone RD-26578 CAR DNA LxH (SEQ ID NO: 409)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCC
CGGAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCAC
CCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCT
GGCCAGGCTCCCAGGCTCCTCATCTATAGCGCATCCACCAGGGCCACTGGTATCCCAGCCA
GGTTCAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGA
AGATTTTGCAGTTTATTACTGTCAGCAGCACCACGTCTGGCCTCTCACTTTTGGCGGAGGG
ACCAAGGTTGAGATCAAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAG
GTAGTACAAAGGGGCAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAG
GTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCCGTGGCATGCACTGG
GTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATAGGGTATGATGGACAGG
AGAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAA
CACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTC
AAGGGGCCGTTGCAGGAGCCGCCATACGATTATGGAATGGACGTATGGGGCCAGGGAACAA
CTGTCACCGTCTCCTCAGCCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTCA
CGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGG
GTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTA
TAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGAC
TCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTC
GCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGG
GCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGA
CAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAG
GGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGA
AAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTAC
GAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

Clone RD-26578 CAR LxH (SEQ ID NO: 410)

MALPVTALLL PLALLLHAAR PEIVMTQSPA TLSVSPGERA TLSCRASQSV
SSNLAWYQQK PGQAPRLLIY SASTRATGIP ARFSGSGSGT EFTLTISSLQ
SEDFAVYYCQ QHHVWPLTFG GGTKVEIKRG STSGSGKPGS GEGSTKGQVQ
LVESGGGVVQ PGRSLRLSCA ASGFTFSSRG MHWVRQAPGK GLEWVAVIGY
DGQEKYYADS VKGRFTISRD NSKNTLYLQM NSLRAEDTAV YYCVKGPLQE
PPYDYGMDVW GQGTTVTVSS AAALDNEKSN GTIIHVKGKH LCPSPLFPGP
SKPFWVLVVV GGVLACYSLL VTVAFIIFWV RSKRSRLLHS DYMNMTPRRP
GPTRKHYQPY APPRDFAAYR SRVKFSRSAD APAYQQGQNQ LYNELNLGRR
EEYDVLDKRR GRDPEMGGKP RRKNPQEGLY NELQKDKMAE AYSEIGMKGE
RRRGKGHDGL YQGLSTATKD TYDALHMQAL PPR

CLAIMS

What is claimed is:

1. An isolated polynucleotide encoding a chimeric antigen receptor (CAR) or T cell receptor (TCR) comprising an antigen binding molecule that specifically binds to B-cell maturation antigen (BCMA), wherein the antigen binding molecule comprises:

(a) a heavy chain variable region (VH) complementarity determining region (CDR) 1 comprising, consisting of, or consisting essentially of the amino acid sequence $GX_2X_3X_4X_5X_6X_7SY$ (SEQ ID NO: 145), wherein:

$X_2$ is not present or G;

$X_3$ is not present or S;

$X_4$ is F, G, I, or Y;

$X_5$ is S or T;

$X_6$ is F or S; and

$X_7$ is S or T; and/or

(b) a VH CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1IX_3X_4X_5X_6X_7X_8X_9X_{10}YX_{12}X_{13}X_{14}X_{15}X_{16}X_{17}$ (SEQ ID NO: 146), wherein:

$X_1$ is A, G, I, S, T, or V;

$X_3$ is I, N, or S;

$X_4$ is G, P, S, or Y;

$X_5$ is D, G, I, or S;

$X_6$ is F, G, or S;

$X_7$ is not present or G or S;

$X_8$ is N, S, or T;

$X_9$ is A, I, K, or T;

$X_{10}$ is N, S, or Y;

$X_{12}$ is A or N;

$X_{13}$ is D, P, or Q;

$X_{14}$ is K or S;

$X_{15}$ is F, L, or V;

$X_{16}$ is K or Q; and

$X_{17}$ is G or S; and/or

(c) a VH CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}DX_{19}$ (SEQ ID NO: 147), wherein:

$X_1$ is A or V;

$X_2$ is K or R;

$X_3$ is not present or D, G, or T;

$X_4$ is not present or A, D, G, P, R, or S;

$X_5$ is not present or E, F, G, L, Q, or T;

$X_6$ is not present or E, M, Q, W, or Y;

$X_7$ is not present or A, E, L, or S;

$X_8$ is not present or G, P, S, or T;

$X_9$ is not present or G, P, or S;

$X_{10}$ is not present or I, L, P, or Y;

$X_{11}$ is not present or W;

$X_{12}$ is not present or H;

$X_{13}$ is not present or E or Y;

$X_{14}$ is not present or D, G, H, P, S, W, or Y;

$X_{15}$ is A, G, L, W, or Y;

$X_{16}$ is not present or A, G, I, P, or V;

$X_{17}$ is F, L, or M; and

$X_{19}$ is I, L, V, or Y; and/or

(d) a light chain variable region (VL) CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2SQX_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}LX_{17}$ (SEQ ID NO: 148), wherein

$X_1$ is K or R;

$X_2$ is A or S;

$X_5$ is G or S;

$X_6$ is I, L, or V;

$X_7$ is L or S;

$X_8$ is not present or H or Y;

$X_9$ is not present or S;

$X_{10}$ is not present or N or S;

$X_{11}$ is not present or G or N;

$X_{12}$ is not present or N;

$X_{13}$ is not present or K or Y;

$X_{14}$ is N, R, or S;

$X_{15}$ is N, W, or Y; and

$X_{17}$ is A or D;

(e) a VL CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2SX_4X_5X_6X_7$ (SEQ ID NO: 149), wherein

$X_1$ is D, G, L, S, or W;

$X_2$ is A or G;

$X_4$ is N, S, or T;

$X_5$ is L or R;

$X_6$ is A, E, or Q; and

$X_7$ is S or T; and/or

(f) a VL CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1QX_3X_4X_5X_6PX_8T$ (SEQ ID NO: 150), wherein

$X_1$ is M or Q;

$X_3$ is F, G, H, I, R, or Y;

$X_4$ is A, F, H, I, L, or Y;

$X_5$ is A, G, H, S, T, V, or Y;

$X_6$ is F, L, T, W, or Y; and

$X_8$ is not present or F, L, P, or W.

2. The polynucleotide of claim 1, wherein the VH CDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 41-48.

3. An isolated polynucleotide encoding a chimeric antigen receptor (CAR) or T cell receptor (TCR) comprising an antigen binding molecule that specifically binds to B-cell maturation antigen (BCMA), wherein the antigen binding molecule comprises a VH CDR3 comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 41-48.

4. The polynucleotide of any one of claims 1 to 3, wherein the VH CDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 9-16.

5. The polynucleotide of any one of claims 1 to 4, wherein the VH CDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 25-32.

6. The polynucleotide of any one of claims 1 to 5, wherein the VL CDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 81-88.

7. The polynucleotide of any one of claims 1 to 6, wherein the VL CDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 97-104.

8. The polynucleotide of any one of claims 1 to 7, wherein the VL CDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 113-120.

9. The polynucleotide of any one of claims 1, 2, and 4 to 8, wherein the VH CDR1, VH CDR2, and VH CDR3 each comprise the amino acid sequence of the VH CDR1, VH CDR2, and VH CDR3 of an antibody in FIG. 1A or FIG. 1B.

10. The polynucleotide of any one of claims 1, 2, and 4 to 9, wherein the VL CDR1, VL CDR2, and VL CDR3 each comprise the amino acid sequence of the VL CDR1, VL CDR2, and VL CDR3 of an antibody in FIG. 1C.

11. The polynucleotide of any one of claims 1 to 10, wherein the antigen binding molecule comprises a heavy chain variable region sequence comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 65-72.

12. The polynucleotide of any one of claims 1 to 11, wherein the antigen binding molecule comprises a light chain variable region sequence comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 137-144.

13. The polynucleotide of any one of claims 1 to 12, wherein the antigen binding molecule comprises:

(a) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 9; a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 25; a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 41; a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 81; a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 97; and a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 113;

(b) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 10; a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 26; a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 42; a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 82; a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 98; and a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 114;

(c) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 11; a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 27; a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 43; a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 83; a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 99; and a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 115;

(d) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 12; a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 28; a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 44; a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 84; a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 100; and a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 116;

(e) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 13; a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 29; a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 45; a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 85; a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 101; and a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 117;

(f) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 14; a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 30; a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 46; a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 86; a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 102; and a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 118;

(g) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 15; a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 31; a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 47; a VL CDR1

region comprising the amino acid sequence of SEQ ID NO: 87; a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 103; and a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 119; or

(h) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 16; a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 32; a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 48; a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 88; a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 104; and a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 120.

14. The polynucleotide of any one of claims 1 to 13, wherein the antigen binding molecule comprises:

(a) a VH comprising the amino acid sequence of SEQ ID NO: 65; and a VL comprising the amino acid sequence of SEQ ID NO: 137;

(b) a VH comprising the amino acid sequence of SEQ ID NO: 66; and a VL comprising the amino acid sequence of SEQ ID NO: 138;

(c) a VH comprising the amino acid sequence of SEQ ID NO: 67; and a VL comprising the amino acid sequence of SEQ ID NO: 139;

(d) a VH comprising the amino acid sequence of SEQ ID NO: 68; and a VL comprising the amino acid sequence of SEQ ID NO: 140;

(e) a VH comprising the amino acid sequence of SEQ ID NO: 69; and a VL comprising the amino acid sequence of SEQ ID NO: 141;

(f) a VH comprising the amino acid sequence of SEQ ID NO: 70; and a VL comprising the amino acid sequence of SEQ ID NO: 142;

(g) a VH comprising the amino acid sequence of SEQ ID NO: 71; and a VL comprising the amino acid sequence of SEQ ID NO: 143; or

(h) a VH comprising the amino acid sequence of SEQ ID NO: 72; and a VL comprising the amino acid sequence of SEQ ID NO: 144.

15. The polynucleotide of claim 14, which 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 form the group consisting of SEQ ID NOs: 57-64.

16. The polynucleotide of claim 14 or 15, which 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 form the group consisting of SEQ ID NOs: 129-136.

17. The polynucleotide of any one of claims 1 to 16, wherein the antigen binding molecule is single chained.

18. The polynucleotide of any one of claims 1 to 17, wherein the antigen binding molecule is selected from the group consisting of scFv, Fab, Fab', Fv, F(ab')2, dAb, and any combination thereof.

19. The polynucleotide of any one of claims 1 to 18, wherein the antigen binding molecule comprises an scFv.

20. The polynucleotide of any one of claims 1 to 19, wherein the VH and the VL are connected by a linker.

21. The polynucleotide of claim 20, wherein the VH is located at the N terminus of the linker and the VL is located at the C terminus of the linker.

22. The polynucleotide of claim 20, wherein the VL is located at the N terminus of the linker and the VH is located at the N terminus of the linker.

23. The polynucleotide of any one of claims 20 to 22, wherein 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.

24. The polynucleotide of any one of claims 20 to 23, wherein the linker comprises an amino acid sequence at least 75%, at least 85%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 174.

25. The polynucleotide of any one of claims 1 to 24, wherein the antigen binding molecule binds to BCMA with a $K_D$ of less than about 1 x $10^{-6}$ M, less than about 1 x $10^{-7}$ M, less than about 1 x $10^{-8}$ M, or less than about 1 x $10^{-9}$ M.

26. The polynucleotide of any one of claims 1 to 25, wherein the TCR further comprises a CDR4.

27. The polynucleotide of any one of claims 1 to 26, wherein the TCR further comprises a constant region.

28. The polynucleotide of any one of claims 1 to 25, wherein the CAR comprises a transmembrane domain.

29. The polynucleotide of claim 28, wherein the transmembrane domain is a transmembrane domain of CD28, 4-1BB/CD137, CD8 alpha, CD4, CD19, CD3 epsilon, CD45, CD5, CD9, CD16, CD22, CD33, CD37, CD64, CD80, CD86, CD134, CD137, CD154, an alpha chain of a T cell receptor, a beta chain of a T cell receptor, a zeta chain of a T cell receptor, or any combination thereof.

30. The polynucleotide of claim 28 or 29, wherein the transmembrane domain is a CD28 transmembrane domain.

31. The polynucleotide of claim 30, wherein the CD28 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: 169.

32. The polynucleotide of claim 31, wherein the CD28 transmembrane 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: 168.

33. The polynucleotide of any one of claims 28 to 32, wherein the CAR comprises a hinge region between the transmembrane domain and the antigen binding molecule.

34. The polynucleotide of claim 33, wherein the hinge region is of IgG1, IgG2, IgG3, IgG4, IgA, IgD, IgE, IgM, CD28, or CD8 alpha.

35. The polynucleotide of claim 33 or 34, wherein the hinge region is of CD28.

36. The polynucleotide of claim 35, wherein the hinge region 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: 167.

37. The polynucleotide of claim 35 or 36, wherein the hinge region 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: 166.

38. The polynucleotide of any one of claims 1 to 37, wherein the CAR or TCR comprises a costimulatory region.

39. The polynucleotide of claim 38, wherein the costimulatory region is a signaling region of CD28, OX-40, 4-1BB/CD137, CD2, CD7, CD27, CD30, CD40, programmed death-1 (PD-1), inducible T cell costimulator (ICOS), lymphocyte function-associated antigen-1 (LFA-1 (CDl la/CD18), CD3 gamma, CD3 delta, CD3 epsilon, CD247, CD276 (B7-H3), LIGHT (tumor necrosis factor superfamily member 14; TNFSF14), NKG2C, Ig alpha (CD79a), DAP-10, Fc gamma receptor, MHC class I molecule, TNF receptor proteins, Immunoglobulin-like proteins, cytokine receptors, integrins, signaling lymphocytic activation molecules (SLAM proteins), activating NK cell receptors, BTLA, a Toll ligand receptor, ICAM-1, B7-H3, CDS, ICAM-1, GITR, BAFFR, LIGHT, HVEM (LIGHTR), KIRDS2, SLAMF7, NKp80 (KLRF1), NKp44, NKp30, NKp46, CD19, CD4, CD8alpha, CD8beta, IL2R beta, IL2R gamma, IL7R alpha, ITGA4, VLA1, CD49a, ITGA4, IA4, CD49D, ITGA6, VLA-6, CD49f, ITGAD, CDl ld, ITGAE, CD103, ITGAL, CDl la, LFA-1, ITGAM, CDl lb, ITGAX, CDl lc, ITGBl, CD29, ITGB2, CD18, LFA-1, ITGB7, NKG2D, TNFR2, TRANCE/RANKL, DNAM1 (CD226), SLAMF4 (CD244, 2B4), CD84, CD96 (Tactile), CEACAM1, CRT AM, Ly9 (CD229), CD160 (BY55), PSGL1, CD100 (SEMA4D), CD69, SLAMF6 (NTB-A, Lyl08), SLAM (SLAMF1, CD150, IPO-3), BLAME (SLAMF8), SELPLG (CD162), LTBR, LAT, GADS, SLP-76, PAG/Cbp, CD19a, a ligand that specifically binds with CD83, or any combination thereof.

40. The polynucleotide of claim 38 or 39, wherein the costimulatory region is a CD28 costimulatory region.

41. The polynucleotide of claim 38 or 39, wherein the costimulatory region is a 4-1BB/CD137 costimulatory region.

42. The polynucleotide of any one of claims 38 to 40, wherein the costimulatory region 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: 171.

43. The polynucleotide of claim 42, wherein the costimulatory region 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: 170.

44. The polynucleotide of any one of claims 1 to 43, wherein the CAR or TCR comprises an activation domain.

45. The polynucleotide of claim 44, wherein the activation domain is a CD3 zeta domain.

46. The polynucleotide of claim 44 or 45, 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: 173.

47. The polynucleotide of claim 45 or 46, wherein 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: 172.

48. The polynucleotide of any one of claims 1 to 47, wherein the CAR or TCR further comprises a leader peptide.

49. The polynucleotide of claim 48, 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: 165.

50. The polynucleotide of claim 48 or 49, wherein 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: 164.

51. A vector comprising the polynucleotide of any one of claims 1 to 50.

52. The vector of claim 51, which is a retroviral vector, a DNA vector, a plasmid, a RNA vector, an adenoviral vector, an adenovirus associated vector, a lentiviral vector, or any combination thereof.

53. A CAR or TCR encoded by the polynucleotide of any one of claims 1 to 50 or the vector of claim 51 or 52.

54. A cell comprising the polynucleotide of any one of claims 1 to 50, the vector of claim 51 or 52, the CAR or TCR of claim 53, or any combination thereof.

55. The cell of claim 54, wherein the cell comprises an immune cell.

56. The cell of claim 55, wherein the cell is a T cell.

57. The cell of claim 56, wherein the T cell is a tumor-infiltrating lymphocyte (TIL), autologous T cell, engineered autologous T cell (eACT), an allogeneic T cell, or any combination thereof.

58. The cell of any one of claims 54 to 57, wherein the cell is an in vitro cell.

59. A composition comprising the polynucleotide of any one of claims 1 to 50, the vector of claim 51 or 52, the CAR or TCR of claim 53, or the cell of any one of claims 54 to 58.

60. The composition of claim 59, which is formulated to be delivered to a subject.

61. A method of making a cell expressing a CAR or TCR comprising transducing a cell with the polynucleotide of any one of claims 1 to 50 under suitable conditions.

62. The method of claim 61, further comprising isolating the cell.

63. Use of the cell of claim 54 in the manufacture of a medicament for inducing an immunity against a tumor.

64. Use of the polynucleotide of any one of claims 1 to 50, the vector of claim 51 or 52, the CAR or TCR of claim 53, the cell of any one of claims 54 to 58, or the composition of claim 59 or 60, in the manufacture of a medicament for treating a cancer in a subject in need thereof.

65. The use of claim 64, wherein the cancer is a hematologic cancer.

66. The use of claim 64, wherein the cancer is of the white blood cells.

67. The use of claims 64, wherein the cancer is of the plasma cells.

68. The use of any one of claims 64 to 67, wherein the cancer is leukemia, lymphoma, or myeloma.

69. The use of anyone of claims 64 to 67, wherein the cancer is 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), chronic or acute leukemia, acute myeloid leukemia, chronic myeloid leukemia, acute lymphoblastic leukemia (ALL) (including non T cell ALL), chronic lymphocytic leukemia (CLL), T-cell lymphoma, one or more of B-cell acute lymphoid leukemia ("BALL"), T-cell acute lymphoid leukemia ("TALL"), acute lymphoid leukemia (ALL), chronic myelogenous leukemia (CML), B cell prolymphocytic leukemia, blastic plasmacytoid dendritic cell neoplasm, Burkitt's lymphoma, diffuse large B cell lymphoma, follicular lymphoma, hairy cell leukemia, small cell- or a large cell-follicular lymphoma, malignant lymphoproliferative conditions, MALT lymphoma, mantle cell lymphoma, Marginal zone lymphoma, myelodysplasia and myelodysplastic syndrome, plasmablastic lymphoma, plasmacytoid dendritic cell neoplasm, Waldenstrom macroglobulinemia, a plasma cell proliferative disorder (e.g., asymptomatic myeloma (smoldering multiple myeloma or indolent myeloma), monoclonal gammapathy of undetermined significance (MGUS), plasmacytomas (e.g., plasma cell dyscrasia, solitary myeloma, solitary plasmacytoma, extramedullary plasmacytoma, and multiple

plasmacytoma), systemic amyloid light chain amyloidosis, POEMS syndrome (also known as Crow-Fukase syndrome, Takatsuki disease, and PEP syndrome), or a combination thereof.

70. The use of any one of claims 64 to 69, wherein the cancer is multiple myeloma.

71. An isolated polynucleotide encoding an antibody or an antigen binding molecule thereof that specifically binds to BCMA, wherein the antibody or the antigen binding molecule thereof comprises:

(a) a heavy chain variable region (VH) complementarity determining region (CDR) 1 comprising, consisting of, or consisting essentially of the amino acid sequence $GX_2X_3X_4X_5X_6X_7SY$ (SEQ ID NO: 145), wherein:

$X_2$ is not present or G;

$X_3$ is not present or S;

$X_4$ is F, G, I, or Y;

$X_5$ is S or T;

$X_6$ is F or S; and

$X_7$ is S or T;

;

(b) a VH CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1IX_3X_4X_5X_6X_7X_8X_9X_{10}YX_{12}X_{13}X_{14}X_{15}X_{16}X_{17}$ (SEQ ID NO: 146), wherein:

$X_1$ is A, G, I, S, T, or V;

$X_3$ is I, N, or S;

$X_4$ is G, P, S, or Y;

$X_5$ is D, G, I, or S;

$X_6$ is F, G, or S;

$X_7$ is not present or G or S;

$X_8$ is N, S, or T;

$X_9$ is A, I, K, or T;

$X_{10}$ is N, S, or Y;

$X_{12}$ is A or N;

$X_{13}$ is D, P, or Q;

$X_{14}$ is K or S;

$X_{15}$ is F, L, or V;

$X_{16}$ is K or Q; and

$X_{17}$ is G or S;

(c) a VH CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}DX_{19}$ (SEQ ID NO: 147), wherein:

$X_1$ is A or V;

$X_2$ is K or R;

$X_3$ is not present or D, G, or T;

$X_4$ is not present or A, D, G, P, R, or S;

$X_5$ is not present or E, F, G, L, Q, or T;

$X_6$ is not present or E, M, Q, W, or Y;

$X_7$ is not present or A, E, L, or S;

$X_8$ is not present or G, P, S, or T;

$X_9$ is not present or G, P, or S;

$X_{10}$ is not present or I, L, P, or Y;

$X_{11}$ is not present or W;

$X_{12}$ is not present or H;

$X_{13}$ is not present or E or Y;

$X_{14}$ is not present or D, G, H, P, S, W, or Y;

$X_{15}$ is A, G, L, W, or Y;

$X_{16}$ is not present or A, G, I, P, or V;

$X_{17}$ is F, L, or M; and

$X_{19}$ is I, L, V, or Y;

(d) a light chain variable region (VL) CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2SQX_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}LX_{17}$ (SEQ ID NO: 148), wherein

$X_1$ is K or R;

$X_2$ is A or S;

$X_5$ is G or S;

$X_6$ is I, L, or V;

$X_7$ is L or S;

$X_8$ is not present or H or Y;

$X_9$ is not present or S;

$X_{10}$ is not present or N or S;

$X_{11}$ is not present or G or N;

$X_{12}$ is not present or N;

$X_{13}$ is not present or K or Y;

$X_{14}$ is N, R, or S;

$X_{15}$ is N, W, or Y; and

$X_{17}$ is A or D;

(e) a VL CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1X_2SX_4X_5X_6X_7$ (SEQ ID NO: 149), wherein

$X_1$ is D, G, L, S, or W;

$X_2$ is A or G;

$X_4$ is N, S, or T;

$X_5$ is L or R;

$X_6$ is A, E, or Q; and

$X_7$ is S or T; and/or

(f) a VL CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence $X_1QX_3X_4X_5X_6PX_8T$ (SEQ ID NO: 150), wherein

$X_1$ is M or Q;

$X_3$ is F, G, H, I, R, or Y;

$X_4$ is A, F, H, I, L, or Y;

$X_5$ is A, G, H, S, T, V, or Y;

$X_6$ is F, L, T, W, or Y; and

$X_8$ is not present or F, L, P, or W.

72. The polynucleotide of claim 71, wherein the VH CDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 41-48.

73. An isolated polynucleotide encoding an antibody or an antigen binding molecule thereof that specifically binds to BCMA, wherein the antibody or the antigen binding molecule thereof comprises a VH CDR3 comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 41-48.

74. The polynucleotide of any one of claims 71 to 73, wherein the VH CDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 9-16.

75. The polynucleotide of any one of claims 71 to 74, wherein the VH CDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 25-32.

76. The polynucleotide of any one of claims 71 to 75, wherein the VL CDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 81-88.

77. The polynucleotide of any one of claims 71 to 76, wherein the VL CDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 97-104.

78. The polynucleotide of any one of claims 71 to 77, wherein the VL CDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 113-120.

79. The polynucleotide of any one of claims 71, 72, and 74 to 78, wherein the VH CDR1, VH CDR2, and VH CDR3 each comprise the amino acid sequence of the VH CDR1, VH CDR2, and VH CDR3 of an antibody in FIG. FIG. 1B.

80. The polynucleotide of any one of claims 71, 72, and 74 to 79, wherein the VL CDR1, VL CDR2, and VL CDR3 each comprise the amino acid sequence of the VL CDR1, VL CDR2, and VL CDR3 of an antibody in FIG. 1C.

81. The polynucleotide of any one of claims 71 to 80, wherein the antibody or antigen binding molecule thereof comprises a heavy chain variable region sequence comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 65-72.

82. The polynucleotide of any one of claims 71 to 81, wherein the antibody or antigen binding molecule thereof comprises a light chain variable region sequence comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 137-144.

83. The polynucleotide of any one of claims 71 to 82, wherein the antibody or antigen binding molecule thereof comprises:

(a) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 9; a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 25; a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 41; a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 81; a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 97; and a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 113;

(b) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 10; a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 26; a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 42; a VL CDR1 region comprising

the amino acid sequence of SEQ ID NO: 82; a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 98; and a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 114;

(c) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 11; a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 27; a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 43; a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 83; a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 99; and a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 115;

(d) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 12; a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 28; a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 44; a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 84; a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 100; and a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 116;

(e) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 13; a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 29; a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 45; a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 85; a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 101; and a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 117;

(f) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 14; a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 30; a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 46; a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 86; a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 102; and a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 118;

(g) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 15; a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 31; a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 47; a VL CDR1
region comprising the amino acid sequence of SEQ ID NO: 87; a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 103; and a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 119; or

(h) a VH CDR1 region comprising the amino acid sequence of SEQ ID NO: 16; a VH CDR2 region comprising the amino acid sequence of SEQ ID NO: 32; a VH CDR3 region comprising the amino acid sequence of SEQ ID NO: 48; a VL CDR1 region comprising the amino acid sequence of SEQ ID NO: 88; a VL CDR2 region comprising the amino acid sequence of SEQ ID NO: 104; and a VL CDR3 region comprising the amino acid sequence of SEQ ID NO: 120.

84. The polynucleotide of any one of claims 71 to 83, wherein the antibody or antigen binding molecule thereof comprises:

(a) a VH comprising the amino acid sequence of SEQ ID NO: 65; and a VL comprising the amino acid sequence of SEQ ID NO: 137;

(b) a VH comprising the amino acid sequence of SEQ ID NO: 66; and a VL comprising the amino acid sequence of SEQ ID NO: 138;

(c) a VH comprising the amino acid sequence of SEQ ID NO: 67; and a VL comprising the amino acid sequence of SEQ ID NO: 139;

(d) a VH comprising the amino acid sequence of SEQ ID NO: 68; and a VL comprising the amino acid sequence of SEQ ID NO: 140;

(e) a VH comprising the amino acid sequence of SEQ ID NO: 69; and a VL comprising the amino acid sequence of SEQ ID NO: 141;

(f) a VH comprising the amino acid sequence of SEQ ID NO: 70; and a VL comprising the amino acid sequence of SEQ ID NO: 142;

(g) a VH comprising the amino acid sequence of SEQ ID NO: 71; and a VL comprising the amino acid sequence of SEQ ID NO: 143; or

(h) a VH comprising the amino acid sequence of SEQ ID NO: 72; and a VL comprising the amino acid sequence of SEQ ID NO: 144.

85. The polynucleotide of claim 84, which 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 form the group consisting of SEQ ID NOs: 57-64.

86. The polynucleotide of claim 84 or 85, which 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 form the group consisting of SEQ ID NOs: 129-136.

87. The polynucleotide of any one of claims 71 to 86, wherein the antibody or antigen binding molecule thereof is single chained.

88. The polynucleotide of any one of claims 71 to 87, wherein the antibody or antigen binding molecule thereof is selected from the group consisting of scFv, Fab, Fab', Fv, F(ab')2, dAb, and any combination thereof.

89. The polynucleotide of any one of claims 71 to 88, wherein the antibody or antigen binding molecule thereof comprises a scFv.

90. The polynucleotide of any one of claims 71 to 89, wherein the VH and the VL are connected by a linker.

91. The polynucleotide of claim 90, wherein the VH is located at the N terminus of the linker and the VL is located at the C terminus of the linker.

92. The polynucleotide of claim 90, wherein the VL is located at the N terminus of the linker and the VH is located at the N terminus of the linker.

93. The polynucleotide of any one of claims 90 to 92, wherein 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.

94. The polynucleotide of any one of claims 90 to 93, wherein the linker comprises an amino acid sequence at least 75%, at least 85%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 174.

95. The polynucleotide of any one of claims 71 to 94, wherein the antibody or antigen binding molecule thereof binds to BCMA with a $K_D$ of less than about 1 x $10^{-6}$ M, less than about 1 x $10^{-7}$ M, less than about 1 x $10^{-8}$ M, or less than about 1 x $10^{-9}$ M.

96. A vector comprising the polynucleotide of any one of claims 71 to 95.

97. The vector of claim 96, which is a retroviral vector, a DNA vector, a plasmid, a RNA vector, an adenoviral vector, an adenovirus associated vector, a lentiviral vector, or any combination thereof.

98. An antibody or an antigen binding molecule thereof encoded by the polynucleotide of any one of claims 71 to 95 or the vector of claim 96 or 97.

99. A polypeptide encoding a chimeric antigen receptor (CAR) or T cell receptor (TCR), wherein the CAR or the TCR comprises the antibody of the antigen binding molecule thereof of claim 98.

100. A cell comprising the polynucleotide of any one of claims 71 to 95, the vector of claim 96 or 97, the antibody or the antigen binding molecule thereof of claim 98, or any combination thereof.

101. The cell of claim 100, wherein the cell comprises an immune cell.

102. The cell of claim 100, wherein the cell is a T cell.

103. The cell of claim 102, wherein the T cell is a tumor-infiltrating lymphocyte (TIL), autologous T cell, engineered autologous T cell (eACT), an allogeneic T cell, or any combination thereof.

104. The cell of any one of claims 100 to 103, wherein the cell is an in vitro cell.

105. A composition comprising the polynucleotide of any one of claims 71 to 95, the vector of claim 96 or 97, the antibody or the antigen binding molecule thereof of claim 98, or the cell of any one of claims 100 to 104.

106. The composition of claim 105, which is formulated to be delivered to a subject.

107. A method of making an antibody or an antigen binding molecule thereof comprising transducing a cell with the polynucleotide of any one of claims 71 to 95 under suitable conditions.

108. The method of claim 107, further comprising isolating the cell.

109. Use of the cell of claim 100 in the manufacture of a medicament for inducing an immunity against a tumor.

110. Use of the polynucleotide of any one of claims 71 to 95, the vector of claim 96 or 97, the antibody or the antigen binding molecule thereof of claim 98, the cell of any one of claims 100 to 104, or the composition of claim 105 or 106, in the manufacture of a medicament for treating a cancer in a subject in need thereof.

111. The use of claim 110, wherein the cancer is a hematologic cancer.

112. The use of claim 110, wherein the cancer is of the white blood cells.

113. The use of claims 110, wherein the cancer is of the plasma cells.

114. The use of any one of claims 110 to 113, wherein the cancer is leukemia, lymphoma, or myeloma.

115. The use of anyone of claims 110 to 114, wherein the cancer is 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), chronic or acute leukemia, acute myeloid leukemia, chronic myeloid leukemia, acute lymphoblastic leukemia (ALL) (including non T cell ALL), chronic lymphocytic leukemia (CLL), T-cell lymphoma, one or more of B-cell acute lymphoid leukemia ("BALL"), T-cell acute lymphoid leukemia ("TALL"), acute lymphoid leukemia (ALL), chronic myelogenous leukemia (CML), B cell prolymphocytic leukemia, blastic plasmacytoid dendritic cell neoplasm, Burkitt's lymphoma, diffuse large B cell lymphoma, follicular lymphoma, hairy cell leukemia, small cell- or a large cell-follicular lymphoma, malignant lymphoproliferative conditions, MALT lymphoma, mantle cell lymphoma, Marginal zone lymphoma, myelodysplasia and myelodysplastic

syndrome, plasmablastic lymphoma, plasmacytoid dendritic cell neoplasm, Waldenstrom macroglobulinemia, a plasma cell proliferative disorder (e.g., asymptomatic myeloma (smoldering multiple myeloma or indolent myeloma), monoclonal gammapathy of undetermined significance (MGUS), plasmacytomas (e.g., plasma cell dyscrasia, solitary myeloma, solitary plasmacytoma, extramedullary plasmacytoma, and multiple plasmacytoma), systemic amyloid light chain amyloidosis, POEMS syndrome (also known as Crow-Fukase syndrome, Takatsuki disease, and PEP syndrome), or a combination thereof.

116. The use of any one of claims 110 to 115, wherein the cancer is multiple myeloma.

117. A sequence comprising any of SEQ ID NO. 271 to SEQ ID NO. 410.

118. A vector comprising at least one sequence set forth in SEQ ID NO. 271 to SEQ ID NO. 410.

119. An immune cell comprising a sequence set forth in any of SEQ ID NO. 271 to SEQ ID NO. 410.

120. An immune cell according to claim 119 for use in treating a patient in need thereof.

121. The immune cell according to claim 120, wherein said patient is preconditioned.

122. The immune cell according to claim 121, wherein said patient is preconditioned with cyclophosphamide and fludarabine.

123. The lentiviral vector according to claim 52 that comprises pGAR, or a derivative thereof.

# ABSTRACT

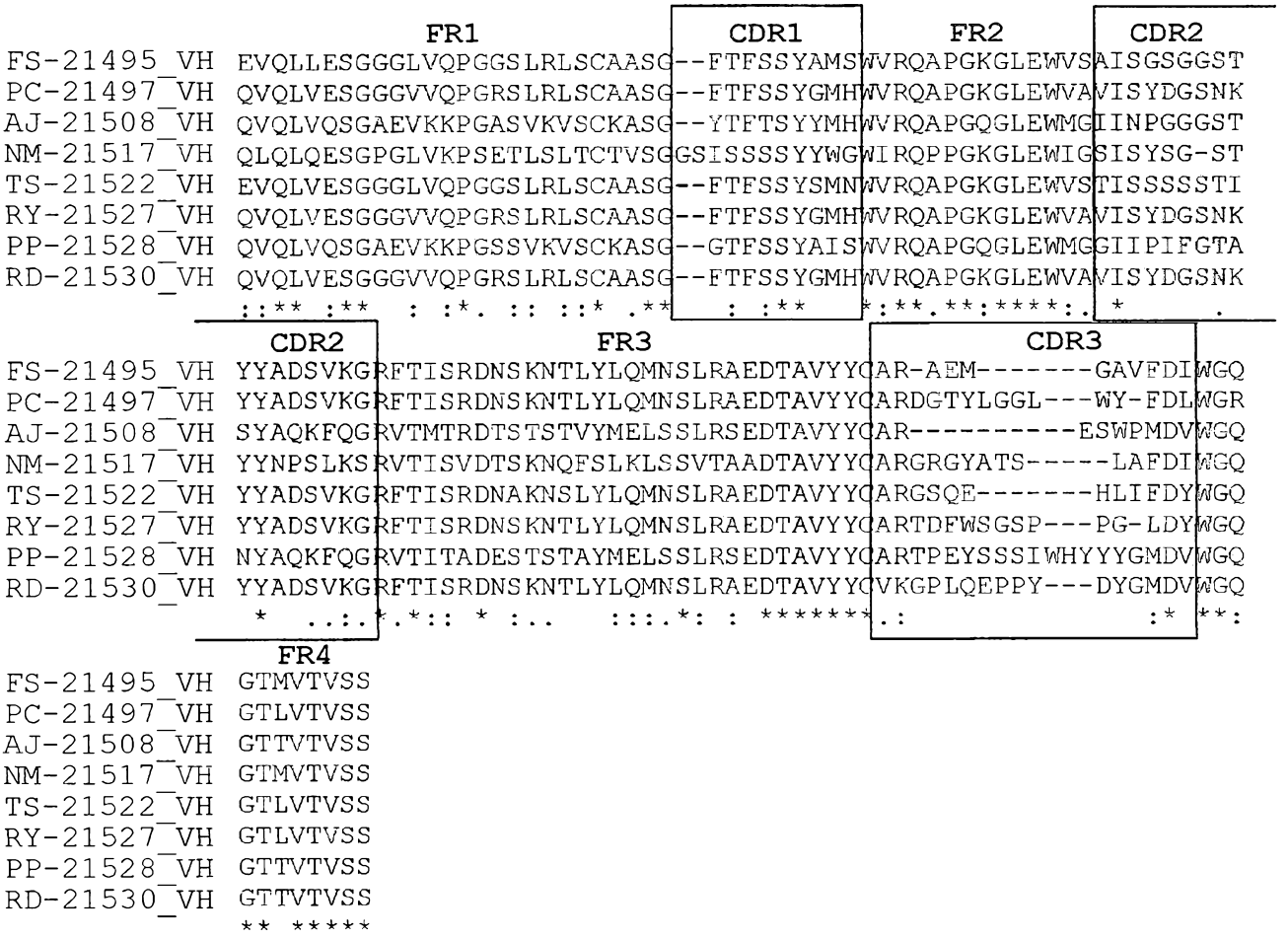
The invention provides antibodies, antigen binding fragments thereof, chimeric antigen receptors (CARs), and engineered T cell receptors, polynucleotides encoding the same, and in vitro cells comprising the same. The polynucleotides, polypeptides, and in vitro cells described herein can be used in an engineered CAR T cell therapy for the treatment of a patient suffering from a cancer. In one embodiment, the polynucleotides, polypeptides, and in vitro cells described herein can be used for the treatment of multiple myeloma.

# FIG. 1A – Anti-BCMA Binding Molecules

## FIG. 1B

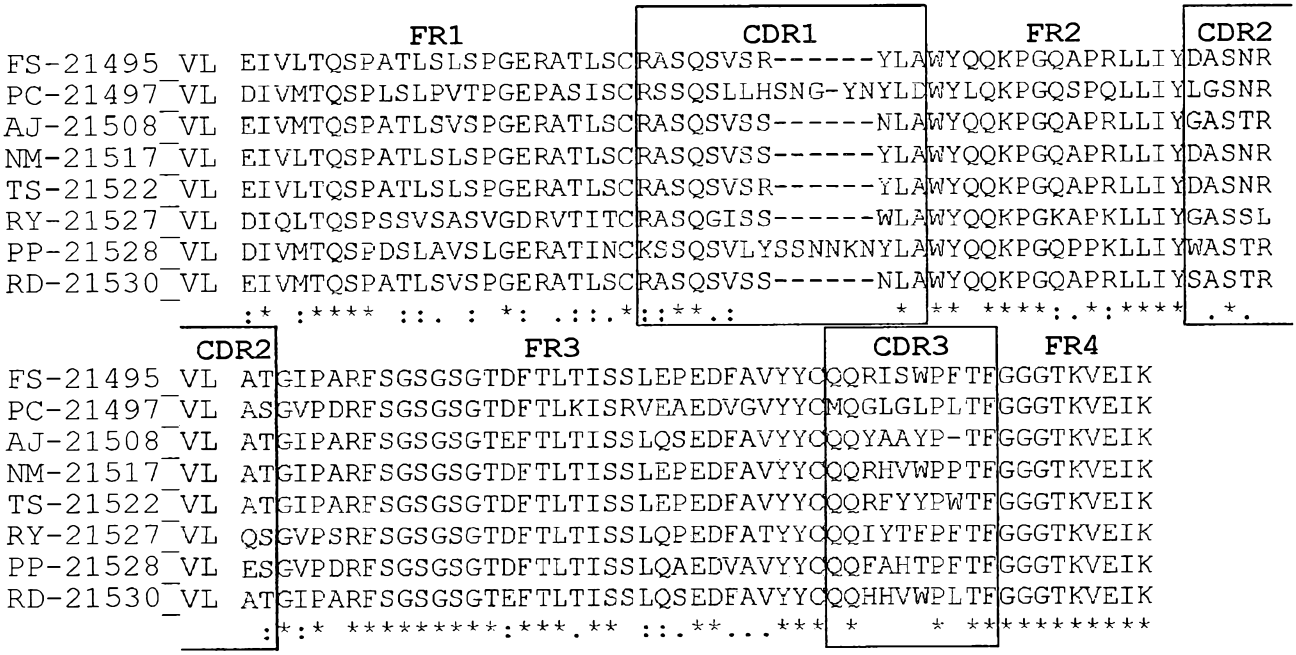
| | SEQ ID NO: | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | VH | FR1 | CDR1 | FR2 | CDR2 | FR3 | CDR3 | FR4 |
| FS-21495 VH | 65 | 1 | 9 | 17 | 25 | 33 | 41 | 49 |
| PC-21497 VH | 66 | 2 | 10 | 18 | 26 | 34 | 42 | 50 |
| AJ-21508 VH | 67 | 3 | 11 | 19 | 27 | 35 | 43 | 51 |
| NM-21517 VH | 68 | 4 | 12 | 20 | 28 | 36 | 44 | 52 |
| TS-21522 VH | 69 | 5 | 13 | 21 | 29 | 37 | 45 | 53 |
| RY-21527 VH | 70 | 6 | 14 | 22 | 30 | 38 | 46 | 54 |
| PP-21528 VH | 71 | 7 | 15 | 23 | 31 | 39 | 47 | 55 |
| RD-21530 VH | 72 | 8 | 16 | 24 | 32 | 40 | 48 | 56 |

# FIG. 1C – Anti-BCMA Binding Molecules



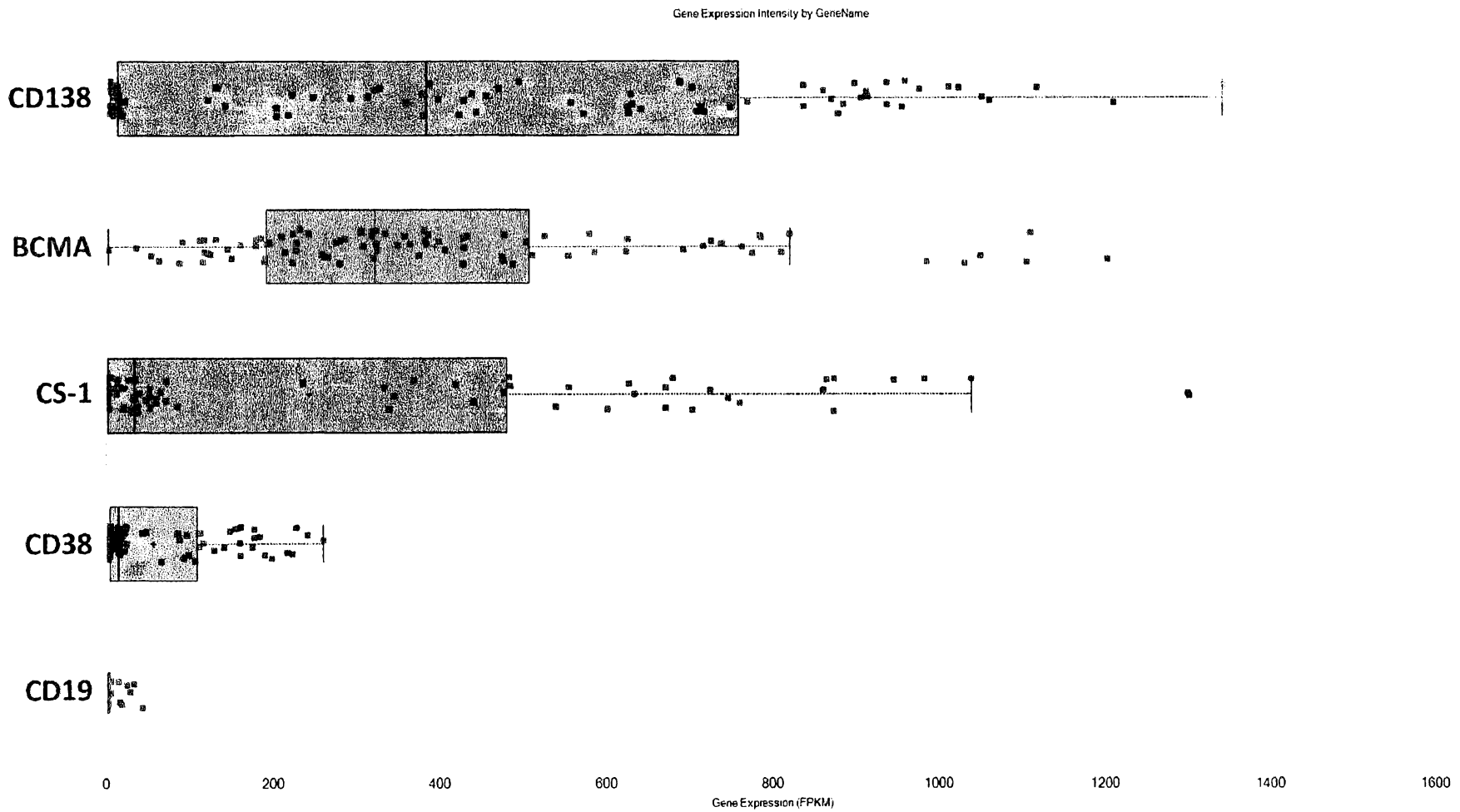

| FIG. 1D | SEQ ID NO: | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | VH | FR1 | CDR1 | FR2 | CDR2 | FR3 | CDR3 | FR4 |
| FS-21495 VH | 65 | 207 | 215 | 223 | 231 | 239 | 247 | 255 |
| PC-21497 VH | 66 | 208 | 216 | 224 | 232 | 240 | 248 | 256 |
| AJ-21508 VH | 67 | 209 | 217 | 225 | 233 | 241 | 249 | 257 |
| NM-21517 VH | 68 | 210 | 218 | 226 | 234 | 242 | 250 | 258 |
| TS-21522 VH | 69 | 211 | 219 | 227 | 235 | 243 | 251 | 259 |
| RY-21527 VH | 70 | 212 | 220 | 228 | 236 | 244 | 252 | 260 |
| PP-21528 VH | 71 | 213 | 221 | 229 | 237 | 245 | 253 | 261 |
| RD-21530 VH | 72 | 214 | 222 | 230 | 238 | 246 | 254 | 262 |

# FIG. 1E – Anti-BCMA Binding Molecules




| FIG. 1F | SEQ ID NO: | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | VL | FR1 | CDR1 | FR2 | CDR2 | FR3 | CDR3 | FR4 |
| FS-21495 VL | 137 | 73 | 81 | 89 | 97 | 105 | 113 | 121 |
| PC-21497 VL | 138 | 74 | 82 | 90 | 98 | 106 | 114 | 122 |
| AJ-21508 VL | 139 | 75 | 83 | 91 | 99 | 107 | 115 | 123 |
| NM-21517 VL | 140 | 76 | 84 | 92 | 100 | 108 | 116 | 124 |
| TS-21522 VL | 141 | 77 | 85 | 93 | 101 | 109 | 117 | 125 |
| RY-21527 VL | 142 | 78 | 86 | 94 | 102 | 110 | 118 | 126 |
| PP-21528 VL | 143 | 79 | 87 | 95 | 103 | 111 | 119 | 127 |
| RD-21530 VL | 144 | 80 | 88 | 96 | 104 | 112 | 120 | 128 |

# FIG. 2A – Gene Expression in Multiple Myeloma Cells




**Gene Expression (Fragments/kilobase of exon/million reads mapped [FPKM])**

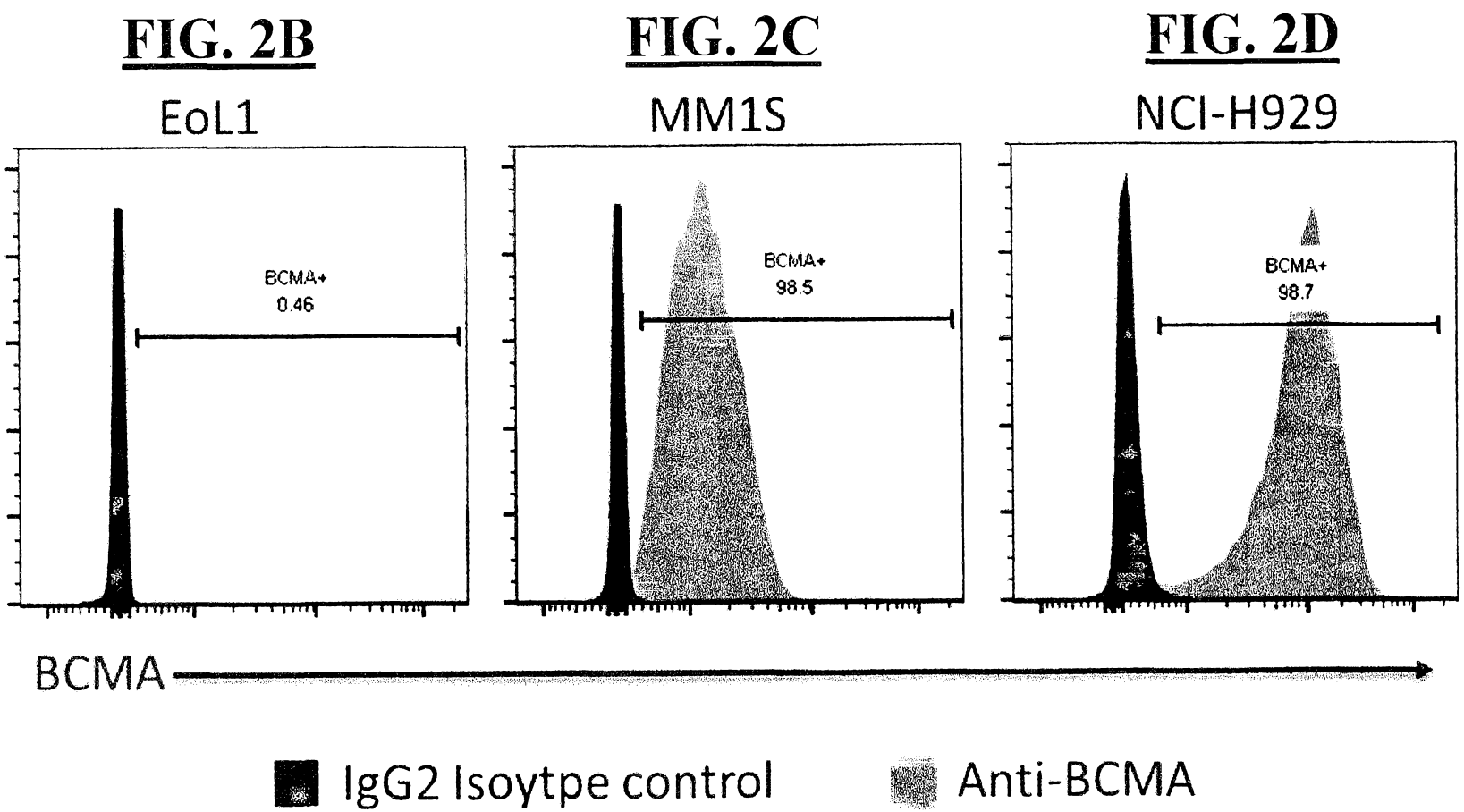
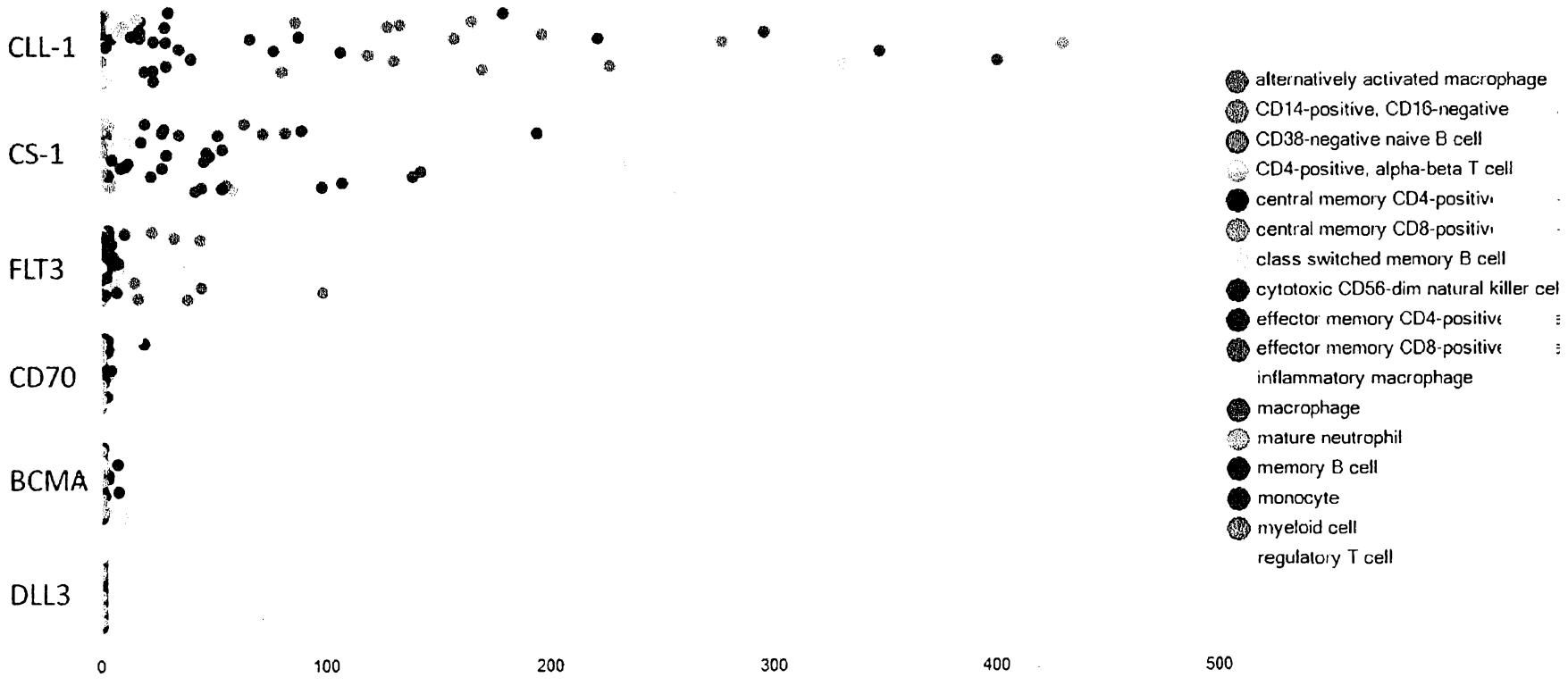


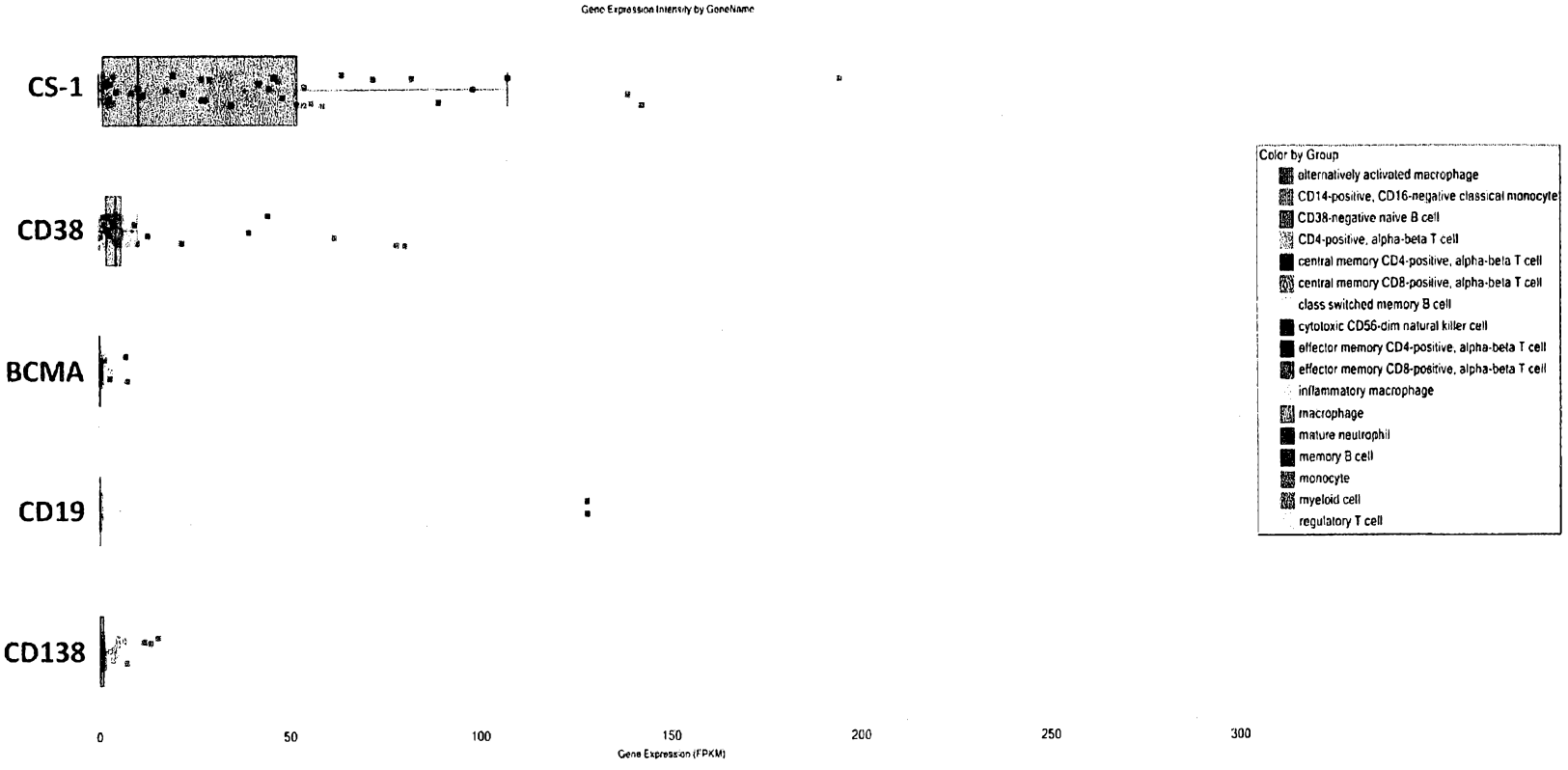
FIG. 2B
EoL1
BCMA+
0.46
FIG. 2C
MM1S
BCMA+
98.5
FIG. 2D
NCI-H929
BCMA+
98.7
BCMA
IgG2 Isoytpe control
Anti-BCMA

# FIG. 2E – Gene Expression in Normal Immune Cells



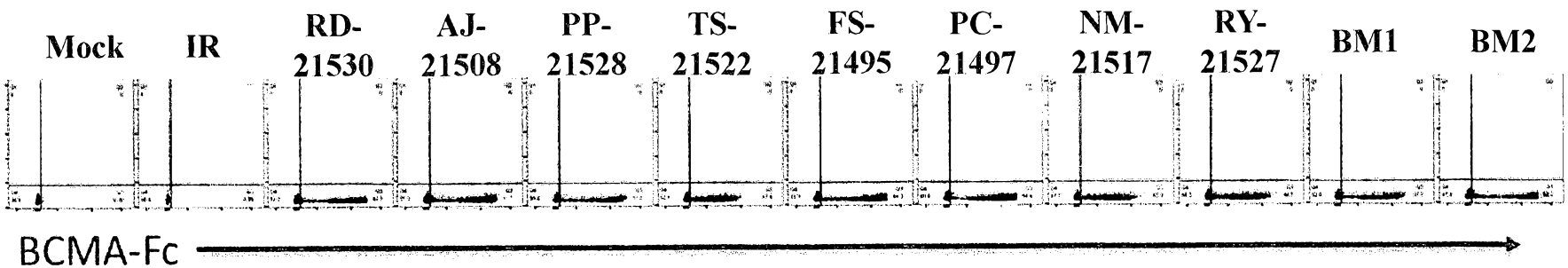

**Gene Expression (Fragments/kilobase of exon/million reads mapped [FPKM])**

# FIG. 2F – Gene Expression in Normal Immune Cells

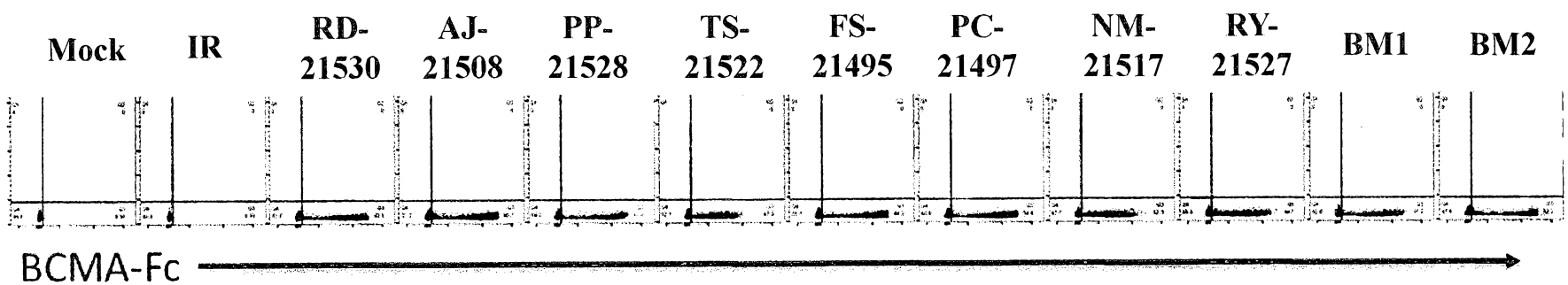



**Gene Expression (Fragments/kilobase of exon/million reads mapped [FPKM])**

# FIG. 3A



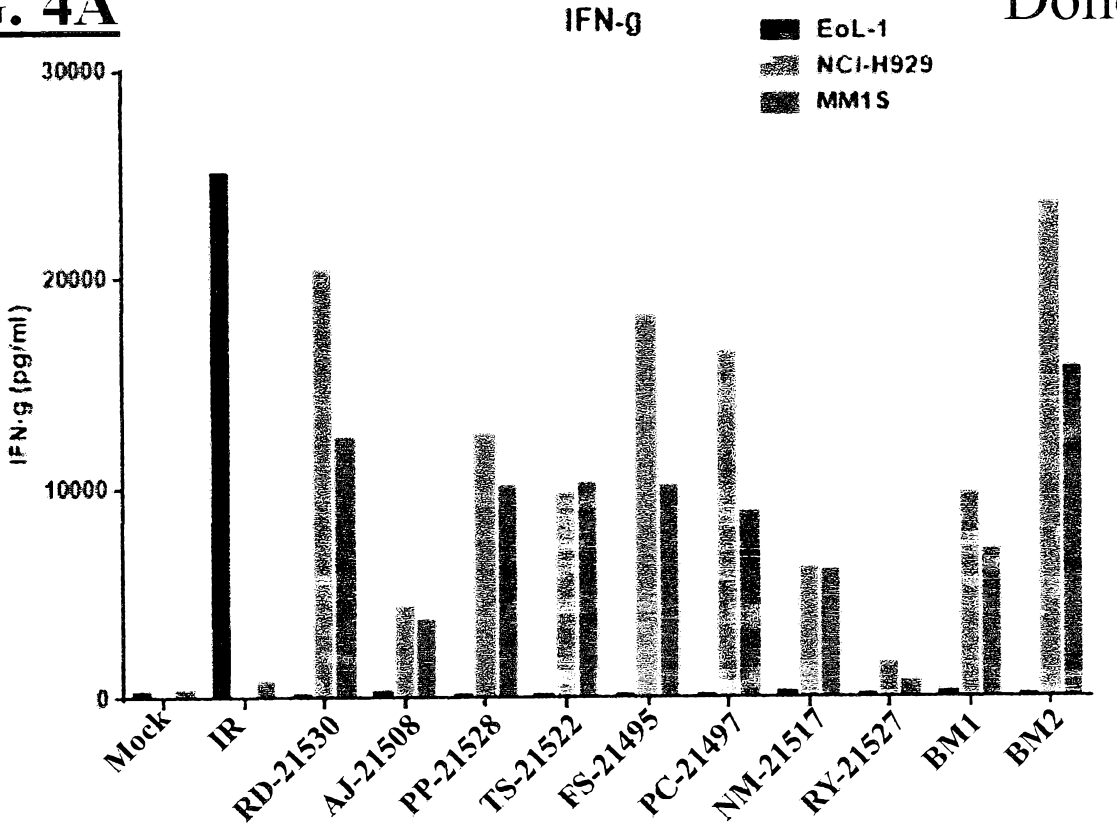

# FIG. 3B




IR = Irrelevant CAR (Negative Control)
BM = Positive Control

# FIG. 4A

Donor 1




# FIG. 4B

Donor 2

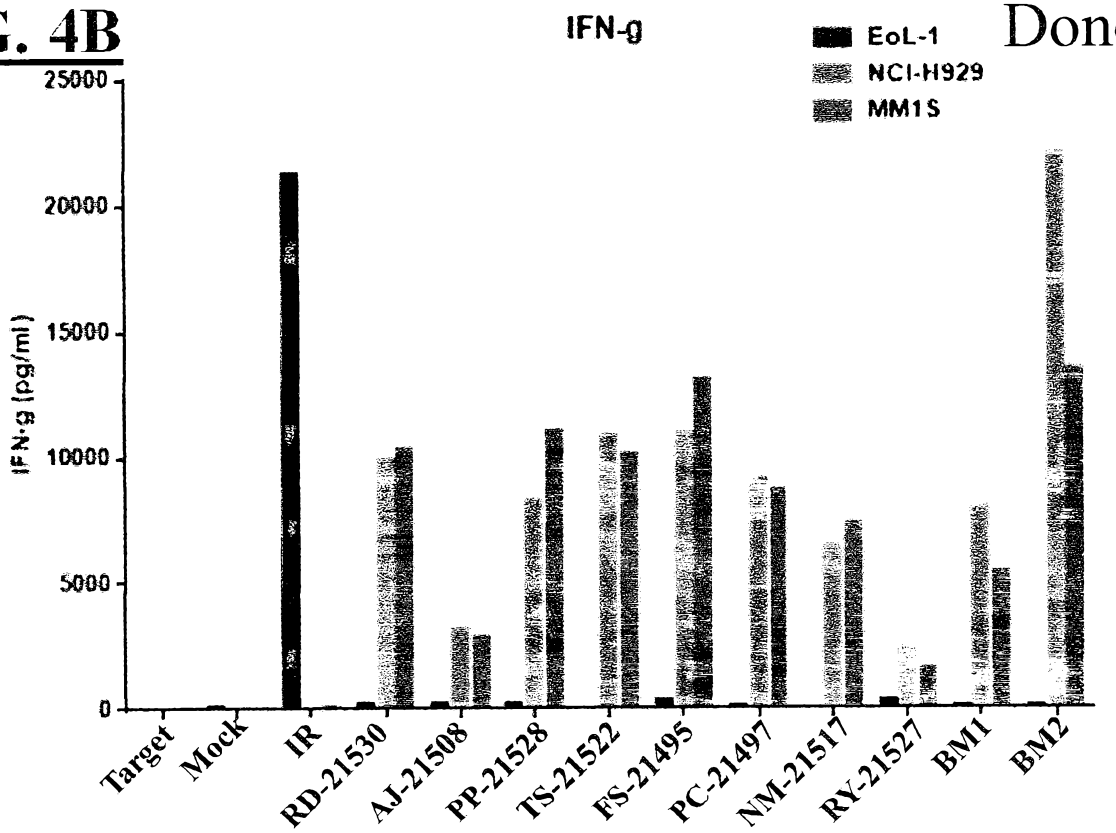


FIG. 4C

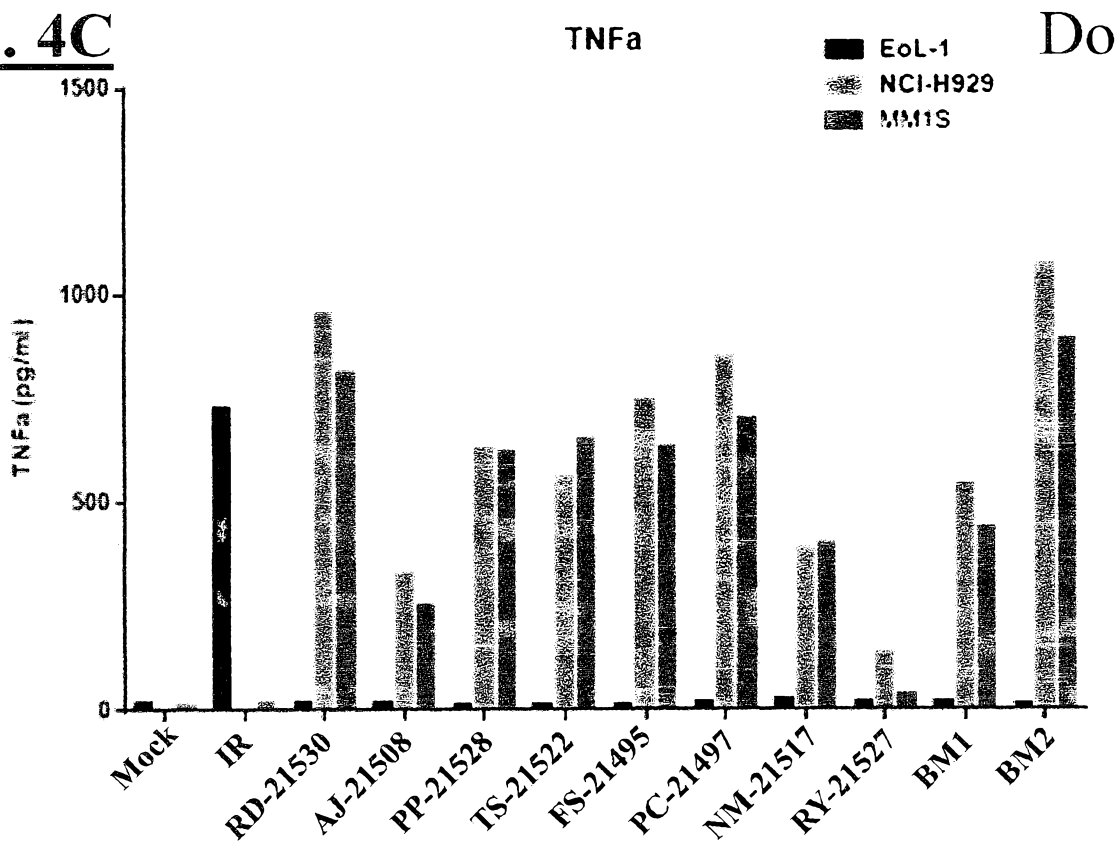

TNFa
EoL-1
NCI-H929
MM1S
Donor 1
TNFa (pg/ml)
1500
1000
500
0
Mock
IR
RD-21530
AJ-21508
PP-21528
TS-21522
FS-21495
PC-21497
NM-21517
RY-21527
BM1
BM2

FIG. 4D

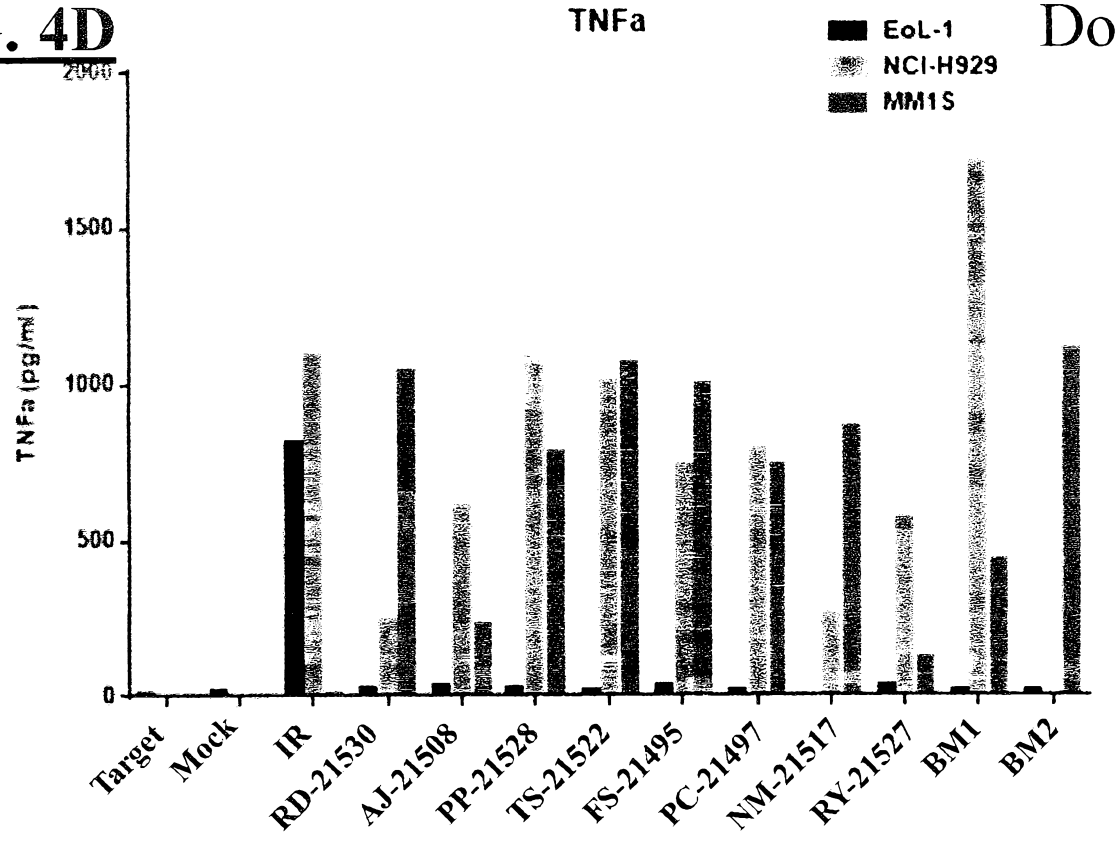

TNFa
EoL-1
NCI-H929
MM1S
Donor 2
TNFa (pg/ml)
2000
1500
1000
500
0
Target
Mock
IR
RD-21530
AJ-21508
PP-21528
TS-21522
FS-21495
PC-21497
NM-21517
RY-21527
BM1
BM2

FIG. 4E

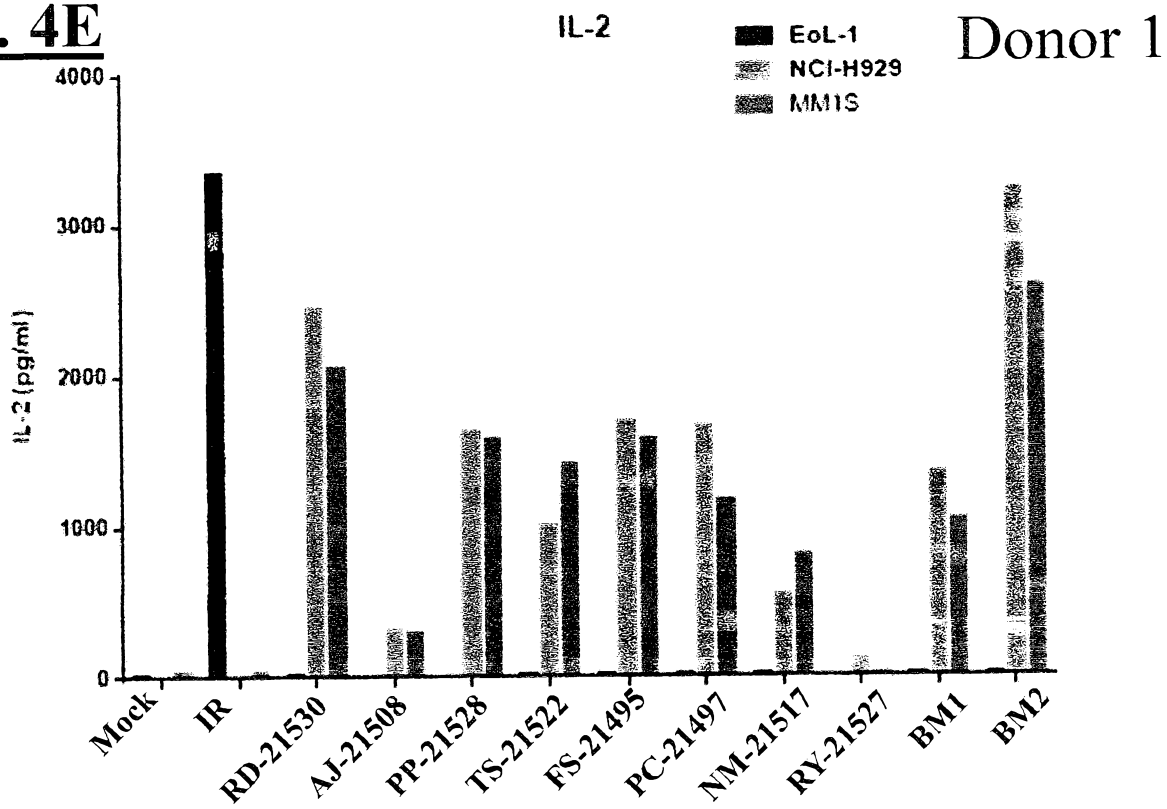
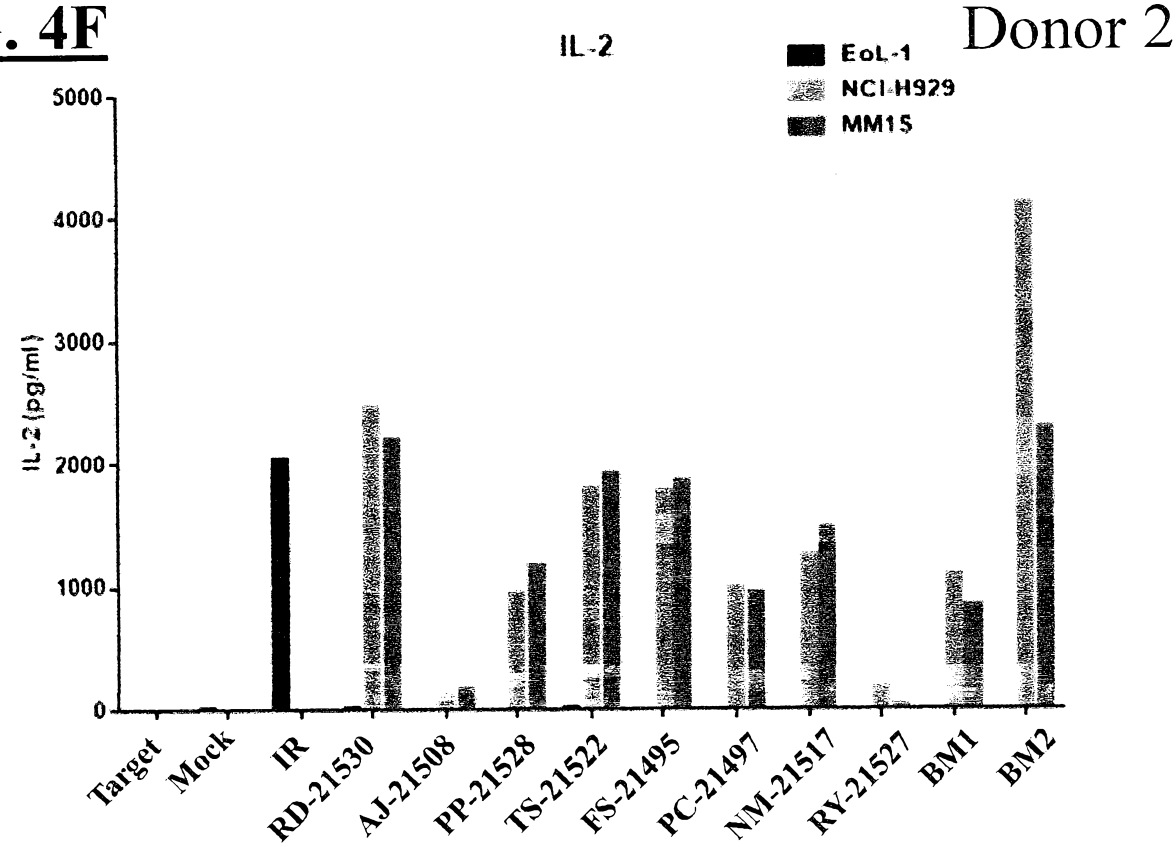
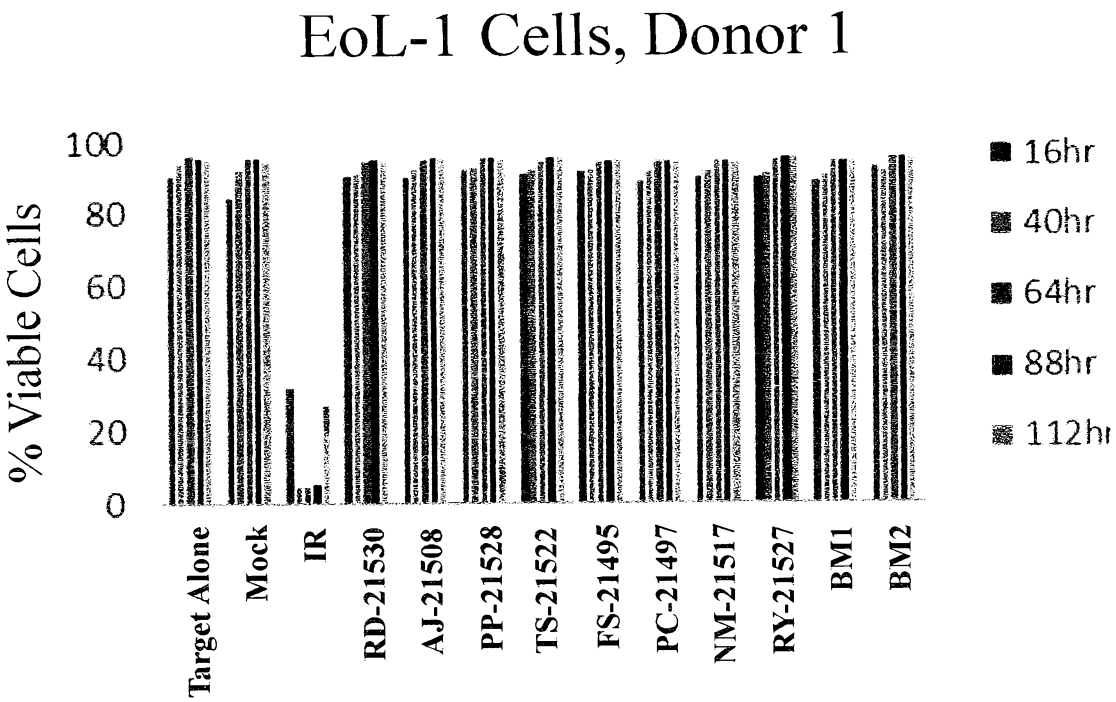

IL-2
EoL-1
NCI-H929
MM1S
Donor 1
IL-2 (pg/ml)
4000
3000
2000
1000
0
Mock
IR
RD-21530
AJ-21508
PP-21528
TS-21522
FS-21495
PC-21497
NM-21517
RY-21527
BM1
BM2

FIG. 4F


IL-2
EoL-1
NCI-H929
MM1S
Donor 2
IL-2 (pg/ml)
5000
4000
3000
2000
1000
0
Target
Mock
IR
RD-21530
AJ-21508
PP-21528
TS-21522
FS-21495
PC-21497
NM-21517
RY-21527
BM1
BM2

19653

# FIG. 5A




# FIG. 5B

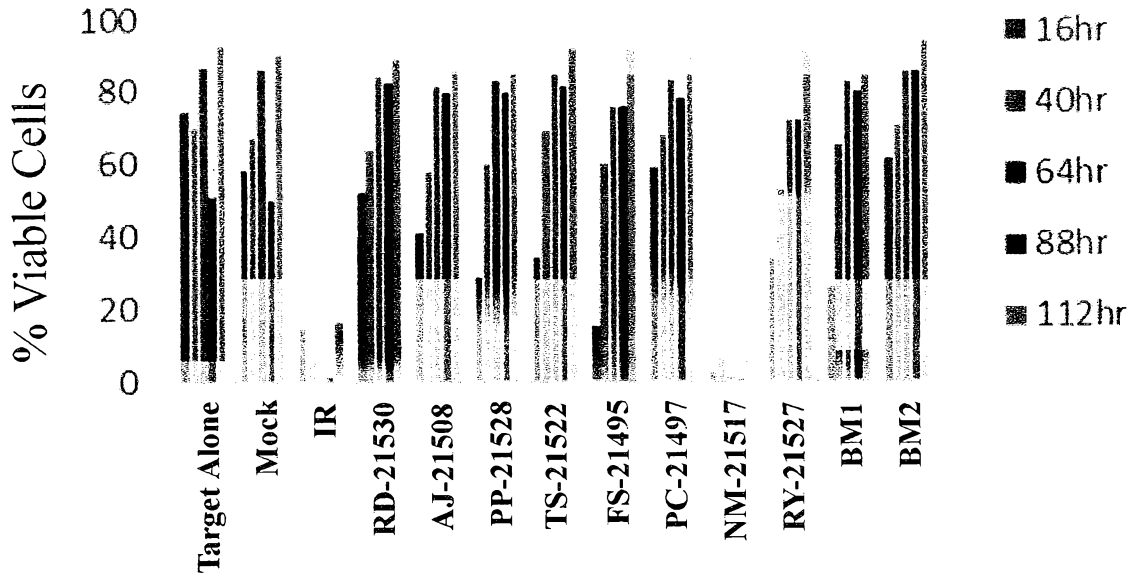


**FIG. 5C**

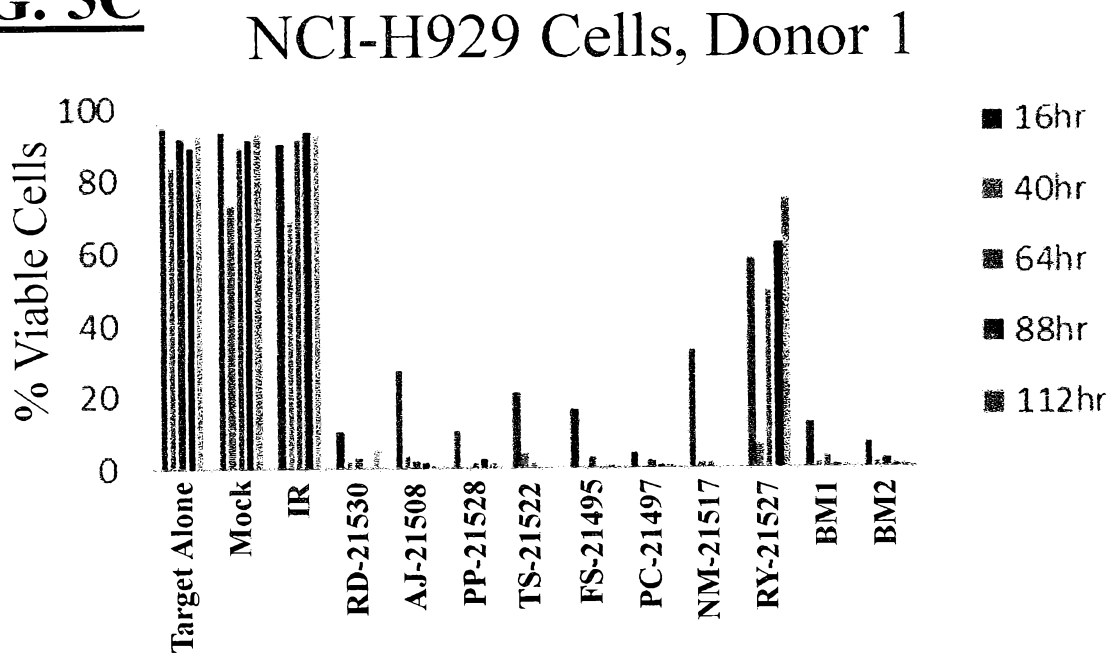

NCI-H929 Cells, Donor 1
% Viable Cells
100
80
60
40
20
0
Target Alone
Mock
IR
RD-21530
AJ-21508
PP-21528
TS-21522
FS-21495
PC-21497
NM-21517
RY-21527
BM1
BM2
16hr
40hr
64hr
88hr
112hr

**FIG. 5D**

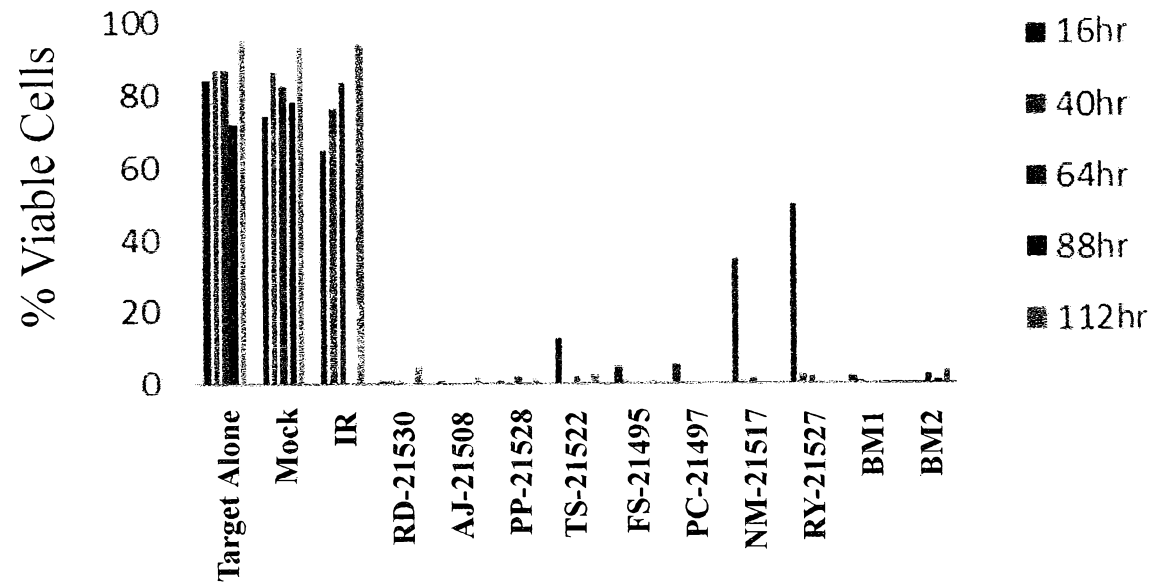

NCI-H929 Cells, Donor 2
% Viable Cells
100
80
60
40
20
0
Target Alone
Mock
IR
RD-21530
AJ-21508
PP-21528
TS-21522
FS-21495
PC-21497
NM-21517
RY-21527
BM1
BM2
16hr
40hr
64hr
88hr
112hr

**FIG. 5E**

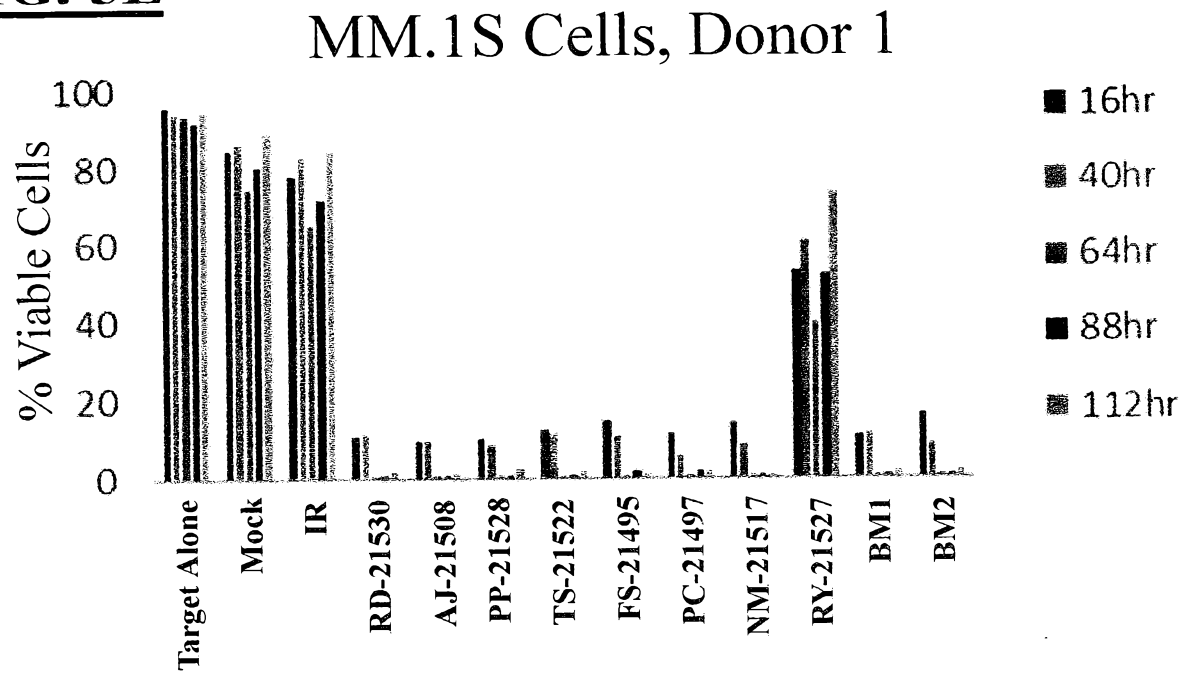
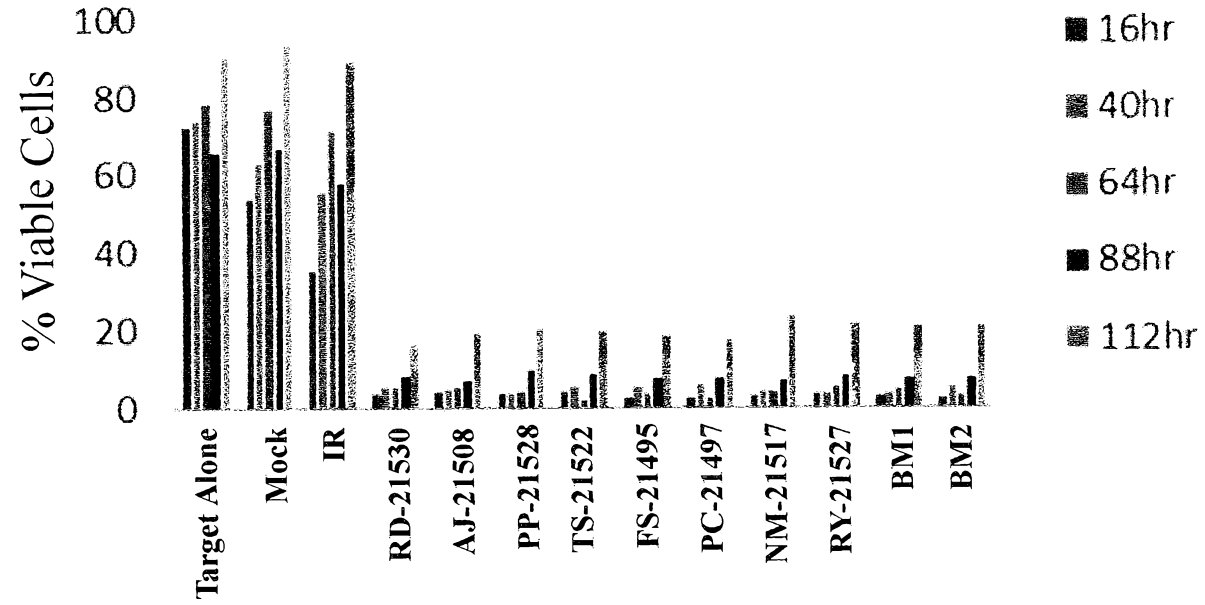
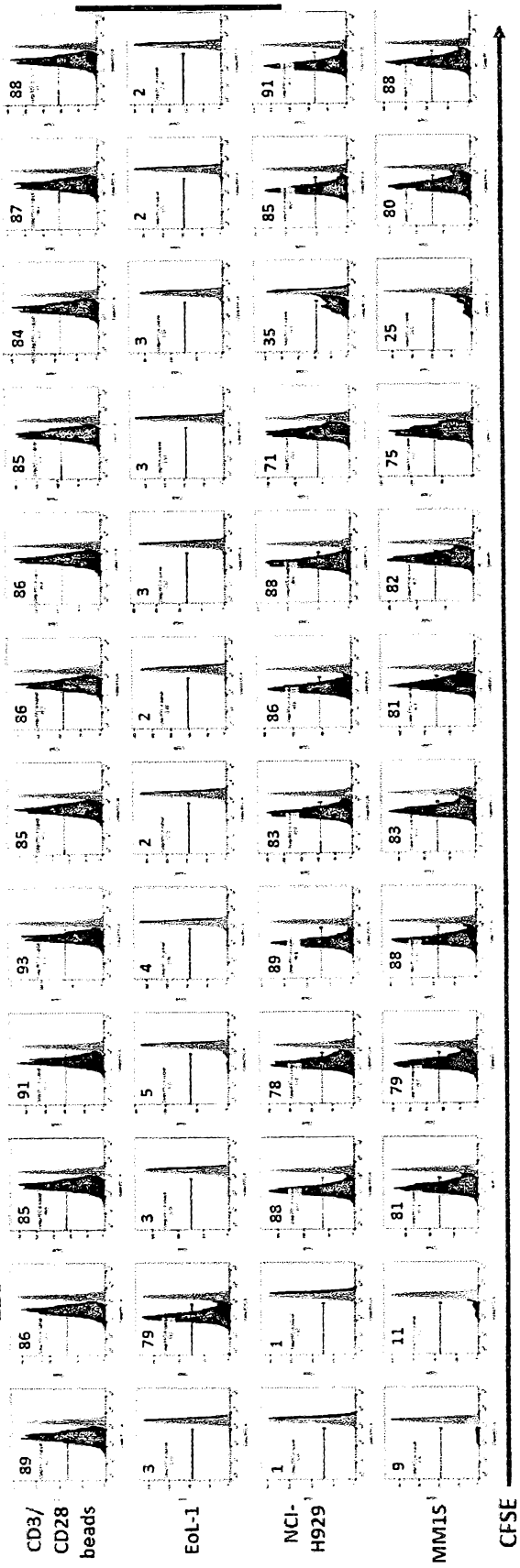

MM.1S Cells, Donor 1
% Viable Cells
100
80
60
40
20
0
16hr
40hr
64hr
88hr
112hr
Target Alone
Mock
IR
RD-21530
AJ-21508
PP-21528
TS-21522
FS-21495
PC-21497
NM-21517
RY-21527
BM1
BM2

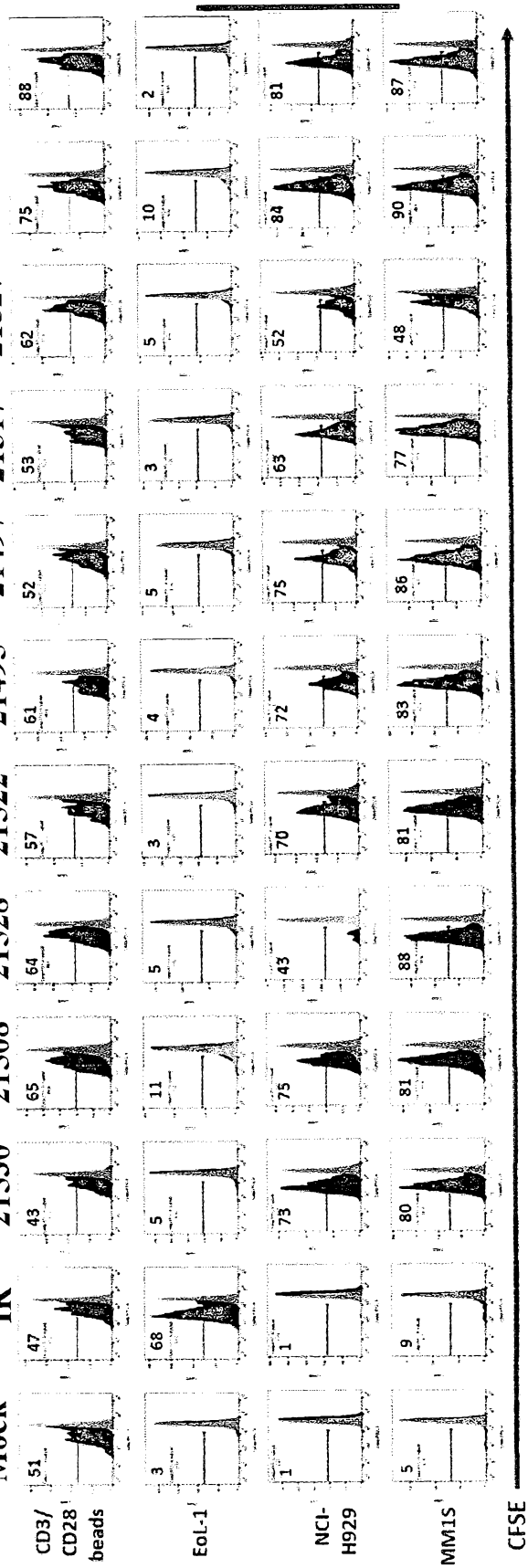
**FIG. 5F**


MM.1S Cells, Donor 2
% Viable Cells
100
80
60
40
20
0
16hr
40hr
64hr
88hr
112hr
Target Alone
Mock
IR
RD-21530
AJ-21508
PP-21528
TS-21522
FS-21495
PC-21497
NM-21517
RY-21527
BM1
BM2

# FIG. 6A


Mock
IR
RD-21530
AJ-21508
PP-21528
TS-21522
FS-21495
PC-21497
NM-21517
RY-21527
BM1
BM2
CD3/CD28 beads
EoL-1
NCI-H929
MM1S
CFSE

# FIG. 6B


Mock
IR
RD-21530
AJ-21508
PP-21528
TS-21522
FS-21495
PC-21497
NM-21517
RY-21527
BM1
BM2
CD3/CD28 beads
EoL-1
NCI-H929
MM1S
CFSE
Unstimulated T cells
T cells + indicated stimulus

## FIG. 7A

**Clone FS-26528 HC DNA (SEQ ID NO: 271)**

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCC
TGTGCAGCCTCTGGATTCACCTTTGACGACTATGCCATGGCATGGGTCCGCCAGGCTCCAGGG
AAGGGGCTGGAGTGGGTCTCAGCTATTAGTGATGCAGGTGACAGAACATACTACGCAGACTCC
GTGAGGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACACTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCAAGAGCCGAGATGGGAGCCGTATTC
GACATATGGGGTCAGGGTACAATGGTCACCGTCTCCTCA

## FIG. 7B

**Clone FS-26528 HC (SEQ ID NO: 272). CDRs 1, 2, and 3 are underlined.**

EVQLLESGGG LVQPGGSLRL SCAASGFTFD DYAMAWVRQA PGKGLEWVSA
ISDAGDRTYY ADSVRGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARAE
MGAVFDIWGQ GTMVTVSS

## FIG. 7C

SCAASGFTFDDYAMA (SEQ ID NO: 273) [HC CDR1]

AISDAGDRTYYADSVRG (SEQ ID NO: 274) [HC CDR2]

ARAEMGAVFDI (SEQ ID NO: 275) [HC CDR3]

## FIG. 7D

**Clone FS-26528 LC DNA (SEQ ID NO: 276)**

GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTC
TCCTGCAGGGCCAGTCAGAGTGTTAGCAGGTACTTAGCCTGGTACCAACAGAAACCTGGCCAG
GCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTCAGT
GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGATTTTGCA
GTTTATTACTGTCAGCAGAGAATCTCCTGGCCTTTCACTTTTGGCGGAGGGACCAAGGTTGAG
ATCAAACGG

## FIG. 7E

**Clone FS-26528 LC (SEQ ID NO: 277). CDRs 1, 2, and 3 are underlined.**

EIVLTQSPAT LSLSPGERAT LSCRASQSVS RYLAWYQQKP GQAPRLLIYD
ASNRATGIPA RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ RISWPFTFGG GTKVEIKR

## FIG. 7F

RASQSVSRYLA (SEQ ID NO: 278) [LC CDR1]

DASNRAT (SEQ ID NO: 279) [LC CDR2]

QQRISWPFT (SEQ ID NO: 280) [LC CDR3]

## FIG. 7G

**Clone FS-26528 CAR DNA HxL (SEQ ID NO: 281)**

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCC
TGTGCAGCCTCTGGATTCACCTTTGACGACTATGCCATGGCATGGGTCCGCCAGGCTCCAGGG
AAGGGGCTGGAGTGGGTCTCAGCTATTAGTGATGCAGGTGACAGAACATACTACGCAGACTCC
GTGAGGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACACTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCAAGAGCCGAGATGGGAGCCGTATTC
GACATATGGGGTCAGGGTACAATGGTCACCGTCTCCTCAGGGTCTACATCCGGCTCCGGGAAG
CCCGGAAGTGGCGAAGGTAGTACAAAGGGGGAAATTGTGTTGACACAGTCTCCAGCCACCCTG
TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGGTAC
TTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGATGCATCCAAC
AGGGCCACTGGCATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACC
ATCAGCAGCCTAGAGCCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGAATCTCCTGGCCT
TTCACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGGCCGCTGCCCTTGATAATGAAAAG
TCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGT
CCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTC
GTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGAT
TACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCA
CCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCG
TATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGAC
GTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCC
CAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGC
ATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCT
ACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 7H

**Clone FS-26528 CAR HxL (SEQ ID NO: 282)**

MALPVTALLL PLALLLHAAR PEVQLLESGG GLVQPGGSLR LSCAASGFTF
DDYAMAWVRQ APGKGLEWVS AISDAGDRTY YADSVRGRFT ISRDNSKNTL
YLQMNSLRAE DTAVYYCARA EMGAVFDIWG QGTMVTVSSG STSGSGKPGS
GEGSTKGEIV LTQSPATLSL SPGERATLSC RASQSVSRYL AWYQQKPGQA
PRLLIYDASN RATGIPARFS GSGSGTDFTL TISSLEPEDF AVYYCQQRIS
WPFTFGGGTK VEIKRAAALD NEKSNGTIIH VKGKHLCPSP LFPGPSKPFW
VLVVVGGVLA CYSLLVTVAF IIFWVRSKRS RLLHSDYMNM TPRRPGPTRK
HYQPYAPPRD FAAYRSRVKF SRSADAPAYQ QGQNQLYNEL NLGRREEYDV
LDKRRGRDPE MGGKPRRKNP QEGLYNELQK DKMAEAYSEI GMKGERRRGK
GHDGLYQGLS TATKDTYDAL HMQALPPR

## FIG. 7F

RASQSVSRYLA (SEQ ID NO: 278) [LC CDR1]

DASNRAT (SEQ ID NO: 279) [LC CDR2]

QQRISWPFT (SEQ ID NO: 280) [LC CDR3]

## FIG. 7G

**Clone FS-26528 CAR DNA HxL (SEQ ID NO: 281)**

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCC
TGTGCAGCCTCTGGATTCACCTTTGACGACTATGCCATGGCATGGGTCCGCCAGGCTCCAGGG
AAGGGGCTGGAGTGGGTCTCAGCTATTAGTGATGCAGGTGACAGAACATACTACGCAGACTCC
GTGAGGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACACTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCAAGAGCCGAGATGGGAGCCGTATTC
GACATATGGGGTCAGGGTACAATGGTCACCGTCTCCTCAGGGTCTACATCCGGCTCCGGGAAG
CCCGGAAGTGGCGAAGGTAGTACAAAGGGGGAAATTGTGTTGACACAGTCTCCAGCCACCCTG
TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGGTAC
TTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGATGCATCCAAC
AGGGCCACTGGCATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACC
ATCAGCAGCCTAGAGCCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGAATCTCCTGGCCT
TTCACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGGCCGCTGCCCTTGATAATGAAAAG
TCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGT
CCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTC
GTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGAT
TACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCA
CCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCG
TATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGAC
GTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCC
CAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGC
ATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCT
ACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 7H

**Clone FS-26528 CAR HxL (SEQ ID NO: 282)**

MALPVTALLL PLALLLHAAR PEVQLLESGG GLVQPGGSLR LSCAASGFTF
DDYAMAWVRQ APGKGLEWVS AISDAGDRTY YADSVRGRFT ISRDNSKNTL
YLQMNSLRAE DTAVYYCARA EMGAVFDIWG QGTMVTVSSG STSGSGKPGS
GEGSTKGEIV LTQSPATLSL SPGERATLSC RASQSVSRYL AWYQQKPGQA
PRLLIYDASN RATGIPARFS GSGSGTDFTL TISSLEPEDF AVYYCQQRIS
WPFTFGGGTK VEIKRAAALD NEKSNGTIIH VKGKHLCPSP LFPGPSKPFW
VLVVVGGVLA CYSLLVTVAF IIFWVRSKRS RLLHSDYMNM TPRRPGPTRK
HYQPYAPPRD FAAYRSRVKF SRSADAPAYQ QGQNQLYNEL NLGRREEYDV
LDKRRGRDPE MGGKPRRKNP QEGLYNELQK DKMAEAYSEI GMKGERRRGK
GHDGLYQGLS TATKDTYDAL HMQALPPR

## FIG. 7I

Clone FS-26528 CAR DNA LxH (SEQ ID NO: 283)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTC
TCCTGCAGGGCCAGTCAGAGTGTTAGCAGGTACTTAGCCTGGTACCAACAGAAACCTGGCCAG
GCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTCAGT
GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGATTTTGCA
GTTTATTACTGTCAGCAGAGAATCTCCTGGCCTTTCACTTTTGGCGGAGGGACCAAGGTTGAG
ATCAAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGG
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCC
TGTGCAGCCTCTGGATTCACCTTTGACGACTATGCCATGGCATGGGTCCGCCAGGCTCCAGGG
AAGGGGCTGGAGTGGGTCTCAGCTATTAGTGATGCAGGTGACAGAACATACTACGCAGACTCC
GTGAGGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACACTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCAAGAGCCGAGATGGGAGCCGTATTC
GACATATGGGGTCAGGGTACAATGGTCACCGTCTCCTCAGCCGCTGCCCTTGATAATGAAAAG
TCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGT
CCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTC
GTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGAT
TACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCA
CCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCG
TATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGAC
GTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCC
CAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGC
ATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCT
ACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 7J

Clone FS-26528 CAR LxH (SEQ ID NO: 284)

MALPVTALLL PLALLLHAAR PEIVLTQSPA TLSLSPGERA TLSCRASQSV
SRYLAWYQQK PGQAPRLLIY DASNRATGIP ARFSGSGSGT DFTLTISSLE
PEDFAVYYCQ QRISWPFTFG GGTKVEIKRG STSGSGKPGS GEGSTKGEVQ
LLESGGGLVQ PGGSLRLSCA ASGFTFDDYA MAWVRQAPGK GLEWVSAISD
AGDRTYYADS VRGRFTISRD NSKNTLYLQM NSLRAEDTAV YYCARAEMGA
VFDIWGQGTM VTVSSAAALD NEKSNGTIIH VKGKHLCPSP LFPGPSKPFW
VLVVVGGVLA CYSLLVTVAF IIFWVRSKRS RLLHSDYMNM TPRRPGPTRK
HYQPYAPPRD FAAYRSRVKF SRSADAPAYQ QGQNQLYNEL NLGRREEYDV
LDKRRGRDPE MGGKPRRKNP QEGLYNELQK DKMAEAYSEI GMKGERRRGK
GHDGLYQGLS TATKDTYDAL HMQALPPR

## FIG. 8A

Clone PC-26534 HC DNA (SEQ ID NO: 285)

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC
TGTGCAGCGTCTGGATTCACCTTCAGTGAGCATGGCATGCACTGGGTCCGCCAGGCTCCAGGC
AAGGGGCTGGAGTGGGTGGCAGCTATATCTTATGATGGAAGGAATAAACACTATGCAGACTCC
GTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCCAGAGACGGTACTTATCTAGGTGGT
CTCTGGTACTTCGACTTATGGGGGAGAGGTACCTTGGTCACCGTCTCCTCA

## FIG. 8B

Clone PC-26534 HC (SEQ ID NO: 286). CDRs 1, 2, and 3 are underlined.

QVQLVESGGG VVQPGRSLRL SCAASGFTFS EHGMHWVRQA PGKGLEWVAA
ISYDGRNKHY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARDG
TYLGGLWYFD LWGRGTLVTV SS

## FIG 8C

FTFSEHGMH (SEQ ID NO: 287) [HC CDR1]

AISYDGRNKHYADSVKG (SEQ ID NO: 288) [HC CDR2]

ARDGTYLGGLWYFDL (SEQ ID NO: 289) [HC CDR3]

## FIG. 8D

Clone PC-26534 LC DNA (SEQ ID NO: 290)

GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCATC
TCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACAACTATTTGGATTGGTACCTG
CAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGGGTTCTAATCGGGCCTCCGGGGTC
CCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAG
GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGGACTCGGCCTCCCTCTCACTTTTGGCGGA
GGGACCAAGGTTGAGATCAAACGG

## FIG. 8E

Clone PC-26534 LC (SEQ ID NO: 291). CDRs 1, 2, and 3 are underlined.

DIVMTQSPLS LPVTPGEPAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ
LLIYLGSNRA SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQGLGLP
LTFGGGTKVE IKR

## FIG. 8F

RSSQSLLHSNGYNYLD (SEQ ID NO: 292) [LC CDR1]

LGSNRAS (SEQ ID NO: 293) [LC CDR2]

MQGLGLPLT (SEQ ID NO: 294) [LC CDR3]

## FIG. 8G

**Clone PC-26534 CAR DNA HxL (SEQ ID NO: 295)**

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC
TGTGCAGCGTCTGGATTCACCTTCAGTGAGCATGGCATGCACTGGGTCCGCCAGGCTCCAGGC
AAGGGGCTGGAGTGGGTGGCAGCTATATCTTATGATGGAAGGAATAAACACTATGCAGACTCC
GTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCCAGAGACGGTACTTATCTAGGTGGT
CTCTGGTACTTCGACTTATGGGGGAGAGGTACCTTGGTCACCGTCTCCTCAGGGTCTACATCC
GGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGATATTGTGATGACTCAGTCT
CCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCATCTCCTGCAGGTCTAGTCAGAGC
CTCCTGCATAGTAATGGATACAACTATTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCA
CAGCTCCTGATCTATTTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTCAGTGGCAGT
GGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATGTTGGGGTTTAT
TACTGCATGCAGGGACTCGGCCTCCCTCTCACTTTTGGCGGAGGGACCAAGGTTGAGATCAAA
CGGGCCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCAC
CTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGT
GGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCC
AAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACA
AGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAG
TTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTC
AACCTGGGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATG
GGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAG
ATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGAC
GGTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCC
CTGCCACCTAGG

## FIG. 8H

**Clone PC-26534 CAR HxL (SEQ ID NO: 296)**

MALPVTALLL PLALLLHAAR PQVQLVESGG GVVQPGRSLR LSCAASGFTF
SEHGMHWVRQ APGKGLEWVA AISYDGRNKH YADSVKGRFT ISRDNSKNTL
YLQMNSLRAE DTAVYYCARD GTYLGGLWYF DLWGRGTLVT VSSGSTSGSG
KPGSGEGSTK GDIVMTQSPL SLPVTPGEPA SISCRSSQSL LHSNGYNYLD
WYLQKPGQSP QLLIYLGSNR ASGVPDRFSG SGSGTDFTLK ISRVEAEDVG
VYYCMQGLGL PLTFGGGTKV EIKRAAALDN EKSNGTIIHV KGKHLCPSPL
FPGPSKPFWV LVVVGGVLAC YSLLVTVAFI IFWVRSKRSR LLHSDYMNMT
PRRPGPTRKH YQPYAPPRDF AAYRSRVKFS RSADAPAYQQ GQNQLYNELN
LGRREEYDVL DKRRGRDPEM GGKPRRKNPQ EGLYNELQKD KMAEAYSEIG
MKGERRRGKG HDGLYQGLST ATKDTYDALH MQALPPR

## FIG. 8I

Clone PC-26534 CAR DNA LxH (SEQ ID NO: 297)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCATC
TCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACAACTATTTGGATTGGTACCTG
CAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGGGTTCTAATCGGGCCTCCGGGGTC
CCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAG
GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGGACTCGGCCTCCCTCTCACTTTTGGCGGA
GGGACCAAGGTTGAGATCAAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAA
GGTAGTACAAAGGGGCAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGG
TCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTGAGCATGGCATGCACTGGGTC
CGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGCTATATCTTATGATGGAAGGAATAAA
CACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCCAGAGACGGT
ACTTATCTAGGTGGTCTCTGGTACTTCGACTTATGGGGGAGAGGTACCTTGGTCACCGTCTCC
TCAGCCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCAC
CTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGT
GGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCC
AAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACA
AGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAG
TTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTC
AACCTGGGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATG
GGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAG
ATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGAC
GGTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCC
CTGCCACCTAGG

## FIG. 8J

Clone PC-26534 CAR LxH (SEQ ID NO: 298)

MALPVTALLL PLALLLHAAR PDIVMTQSPL SLPVTPGEPA SISCRSSQSL
LHSNGYNYLD WYLQKPGQSP QLLIYLGSNR ASGVPDRFSG SGSGTDFTLK
ISRVEAEDVG VYYCMQGLGL PLTFGGGTKV EIKRGSTSGS GKPGSGEGST
KGQVQLVESG GGVVQPGRSL RLSCAASGFT FSEHGMHWVR QAPGKGLEWV
AAISYDGRNK HYADSVKGRF TISRDNSKNT LYLQMNSLRA EDTAVYYCAR
DGTYLGGLWY FDLWGRGTLV TVSSAAALDN EKSNGTIIHV KGKHLCPSPL
FPGPSKPFWV LVVVGGVLAC YSLLVTVAFI IFWVRSKRSR LLHSDYMNMT
PRRPGPTRKH YQPYAPPRDF AAYRSRVKFS RSADAPAYQQ GQNQLYNELN
LGRREEYDVL DKRRGRDPEM GGKPRRKNPQ EGLYNELQKD KMAEAYSEIG
MKGERRRGKG HDGLYQGLST ATKDTYDALH MQALPPR

## FIG. 9A

Clone AJ-26545 HC DNA (SEQ ID NO: 299)

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCC
TGCAGGGCATCTGGATACACCTTCATGGAGCACTATATGCACTGGGTGCGACAGGCCCCTGGA
CAAGGGCTTGAGTGGATGGGAGTAATCGGGCCTAGTGGTGGTAAGACAAGCTACGCACAGAAG
TTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGC
AGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGAGAGAATTGGCCAATGGACGTA
TGGGGCCAGGGAACAACTGTCACCGTCTCCTCA

## FIG. 9B

Clone AJ-26545 HC (SEQ ID NO: 300). CDRs 1, 2, and 3 are underlined.

QVQLVQSGAE VKKPGASVKV SCRASGYTFM EHYMHWVRQA PGQGLEWMGV
IGPSGGKTSY AQKFQGRVTM TRDTSTSTVY MELSSLRSED TAVYYCARES
WPMDVWGQGT TVTVSS

## FIG. 9C

YTFMEHYMH (SEQ ID NO: 301) (HC CDR1)

VIGPSGGKTSYAQKFQG (SEQ ID NO: 302) (HC CDR2)

ARESWPMDV (SEQ ID NO: 303) (HC CDR3)

## FIG. 9D

Clone AJ-26545 LC DNA (SEQ ID NO: 304)

GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTC
TCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAG
GCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGT
GGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCA
GTTTATTACTGTCAGCAGTACGCCGCCTACCCTACTTTTGGCGGAGGGACCAAGGTTGAGATC
AAACGG

## FIG. 9E

Clone AJ-26545 LC (SEQ ID NO: 305). CDRs 1, 2, and 3 are underlined.

EIVMTQSPAT LSVSPGERAT LSCRASQSVS SNLAWYQQKP GQAPRLLIYG
ASTRATGIPA RFSGSGSGTE FTLTISSLQS EDFAVYYCQQ YAAYPTFGGG TKVEIKR

## FIG. 9F

RASQSVSSNLA (SEQ ID NO: 306) (LC CDR1)

GASTRAT (SEQ ID NO: 307) (LC CDR2)

QQYAAYPT (SEQ ID NO: 308) (LC CDR3)

## FIG. 9G

**Clone AJ-26545 CAR DNA HxL (SEQ ID NO: 309)**

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCC
TGCAGGGCATCTGGATACACCTTCATGGAGCACTATATGCACTGGGTGCGACAGGCCCCTGGA
CAAGGGCTTGAGTGGATGGGAGTAATCGGGCCTAGTGGTGGTAAGACAAGCTACGCACAGAAG
TTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGC
AGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGAGAGAATTGGCCAATGGACGTA
TGGGGCCAGGGAACAACTGTCACCGTCTCCTCAGGGTCTACATCCGGCTCCGGGAAGCCCGGA
AGTGGCGAAGGTAGTACAAAGGGGGAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTG
TCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCC
TGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCC
ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGC
AGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACGCCGCCTACCCTACTTTT
GGCGGAGGGACCAAGGTTGAGATCAAACGGGCCGCTGCCCTTGATAATGAAAAGTCAAACGGA
ACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAG
CCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTG
GCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAAT
ATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGAT
TTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAG
GGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGAC
AAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGT
CTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGA
GAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGAT
ACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 9H

**Clone AJ-26545 CAR HxL (SEQ ID NO: 310)**

MALPVTALLL PLALLLHAAR PQVQLVQSGA EVKKPGASVK VSCRASGYTF
MEHYMHWVRQ APGQGLEWMG VIGPSGGKTS YAQKFQGRVT MTRDTSTSTV
YMELSSLRSE DTAVYYCARE SWPMDVWGQG TTVTVSSGST SGSGKPGSGE
GSTKGEIVMT QSPATLSVSP GERATLSCRA SQSVSSNLAW YQQKPGQAPR
LLIYGASTRA TGIPARFSGS GSGTEFTLTI SSLQSEDFAV YYCQQYAAYP
TFGGGTKVEI KRAAALDNEK SNGTIIHVKG KHLCPSPLFP GPSKPFWVLV
VVGGVLACYS LLVTVAFIIF WVRSKRSRLL HSDYMNMTPR RPGPTRKHYQ
PYAPPRDFAA YRSRVKFSRS ADAPAYQQGQ NQLYNELNLG RREEYDVLDK
RRGRDPEMGG KPRRKNPQEG LYNELQKDKM AEAYSEIGMK GERRRGKGHD
GLYQGLSTAT KDTYDALHMQ ALPPR

## FIG. 9I

Clone AJ-26545 CAR DNA LxH (SEQ ID NO: 311)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTC
TCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAG
GCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGT
GGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCA
GTTTATTACTGTCAGCAGTACGCCGCCTACCCTACTTTTGGCGGAGGGACCAAGGTTGAGATC
AAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGCAG
GTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGC
AGGGCATCTGGATACACCTTCATGGAGCACTATATGCACTGGGTGCGACAGGCCCCTGGACAA
GGGCTTGAGTGGATGGGAGTAATCGGGCCTAGTGGTGGTAAGACAAGCTACGCACAGAAGTTC
CAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGC
CTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGAGAGAATTGGCCAATGGACGTATGG
GGCCAGGGAACAACTGTCACCGTCTCCTCAGCCGCTGCCCTTGATAATGAAAAGTCAAACGGA
ACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAG
CCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTG
GCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAAT
ATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGAT
TTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAG
GGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGAC
AAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGT
CTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGA
GAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGAT
ACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 9J

Clone AJ-26545 CAR LxH (SEQ ID NO: 312)

MALPVTALLL PLALLLHAAR PEIVMTQSPA TLSVSPGERA TLSCRASQSV
SSNLAWYQQK PGQAPRLLIY GASTRATGIP ARFSGSGSGT EFTLTISSLQ
SEDFAVYYCQ QYAAYPTFGG GTKVEIKRGS TSGSGKPGSG EGSTKGQVQL
VQSGAEVKKP GASVKVSCRA SGYTFMEHYM HWVRQAPGQG LEWMGVIGPS
GGKTSYAQKF QGRVTMTRDT STSTVYMELS SLRSEDTAVY YCARESWPMD
VWGQGTTVTV SSAAALDNEK SNGTIIHVKG KHLCPSPLFP GPSKPFWVLV
VVGGVLACYS LLVTVAFIIF WVRSKRSRLL HSDYMNMTPR RPGPTRKHYQ
PYAPPRDFAA YRSRVKFSRS ADAPAYQQGQ NQLYNELNLG RREEYDVLDK
RRGRDPEMGG KPRRKNPQEG LYNELQKDKM AEAYSEIGMK GERRRGKGHD
GLYQGLSTAT KDTYDALHMQ ALPPR

## FIG. 10A

Clone AJ-26554 HC DNA (SEQ ID NO: 313)

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCC
TGCAAGGCATCTGGATACACCTTCACGGAGCACTATATGCACTGGGTGCGACAGGCCCCTGGA
CAAAGGCTTGAGTGGATGGGAGTAATCGGGCCTAGTGGTGGTAAGACAAGCTACGCACAGAAG
TTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGC
AGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGAGAGAGTTGGCCAATGGACGTA
TGGGGCCAGGGAACAACTGTCACCGTCTCCTCA

## FIG. 10B

Clone AJ-26554 HC (SEQ ID NO: 314). CDRs 1, 2, and 3 are underlined.

QVQLVQSGAE VKKPGASVKV SCKASGYTFT EHYMHWVRQA PGQRLEWMGV
IGPSGGKTSY AQKFQGRVTM TRDTSTSTVY MELSSLRSED TAVYYCARES
WPMDVWGQGT TVTVSS

## FIG. 10C

YTFTEHYMH (SEQ ID NO: 315) (HC CDR1)

VIGPSGGKTSYAQKFQG (SEQ ID NO: 316) (HC CDR2)

ARESWPMDV (SEQ ID NO: 317) (HC CDR3)

## FIG. 10D

Clone AJ-26554 LC DNA (SEQ ID NO: 318)

GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTC
TCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAG
GCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGT
GGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCA
GTTTATTACTGTCAGCAGTACGCCGCCTACCCTACTTTTGGCGGAGGGACCAAGGTTGAGATC
AAACGG

## FIG. 10E

Clone AJ-26554 LC (SEQ ID NO: 319). CDRs 1, 2, and 3 are underlined.

EIVMTQSPAT LSVSPGERAT LSCRASQSVS SNLAWYQQKP GQAPRLLIYG
ASTRATGIPA RFSGSGSGTE FTLTISSLQS EDFAVYYCQQ YAAYPTFGGG TKVEIKR

## FIG. 10F

RASQSVSSNLA (SEQ ID NO: 320) (LC CDR1)

GASTRAT (SEQ ID NO: 321) (LC CDR2)

QQYAAYPT (SEQ ID NO: 322) (LC CDR3)

## FIG. 10G

**Clone AJ-26554 CAR DNA HxL (SEQ ID NO: 323)**

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCC
TGCAAGGCATCTGGATACACCTTCACGGAGCACTATATGCACTGGGTGCGACAGGCCCCTGGA
CAAAGGCTTGAGTGGATGGGAGTAATCGGGCCTAGTGGTGGTAAGACAAGCTACGCACAGAAG
TTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGC
AGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGAGAGAGTTGGCCAATGGACGTA
TGGGGCCAGGGAACAACTGTCACCGTCTCCTCAGGGTCTACATCCGGCTCCGGGAAGCCCGGA
AGTGGCGAAGGTAGTACAAAGGGGGAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTG
TCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCC
TGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCC
ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGC
AGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACGCCGCCTACCCTACTTTT
GGCGGAGGGACCAAGGTTGAGATCAAACGGGCCGCTGCCCTTGATAATGAAAAGTCAAACGGA
ACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAG
CCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTG
GCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAAT
ATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGAT
TTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAG
GGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGAC
AAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGT
CTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGA
GAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGAT
ACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 10H

**Clone AJ-26554 CAR HxL (SEQ ID NO: 324)**

MALPVTALLL PLALLLHAAR PQVQLVQSGA EVKKPGASVK VSCKASGYTF
TEHYMHWVRQ APGQRLEWMG VIGPSGGKTS YAQKFQGRVT MTRDTSTSTV
YMELSSLRSE DTAVYYCARE SWPMDVWGQG TTVTVSSGST SGSGKPGSGE
GSTKGEIVMT QSPATLSVSP GERATLSCRA SQSVSSNLAW YQQKPGQAPR
LLIYGASTRA TGIPARFSGS GSGTEFTLTI SSLQSEDFAV YYCQQYAAYP
TFGGGTKVEI KRAAALDNEK SNGTIIHVKG KHLCPSPLFP GPSKPFWVLV
VVGGVLACYS LLVTVAFIIF WVRSKRSRLL HSDYMNMTPR RPGPTRKHYQ
PYAPPRDFAA YRSRVKFSRS ADAPAYQQGQ NQLYNELNLG RREEYDVLDK
RRGRDPEMGG KPRRKNPQEG LYNELQKDKM AEAYSEIGMK GERRRGKGHD
GLYQGLSTAT KDTYDALHMQ ALPPR

## FIG. 10I

Clone AJ-26554 CAR DNA LxH (SEQ ID NO: 325)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTC
TCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAG
GCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGT
GGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCA
GTTTATTACTGTCAGCAGTACGCCGCCTACCCTACTTTTGGCGGAGGGACCAAGGTTGAGATC
AAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGCAG
GTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGC
AAGGCATCTGGATACACCTTCACGGAGCACTATATGCACTGGGTGCGACAGGCCCCTGGACAA
AGGCTTGAGTGGATGGGAGTAATCGGGCCTAGTGGTGGTAAGACAAGCTACGCACAGAAGTTC
CAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGC
CTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGAGAGAGTTGGCCAATGGACGTATGG
GGCCAGGGAACAACTGTCACCGTCTCCTCAGCCGCTGCCCTTGATAATGAAAAGTCAAACGGA
ACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAG
CCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTG
GCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAAT
ATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGAT
TTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAG
GGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGAC
AAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGT
CTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGA
GAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGAT
ACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 10J

Clone AJ-26554 CAR LxH (SEQ ID NO: 326)

MALPVTALLL PLALLLHAAR PEIVMTQSPA TLSVSPGERA TLSCRASQSV
SSNLAWYQQK PGQAPRLLIY GASTRATGIP ARFSGSGSGT EFTLTISSLQ
SEDFAVYYCQ QYAAYPTFGG GTKVEIKRGS TSGSGKPGSG EGSTKGQVQL
VQSGAEVKKP GASVKVSCKA SGYTFTEHYM HWVRQAPGQR LEWMGVIGPS
GGKTSYAQKF QGRVTMTRDT STSTVYMELS SLRSEDTAVY YCARESWPMD
VWGQGTTVTV SSAAALDNEK SNGTIIHVKG KHLCPSPLFP GPSKPFWVLV
VVGGVLACYS LLVTVAFIIF WVRSKRSRLL HSDYMNMTPR RPGPTRKHYQ
PYAPPRDFAA YRSRVKFSRS ADAPAYQQGQ NQLYNELNLG RREEYDVLDK
RRGRDPEMGG KPRRKNPQEG LYNELQKDKM AEAYSEIGMK GERRRGKGHD
GLYQGLSTAT KDTYDALHMQ ALPPR

## FIG. 11A

Clone NM-26562 HC DNA (SEQ ID NO: 327)

CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACC
TGTACTGTCTCTGGTGGCTCCATCGGGAGTGGTGGTAGTTACTGGAGCTGGATCCGCCAGCAC
CCAGGGAAGGGCCTGGAGTGGATTGGGTTGATCTATTACGATGGGAGCACCTACTACAACCCG
TCCCTCAAGAGTCGAGTTACCATATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAAGCTG
AGTTCTGTGACCGCCGCAGACACGGCGGTGTACTACTGCGCCAGAGGCAGGGGATATGAGACT
TCTTTAGCCTTCGATATCTGGGGTCAGGGTACAATGGTCACCGTCTCCTCA

## FIG. 11B

Clone NM-26562 HC (SEQ ID NO: 328). CDRs 1, 2, and 3 are underlined.

QVQLQESGPG LVKPSQTLSL TCTVSGGSIG SGGSYWSWIR QHPGKGLEWI
GLIYYDGSTY YNPSLKSRVT ISVDTSKNQF SLKLSSVTAA DTAVYYCARG
RGYETSLAFD IWGQGTMVTV SS

## FIG. 11C

GSIGSGGSYWS (SEQ ID NO: 329) (HC CDR1)

LIYYDGSTYYNPSLKS (SEQ ID NO: 330) (HC CDR2)

ARGRGYETSLAFDI (SEQ ID NO: 331) (HC CDR3)

## FIG. 11D

Clone NM-26562 LC DNA (SEQ ID NO: 332)

GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTC
TCCTGCAGGGCCAGTCAGAGTGTTAGCAGCTACTTAGCCTGGTACCAACAGAAACCTGGCCAG
GCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTCAGT
GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGATTTTGCA
GTTTATTACTGTCAGCAGAGACACGTCTGGCCTCCTACTTTTGGCGGAGGGACCAAGGTTGAG
ATCAAACGG

## FIG. 11E

Clone NM-26562 LC (SEQ ID NO: 333). CDRs 1, 2, and 3 are underlined.

EIVLTQSPAT LSLSPGERAT LSCRASQSVS SYLAWYQQKP GQAPRLLIYD
ASNRATGIPA RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ RHVWPPTFGG GTKVEIKR

## FIG. 11F

RASQSVSSYLA (SEQ ID NO: 334) (LC CDR1)

DASNRAT (SEQ ID NO: 335) (LC CDR2)

QQRHVWPPT (SEQ ID NO: 336) (LC CDR3)

## FIG. 11G

Clone NM-26562 CAR DNA HxL (SEQ ID NO: 337)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACC
TGTACTGTCTCTGGTGGCTCCATCGGGAGTGGTGGTAGTTACTGGAGCTGGATCCGCCAGCAC
CCAGGGAAGGGCCTGGAGTGGATTGGGTTGATCTATTACGATGGGAGCACCTACTACAACCCG
TCCCTCAAGAGTCGAGTTACCATATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAAGCTG
AGTTCTGTGACCGCCGCAGACACGGCGGTGTACTACTGCGCCAGAGGCAGGGGATATGAGACT
TCTTTAGCCTTCGATATCTGGGGTCAGGGTACAATGGTCACCGTCTCCTCAGGGTCTACATCC
GGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGAAATTGTGTTGACACAGTCT
CCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGT
GTTAGCAGCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT
GATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGAC
TTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGA
CACGTCTGGCCTCCTACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGGCCGCTGCCCTT
GATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCC
TTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGT
TACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTG
CTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAG
CCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCA
GATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGG
GAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGA
CGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTAT
TCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGA
CTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 11H

Clone NM-26562 CAR HxL (SEQ ID NO: 338)

MALPVTALLL PLALLLHAAR PQVQLQESGP GLVKPSQTLS LTCTVSGGSI
GSGGSYWSWI RQHPGKGLEW IGLIYYDGST YYNPSLKSRV TISVDTSKNQ
FSLKLSSVTA ADTAVYYCAR GRGYETSLAF DIWGQGTMVT VSSGSTSGSG
KPGSGEGSTK GEIVLTQSPA TLSLSPGERA TLSCRASQSV SSYLAWYQQK
PGQAPRLLIY DASNRATGIP ARFSGSGSGT DFTLTISSLE PEDFAVYYCQ
QRHVWPPTFG GGTKVEIKRA AALDNEKSNG TIIHVKGKHL CPSPLFPGPS
KPFWVLVVVG GVLACYSLLV TVAFIIFWVR SKRSRLLHSD YMNMTPRRPG
PTRKHYQPYA PPRDFAAYRS RVKFSRSADA PAYQQGQNQL YNELNLGRRE
EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA YSEIGMKGER
RRGKGHDGLY QGLSTATKDT YDALHMQALP PR

## FIG. 11I

Clone NM-26562 CAR DNA LxH (SEQ ID NO: 339)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTC
TCCTGCAGGGCCAGTCAGAGTGTTAGCAGCTACTTAGCCTGGTACCAACAGAAACCTGGCCAG
GCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTCAGT
GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGATTTTGCA
GTTTATTACTGTCAGCAGAGACACGTCTGGCCTCCTACTTTTGGCGGAGGGACCAAGGTTGAG
ATCAAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGG
CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACC
TGTACTGTCTCTGGTGGCTCCATCGGGAGTGGTGGTAGTTACTGGAGCTGGATCCGCCAGCAC
CCAGGGAAGGGCCTGGAGTGGATTGGGTTGATCTATTACGATGGGAGCACCTACTACAACCCG
TCCCTCAAGAGTCGAGTTACCATATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAAGCTG
AGTTCTGTGACCGCCGCAGACACGGCGGTGTACTACTGCGCCAGAGGCAGGGGATATGAGACT
TCTTTAGCCTTCGATATCTGGGGTCAGGGTACAATGGTCACCGTCTCCTCAGCCGCTGCCCTT
GATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCC
TTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGT
TACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTG
CTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAG
CCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCA
GATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGG
GAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGA
CGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTAT
TCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGA
CTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 11J

Clone NM-26562 CAR LxH (SEQ ID NO: 340)

MALPVTALLL PLALLLHAAR PEIVLTQSPA TLSLSPGERA TLSCRASQSV
SSYLAWYQQK PGQAPRLLIY DASNRATGIP ARFSGSGSGT DFTLTISSLE
PEDFAVYYCQ QRHVWPPTFG GGTKVEIKRG STSGSGKPGS GEGSTKGQVQ
LQESGPGLVK PSQTLSLTCT VSGGSIGSGG SYWSWIRQHP GKGLEWIGLI
YYDGSTYYNP SLKSRVTISV DTSKNQFSLK LSSVTAADTA VYYCARGRGY
ETSLAFDIWG QGTMVTVSSA AALDNEKSNG TIIHVKGKHL CPSPLFPGPS
KPFWVLVVVG GVLACYSLLV TVAFIIFWVR SKRSRLLHSD YMNMTPRRPG
PTRKHYQPYA PPRDFAAYRS RVKFSRSADA PAYQQGQNQL YNELNLGRRE
EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA YSEIGMKGER
RRGKGHDGLY QGLSTATKDT YDALHMQALP PR

## FIG. 12A

Clone TS-26564 HC DNA (SEQ ID NO: 341)

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCC
TGTGCAGCCTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCGCCAGGCTCCAGGG
AAGGGGCTGGAGTGGGTTTCAACCATTAGTAGTAGTAGTAGTATCATATACTACGCAGACTCT
GTGAAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACTCACTGTATCTGCAAATGAAC
AGCCTGAGAGCTGAGGACACGGCGGTGTACTACTGCGCCAGAGGTTCTCAGGAGCACCTGATT
TTCGATTATTGGGGACAGGGTACATTGGTCACCGTCTCCTCA

## FIG. 12B

Clone TS-26564 HC (SEQ ID NO: 342). CDRs 1, 2, and 3 are underlined.

EVQLVESGGG LVQPGGSLRL SCAASGFTFS SYSMNWVRQA PGKGLEWVST
ISSSSSIIYY ADSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARGS
QEHLIFDYWG QGTLVTVSS

## FIG. 12C

FTFSSYSMN (SEQ ID NO: 343) (HC CDR1)

TISSSSSIIYYADSVKG (SEQ ID NO: 344) (HC CDR2)

ARGSQEHLIFDY (SEQ ID NO: 345) (HC CDR3)

## FIG. 12D

Clone TS-26564 LC DNA (SEQ ID NO: 346)

GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTC
TCCTGCAGGGCCAGTCAGAGTGTTAGCAGGTACTTAGCCTGGTACCAACAGAAACCTGGCCAG
GCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTCAGT
GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGATTTTGCA
GTTTATTACTGTCAGCAGAGATTCTACTACCCTTGGACTTTTGGCGGAGGGACCAAGGTTGAG
ATCAAACGG

## FIG. 12E

Clone TS-26564 LC (SEQ ID NO: 347). CDRs 1, 2, and 3 are underlined.

EIVLTQSPAT LSLSPGERAT LSCRASQSVS RYLAWYQQKP GQAPRLLIYD
ASNRATGIPA RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ RFYYPWTFGG GTKVEIKR

## FIG. 12F

RASQSVSRYLA (SEQ ID NO: 347) (LC CDR1)

DASNRAT (SEQ ID NO: 349) (LC CDR2)

QQRFYYPWT (SEQ ID NO: 350) (LC CDR3)

## IG. 12G

Clone TS-26564 CAR DNA HxL (SEQ ID NO: 351)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCC
TGTGCAGCCTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCGCCAGGCTCCAGGG
AAGGGGCTGGAGTGGGTTTCAACCATTAGTAGTAGTAGTAGTATCATATACTACGCAGACTCT
GTGAAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACTCACTGTATCTGCAAATGAAC
AGCCTGAGAGCTGAGGACACGGCGGTGTACTACTGCGCCAGAGGTTCTCAGGAGCACCTGATT
TTCGATTATTGGGGACAGGGTACATTGGTCACCGTCTCCTCAGGGTCTACATCCGGCTCCGGG
AAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGAAATTGTGTTGACACAGTCTCCAGCCACC
CTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGG
TACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGATGCATCC
AACAGGGCCACTGGCATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTC
ACCATCAGCAGCCTAGAGCCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGATTCTACTAC
CCTTGGACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGGCCGCTGCCCTTGATAATGAA
AAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCT
GGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTG
CTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGC
GATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCA
CCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCA
GCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTAT
GACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAAC
CCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATA
GGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACT
GCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 12H

Clone TS-26564 CAR HxL (SEQ ID NO: 352)

MALPVTALLL PLALLLHAAR PEVQLVESGG GLVQPGGSLR LSCAASGFTF
SSYSMNWVRQ APGKGLEWVS TISSSSSIIY YADSVKGRFT ISRDNAKNSL
YLQMNSLRAE DTAVYYCARG SQEHLIFDYW GQGTLVTVSS GSTSGSGKPG
SGEGSTKGEI VLTQSPATLS LSPGERATLS CRASQSVSRY LAWYQQKPGQ
APRLLIYDAS NRATGIPARF SGSGSGTDFT LTISSLEPED FAVYYCQQRF
YYPWTFGGGT KVEIKRAAAL DNEKSNGTII HVKGKHLCPS PLFPGPSKPF
WVLVVVGGVL ACYSLLVTVA FIIFWVRSKR SRLLHSDYMN MTPRRPGPTR
KHYQPYAPPR DFAAYRSRVK FSRSADAPAY QQGQNQLYNE LNLGRREEYD
VLDKRRGRDP EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRG
KGHDGLYQGL STATKDTYDA LHMQALPPR

## FIG. 12I

Clone TS-26564 CAR DNA LxH (SEQ ID NO: 353)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTC
TCCTGCAGGGCCAGTCAGAGTGTTAGCAGGTACTTAGCCTGGTACCAACAGAAACCTGGCCAG
GCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTCAGT
GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGATTTTGCA
GTTTATTACTGTCAGCAGAGATTCTACTACCCTTGGACTTTTGGCGGAGGGACCAAGGTTGAG
ATCAAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGG
GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCC
TGTGCAGCCTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCGCCAGGCTCCAGGG
AAGGGGCTGGAGTGGGTTTCAACCATTAGTAGTAGTAGTAGTATCATATACTACGCAGACTCT
GTGAAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACTCACTGTATCTGCAAATGAAC
AGCCTGAGAGCTGAGGACACGGCGGTGTACTACTGCGCCAGAGGTTCTCAGGAGCACCTGATT
TTCGATTATTGGGGACAGGGTACATTGGTCACCGTCTCCTCAGCCGCTGCCCTTGATAATGAA
AAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCT
GGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTG
CTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGC
GATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCA
CCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCA
GCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTAT
GACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAAC
CCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATA
GGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACT
GCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 12J

Clone TS-26564 CAR LxH (SEQ ID NO: 354)

MALPVTALLL PLALLLHAAR PEIVLTQSPA TLSLSPGERA TLSCRASQSV
SRYLAWYQQK PGQAPRLLIY DASNRATGIP ARFSGSGSGT DFTLTISSLE
PEDFAVYYCQ QRFYYPWTFG GGTKVEIKRG STSGSGKPGS GEGSTKGEVQ
LVESGGGLVQ PGGSLRLSCA ASGFTFSSYS MNWVRQAPGK GLEWVSTISS
SSSIIYYADS VKGRFTISRD NAKNSLYLQM NSLRAEDTAV YYCARGSQEH
LIFDYWGQGT LVTVSSAAAL DNEKSNGTII HVKGKHLCPS PLFPGPSKPF
WVLVVVGGVL ACYSLLVTVA FIIFWVRSKR SRLLHSDYMN MTPRRPGPTR
KHYQPYAPPR DFAAYRSRVK FSRSADAPAY QQGQNQLYNE LNLGRREEYD
VLDKRRGRDP EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRG
KGHDGLYQGL STATKDTYDA LHMQALPPR

## FIG. 13A

**Clone RY-26568 HC DNA (SEQ ID NO: 355)**

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC
TGTGCAGCGTCTGGATTCACCTTCGGGAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGC
AAGGGGCTGGAGTGGGTGGCAGTTATACATTATGATGGAAGTGTTGAATACTATGCAGACTCC
GTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGGACACGCTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCCAGAACTGACTTCTGGAGCGGATCC
CCTCCAAGCTTAGATTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA

## FIG. 13B

**Clone RY-26568 HC (SEQ ID NO: 356). CDRs 1, 2, and 3 are underlined.**

QVQLVESGGG VVQPGRSLRL SCAASGFTFG SYGMHWVRQA PGKGLEWVAV
IHYDGSVEYY ADSVKGRFTI SRDNSKDTLY LQMNSLRAED TAVYYCARTD
FWSGSPPSLD YWGQGTLVTV SS

## FIG. 13C

FTFGSYGMH (SEQ ID NO: 357) (HC CDR1)

VIHYDGSVEYYADSVKG (SEQ ID NO: 358) (HC CDR2)

ARTDFWSGSPPSLDY (SEQ ID NO: 359) (HC CDR3)

## FIG. 13D

**Clone RY-26568 LC DNA (SEQ ID NO: 360)**

GACATCCAGTTGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATC
ACTTGTCGGGCGAGTCGGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAA
GCCCCTAAGCTCCTGATCTATGGTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGC
GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCA
ACTTATTACTGTCAGCAGATATACACCTTCCCTTTCACTTTTGGCGGAGGGACCAAGGTTGAG
ATCAAACGG

## FIG. 13E

**Clone RY-26568 LC (SEQ ID NO: 361). CDRs 1, 2, and 3 are underlined.**

DIQLTQSPSS VSASVGDRVT ITCRASRGIS SWLAWYQQKP GKAPKLLIYG
ASSLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ IYTFPFTFGG GTKVEIKR

## FIG. 13F

RASRGISSWLA (SEQ ID NO: 362) (LC CDR1)

GASSLQS (SEQ ID NO: 363) (LC CDR2)

QQIYTFPFT (SEQ ID NO: 364) (LC CDR3)

## FIG. 13G

Clone RY-26568 CAR DNA HxL (SEQ ID NO: 365)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC
TGTGCAGCGTCTGGATTCACCTTCGGGAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGC
AAGGGGCTGGAGTGGGTGGCAGTTATACATTATGATGGAAGTGTTGAATACTATGCAGACTCC
GTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGGACACGCTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCCAGAACTGACTTCTGGAGCGGATCC
CCTCCAAGCTTAGATTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCAGGGTCTACATCC
GGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGACATCCAGTTGACCCAGTCT
CCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGTCGGGCGAGTCGGGGT
ATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTAT
GGTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAT
TTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCAGCAGATA
TACACCTTCCCTTTCACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGGCCGCTGCCCTT
GATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCC
TTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGT
TACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTG
CTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAG
CCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCA
GATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGG
GAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGA
CGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTAT
TCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGA
CTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 13H

Clone RY-26568 CAR HxL (SEQ ID NO: 366)

MALPVTALLL PLALLLHAAR PQVQLVESGG GVVQPGRSLR LSCAASGFTF
GSYGMHWVRQ APGKGLEWVA VIHYDGSVEY YADSVKGRFT ISRDNSKDTL
YLQMNSLRAE DTAVYYCART DFWSGSPPSL DYWGQGTLVT VSSGSTSGSG
KPGSGEGSTK GDIQLTQSPS SVSASVGDRV TITCRASRGI SSWLAWYQQK
PGKAPKLLIY GASSLQSGVP SRFSGSGSGT DFTLTISSLQ PEDFATYYCQ
QIYTFPFTFG GGTKVEIKRA AALDNEKSNG TIIHVKGKHL CPSPLFPGPS
KPFWVLVVVG GVLACYSLLV TVAFIIFWVR SKRSRLLHSD YMNMTPRRPG
PTRKHYQPYA PPRDFAAYRS RVKFSRSADA PAYQQGQNQL YNELNLGRRE
EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA YSEIGMKGER
RRGKGHDGLY QGLSTATKDT YDALHMQALP PR

## FIG. 13I

Clone RY-26568 CAR DNA LxH (SEQ ID NO: 367)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
GACATCCAGTTGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATC
ACTTGTCGGGCGAGTCGGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAA
GCCCCTAAGCTCCTGATCTATGGTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGC
GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCA
ACTTATTACTGTCAGCAGATATACACCTTCCCTTTCACTTTTGGCGGAGGGACCAAGGTTGAG
ATCAAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGG
CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC
TGTGCAGCGTCTGGATTCACCTTCGGGAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGC
AAGGGGCTGGAGTGGGTGGCAGTTATACATTATGATGGAAGTGTTGAATACTATGCAGACTCC
GTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGGACACGCTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCCAGAACTGACTTCTGGAGCGGATCC
CCTCCAAGCTTAGATTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCAGCCGCTGCCCTT
GATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCC
TTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGT
TACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTG
CTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAG
CCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCA
GATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGG
GAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGA
CGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTAT
TCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGA
CTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 13J

Clone RY-26568 CAR LxH (SEQ ID NO: 368)

MALPVTALLL PLALLLHAAR PDIQLTQSPS SVSASVGDRV TITCRASRGI
SSWLAWYQQK PGKAPKLLIY GASSLQSGVP SRFSGSGSGT DFTLTISSLQ
PEDFATYYCQ QIYTFPFTFG GGTKVEIKRG STSGSGKPGS GEGSTKGQVQ
LVESGGGVVQ PGRSLRLSCA ASGFTFGSYG MHWVRQAPGK GLEWVAVIHY
DGSVEYYADS VKGRFTISRD NSKDTLYLQM NSLRAEDTAV YYCARTDFWS
GSPPSLDYWG QGTLVTVSSA AALDNEKSNG TIIHVKGKHL CPSPLFPGPS
KPFWVLVVVG GVLACYSLLV TVAFIIFWVR SKRSRLLHSD YMNMTPRRPG
PTRKHYQPYA PPRDFAAYRS RVKFSRSADA PAYQQGQNQL YNELNLGRRE
EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA YSEIGMKGER
RRGKGHDGLY QGLSTATKDT YDALHMQALP PR

## FIG. 14A

Clone PP-26575 HC DNA (SEQ ID NO: 369)

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCC
TGCAAGGCTTCTGGAGGCACCCTCAGCAGCCTGGCTATCAGCTGGGTGCGACAGGCCCCTGGA
CAAGGGCTTGAGTGGATGGGAGGGGTCATCCCTATCTTGGGTCGGGCAAACTACGCACAGAAG
TTCCAGGGCAGAGTCACGATTACCGCGGACGAGTCCACGAGCACAGCCTACATGGAGCTGAGC
AGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGAACTCCTGAATACTCCTCCAGC
ATATGGCACTATTACTACGGCATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA

## FIG. 14B

Clone PP-26575 HC (SEQ ID NO: 370). CDRs 1, 2, and 3 are underlined.

QVQLVQSGAE VKKPGSSVKV SCKASGGTLS SLAISWVRQA PGQGLEWMGG
VIPILGRANY AQKFQGRVTI TADESTSTAY MELSSLRSED TAVYYCARTP
EYSSSIWHYY YGMDVWGQGT TVTVSS

## FIG. 14C

GTLSSLAIS (SEQ ID NO: 371) (HC CDR1)

GVIPILGRANYAQKFQG (SEQ ID NO: 372) (HC CDR2)

ARTPEYSSSIWHYYYGMDV (SEQ ID NO: 373) (HC CDR3)

## FIG. 14D

Clone PP-26575 LC DNA (SEQ ID NO: 374)

GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATC
AACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCTTGGTAC
CAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG
GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG
CAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTTCGCCCACACTCCTTTCACTTTTGGC
GGAGGGACCAAGGTTGAGATCAAACGG

## FIG. 14E

Clone PP-26575 LC (SEQ ID NO: 375). CDRs 1, 2, and 3 are underlined.

DIVMTQSPDS LAVSLGERAT INCKSSQSVL YSSNNKNYLA WYQQKPGQPP
KLLIYWASTR ESGVPDRFSG SGSGTDFTLT ISSLQAEDVA VYYCQQFAHT
PFTFGGGTKV EIKR

## FIG. 14F

KSSQSVLYSSNNKNYLA (SEQ ID NO: 376) (LC CDR1)

WASTRES (SEQ ID NO: 377) (LC CDR2)

QQFAHTPFT (SEQ ID NO: 378) (LC CDR3)

## FIG. 14G

Clone PP-26575 CAR DNA HxL (SEQ ID NO: 379)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCC
TGCAAGGCTTCTGGAGGCACCCTCAGCAGCCTGGCTATCAGCTGGGTGCGACAGGCCCCTGGA
CAAGGGCTTGAGTGGATGGGAGGGGTCATCCCTATCTTGGGTCGGGCAAACTACGCACAGAAG
TTCCAGGGCAGAGTCACGATTACCGCGGACGAGTCCACGAGCACAGCCTACATGGAGCTGAGC
AGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGAACTCCTGAATACTCCTCCAGC
ATATGGCACTATTACTACGGCATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA
GGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGACATCGTG
ATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAG
TCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCTTGGTACCAGCAGAAA
CCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC
CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAA
GATGTGGCAGTTTATTACTGTCAGCAGTTCGCCCACACTCCTTTCACTTTTGGCGGAGGGACC
AAGGTTGAGATCAAACGGGCCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTCAC
GTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTG
TTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATC
TTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACGC
CGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCTGCCTAT
CGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAA
CTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGA
CGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAG
CTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGG
GGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCT
CTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 14H

Clone PP-26575 CAR HxL (SEQ ID NO: 380)

MALPVTALLL PLALLLHAAR PQVQLVQSGA EVKKPGSSVK VSCKASGGTL
SSLAISWVRQ APGQGLEWMG GVIPILGRAN YAQKFQGRVT ITADESTSTA
YMELSSLRSE DTAVYYCART PEYSSSIWHY YYGMDVWGQG TTVTVSSGST
SGSGKPGSGE GSTKGDIVMT QSPDSLAVSL GERATINCKS SQSVLYSSNN
KNYLAWYQQK PGQPPKLLIY WASTRESGVP DRFSGSGSGT DFTLTISSLQ
AEDVAVYYCQ QFAHTPFTFG GGTKVEIKRA AALDNEKSNG TIIHVKGKHL
CPSPLFPGPS KPFWVLVVVG GVLACYSLLV TVAFIIFWVR SKRSRLLHSD
YMNMTPRRPG PTRKHYQPYA PPRDFAAYRS RVKFSRSADA PAYQQGQNQL
YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA
YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR

## FIG. 14I

Clone PP-26575 CAR DNA LxH (SEQ ID NO: 381)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATC
AACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCTTGGTAC
CAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG
GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG
CAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTTCGCCCACACTCCTTTCACTTTTGGC
GGAGGGACCAAGGTTGAGATCAAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGC
GAAGGTAGTACAAAGGGGCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGG
TCCTCGGTGAAGGTCTCCTGCAAGGCTTCTGGAGGCACCCTCAGCAGCCTGGCTATCAGCTGG
GTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAGGGGTCATCCCTATCTTGGGTCGG
GCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAGTCCACGAGCACA
GCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGAACT
CCTGAATACTCCTCCAGCATATGGCACTATTACTACGGCATGGACGTATGGGGCCAGGGAACA
ACTGTCACCGTCTCCTCAGCCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTCAC
GTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTG
TTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATC
TTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACGC
CGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCTGCCTAT
CGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAA
CTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGA
CGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAG
CTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGG
GGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCT
CTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 14J

Clone PP-26575 CAR LxH (SEQ ID NO: 382)

MALPVTALLL PLALLLHAAR PDIVMTQSPD SLAVSLGERA TINCKSSQSV
LYSSNNKNYL AWYQQKPGQP PKLLIYWAST RESGVPDRFS GSGSGTDFTL
TISSLQAEDV AVYYCQQFAH TPFTFGGGTK VEIKRGSTSG SGKPGSGEGS
TKGQVQLVQS GAEVKKPGSS VKVSCKASGG TLSSLAISWV RQAPGQGLEW
MGGVIPILGR ANYAQKFQGR VTITADESTS TAYMELSSLR SEDTAVYYCA
RTPEYSSSIW HYYYGMDVWG QGTTVTVSSA AALDNEKSNG TIIHVKGKHL
CPSPLFPGPS KPFWVLVVVG GVLACYSLLV TVAFIIFWVR SKRSRLLHSD
YMNMTPRRPG PTRKHYQPYA PPRDFAAYRS RVKFSRSADA PAYQQGQNQL
YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA
YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR

## FIG. 15A

Clone RD-26576 HC DNA (SEQ ID NO: 383)

CAGGTGCGGCTGGTGGAGTCTGGGGGGGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC
TGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATACACTGGGTCCGCCAGGCTCCAGGC
AAGGGGCTGGAGTGGGTGGCAGTTATAGGGTATGATGGACAGGAGAAATACTATGCAGACTCC
GTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAAGGGGCCGTTGCAGGAGCCGCCA
TACGCTTTTGGGATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA

## FIG. 15B

Clone RD-26576 HC (SEQ ID NO: 384). CDRs 1, 2, and 3 are underlined.

QVRLVESGGG VVQPGRSLRL SCAASGFTFS SYGIHWVRQA PGKGLEWVAV
IGYDGQEKYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKGP
LQEPPYAFGM DVWGQGTTVT VSS

## FIG. 15C

FTFSSYGIH (SEQ ID NO: 385) (HC CDR1)

VIGYDGQEKYYADSVKG (SEQ ID NO: 386) (HC CDR2)

VKGPLQEPPYAFGMDV (SEQ ID NO: 387) (HC CDR3)

## FIG. 15D

Clone RD-26576 LC DNA (SEQ ID NO: 388)

GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTC
TCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAG
GCTCCCAGGCTCCTCATCTATAGCGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGT
GGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCA
GTTTATTACTGTCAGCAGCACCACGTCTGGCCTCTCACTTTTGGCGGAGGGACCAAGGTTGAG
ATCAAACGG

## FIG. 15E

Clone RD-26576 LC (SEQ ID NO: 389). CDRs 1, 2, and 3 are underlined.

EIVMTQSPAT LSVSPGERAT LSCRASQSVS SNLAWYQQKP GQAPRLLIYS
ASTRATGIPA RFSGSGSGTE FTLTISSLQS EDFAVYYCQQ HHVWPLTFGG GTKVEIKR

## FIG. 15F

RASQSVSSNLA (SEQ ID NO: 390) (LC CDR1)

SASTRAT (SEQ ID NO: 391) (LC CDR2)

QQHHVWPLT (SEQ ID NO: 392) (LC CDR3)

## FIG. 15G

**Clone RD-26576 CAR DNA HxL (SEQ ID NO: 393)**

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
CAGGTGCGGCTGGTGGAGTCTGGGGGGGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC
TGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATACACTGGGTCCGCCAGGCTCCAGGC
AAGGGGCTGGAGTGGGTGGCAGTTATAGGGTATGATGGACAGGAGAAATACTATGCAGACTCC
GTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAAGGGGCCGTTGCAGGAGCCGCCA
TACGCTTTTGGGATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCAGGGTCTACA
TCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGAAATAGTGATGACGCAG
TCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAG
AGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATC
TATAGCGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACA
GAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAG
CACCACGTCTGGCCTCTCACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGGCCGCTGCC
CTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCA
CCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCT
TGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGC
CTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTAC
CAGCCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCT
GCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGC
AGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCA
AGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCC
TATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAG
GGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 15H

**Clone RD-26576 CAR HxL (SEQ ID NO: 394)**

MALPVTALLL PLALLLHAAR PQVRLVESGG GVVQPGRSLR LSCAASGFTF
SSYGIHWVRQ APGKGLEWVA VIGYDGQEKY YADSVKGRFT ISRDNSKNTL
YLQMNSLRAE DTAVYYCVKG PLQEPPYAFG MDVWGQGTTV TVSSGSTSGS
GKPGSGEGST KGEIVMTQSP ATLSVSPGER ATLSCRASQS VSSNLAWYQQ
KPGQAPRLLI YSASTRATGI PARFSGSGSG TEFTLTISSL QSEDFAVYYC
QQHHVWPLTF GGGTKVEIKR AAALDNEKSN GTIIHVKGKH LCPSPLFPGP
SKPFWVLVVV GGVLACYSLL VTVAFIIFWV RSKRSRLLHS DYMNMTPRRP
GPTRKHYQPY APPRDFAAYR SRVKFSRSAD APAYQQGQNQ LYNELNLGRR
EEYDVLDKRR GRDPEMGGKP RRKNPQEGLY NELQKDKMAE AYSEIGMKGE
RRRGKGHDGL YQGLSTATKD TYDALHMQAL PPR

## FIG. 15I

Clone RD-26576 CAR DNA LxH (SEQ ID NO: 395)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTC
TCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAG
GCTCCCAGGCTCCTCATCTATAGCGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGT
GGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCA
GTTTATTACTGTCAGCAGCACCACGTCTGGCCTCTCACTTTTGGCGGAGGGACCAAGGTTGAG
ATCAAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGG
CAGGTGCGGCTGGTGGAGTCTGGGGGGGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC
TGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATACACTGGGTCCGCCAGGCTCCAGGC
AAGGGGCTGGAGTGGGTGGCAGTTATAGGGTATGATGGACAGGAGAAATACTATGCAGACTCC
GTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAAGGGGCCGTTGCAGGAGCCGCCA
TACGCTTTTGGGATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCAGCCGCTGCC
CTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCA
CCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCT
TGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGC
CTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTAC
CAGCCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCT
GCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGC
AGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCA
AGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCC
TATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAG
GGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 15J

Clone RD-26576 CAR LxH (SEQ ID NO: 396)

MALPVTALLL PLALLLHAAR PEIVMTQSPA TLSVSPGERA TLSCRASQSV
SSNLAWYQQK PGQAPRLLIY SASTRATGIP ARFSGSGSGT EFTLTISSLQ
SEDFAVYYCQ QHHVWPLTFG GGTKVEIKRG STSGSGKPGS GEGSTKGQVR
LVESGGGVVQ PGRSLRLSCA ASGFTFSSYG IHWVRQAPGK GLEWVAVIGY
DGQEKYYADS VKGRFTISRD NSKNTLYLQM NSLRAEDTAV YYCVKGPLQE
PPYAFGMDVW GQGTTVTVSS AAALDNEKSN GTIIHVKGKH LCPSPLFPGP
SKPFWVLVVV GGVLACYSLL VTVAFIIFWV RSKRSRLLHS DYMNMTPRRP
GPTRKHYQPY APPRDFAAYR SRVKFSRSAD APAYQQGQNQ LYNELNLGRR
EEYDVLDKRR GRDPEMGGKP RRKNPQEGLY NELQKDKMAE AYSEIGMKGE
RRRGKGHDGL YQGLSTATKD TYDALHMQAL PPR

## FIG. 16A

Clone RD-26578 HC DNA (SEQ ID NO: 397)

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC
TGTGCAGCGTCTGGATTCACCTTCAGTAGCCGTGGCATGCACTGGGTCCGCCAGGCTCCAGGC
AAGGGGCTGGAGTGGGTGGCAGTTATAGGGTATGATGGACAGGAGAAATACTATGCAGACTCC
GTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAAGGGGCCGTTGCAGGAGCCGCCA
TACGATTATGGAATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA

## FIG. 16B

Clone RD-26578 HC (SEQ ID NO: 398) CDRs 1, 2, and 3 are underlined.

QVQLVESGGG VVQPGRSLRL SCAASGFTFS SRGMHWVRQA PGKGLEWVAV
IGYDGQEKYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKGP
LQEPPYDYGM DVWGQGTTVT VSS

## FIG. 16C

FTFSSRGMH (SEQ ID NO: 399) (HC CDR1)

VIGYDGQEKYYADSVKG (SEQ ID NO: 400) (HC CDR2)

VKGPLQEPPYDYGMDV (SEQ ID NO: 401) (HC CDR3)

## FIG. 16D

Clone RD-26578 LC DNA (SEQ ID NO: 402)

GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTC
TCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAG
GCTCCCAGGCTCCTCATCTATAGCGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGT
GGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCA
GTTTATTACTGTCAGCAGCACCACGTCTGGCCTCTCACTTTTGGCGGAGGGACCAAGGTTGAG
ATCAAACGG

## FIG. 16E

Clone RD-26578 LC (SEQ ID NO: 403). CDRs 1, 2, and 3 are underlined.

EIVMTQSPAT LSVSPGERAT LSCRASQSVS SNLAWYQQKP GQAPRLLIYS
ASTRATGIPA RFSGSGSGTE FTLTISSLQS EDFAVYYCQQ HHVWPLTFGG GTKVEIKR

## FIG. 16F

RASQSVSSNLA (SEQ ID NO: 404) (LC CDR1)

SASTRAT (SEQ ID NO: 405) (LC CDR2)

QQHHVWPLT (SEQ ID NO: 406) (LC CDR3)

## FIG. 16G

**Clone RD-26578 CAR DNA HxL (SEQ ID NO: 407)**

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC
TGTGCAGCGTCTGGATTCACCTTCAGTAGCCGTGGCATGCACTGGGTCCGCCAGGCTCCAGGC
AAGGGGCTGGAGTGGGTGGCAGTTATAGGGTATGATGGACAGGAGAAATACTATGCAGACTCC
GTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAAGGGGCCGTTGCAGGAGCCGCCA
TACGATTATGGAATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCAGGGTCTACA
TCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGAAATAGTGATGACGCAG
TCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAG
AGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATC
TATAGCGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACA
GAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAG
CACCACGTCTGGCCTCTCACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGGCCGCTGCC
CTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCA
CCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCT
TGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGC
CTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTAC
CAGCCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCT
GCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGC
AGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCA
AGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCC
TATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAG
GGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

FIG. 16H

Clone RD-26578 CAR HxL (SEQ ID NO: 408)

MALPVTALLL PLALLLHAAR PQVQLVESGG GVVQPGRSLR LSCAASGFTF
SSRGMHWVRQ APGKGLEWVA VIGYDGQEKY YADSVKGRFT ISRDNSKNTL
YLQMNSLRAE DTAVYYCVKG PLQEPPYDYG MDVWGQGTTV TVSSGSTSGS
GKPGSGEGST KGEIVMTQSP ATLSVSPGER ATLSCRASQS VSSNLAWYQQ
KPGQAPRLLI YSASTRATGI PARFSGSGSG TEFTLTISSL QSEDFAVYYC
QQHHVWPLTF GGGTKVEIKR AAALDNEKSN GTIIHVKGKH LCPSPLFPGP
SKPFWVLVVV GGVLACYSLL VTVAFIIFWV RSKRSRLLHS DYMNMTPRRP
GPTRKHYQPY APPRDFAAYR SRVKFSRSAD APAYQQGQNQ LYNELNLGRR
EEYDVLDKRR GRDPEMGGKP RRKNPQEGLY NELQKDKMAE AYSEIGMKGE
RRRGKGHDGL YQGLSTATKD TYDALHMQAL PPR

FIG. 16I

Clone RD-26578 CAR DNA LxH (SEQ ID NO: 409)

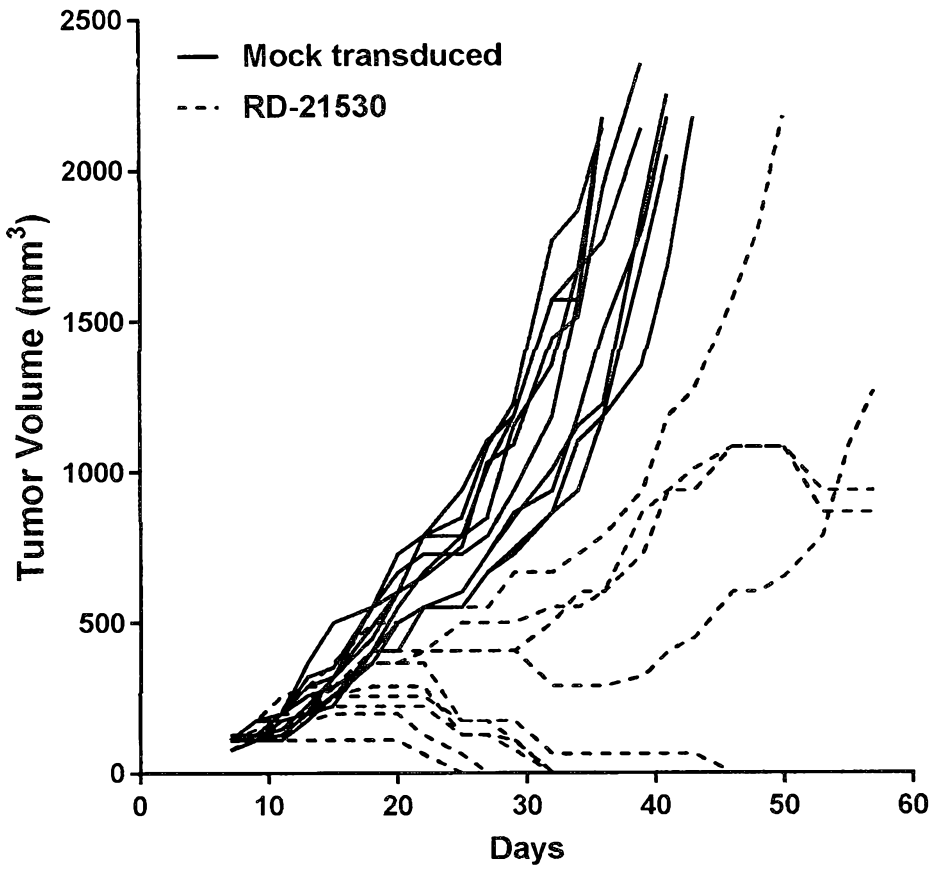
ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTC
TCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAG
GCTCCCAGGCTCCTCATCTATAGCGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGT
GGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCA
GTTTATTACTGTCAGCAGCACCACGTCTGGCCTCTCACTTTTGGCGGAGGGACCAAGGTTGAG
ATCAAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGG
CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC
TGTGCAGCGTCTGGATTCACCTTCAGTAGCCGTGGCATGCACTGGGTCCGCCAGGCTCCAGGC
AAGGGGCTGGAGTGGGTGGCAGTTATAGGGTATGATGGACAGGAGAAATACTATGCAGACTCC
GTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAAGGGGCCGTTGCAGGAGCCGCCA
TACGATTATGGAATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCAGCCGCTGCC
CTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCA
CCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCT
TGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGC
CTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTAC
CAGCCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCT
GCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGC
AGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCA
AGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCC
TATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAG
GGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

FIG. 16J

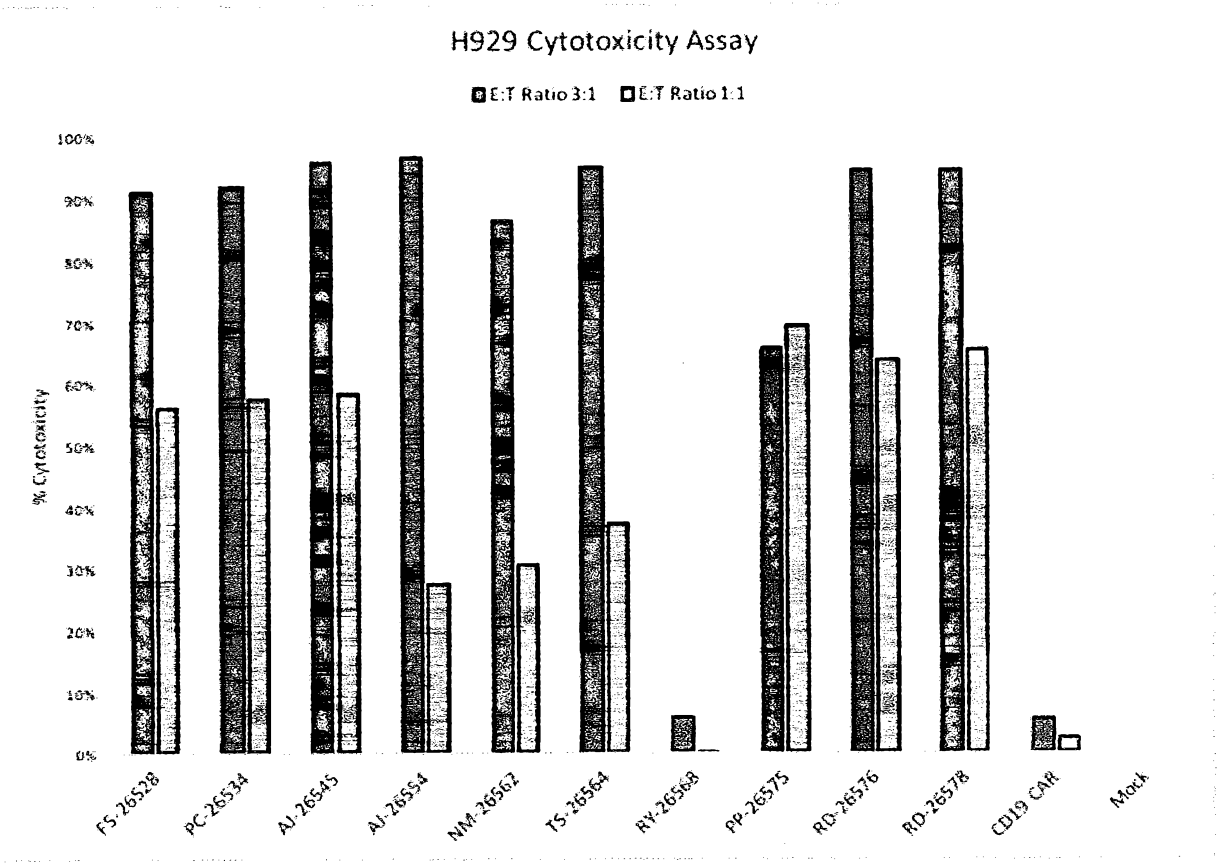
Clone RD-26578 CAR LxH (SEQ ID NO: 410)

MALPVTALLL PLALLLHAAR PEIVMTQSPA TLSVSPGERA TLSCRASQSV
SSNLAWYQQK PGQAPRLLIY SASTRATGIP ARFSGSGSGT EFTLTISSLQ
SEDFAVYYCQ QHHVWPLTFG GGTKVEIKRG STSGSGKPGS GEGSTKGQVQ
LVESGGGVVQ PGRSLRLSCA ASGFTFSSRG MHWVRQAPGK GLEWVAVIGY
DGQEKYYADS VKGRFTISRD NSKNTLYLQM NSLRAEDTAV YYCVKGPLQE
PPYDYGMDVW GQGTTVTVSS AAALDNEKSN GTIIHVKGKH LCPSPLFPGP
SKPFWVLVVV GGVLACYSLL VTVAFIIFWV RSKRSRLLHS DYMNMTPRRP
GPTRKHYQPY APPRDFAAYR SRVKFSRSAD APAYQQGQNQ LYNELNLGRR
EEYDVLDKRR GRDPEMGGKP RRKNPQEGLY NELQKDKMAE AYSEIGMKGE
RRRGKGHDGL YQGLSTATKD TYDALHMQAL PPR

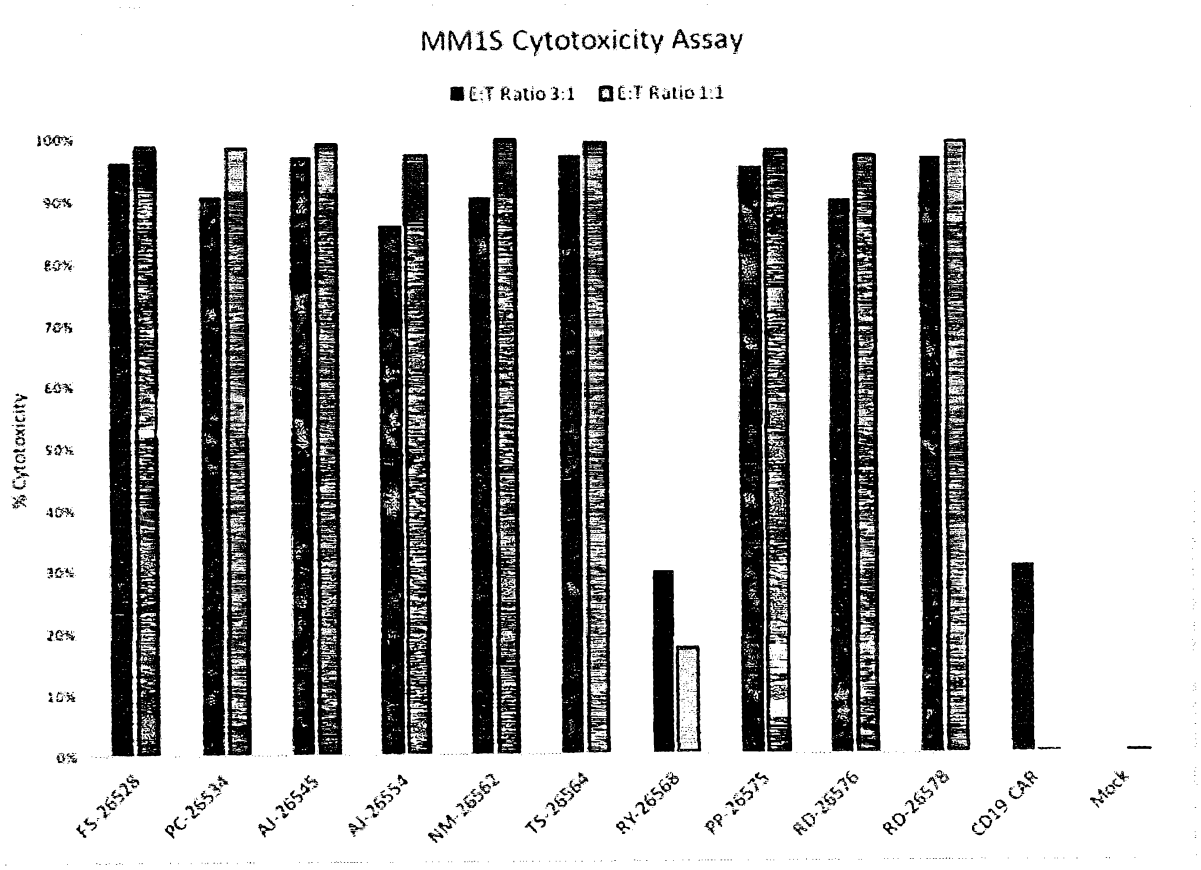
# FIG. 17


Mock transduced
RD-21530
Tumor Volume (mm3)
2500
2000
1500
1000
500
0
0
10
20
30
40
50
60
Days

# FIG. 18A


H929 Cytotoxicity Assay
E:T Ratio 3:1
E:T Ratio 1:1
% Cytotoxicity
100%
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
FS-26528
PC-26534
AJ-26545
AJ-26554
NM-26562
TS-26564
RY-26568
PP-26575
RD-26576
RD-26578
CD19 CAR
Mock

# FIG. 18B


MM1S Cytotoxicity Assay
E:T Ratio 3:1
E:T Ratio 1:1
% Cytotoxicity
100%
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
FS-26528
PC-26534
AJ-26545
AJ-26554
NM-26562
TS-26564
RY-26568
PP-26575
RD-26576
RD-26578
CD19 CAR
Mock

SEQUENCE LISTING

<110> KITE PHARMA, INC.

<120> BCMA BINDING MOLECULES AND METHODS OF USE THEREOF

<130> K-1030.02US

<140> 15/476,309
<141> 2017-03-31

<150> 62/317,334
<151> 2016-04-01

<160> 413

<170> PatentIn version 3.5

<210> 1
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR1 peptide

<400> 1
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
20 25

<210> 2
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR1 peptide

<400> 2
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
20 25

<210> 3
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR1 peptide

<400> 3
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
20 25

<210> 4
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR1 peptide

<400> 4
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
20 25

<210> 5
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR1 peptide

<400> 5
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
20 25

<210> 6
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR1 peptide

<400> 6
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
20 25

<210> 7
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR1 peptide

<400> 7
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
20 25

<210> 8
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR1 peptide

<400> 8
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
20 25

<210> 9
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic VH CDR1 peptide

<400> 9
Gly Phe Thr Phe Ser Ser Tyr
1 5

<210> 10
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic VH CDR1 peptide

<400> 10
Gly Phe Thr Phe Ser Ser Tyr
1 5

<210> 11
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic VH CDR1 peptide

<400> 11
Gly Tyr Thr Phe Thr Ser Tyr
1 5

<210> 12
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR1 peptide

<400> 12
Gly Gly Ser Ile Ser Ser Ser Ser Tyr
1 5

<210> 13
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR1 peptide

<400> 13
Gly Phe Thr Phe Ser Ser Tyr
1 5

<210> 14
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR1 peptide

<400> 14
Gly Phe Thr Phe Ser Ser Tyr
1 5

<210> 15
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR1 peptide

<400> 15
Gly Gly Thr Phe Ser Ser Tyr
1 5

<210> 16
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR1 peptide

<400> 16
Gly Phe Thr Phe Ser Ser Tyr
1 5

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

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 17
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
1 5 10 15

Ser

<210> 18
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 18
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
1 5 10 15

Ala

<210> 19
<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 19
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
1 5 10 15

Gly

<210> 20
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 20
Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
1 5 10 15

Gly

<210> 21
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 21
Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
1 5 10 15

Ser

<210> 22
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 22
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
1 5 10 15

Ala

<210> 23
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 23
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
1 5 10 15

Gly

<210> 24
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 24
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
1 5 10 15

Ala

<210> 25
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR2 peptide

<400> 25
Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 26
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR2 peptide

<400> 26
Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 27
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR2 peptide

<400> 27
Ile Ile Asn Pro Gly Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 28
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR2 peptide

<400> 28
Ser Ile Ser Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 29
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR2 peptide

<400> 29
Thr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 30
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR2 peptide

<400> 30
Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 31
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR2 peptide

<400> 31
Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 32
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR2 peptide

<400> 32
Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 33
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR3 polypeptide

<400> 33
Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
20 25 30

<210> 34
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR3 polypeptide

<400> 34
Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
20 25 30

<210> 35
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR3 polypeptide

<400> 35
Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu
1 5 10 15

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

<210> 36
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR3 polypeptide

<400> 36
Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys
1 5 10 15

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
20 25 30

<210> 37
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR3 polypeptide

<400> 37
Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
20 25 30

<210> 38
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR3 polypeptide

<400> 38
Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
20 25 30

<210> 39
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR3 polypeptide

<400> 39

Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

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

<210> 40
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR3 polypeptide

<400> 40
Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
20 25 30

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

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3 peptide

<400> 41
Ala Arg Ala Glu Met Gly Ala Val Phe Asp Ile
1 5 10

<210> 42
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3 peptide

<400> 42
Ala Arg Asp Gly Thr Tyr Leu Gly Gly Leu Trp Tyr Phe Asp Leu
1 5 10 15

<210> 43
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3 peptide

<400> 43
Ala Arg Glu Ser Trp Pro Met Asp Val
1 5

<210> 44
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3 peptide

<400> 44
Ala Arg Gly Arg Gly Tyr Ala Thr Ser Leu Ala Phe Asp Ile
1 5 10

<210> 45
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3 peptide

<400> 45
Ala Arg Gly Ser Gln Glu His Leu Ile Phe Asp Tyr
1 5 10

<210> 46
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3 peptide

<400> 46
Ala Arg Thr Asp Phe Trp Ser Gly Ser Pro Pro Gly Leu Asp Tyr
1 5 10 15

<210> 47
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3 peptide

<400> 47
Ala Arg Thr Pro Glu Tyr Ser Ser Ser Ile Trp His Tyr Tyr Tyr Gly
1 5 10 15

Met Asp Val

<210> 48
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3 peptide

<400> 48
Val Lys Gly Pro Leu Gln Glu Pro Pro Tyr Asp Tyr Gly Met Asp Val
1 5 10 15

<210> 49
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR4 peptide

<400> 49
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
1 5 10

<210> 50
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR4 peptide

<400> 50
Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 51
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR4 peptide

<400> 51
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
1 5 10

<210> 52
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR4 peptide

<400> 52
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
1 5 10

<210> 53
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR4 peptide

<400> 53

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 54
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR4 peptide

<400> 54
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 55
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR4 peptide

<400> 55
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
1 5 10

<210> 56
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR4 peptide

<400> 56
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
1 5 10

<210> 57
<211> 354
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
VH polynucleotide

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tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggcggtgt actactgcgc aagagccgag 300

atgggagccg tattcgacat atggggtcag ggtacaatgg tcaccgtctc ctca 354

<210> 58
<211> 366
<212> DNA
<213> Artificial Sequence

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

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tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatcgtatg atggaagtaa taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggcggtgt actactgcgc cagagacggt 300

acttatctag gtggtctctg gtacttcgac ttatggggga gaggtacctt ggtcaccgtc 360

tcctca 366

<210> 59
<211> 348
<212> DNA
<213> Artificial Sequence

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

<400> 59

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tcctgcaagg catctggata caccttcacc agctactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaata atcaaccctg gtggtggtag cacaagctac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

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<210> 60
<211> 366
<212> DNA
<213> Artificial Sequence

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

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acctgcactg tctctggtgg ctccatcagc agtagtagtt actactgggg ctggatccgc 120

cagcccccag ggaaggggct ggagtggatt gggagtatct cctatagtgg gagcacctac 180

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aggggatatg caaccagctt agccttcgat atctggggtc agggtacaat ggtcaccgtc 360

tcctca 366

<210> 61
<211> 357
<212> DNA
<213> Artificial Sequence

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

<400> 61
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ccagggaagg ggctggagtg ggtttcaacc attagtagta gtagtagtac catatactac 180

gcagactctg tgaagggccg attcaccatc tccagagaca atgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agctgaggac acggcggtgt actactgcgc cagaggttct 300

caggagcacc tgattttcga ttattgggga cagggtacat tggtcaccgt ctcctca 357

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

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

<400> 62
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatcgtatg atggaagtaa taaatactat 180

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ctgcaaatga acagcctgag agccgaggac acggcggtgt actactgcgc cagaactgac 300

ttctggagcg gatcccctcc aggcttagat tactggggac agggtacatt ggtcaccgtc 360

tcctca 366

<210> 63
<211> 378
<212> DNA
<213> Artificial Sequence

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

<400> 63
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 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> 64
<211> 369
<212> DNA
<213> Artificial Sequence

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

<400> 64
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ccaggcaagg ggctggagtg ggtggcagtt atatcgtatg atggaagtaa taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggcggtgt actactgcgt caaggggccg 300

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gtctcctca 369

<210> 65
<211> 118
<212> PRT
<213> Artificial Sequence

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

<400> 65
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> 66
<211> 122
<212> PRT
<213> Artificial Sequence

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

<400> 66
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> 67
<211> 116
<212> PRT
<213> Artificial Sequence

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

<400> 67
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> 68
<211> 122
<212> PRT
<213> Artificial Sequence

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

<400> 68
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> 69
<211> 119
<212> PRT
<213> Artificial Sequence

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

<400> 69
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> 70
<211> 122
<212> PRT
<213> Artificial Sequence

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

<400> 70
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> 71
<211> 126
<212> PRT
<213> Artificial Sequence

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

<400> 71
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> 72
<211> 123
<212> PRT
<213> Artificial Sequence

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

<400> 72
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> 73
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR1 peptide

<400> 73
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
20

<210> 74
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR1 peptide

<400> 74
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
20

<210> 75
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR1 peptide

<400> 75
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
20

<210> 76
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR1 peptide

<400> 76
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
20

<210> 77
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR1 peptide

<400> 77
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
20

<210> 78
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR1 peptide

<400> 78

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
20

<210> 79
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR1 peptide

<400> 79
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
20

<210> 80
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR1 peptide

<400> 80
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
20

<210> 81
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR1 peptide

<400> 81
Arg Ala Ser Gln Ser Val Ser Arg Tyr Leu Ala
1 5 10

<210> 82
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR1 peptide

<400> 82
Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp
1 5 10 15

<210> 83
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR1 peptide

<400> 83
Arg Ala Ser Gln Ser Val Ser Ser Asn Leu Ala
1 5 10

<210> 84
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR1 peptide

<400> 84
Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
1 5 10

<210> 85
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR1 peptide

<400> 85
Arg Ala Ser Gln Ser Val Ser Arg Tyr Leu Ala
1 5 10

<210> 86
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR1peptide

<400> 86
Arg Ala Ser Gln Gly Ile Ser Ser Trp Leu Ala
1 5 10

<210> 87
<211> 17
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR1 peptide

<400> 87
Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 88
<211> 11
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<220>
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VL CDR1 peptide

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Arg Ala Ser Gln Ser Val Ser Ser Asn Leu Ala
1 5 10

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VL FR2 peptide

<400> 89
Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
1 5 10 15

<210> 90
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR2 peptide

<400> 90
Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr
1 5 10 15

<210> 91
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR2 peptide

<400> 91
Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
1 5 10 15

<210> 92
<211> 15
<212> PRT
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<220>

<223> Description of Artificial Sequence: Synthetic
VL FR2 peptide

<400> 92
Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
1 5 10 15

<210> 93
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR2 peptide

<400> 93
Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
1 5 10 15

<210> 94
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR2 peptide

<400> 94
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
1 5 10 15

<210> 95
<211> 15
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
VL FR2 peptide

<400> 95
Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
1 5 10 15

<210> 96
<211> 15

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR2 peptide

<400> 96
Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
1 5 10 15

<210> 97
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR2 peptide

<400> 97
Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 98
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR2 peptide

<400> 98
Leu Gly Ser Asn Arg Ala Ser
1 5

<210> 99
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR2 peptide

<400> 99
Gly Ala Ser Thr Arg Ala Thr
1 5

<210> 100
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR2 peptide

<400> 100
Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 101
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR2 peptide

<400> 101
Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 102
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR2 peptide

<400> 102
Gly Ala Ser Ser Leu Gln Ser
1 5

<210> 103
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR2 peptide

<400> 103
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 104
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR2 peptide

<400> 104
Ser Ala Ser Thr Arg Ala Thr
1 5

<210> 105
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR3 polypeptide

<400> 105
Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
20 25 30

<210> 106
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR3 polypeptide

<400> 106
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys
20 25 30

<210> 107
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR3 polypeptide

<400> 107
Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys
20 25 30

<210> 108
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR3 polypeptide

<400> 108
Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
20 25 30

<210> 109
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR3 polypeptide

<400> 109
Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
20 25 30

<210> 110
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR3 polypeptide

<400> 110
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
20 25 30

<210> 111
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR3 polypeptide

<400> 111
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

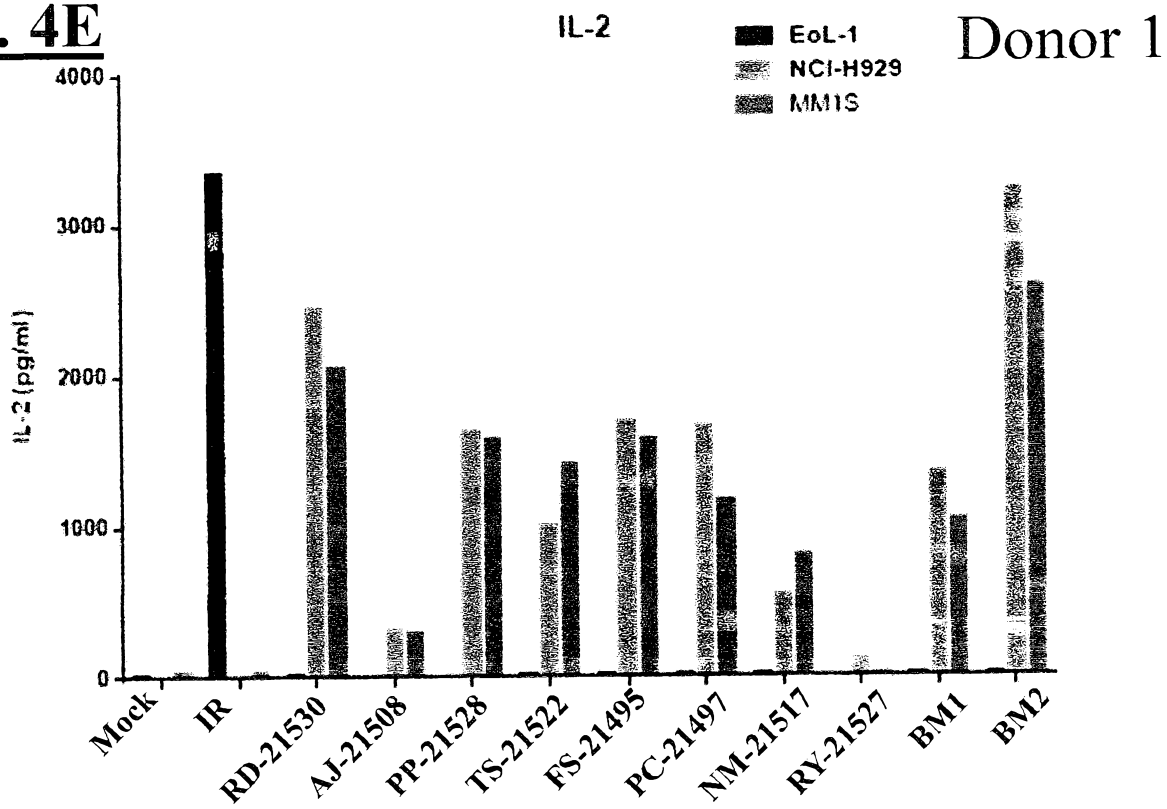
Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
20 25 30

<210> 112
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR3 polypeptide

<400> 112

FIG. 4E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EoL-1
NCI-H929
MM1S
Donor 1
IL-2 (pg/ml)
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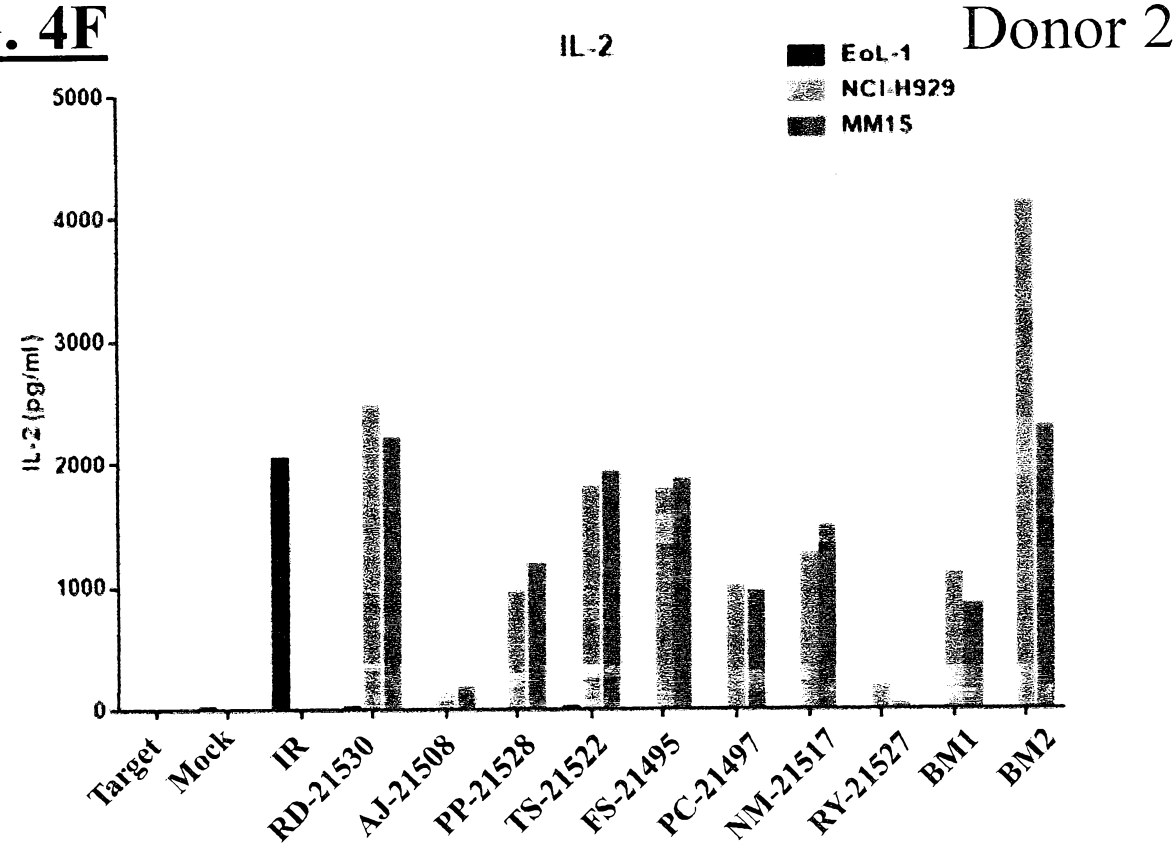
2000
1000
0
Mock
IR
RD-21530
AJ-21508
PP-21528
TS-21522
FS-21495
PC-21497
NM-21517
RY-21527
BM1
BM2

FIG. 4F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EoL-1
NCI-H929
MM1S
Donor 2
IL-2 (pg/ml)
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4000
3000
2000
1000
0
Target
Mock
IR
RD-21530
AJ-21508
PP-21528
TS-21522
FS-21495
PC-21497
NM-21517
RY-21527
BM1
BM2

**FIG. 5A**

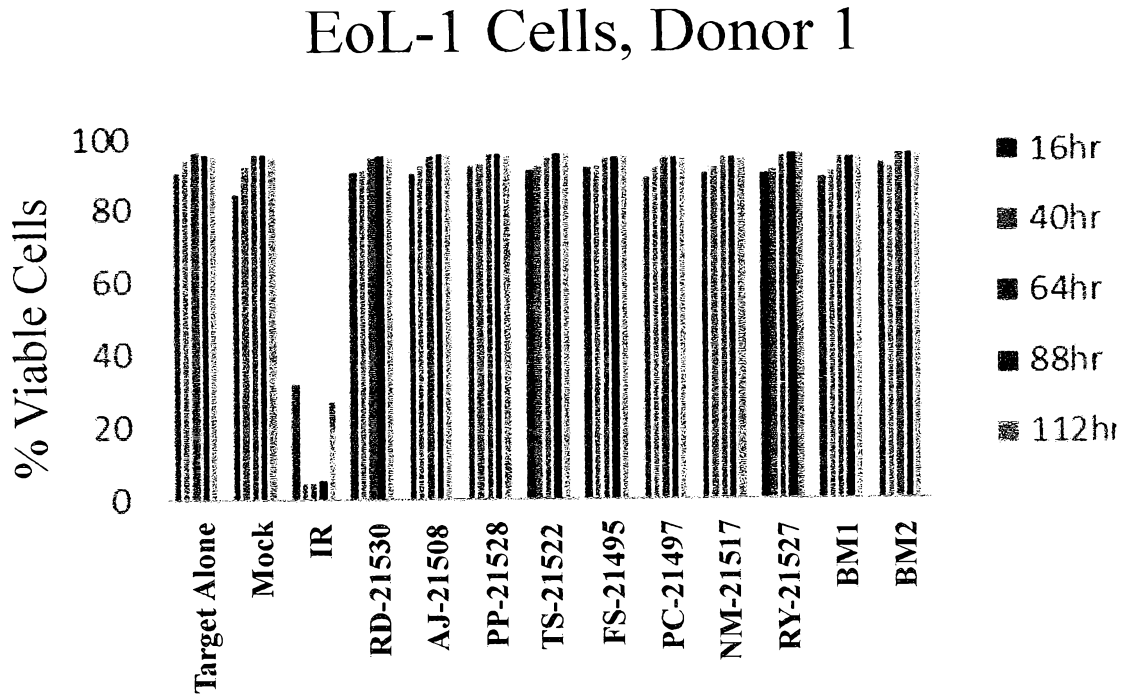

EoL-1 Cells, Donor 1
% Viable Cells
100
80
60
40
20
0
Target Alone
Mock
IR
RD-21530
AJ-21508
PP-21528
TS-21522
FS-21495
PC-21497
NM-21517
RY-21527
BM1
BM2
16hr
40hr
64hr
88hr
112hr

**FIG. 5B**

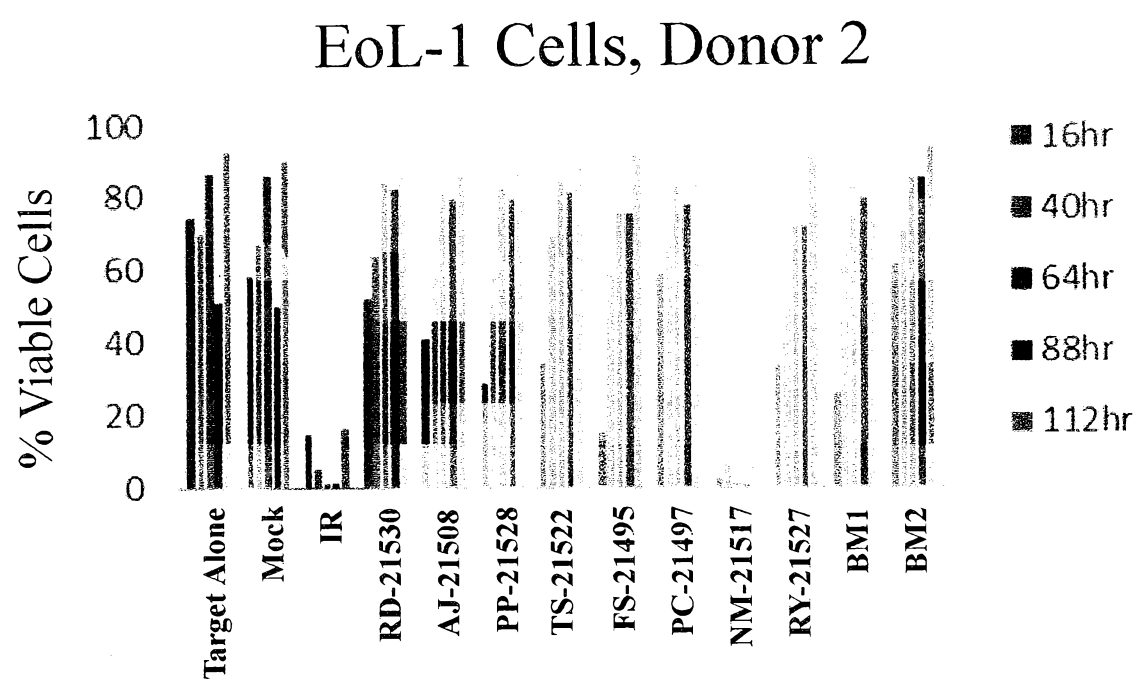

EoL-1 Cells, Donor 2
% Viable Cells
100
80
60
40
20
0
Target Alone
Mock
IR
RD-21530
AJ-21508
PP-21528
TS-21522
FS-21495
PC-21497
NM-21517
RY-21527
BM1
BM2
16hr
40hr
64hr
88hr
112hr

**FIG. 5C**

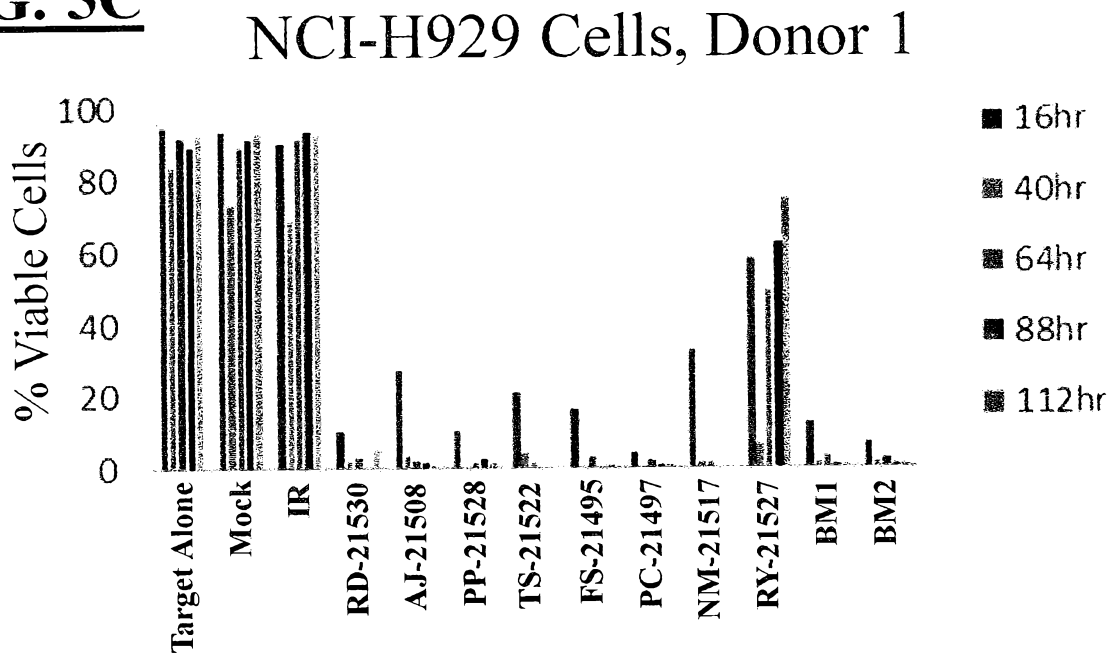

NCI-H929 Cells, Donor 1
% Viable Cells
100
80
60
40
20
0
Target Alone
Mock
IR
RD-21530
AJ-21508
PP-21528
TS-21522
FS-21495
PC-21497
NM-21517
RY-21527
BM1
BM2
16hr
40hr
64hr
88hr
112hr

**FIG. 5D**

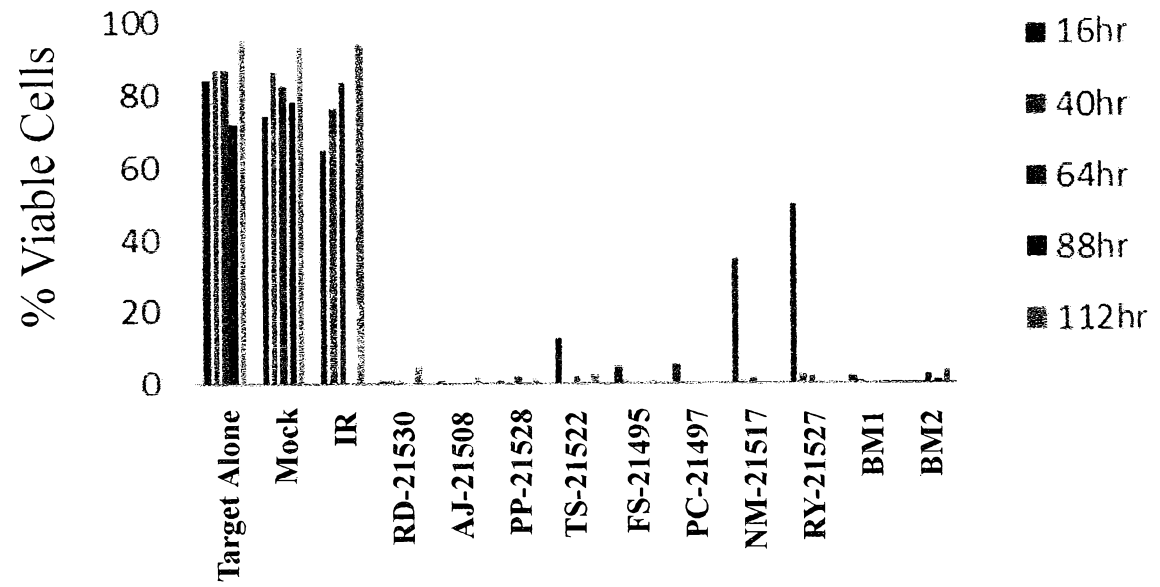

NCI-H929 Cells, Donor 2
% Viable Cells
100
80
60
40
20
0
Target Alone
Mock
IR
RD-21530
AJ-21508
PP-21528
TS-21522
FS-21495
PC-21497
NM-21517
RY-21527
BM1
BM2
16hr
40hr
64hr
88hr
112hr

**FIG. 5E**

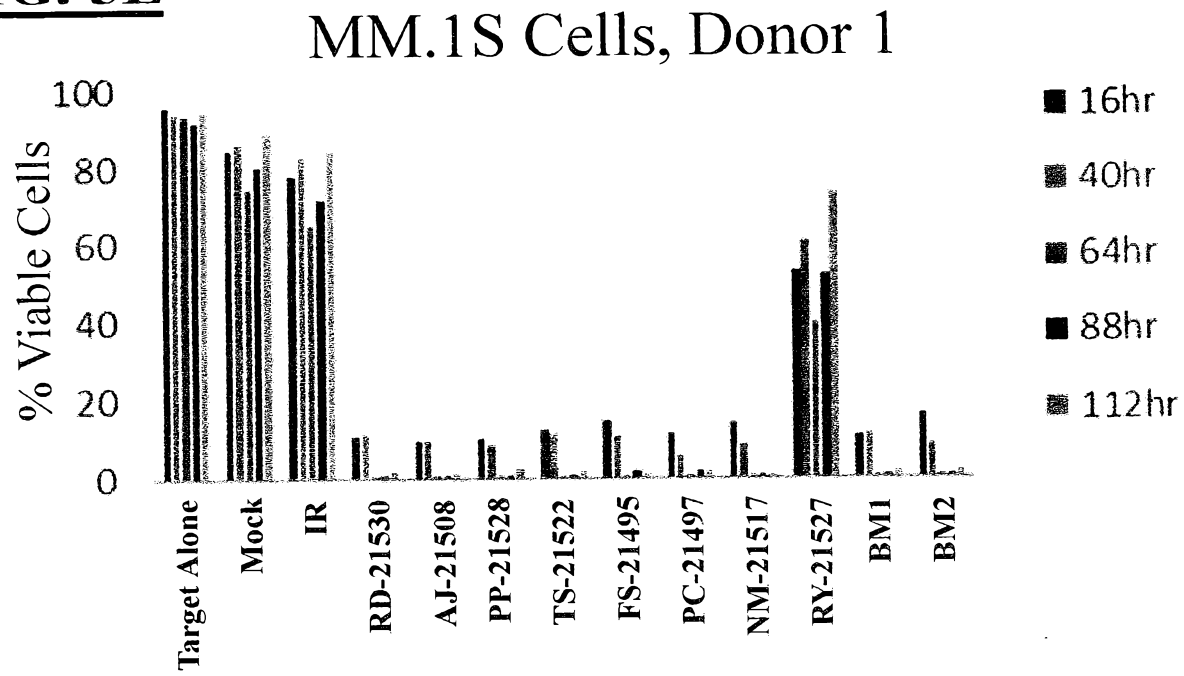
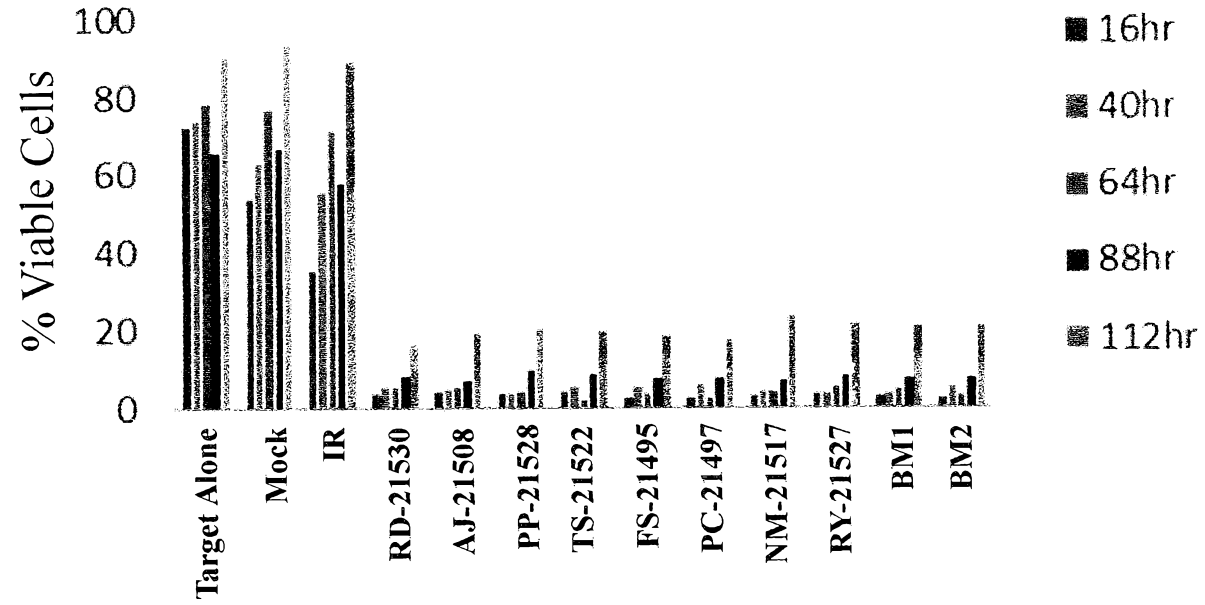
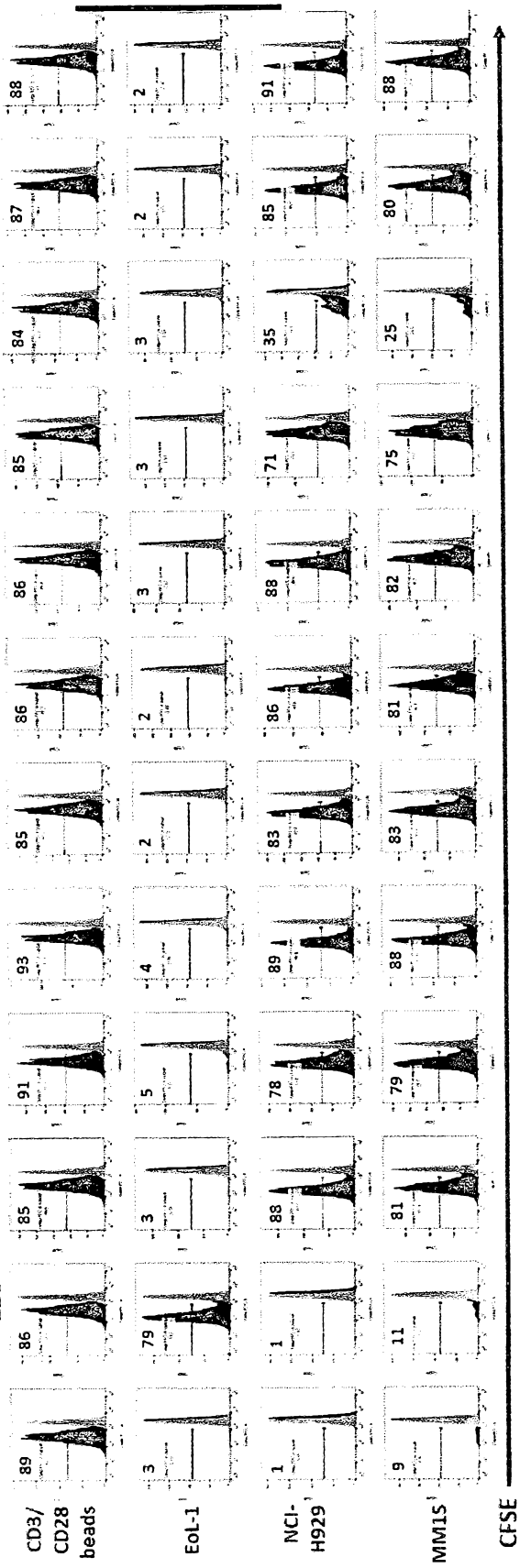

MM.1S Cells, Donor 1
% Viable Cells
100
80
60
40
20
0
16hr
40hr
64hr
88hr
112hr
Target Alone
Mock
IR
RD-21530
AJ-21508
PP-21528
TS-21522
FS-21495
PC-21497
NM-21517
RY-21527
BM1
BM2

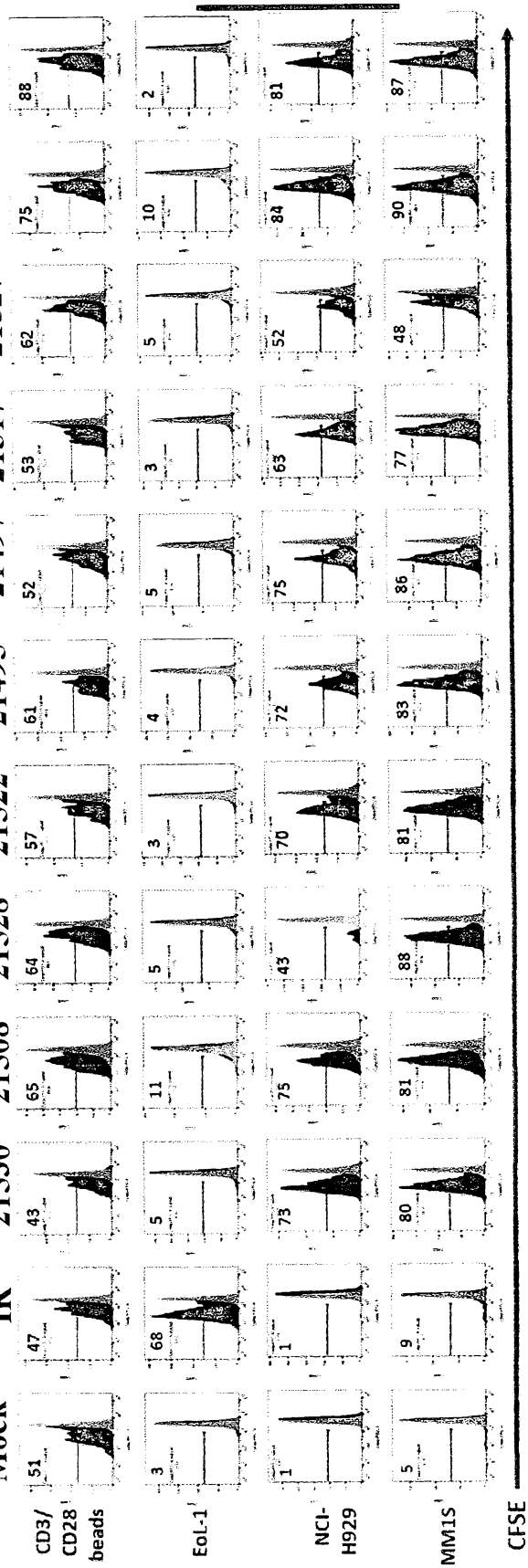
**FIG. 5F**


MM.1S Cells, Donor 2
% Viable Cells
100
80
60
40
20
0
16hr
40hr
64hr
88hr
112hr
Target Alone
Mock
IR
RD-21530
AJ-21508
PP-21528
TS-21522
FS-21495
PC-21497
NM-21517
RY-21527
BM1
BM2

# FIG. 6A


Mock
IR
RD-21530
AJ-21508
PP-21528
TS-21522
FS-21495
PC-21497
NM-21517
RY-21527
BM1
BM2
CD3/CD28 beads
EoL-1
NCI-H929
MM1S
CFSE

# FIG. 6B


Mock
IR
RD-21530
AJ-21508
PP-21528
TS-21522
FS-21495
PC-21497
NM-21517
RY-21527
BM1
BM2
CD3/CD28 beads
EoL-1
NCI-H929
MM1S
CFSE
Unstimulated T cells
T cells + indicated stimulus

## FIG. 7A

**Clone FS-26528 HC DNA (SEQ ID NO: 271)**

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCC
TGTGCAGCCTCTGGATTCACCTTTGACGACTATGCCATGGCATGGGTCCGCCAGGCTCCAGGG
AAGGGGCTGGAGTGGGTCTCAGCTATTAGTGATGCAGGTGACAGAACATACTACGCAGACTCC
GTGAGGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACACTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCAAGAGCCGAGATGGGAGCCGTATTC
GACATATGGGGTCAGGGTACAATGGTCACCGTCTCCTCA

## FIG. 7B

**Clone FS-26528 HC (SEQ ID NO: 272). CDRs 1, 2, and 3 are underlined.**

EVQLLESGGG LVQPGGSLRL SCAASGFTFD DYAMAWVRQA PGKGLEWVSA
ISDAGDRTYY ADSVRGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARAE
MGAVFDIWGQ GTMVTVSS

## FIG. 7C

SCAASGFTFDDYAMA (SEQ ID NO: 273) [HC CDR1]

AISDAGDRTYYADSVRG (SEQ ID NO: 274) [HC CDR2]

ARAEMGAVFDI (SEQ ID NO: 275) [HC CDR3]

## FIG. 7D

**Clone FS-26528 LC DNA (SEQ ID NO: 276)**

GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTC
TCCTGCAGGGCCAGTCAGAGTGTTAGCAGGTACTTAGCCTGGTACCAACAGAAACCTGGCCAG
GCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTCAGT
GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGATTTTGCA
GTTTATTACTGTCAGCAGAGAATCTCCTGGCCTTTCACTTTTGGCGGAGGGACCAAGGTTGAG
ATCAAACGG

## FIG. 7E

**Clone FS-26528 LC (SEQ ID NO: 277). CDRs 1, 2, and 3 are underlined.**

EIVLTQSPAT LSLSPGERAT LSCRASQSVS RYLAWYQQKP GQAPRLLIYD
ASNRATGIPA RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ RISWPFTFGG GTKVEIKR

## FIG. 7F

RASQSVSRYLA (SEQ ID NO: 278) [LC CDR1]

DASNRAT (SEQ ID NO: 279) [LC CDR2]

QQRISWPFT (SEQ ID NO: 280) [LC CDR3]

## FIG. 7G

**Clone FS-26528 CAR DNA HxL (SEQ ID NO: 281)**

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCC
TGTGCAGCCTCTGGATTCACCTTTGACGACTATGCCATGGCATGGGTCCGCCAGGCTCCAGGG
AAGGGGCTGGAGTGGGTCTCAGCTATTAGTGATGCAGGTGACAGAACATACTACGCAGACTCC
GTGAGGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACACTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCAAGAGCCGAGATGGGAGCCGTATTC
GACATATGGGGTCAGGGTACAATGGTCACCGTCTCCTCAGGGTCTACATCCGGCTCCGGGAAG
CCCGGAAGTGGCGAAGGTAGTACAAAGGGGGAAATTGTGTTGACACAGTCTCCAGCCACCCTG
TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGGTAC
TTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGATGCATCCAAC
AGGGCCACTGGCATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACC
ATCAGCAGCCTAGAGCCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGAATCTCCTGGCCT
TTCACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGGCCGCTGCCCTTGATAATGAAAAG
TCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGT
CCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTC
GTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGAT
TACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCA
CCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCG
TATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGAC
GTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCC
CAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGC
ATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCT
ACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 7H

**Clone FS-26528 CAR HxL (SEQ ID NO: 282)**

MALPVTALLL PLALLLHAAR PEVQLLESGG GLVQPGGSLR LSCAASGFTF
DDYAMAWVRQ APGKGLEWVS AISDAGDRTY YADSVRGRFT ISRDNSKNTL
YLQMNSLRAE DTAVYYCARA EMGAVFDIWG QGTMVTVSSG STSGSGKPGS
GEGSTKGEIV LTQSPATLSL SPGERATLSC RASQSVSRYL AWYQQKPGQA
PRLLIYDASN RATGIPARFS GSGSGTDFTL TISSLEPEDF AVYYCQQRIS
WPFTFGGGTK VEIKRAAALD NEKSNGTIIH VKGKHLCPSP LFPGPSKPFW
VLVVVGGVLA CYSLLVTVAF IIFWVRSKRS RLLHSDYMNM TPRRPGPTRK
HYQPYAPPRD FAAYRSRVKF SRSADAPAYQ QGQNQLYNEL NLGRREEYDV
LDKRRGRDPE MGGKPRRKNP QEGLYNELQK DKMAEAYSEI GMKGERRRGK
GHDGLYQGLS TATKDTYDAL HMQALPPR

## FIG. 7F

RASQSVSRYLA (SEQ ID NO: 278) [LC CDR1]

DASNRAT (SEQ ID NO: 279) [LC CDR2]

QQRISWPFT (SEQ ID NO: 280) [LC CDR3]

## FIG. 7G

**Clone FS-26528 CAR DNA HxL (SEQ ID NO: 281)**

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCC
TGTGCAGCCTCTGGATTCACCTTTGACGACTATGCCATGGCATGGGTCCGCCAGGCTCCAGGG
AAGGGGCTGGAGTGGGTCTCAGCTATTAGTGATGCAGGTGACAGAACATACTACGCAGACTCC
GTGAGGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACACTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCAAGAGCCGAGATGGGAGCCGTATTC
GACATATGGGGTCAGGGTACAATGGTCACCGTCTCCTCAGGGTCTACATCCGGCTCCGGGAAG
CCCGGAAGTGGCGAAGGTAGTACAAAGGGGGAAATTGTGTTGACACAGTCTCCAGCCACCCTG
TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGGTAC
TTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGATGCATCCAAC
AGGGCCACTGGCATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACC
ATCAGCAGCCTAGAGCCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGAATCTCCTGGCCT
TTCACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGGCCGCTGCCCTTGATAATGAAAAG
TCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGT
CCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTC
GTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGAT
TACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCA
CCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCG
TATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGAC
GTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCC
CAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGC
ATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCT
ACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 7H

**Clone FS-26528 CAR HxL (SEQ ID NO: 282)**

MALPVTALLL PLALLLHAAR PEVQLLESGG GLVQPGGSLR LSCAASGFTF
DDYAMAWVRQ APGKGLEWVS AISDAGDRTY YADSVRGRFT ISRDNSKNTL
YLQMNSLRAE DTAVYYCARA EMGAVFDIWG QGTMVTVSSG STSGSGKPGS
GEGSTKGEIV LTQSPATLSL SPGERATLSC RASQSVSRYL AWYQQKPGQA
PRLLIYDASN RATGIPARFS GSGSGTDFTL TISSLEPEDF AVYYCQQRIS
WPFTFGGGTK VEIKRAAALD NEKSNGTIIH VKGKHLCPSP LFPGPSKPFW
VLVVVGGVLA CYSLLVTVAF IIFWVRSKRS RLLHSDYMNM TPRRPGPTRK
HYQPYAPPRD FAAYRSRVKF SRSADAPAYQ QGQNQLYNEL NLGRREEYDV
LDKRRGRDPE MGGKPRRKNP QEGLYNELQK DKMAEAYSEI GMKGERRRGK
GHDGLYQGLS TATKDTYDAL HMQALPPR

## FIG. 7I

Clone FS-26528 CAR DNA LxH (SEQ ID NO: 283)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTC
TCCTGCAGGGCCAGTCAGAGTGTTAGCAGGTACTTAGCCTGGTACCAACAGAAACCTGGCCAG
GCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTCAGT
GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGATTTTGCA
GTTTATTACTGTCAGCAGAGAATCTCCTGGCCTTTCACTTTTGGCGGAGGGACCAAGGTTGAG
ATCAAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGG
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCC
TGTGCAGCCTCTGGATTCACCTTTGACGACTATGCCATGGCATGGGTCCGCCAGGCTCCAGGG
AAGGGGCTGGAGTGGGTCTCAGCTATTAGTGATGCAGGTGACAGAACATACTACGCAGACTCC
GTGAGGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACACTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCAAGAGCCGAGATGGGAGCCGTATTC
GACATATGGGGTCAGGGTACAATGGTCACCGTCTCCTCAGCCGCTGCCCTTGATAATGAAAAG
TCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGT
CCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTC
GTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGAT
TACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCA
CCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCG
TATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGAC
GTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCC
CAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGC
ATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCT
ACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 7J

Clone FS-26528 CAR LxH (SEQ ID NO: 284)

MALPVTALLL PLALLLHAAR PEIVLTQSPA TLSLSPGERA TLSCRASQSV
SRYLAWYQQK PGQAPRLLIY DASNRATGIP ARFSGSGSGT DFTLTISSLE
PEDFAVYYCQ QRISWPFTFG GGTKVEIKRG STSGSGKPGS GEGSTKGEVQ
LLESGGGLVQ PGGSLRLSCA ASGFTFDDYA MAWVRQAPGK GLEWVSAISD
AGDRTYYADS VRGRFTISRD NSKNTLYLQM NSLRAEDTAV YYCARAEMGA
VFDIWGQGTM VTVSSAAALD NEKSNGTIIH VKGKHLCPSP LFPGPSKPFW
VLVVVGGVLA CYSLLVTVAF IIFWVRSKRS RLLHSDYMNM TPRRPGPTRK
HYQPYAPPRD FAAYRSRVKF SRSADAPAYQ QGQNQLYNEL NLGRREEYDV
LDKRRGRDPE MGGKPRRKNP QEGLYNELQK DKMAEAYSEI GMKGERRRGK
GHDGLYQGLS TATKDTYDAL HMQALPPR

## FIG. 8A

Clone PC-26534 HC DNA (SEQ ID NO: 285)

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC
TGTGCAGCGTCTGGATTCACCTTCAGTGAGCATGGCATGCACTGGGTCCGCCAGGCTCCAGGC
AAGGGGCTGGAGTGGGTGGCAGCTATATCTTATGATGGAAGGAATAAACACTATGCAGACTCC
GTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCCAGAGACGGTACTTATCTAGGTGGT
CTCTGGTACTTCGACTTATGGGGGAGAGGTACCTTGGTCACCGTCTCCTCA

## FIG. 8B

Clone PC-26534 HC (SEQ ID NO: 286). CDRs 1, 2, and 3 are underlined.

QVQLVESGGG VVQPGRSLRL SCAASGFTFS EHGMHWVRQA PGKGLEWVAA
ISYDGRNKHY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARDG
TYLGGLWYFD LWGRGTLVTV SS

## FIG 8C

FTFSEHGMH (SEQ ID NO: 287) [HC CDR1]

AISYDGRNKHYADSVKG (SEQ ID NO: 288) [HC CDR2]

ARDGTYLGGLWYFDL (SEQ ID NO: 289) [HC CDR3]

## FIG. 8D

Clone PC-26534 LC DNA (SEQ ID NO: 290)

GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCATC
TCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACAACTATTTGGATTGGTACCTG
CAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGGGTTCTAATCGGGCCTCCGGGGTC
CCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAG
GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGGACTCGGCCTCCCTCTCACTTTTGGCGGA
GGGACCAAGGTTGAGATCAAACGG

## FIG. 8E

Clone PC-26534 LC (SEQ ID NO: 291). CDRs 1, 2, and 3 are underlined.

DIVMTQSPLS LPVTPGEPAS ISCRSSQSLL HSNGYNYLDW YLQKPGQSPQ
LLIYLGSNRA SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQGLGLP
LTFGGGTKVE IKR

## FIG. 8F

RSSQSLLHSNGYNYLD (SEQ ID NO: 292) [LC CDR1]

LGSNRAS (SEQ ID NO: 293) [LC CDR2]

MQGLGLPLT (SEQ ID NO: 294) [LC CDR3]

## FIG. 8G

**Clone PC-26534 CAR DNA HxL (SEQ ID NO: 295)**

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC
TGTGCAGCGTCTGGATTCACCTTCAGTGAGCATGGCATGCACTGGGTCCGCCAGGCTCCAGGC
AAGGGGCTGGAGTGGGTGGCAGCTATATCTTATGATGGAAGGAATAAACACTATGCAGACTCC
GTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCCAGAGACGGTACTTATCTAGGTGGT
CTCTGGTACTTCGACTTATGGGGGAGAGGTACCTTGGTCACCGTCTCCTCAGGGTCTACATCC
GGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGATATTGTGATGACTCAGTCT
CCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCATCTCCTGCAGGTCTAGTCAGAGC
CTCCTGCATAGTAATGGATACAACTATTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCA
CAGCTCCTGATCTATTTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTCAGTGGCAGT
GGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATGTTGGGGTTTAT
TACTGCATGCAGGGACTCGGCCTCCCTCTCACTTTTGGCGGAGGGACCAAGGTTGAGATCAAA
CGGGCCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCAC
CTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGT
GGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCC
AAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACA
AGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAG
TTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTC
AACCTGGGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATG
GGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAG
ATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGAC
GGTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCC
CTGCCACCTAGG

## FIG. 8H

**Clone PC-26534 CAR HxL (SEQ ID NO: 296)**

MALPVTALLL PLALLLHAAR PQVQLVESGG GVVQPGRSLR LSCAASGFTF
SEHGMHWVRQ APGKGLEWVA AISYDGRNKH YADSVKGRFT ISRDNSKNTL
YLQMNSLRAE DTAVYYCARD GTYLGGLWYF DLWGRGTLVT VSSGSTSGSG
KPGSGEGSTK GDIVMTQSPL SLPVTPGEPA SISCRSSQSL LHSNGYNYLD
WYLQKPGQSP QLLIYLGSNR ASGVPDRFSG SGSGTDFTLK ISRVEAEDVG
VYYCMQGLGL PLTFGGGTKV EIKRAAALDN EKSNGTIIHV KGKHLCPSPL
FPGPSKPFWV LVVVGGVLAC YSLLVTVAFI IFWVRSKRSR LLHSDYMNMT
PRRPGPTRKH YQPYAPPRDF AAYRSRVKFS RSADAPAYQQ GQNQLYNELN
LGRREEYDVL DKRRGRDPEM GGKPRRKNPQ EGLYNELQKD KMAEAYSEIG
MKGERRRGKG HDGLYQGLST ATKDTYDALH MQALPPR

## FIG. 8I

Clone PC-26534 CAR DNA LxH (SEQ ID NO: 297)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCATC
TCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACAACTATTTGGATTGGTACCTG
CAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGGGTTCTAATCGGGCCTCCGGGGTC
CCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAG
GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGGACTCGGCCTCCCTCTCACTTTTGGCGGA
GGGACCAAGGTTGAGATCAAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAA
GGTAGTACAAAGGGGCAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGG
TCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTGAGCATGGCATGCACTGGGTC
CGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGCTATATCTTATGATGGAAGGAATAAA
CACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCCAGAGACGGT
ACTTATCTAGGTGGTCTCTGGTACTTCGACTTATGGGGGAGAGGTACCTTGGTCACCGTCTCC
TCAGCCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCAC
CTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGT
GGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCC
AAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACA
AGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAG
TTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTC
AACCTGGGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATG
GGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAG
ATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGAC
GGTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCC
CTGCCACCTAGG

## FIG. 8J

Clone PC-26534 CAR LxH (SEQ ID NO: 298)

MALPVTALLL PLALLLHAAR PDIVMTQSPL SLPVTPGEPA SISCRSSQSL
LHSNGYNYLD WYLQKPGQSP QLLIYLGSNR ASGVPDRFSG SGSGTDFTLK
ISRVEAEDVG VYYCMQGLGL PLTFGGGTKV EIKRGSTSGS GKPGSGEGST
KGQVQLVESG GGVVQPGRSL RLSCAASGFT FSEHGMHWVR QAPGKGLEWV
AAISYDGRNK HYADSVKGRF TISRDNSKNT LYLQMNSLRA EDTAVYYCAR
DGTYLGGLWY FDLWGRGTLV TVSSAAALDN EKSNGTIIHV KGKHLCPSPL
FPGPSKPFWV LVVVGGVLAC YSLLVTVAFI IFWVRSKRSR LLHSDYMNMT
PRRPGPTRKH YQPYAPPRDF AAYRSRVKFS RSADAPAYQQ GQNQLYNELN
LGRREEYDVL DKRRGRDPEM GGKPRRKNPQ EGLYNELQKD KMAEAYSEIG
MKGERRRGKG HDGLYQGLST ATKDTYDALH MQALPPR

## FIG. 9A

Clone AJ-26545 HC DNA (SEQ ID NO: 299)
CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCC
TGCAGGGCATCTGGATACACCTTCATGGAGCACTATATGCACTGGGTGCGACAGGCCCCTGGA
CAAGGGCTTGAGTGGATGGGAGTAATCGGGCCTAGTGGTGGTAAGACAAGCTACGCACAGAAG
TTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGC
AGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGAGAGAATTGGCCAATGGACGTA
TGGGGCCAGGGAACAACTGTCACCGTCTCCTCA

## FIG. 9B

Clone AJ-26545 HC (SEQ ID NO: 300). CDRs 1, 2, and 3 are underlined.
QVQLVQSGAE VKKPGASVKV SCRASGYTFM EHYMHWVRQA PGQGLEWMGV
IGPSGGKTSY AQKFQGRVTM TRDTSTSTVY MELSSLRSED TAVYYCARES
WPMDVWGQGT TVTVSS

## FIG. 9C

YTFMEHYMH (SEQ ID NO: 301) (HC CDR1)

VIGPSGGKTSYAQKFQG (SEQ ID NO: 302) (HC CDR2)

ARESWPMDV (SEQ ID NO: 303) (HC CDR3)

## FIG. 9D

Clone AJ-26545 LC DNA (SEQ ID NO: 304)
GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTC
TCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAG
GCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGT
GGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCA
GTTTATTACTGTCAGCAGTACGCCGCCTACCCTACTTTTGGCGGAGGGACCAAGGTTGAGATC
AAACGG

## FIG. 9E

Clone AJ-26545 LC (SEQ ID NO: 305). CDRs 1, 2, and 3 are underlined.
EIVMTQSPAT LSVSPGERAT LSCRASQSVS SNLAWYQQKP GQAPRLLIYG
ASTRATGIPA RFSGSGSGTE FTLTISSLQS EDFAVYYCQQ YAAYPTFGGG TKVEIKR

## FIG. 9F

RASQSVSSNLA (SEQ ID NO: 306) (LC CDR1)

GASTRAT (SEQ ID NO: 307) (LC CDR2)

QQYAAYPT (SEQ ID NO: 308) (LC CDR3)

## FIG. 9G

**Clone AJ-26545 CAR DNA HxL (SEQ ID NO: 309)**

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCC
TGCAGGGCATCTGGATACACCTTCATGGAGCACTATATGCACTGGGTGCGACAGGCCCCTGGA
CAAGGGCTTGAGTGGATGGGAGTAATCGGGCCTAGTGGTGGTAAGACAAGCTACGCACAGAAG
TTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGC
AGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGAGAGAATTGGCCAATGGACGTA
TGGGGCCAGGGAACAACTGTCACCGTCTCCTCAGGGTCTACATCCGGCTCCGGGAAGCCCGGA
AGTGGCGAAGGTAGTACAAAGGGGGAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTG
TCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCC
TGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCC
ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGC
AGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACGCCGCCTACCCTACTTTT
GGCGGAGGGACCAAGGTTGAGATCAAACGGGCCGCTGCCCTTGATAATGAAAAGTCAAACGGA
ACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAG
CCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTG
GCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAAT
ATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGAT
TTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAG
GGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGAC
AAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGT
CTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGA
GAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGAT
ACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 9H

**Clone AJ-26545 CAR HxL (SEQ ID NO: 310)**

MALPVTALLL PLALLLHAAR PQVQLVQSGA EVKKPGASVK VSCRASGYTF
MEHYMHWVRQ APGQGLEWMG VIGPSGGKTS YAQKFQGRVT MTRDTSTSTV
YMELSSLRSE DTAVYYCARE SWPMDVWGQG TTVTVSSGST SGSGKPGSGE
GSTKGEIVMT QSPATLSVSP GERATLSCRA SQSVSSNLAW YQQKPGQAPR
LLIYGASTRA TGIPARFSGS GSGTEFTLTI SSLQSEDFAV YYCQQYAAYP
TFGGGTKVEI KRAAALDNEK SNGTIIHVKG KHLCPSPLFP GPSKPFWVLV
VVGGVLACYS LLVTVAFIIF WVRSKRSRLL HSDYMNMTPR RPGPTRKHYQ
PYAPPRDFAA YRSRVKFSRS ADAPAYQQGQ NQLYNELNLG RREEYDVLDK
RRGRDPEMGG KPRRKNPQEG LYNELQKDKM AEAYSEIGMK GERRRGKGHD
GLYQGLSTAT KDTYDALHMQ ALPPR

## FIG. 9I

Clone AJ-26545 CAR DNA LxH (SEQ ID NO: 311)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTC
TCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAG
GCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGT
GGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCA
GTTTATTACTGTCAGCAGTACGCCGCCTACCCTACTTTTGGCGGAGGGACCAAGGTTGAGATC
AAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGCAG
GTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGC
AGGGCATCTGGATACACCTTCATGGAGCACTATATGCACTGGGTGCGACAGGCCCCTGGACAA
GGGCTTGAGTGGATGGGAGTAATCGGGCCTAGTGGTGGTAAGACAAGCTACGCACAGAAGTTC
CAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGC
CTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGAGAGAATTGGCCAATGGACGTATGG
GGCCAGGGAACAACTGTCACCGTCTCCTCAGCCGCTGCCCTTGATAATGAAAAGTCAAACGGA
ACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAG
CCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTG
GCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAAT
ATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGAT
TTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAG
GGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGAC
AAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGT
CTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGA
GAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGAT
ACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 9J

Clone AJ-26545 CAR LxH (SEQ ID NO: 312)

MALPVTALLL PLALLLHAAR PEIVMTQSPA TLSVSPGERA TLSCRASQSV
SSNLAWYQQK PGQAPRLLIY GASTRATGIP ARFSGSGSGT EFTLTISSLQ
SEDFAVYYCQ QYAAYPTFGG GTKVEIKRGS TSGSGKPGSG EGSTKGQVQL
VQSGAEVKKP GASVKVSCRA SGYTFMEHYM HWVRQAPGQG LEWMGVIGPS
GGKTSYAQKF QGRVTMTRDT STSTVYMELS SLRSEDTAVY YCARESWPMD
VWGQGTTVTV SSAAALDNEK SNGTIIHVKG KHLCPSPLFP GPSKPFWVLV
VVGGVLACYS LLVTVAFIIF WVRSKRSRLL HSDYMNMTPR RPGPTRKHYQ
PYAPPRDFAA YRSRVKFSRS ADAPAYQQGQ NQLYNELNLG RREEYDVLDK
RRGRDPEMGG KPRRKNPQEG LYNELQKDKM AEAYSEIGMK GERRRGKGHD
GLYQGLSTAT KDTYDALHMQ ALPPR

## FIG. 10A

Clone AJ-26554 HC DNA (SEQ ID NO: 313)

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCC
TGCAAGGCATCTGGATACACCTTCACGGAGCACTATATGCACTGGGTGCGACAGGCCCCTGGA
CAAAGGCTTGAGTGGATGGGAGTAATCGGGCCTAGTGGTGGTAAGACAAGCTACGCACAGAAG
TTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGC
AGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGAGAGAGTTGGCCAATGGACGTA
TGGGGCCAGGGAACAACTGTCACCGTCTCCTCA

## FIG. 10B

Clone AJ-26554 HC (SEQ ID NO: 314). CDRs 1, 2, and 3 are underlined.

QVQLVQSGAE VKKPGASVKV SCKASGYTFT EHYMHWVRQA PGQRLEWMGV
IGPSGGKTSY AQKFQGRVTM TRDTSTSTVY MELSSLRSED TAVYYCARES
WPMDVWGQGT TVTVSS

## FIG. 10C

YTFTEHYMH (SEQ ID NO: 315) (HC CDR1)

VIGPSGGKTSYAQKFQG (SEQ ID NO: 316) (HC CDR2)

ARESWPMDV (SEQ ID NO: 317) (HC CDR3)

## FIG. 10D

Clone AJ-26554 LC DNA (SEQ ID NO: 318)

GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTC
TCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAG
GCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGT
GGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCA
GTTTATTACTGTCAGCAGTACGCCGCCTACCCTACTTTTGGCGGAGGGACCAAGGTTGAGATC
AAACGG

## FIG. 10E

Clone AJ-26554 LC (SEQ ID NO: 319). CDRs 1, 2, and 3 are underlined.

EIVMTQSPAT LSVSPGERAT LSCRASQSVS SNLAWYQQKP GQAPRLLIYG
ASTRATGIPA RFSGSGSGTE FTLTISSLQS EDFAVYYCQQ YAAYPTFGGG TKVEIKR

## FIG. 10F

RASQSVSSNLA (SEQ ID NO: 320) (LC CDR1)

GASTRAT (SEQ ID NO: 321) (LC CDR2)

QQYAAYPT (SEQ ID NO: 322) (LC CDR3)

## FIG. 10G

**Clone AJ-26554 CAR DNA HxL (SEQ ID NO: 323)**

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCC
TGCAAGGCATCTGGATACACCTTCACGGAGCACTATATGCACTGGGTGCGACAGGCCCCTGGA
CAAAGGCTTGAGTGGATGGGAGTAATCGGGCCTAGTGGTGGTAAGACAAGCTACGCACAGAAG
TTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGC
AGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGAGAGAGTTGGCCAATGGACGTA
TGGGGCCAGGGAACAACTGTCACCGTCTCCTCAGGGTCTACATCCGGCTCCGGGAAGCCCGGA
AGTGGCGAAGGTAGTACAAAGGGGGAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTG
TCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCC
TGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCC
ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGC
AGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACGCCGCCTACCCTACTTTT
GGCGGAGGGACCAAGGTTGAGATCAAACGGGCCGCTGCCCTTGATAATGAAAAGTCAAACGGA
ACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAG
CCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTG
GCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAAT
ATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGAT
TTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAG
GGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGAC
AAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGT
CTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGA
GAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGAT
ACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 10H

**Clone AJ-26554 CAR HxL (SEQ ID NO: 324)**

MALPVTALLL PLALLLHAAR PQVQLVQSGA EVKKPGASVK VSCKASGYTF
TEHYMHWVRQ APGQRLEWMG VIGPSGGKTS YAQKFQGRVT MTRDTSTSTV
YMELSSLRSE DTAVYYCARE SWPMDVWGQG TTVTVSSGST SGSGKPGSGE
GSTKGEIVMT QSPATLSVSP GERATLSCRA SQSVSSNLAW YQQKPGQAPR
LLIYGASTRA TGIPARFSGS GSGTEFTLTI SSLQSEDFAV YYCQQYAAYP
TFGGGTKVEI KRAAALDNEK SNGTIIHVKG KHLCPSPLFP GPSKPFWVLV
VVGGVLACYS LLVTVAFIIF WVRSKRSRLL HSDYMNMTPR RPGPTRKHYQ
PYAPPRDFAA YRSRVKFSRS ADAPAYQQGQ NQLYNELNLG RREEYDVLDK
RRGRDPEMGG KPRRKNPQEG LYNELQKDKM AEAYSEIGMK GERRRGKGHD
GLYQGLSTAT KDTYDALHMQ ALPPR

## FIG. 10I

Clone AJ-26554 CAR DNA LxH (SEQ ID NO: 325)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTC
TCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAG
GCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGT
GGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCA
GTTTATTACTGTCAGCAGTACGCCGCCTACCCTACTTTTGGCGGAGGGACCAAGGTTGAGATC
AAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGCAG
GTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGC
AAGGCATCTGGATACACCTTCACGGAGCACTATATGCACTGGGTGCGACAGGCCCCTGGACAA
AGGCTTGAGTGGATGGGAGTAATCGGGCCTAGTGGTGGTAAGACAAGCTACGCACAGAAGTTC
CAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGC
CTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGAGAGAGTTGGCCAATGGACGTATGG
GGCCAGGGAACAACTGTCACCGTCTCCTCAGCCGCTGCCCTTGATAATGAAAAGTCAAACGGA
ACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAG
CCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTG
GCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAAT
ATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGAT
TTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAG
GGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGAC
AAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGT
CTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGA
GAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGAT
ACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 10J

Clone AJ-26554 CAR LxH (SEQ ID NO: 326)

MALPVTALLL PLALLLHAAR PEIVMTQSPA TLSVSPGERA TLSCRASQSV
SSNLAWYQQK PGQAPRLLIY GASTRATGIP ARFSGSGSGT EFTLTISSLQ
SEDFAVYYCQ QYAAYPTFGG GTKVEIKRGS TSGSGKPGSG EGSTKGQVQL
VQSGAEVKKP GASVKVSCKA SGYTFTEHYM HWVRQAPGQR LEWMGVIGPS
GGKTSYAQKF QGRVTMTRDT STSTVYMELS SLRSEDTAVY YCARESWPMD
VWGQGTTVTV SSAAALDNEK SNGTIIHVKG KHLCPSPLFP GPSKPFWVLV
VVGGVLACYS LLVTVAFIIF WVRSKRSRLL HSDYMNMTPR RPGPTRKHYQ
PYAPPRDFAA YRSRVKFSRS ADAPAYQQGQ NQLYNELNLG RREEYDVLDK
RRGRDPEMGG KPRRKNPQEG LYNELQKDKM AEAYSEIGMK GERRRGKGHD
GLYQGLSTAT KDTYDALHMQ ALPPR

## FIG. 11A

Clone NM-26562 HC DNA (SEQ ID NO: 327)

CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACC
TGTACTGTCTCTGGTGGCTCCATCGGGAGTGGTGGTAGTTACTGGAGCTGGATCCGCCAGCAC
CCAGGGAAGGGCCTGGAGTGGATTGGGTTGATCTATTACGATGGGAGCACCTACTACAACCCG
TCCCTCAAGAGTCGAGTTACCATATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAAGCTG
AGTTCTGTGACCGCCGCAGACACGGCGGTGTACTACTGCGCCAGAGGCAGGGGATATGAGACT
TCTTTAGCCTTCGATATCTGGGGTCAGGGTACAATGGTCACCGTCTCCTCA

## FIG. 11B

Clone NM-26562 HC (SEQ ID NO: 328). CDRs 1, 2, and 3 are underlined.

QVQLQESGPG LVKPSQTLSL TCTVSGGSIG SGGSYWSWIR QHPGKGLEWI
GLIYYDGSTY YNPSLKSRVT ISVDTSKNQF SLKLSSVTAA DTAVYYCARG
RGYETSLAFD IWGQGTMVTV SS

## FIG. 11C

GSIGSGGSYWS (SEQ ID NO: 329) (HC CDR1)

LIYYDGSTYYNPSLKS (SEQ ID NO: 330) (HC CDR2)

ARGRGYETSLAFDI (SEQ ID NO: 331) (HC CDR3)

## FIG. 11D

Clone NM-26562 LC DNA (SEQ ID NO: 332)

GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTC
TCCTGCAGGGCCAGTCAGAGTGTTAGCAGCTACTTAGCCTGGTACCAACAGAAACCTGGCCAG
GCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTCAGT
GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGATTTTGCA
GTTTATTACTGTCAGCAGAGACACGTCTGGCCTCCTACTTTTGGCGGAGGGACCAAGGTTGAG
ATCAAACGG

## FIG. 11E

Clone NM-26562 LC (SEQ ID NO: 333). CDRs 1, 2, and 3 are underlined.

EIVLTQSPAT LSLSPGERAT LSCRASQSVS SYLAWYQQKP GQAPRLLIYD
ASNRATGIPA RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ RHVWPPTFGG GTKVEIKR

## FIG. 11F

RASQSVSSYLA (SEQ ID NO: 334) (LC CDR1)

DASNRAT (SEQ ID NO: 335) (LC CDR2)

QQRHVWPPT (SEQ ID NO: 336) (LC CDR3)

## FIG. 11G

Clone NM-26562 CAR DNA HxL (SEQ ID NO: 337)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACC
TGTACTGTCTCTGGTGGCTCCATCGGGAGTGGTGGTAGTTACTGGAGCTGGATCCGCCAGCAC
CCAGGGAAGGGCCTGGAGTGGATTGGGTTGATCTATTACGATGGGAGCACCTACTACAACCCG
TCCCTCAAGAGTCGAGTTACCATATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAAGCTG
AGTTCTGTGACCGCCGCAGACACGGCGGTGTACTACTGCGCCAGAGGCAGGGGATATGAGACT
TCTTTAGCCTTCGATATCTGGGGTCAGGGTACAATGGTCACCGTCTCCTCAGGGTCTACATCC
GGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGAAATTGTGTTGACACAGTCT
CCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGT
GTTAGCAGCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT
GATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGAC
TTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGA
CACGTCTGGCCTCCTACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGGCCGCTGCCCTT
GATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCC
TTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGT
TACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTG
CTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAG
CCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCA
GATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGG
GAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGA
CGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTAT
TCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGA
CTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 11H

Clone NM-26562 CAR HxL (SEQ ID NO: 338)

MALPVTALLL PLALLLHAAR PQVQLQESGP GLVKPSQTLS LTCTVSGGSI
GSGGSYWSWI RQHPGKGLEW IGLIYYDGST YYNPSLKSRV TISVDTSKNQ
FSLKLSSVTA ADTAVYYCAR GRGYETSLAF DIWGQGTMVT VSSGSTSGSG
KPGSGEGSTK GEIVLTQSPA TLSLSPGERA TLSCRASQSV SSYLAWYQQK
PGQAPRLLIY DASNRATGIP ARFSGSGSGT DFTLTISSLE PEDFAVYYCQ
QRHVWPPTFG GGTKVEIKRA AALDNEKSNG TIIHVKGKHL CPSPLFPGPS
KPFWVLVVVG GVLACYSLLV TVAFIIFWVR SKRSRLLHSD YMNMTPRRPG
PTRKHYQPYA PPRDFAAYRS RVKFSRSADA PAYQQGQNQL YNELNLGRRE
EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA YSEIGMKGER
RRGKGHDGLY QGLSTATKDT YDALHMQALP PR

## FIG. 11I

Clone NM-26562 CAR DNA LxH (SEQ ID NO: 339)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTC
TCCTGCAGGGCCAGTCAGAGTGTTAGCAGCTACTTAGCCTGGTACCAACAGAAACCTGGCCAG
GCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTCAGT
GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGATTTTGCA
GTTTATTACTGTCAGCAGAGACACGTCTGGCCTCCTACTTTTGGCGGAGGGACCAAGGTTGAG
ATCAAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGG
CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACC
TGTACTGTCTCTGGTGGCTCCATCGGGAGTGGTGGTAGTTACTGGAGCTGGATCCGCCAGCAC
CCAGGGAAGGGCCTGGAGTGGATTGGGTTGATCTATTACGATGGGAGCACCTACTACAACCCG
TCCCTCAAGAGTCGAGTTACCATATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAAGCTG
AGTTCTGTGACCGCCGCAGACACGGCGGTGTACTACTGCGCCAGAGGCAGGGGATATGAGACT
TCTTTAGCCTTCGATATCTGGGGTCAGGGTACAATGGTCACCGTCTCCTCAGCCGCTGCCCTT
GATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCC
TTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGT
TACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTG
CTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAG
CCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCA
GATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGG
GAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGA
CGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTAT
TCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGA
CTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 11J

Clone NM-26562 CAR LxH (SEQ ID NO: 340)

MALPVTALLL PLALLLHAAR PEIVLTQSPA TLSLSPGERA TLSCRASQSV
SSYLAWYQQK PGQAPRLLIY DASNRATGIP ARFSGSGSGT DFTLTISSLE
PEDFAVYYCQ QRHVWPPTFG GGTKVEIKRG STSGSGKPGS GEGSTKGQVQ
LQESGPGLVK PSQTLSLTCT VSGGSIGSGG SYWSWIRQHP GKGLEWIGLI
YYDGSTYYNP SLKSRVTISV DTSKNQFSLK LSSVTAADTA VYYCARGRGY
ETSLAFDIWG QGTMVTVSSA AALDNEKSNG TIIHVKGKHL CPSPLFPGPS
KPFWVLVVVG GVLACYSLLV TVAFIIFWVR SKRSRLLHSD YMNMTPRRPG
PTRKHYQPYA PPRDFAAYRS RVKFSRSADA PAYQQGQNQL YNELNLGRRE
EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA YSEIGMKGER
RRGKGHDGLY QGLSTATKDT YDALHMQALP PR

## FIG. 12A

Clone TS-26564 HC DNA (SEQ ID NO: 341)

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCC
TGTGCAGCCTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCGCCAGGCTCCAGGG
AAGGGGCTGGAGTGGGTTTCAACCATTAGTAGTAGTAGTAGTATCATATACTACGCAGACTCT
GTGAAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACTCACTGTATCTGCAAATGAAC
AGCCTGAGAGCTGAGGACACGGCGGTGTACTACTGCGCCAGAGGTTCTCAGGAGCACCTGATT
TTCGATTATTGGGGACAGGGTACATTGGTCACCGTCTCCTCA

## FIG. 12B

Clone TS-26564 HC (SEQ ID NO: 342). CDRs 1, 2, and 3 are underlined.

EVQLVESGGG LVQPGGSLRL SCAASGFTFS SYSMNWVRQA PGKGLEWVST
ISSSSSIIYY ADSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARGS
QEHLIFDYWG QGTLVTVSS

## FIG. 12C

FTFSSYSMN (SEQ ID NO: 343) (HC CDR1)

TISSSSSIIYYADSVKG (SEQ ID NO: 344) (HC CDR2)

ARGSQEHLIFDY (SEQ ID NO: 345) (HC CDR3)

## FIG. 12D

Clone TS-26564 LC DNA (SEQ ID NO: 346)

GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTC
TCCTGCAGGGCCAGTCAGAGTGTTAGCAGGTACTTAGCCTGGTACCAACAGAAACCTGGCCAG
GCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTCAGT
GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGATTTTGCA
GTTTATTACTGTCAGCAGAGATTCTACTACCCTTGGACTTTTGGCGGAGGGACCAAGGTTGAG
ATCAAACGG

## FIG. 12E

Clone TS-26564 LC (SEQ ID NO: 347). CDRs 1, 2, and 3 are underlined.

EIVLTQSPAT LSLSPGERAT LSCRASQSVS RYLAWYQQKP GQAPRLLIYD
ASNRATGIPA RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ RFYYPWTFGG GTKVEIKR

## FIG. 12F

RASQSVSRYLA (SEQ ID NO: 347) (LC CDR1)

DASNRAT (SEQ ID NO: 349) (LC CDR2)

QQRFYYPWT (SEQ ID NO: 350) (LC CDR3)

## IG. 12G

Clone TS-26564 CAR DNA HxL (SEQ ID NO: 351)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCC
TGTGCAGCCTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCGCCAGGCTCCAGGG
AAGGGGCTGGAGTGGGTTTCAACCATTAGTAGTAGTAGTAGTATCATATACTACGCAGACTCT
GTGAAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACTCACTGTATCTGCAAATGAAC
AGCCTGAGAGCTGAGGACACGGCGGTGTACTACTGCGCCAGAGGTTCTCAGGAGCACCTGATT
TTCGATTATTGGGGACAGGGTACATTGGTCACCGTCTCCTCAGGGTCTACATCCGGCTCCGGG
AAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGAAATTGTGTTGACACAGTCTCCAGCCACC
CTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGG
TACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGATGCATCC
AACAGGGCCACTGGCATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTC
ACCATCAGCAGCCTAGAGCCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGATTCTACTAC
CCTTGGACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGGCCGCTGCCCTTGATAATGAA
AAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCT
GGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTG
CTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGC
GATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCA
CCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCA
GCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTAT
GACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAAC
CCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATA
GGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACT
GCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 12H

Clone TS-26564 CAR HxL (SEQ ID NO: 352)

MALPVTALLL PLALLLHAAR PEVQLVESGG GLVQPGGSLR LSCAASGFTF
SSYSMNWVRQ APGKGLEWVS TISSSSSIIY YADSVKGRFT ISRDNAKNSL
YLQMNSLRAE DTAVYYCARG SQEHLIFDYW GQGTLVTVSS GSTSGSGKPG
SGEGSTKGEI VLTQSPATLS LSPGERATLS CRASQSVSRY LAWYQQKPGQ
APRLLIYDAS NRATGIPARF SGSGSGTDFT LTISSLEPED FAVYYCQQRF
YYPWTFGGGT KVEIKRAAAL DNEKSNGTII HVKGKHLCPS PLFPGPSKPF
WVLVVVGGVL ACYSLLVTVA FIIFWVRSKR SRLLHSDYMN MTPRRPGPTR
KHYQPYAPPR DFAAYRSRVK FSRSADAPAY QQGQNQLYNE LNLGRREEYD
VLDKRRGRDP EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRG
KGHDGLYQGL STATKDTYDA LHMQALPPR

## FIG. 12I

Clone TS-26564 CAR DNA LxH (SEQ ID NO: 353)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTC
TCCTGCAGGGCCAGTCAGAGTGTTAGCAGGTACTTAGCCTGGTACCAACAGAAACCTGGCCAG
GCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTTCAGT
GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGATTTTGCA
GTTTATTACTGTCAGCAGAGATTCTACTACCCTTGGACTTTTGGCGGAGGGACCAAGGTTGAG
ATCAAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGG
GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCC
TGTGCAGCCTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCGCCAGGCTCCAGGG
AAGGGGCTGGAGTGGGTTTCAACCATTAGTAGTAGTAGTAGTATCATATACTACGCAGACTCT
GTGAAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACTCACTGTATCTGCAAATGAAC
AGCCTGAGAGCTGAGGACACGGCGGTGTACTACTGCGCCAGAGGTTCTCAGGAGCACCTGATT
TTCGATTATTGGGGACAGGGTACATTGGTCACCGTCTCCTCAGCCGCTGCCCTTGATAATGAA
AAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCT
GGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTG
CTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGC
GATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCA
CCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCA
GCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTAT
GACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAAC
CCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATA
GGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACT
GCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 12J

Clone TS-26564 CAR LxH (SEQ ID NO: 354)

MALPVTALLL PLALLLHAAR PEIVLTQSPA TLSLSPGERA TLSCRASQSV
SRYLAWYQQK PGQAPRLLIY DASNRATGIP ARFSGSGSGT DFTLTISSLE
PEDFAVYYCQ QRFYYPWTFG GGTKVEIKRG STSGSGKPGS GEGSTKGEVQ
LVESGGGLVQ PGGSLRLSCA ASGFTFSSYS MNWVRQAPGK GLEWVSTISS
SSSIIYYADS VKGRFTISRD NAKNSLYLQM NSLRAEDTAV YYCARGSQEH
LIFDYWGQGT LVTVSSAAAL DNEKSNGTII HVKGKHLCPS PLFPGPSKPF
WVLVVVGGVL ACYSLLVTVA FIIFWVRSKR SRLLHSDYMN MTPRRPGPTR
KHYQPYAPPR DFAAYRSRVK FSRSADAPAY QQGQNQLYNE LNLGRREEYD
VLDKRRGRDP EMGGKPRRKN PQEGLYNELQ KDKMAEAYSE IGMKGERRRG
KGHDGLYQGL STATKDTYDA LHMQALPPR

## FIG. 13A

**Clone RY-26568 HC DNA (SEQ ID NO: 355)**

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC
TGTGCAGCGTCTGGATTCACCTTCGGGAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGC
AAGGGGCTGGAGTGGGTGGCAGTTATACATTATGATGGAAGTGTTGAATACTATGCAGACTCC
GTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGGACACGCTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCCAGAACTGACTTCTGGAGCGGATCC
CCTCCAAGCTTAGATTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA

## FIG. 13B

**Clone RY-26568 HC (SEQ ID NO: 356). CDRs 1, 2, and 3 are underlined.**

QVQLVESGGG VVQPGRSLRL SCAASGFTFG SYGMHWVRQA PGKGLEWVAV
IHYDGSVEYY ADSVKGRFTI SRDNSKDTLY LQMNSLRAED TAVYYCARTD
FWSGSPPSLD YWGQGTLVTV SS

## FIG. 13C

FTFGSYGMH (SEQ ID NO: 357) (HC CDR1)

VIHYDGSVEYYADSVKG (SEQ ID NO: 358) (HC CDR2)

ARTDFWSGSPPSLDY (SEQ ID NO: 359) (HC CDR3)

## FIG. 13D

**Clone RY-26568 LC DNA (SEQ ID NO: 360)**

GACATCCAGTTGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATC
ACTTGTCGGGCGAGTCGGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAA
GCCCCTAAGCTCCTGATCTATGGTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGC
GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCA
ACTTATTACTGTCAGCAGATATACACCTTCCCTTTCACTTTTGGCGGAGGGACCAAGGTTGAG
ATCAAACGG

## FIG. 13E

**Clone RY-26568 LC (SEQ ID NO: 361). CDRs 1, 2, and 3 are underlined.**

DIQLTQSPSS VSASVGDRVT ITCRASRGIS SWLAWYQQKP GKAPKLLIYG
ASSLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ IYTFPFTFGG GTKVEIKR

## FIG. 13F

RASRGISSWLA (SEQ ID NO: 362) (LC CDR1)

GASSLQS (SEQ ID NO: 363) (LC CDR2)

QQIYTFPFT (SEQ ID NO: 364) (LC CDR3)

## FIG. 13G

Clone RY-26568 CAR DNA HxL (SEQ ID NO: 365)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC
TGTGCAGCGTCTGGATTCACCTTCGGGAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGC
AAGGGGCTGGAGTGGGTGGCAGTTATACATTATGATGGAAGTGTTGAATACTATGCAGACTCC
GTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGGACACGCTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCCAGAACTGACTTCTGGAGCGGATCC
CCTCCAAGCTTAGATTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCAGGGTCTACATCC
GGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGACATCCAGTTGACCCAGTCT
CCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGTCGGGCGAGTCGGGGT
ATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTAT
GGTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAT
TTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCAGCAGATA
TACACCTTCCCTTTCACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGGCCGCTGCCCTT
GATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCC
TTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGT
TACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTG
CTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAG
CCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCA
GATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGG
GAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGA
CGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTAT
TCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGA
CTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 13H

Clone RY-26568 CAR HxL (SEQ ID NO: 366)

MALPVTALLL PLALLLHAAR PQVQLVESGG GVVQPGRSLR LSCAASGFTF
GSYGMHWVRQ APGKGLEWVA VIHYDGSVEY YADSVKGRFT ISRDNSKDTL
YLQMNSLRAE DTAVYYCART DFWSGSPPSL DYWGQGTLVT VSSGSTSGSG
KPGSGEGSTK GDIQLTQSPS SVSASVGDRV TITCRASRGI SSWLAWYQQK
PGKAPKLLIY GASSLQSGVP SRFSGSGSGT DFTLTISSLQ PEDFATYYCQ
QIYTFPFTFG GGTKVEIKRA AALDNEKSNG TIIHVKGKHL CPSPLFPGPS
KPFWVLVVVG GVLACYSLLV TVAFIIFWVR SKRSRLLHSD YMNMTPRRPG
PTRKHYQPYA PPRDFAAYRS RVKFSRSADA PAYQQGQNQL YNELNLGRRE
EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA YSEIGMKGER
RRGKGHDGLY QGLSTATKDT YDALHMQALP PR

## FIG. 13I

Clone RY-26568 CAR DNA LxH (SEQ ID NO: 367)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
GACATCCAGTTGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATC
ACTTGTCGGGCGAGTCGGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAA
GCCCCTAAGCTCCTGATCTATGGTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGC
GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCA
ACTTATTACTGTCAGCAGATATACACCTTCCCTTTCACTTTTGGCGGAGGGACCAAGGTTGAG
ATCAAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGG
CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC
TGTGCAGCGTCTGGATTCACCTTCGGGAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGC
AAGGGGCTGGAGTGGGTGGCAGTTATACATTATGATGGAAGTGTTGAATACTATGCAGACTCC
GTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGGACACGCTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGCCAGAACTGACTTCTGGAGCGGATCC
CCTCCAAGCTTAGATTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCAGCCGCTGCCCTT
GATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCACCC
TTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCTTGT
TACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGCCTG
CTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTACCAG
CCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCTGCA
GATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGCAGG
GAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCAAGA
CGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCCTAT
TCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAGGGA
CTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 13J

Clone RY-26568 CAR LxH (SEQ ID NO: 368)

MALPVTALLL PLALLLHAAR PDIQLTQSPS SVSASVGDRV TITCRASRGI
SSWLAWYQQK PGKAPKLLIY GASSLQSGVP SRFSGSGSGT DFTLTISSLQ
PEDFATYYCQ QIYTFPFTFG GGTKVEIKRG STSGSGKPGS GEGSTKGQVQ
LVESGGGVVQ PGRSLRLSCA ASGFTFGSYG MHWVRQAPGK GLEWVAVIHY
DGSVEYYADS VKGRFTISRD NSKDTLYLQM NSLRAEDTAV YYCARTDFWS
GSPPSLDYWG QGTLVTVSSA AALDNEKSNG TIIHVKGKHL CPSPLFPGPS
KPFWVLVVVG GVLACYSLLV TVAFIIFWVR SKRSRLLHSD YMNMTPRRPG
PTRKHYQPYA PPRDFAAYRS RVKFSRSADA PAYQQGQNQL YNELNLGRRE
EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA YSEIGMKGER
RRGKGHDGLY QGLSTATKDT YDALHMQALP PR

## FIG. 14A

Clone PP-26575 HC DNA (SEQ ID NO: 369)

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCC
TGCAAGGCTTCTGGAGGCACCCTCAGCAGCCTGGCTATCAGCTGGGTGCGACAGGCCCCTGGA
CAAGGGCTTGAGTGGATGGGAGGGGTCATCCCTATCTTGGGTCGGGCAAACTACGCACAGAAG
TTCCAGGGCAGAGTCACGATTACCGCGGACGAGTCCACGAGCACAGCCTACATGGAGCTGAGC
AGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGAACTCCTGAATACTCCTCCAGC
ATATGGCACTATTACTACGGCATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA

## FIG. 14B

Clone PP-26575 HC (SEQ ID NO: 370). CDRs 1, 2, and 3 are underlined.

QVQLVQSGAE VKKPGSSVKV SCKASGGTLS SLAISWVRQA PGQGLEWMGG
VIPILGRANY AQKFQGRVTI TADESTSTAY MELSSLRSED TAVYYCARTP
EYSSSIWHYY YGMDVWGQGT TVTVSS

## FIG. 14C

GTLSSLAIS (SEQ ID NO: 371) (HC CDR1)

GVIPILGRANYAQKFQG (SEQ ID NO: 372) (HC CDR2)

ARTPEYSSSIWHYYYGMDV (SEQ ID NO: 373) (HC CDR3)

## FIG. 14D

Clone PP-26575 LC DNA (SEQ ID NO: 374)

GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATC
AACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCTTGGTAC
CAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG
GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG
CAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTTCGCCCACACTCCTTTCACTTTTGGC
GGAGGGACCAAGGTTGAGATCAAACGG

## FIG. 14E

Clone PP-26575 LC (SEQ ID NO: 375). CDRs 1, 2, and 3 are underlined.

DIVMTQSPDS LAVSLGERAT INCKSSQSVL YSSNNKNYLA WYQQKPGQPP
KLLIYWASTR ESGVPDRFSG SGSGTDFTLT ISSLQAEDVA VYYCQQFAHT
PFTFGGGTKV EIKR

## FIG. 14F

KSSQSVLYSSNNKNYLA (SEQ ID NO: 376) (LC CDR1)

WASTRES (SEQ ID NO: 377) (LC CDR2)

QQFAHTPFT (SEQ ID NO: 378) (LC CDR3)

## FIG. 14G

Clone PP-26575 CAR DNA HxL (SEQ ID NO: 379)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCC
TGCAAGGCTTCTGGAGGCACCCTCAGCAGCCTGGCTATCAGCTGGGTGCGACAGGCCCCTGGA
CAAGGGCTTGAGTGGATGGGAGGGGTCATCCCTATCTTGGGTCGGGCAAACTACGCACAGAAG
TTCCAGGGCAGAGTCACGATTACCGCGGACGAGTCCACGAGCACAGCCTACATGGAGCTGAGC
AGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGAACTCCTGAATACTCCTCCAGC
ATATGGCACTATTACTACGGCATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA
GGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGACATCGTG
ATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAG
TCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCTTGGTACCAGCAGAAA
CCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC
CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAA
GATGTGGCAGTTTATTACTGTCAGCAGTTCGCCCACACTCCTTTCACTTTTGGCGGAGGGACC
AAGGTTGAGATCAAACGGGCCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTCAC
GTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTG
TTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATC
TTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACGC
CGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCTGCCTAT
CGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAA
CTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGA
CGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAG
CTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGG
GGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCT
CTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 14H

Clone PP-26575 CAR HxL (SEQ ID NO: 380)

MALPVTALLL PLALLLHAAR PQVQLVQSGA EVKKPGSSVK VSCKASGGTL
SSLAISWVRQ APGQGLEWMG GVIPILGRAN YAQKFQGRVT ITADESTSTA
YMELSSLRSE DTAVYYCART PEYSSSIWHY YYGMDVWGQG TTVTVSSGST
SGSGKPGSGE GSTKGDIVMT QSPDSLAVSL GERATINCKS SQSVLYSSNN
KNYLAWYQQK PGQPPKLLIY WASTRESGVP DRFSGSGSGT DFTLTISSLQ
AEDVAVYYCQ QFAHTPFTFG GGTKVEIKRA AALDNEKSNG TIIHVKGKHL
CPSPLFPGPS KPFWVLVVVG GVLACYSLLV TVAFIIFWVR SKRSRLLHSD
YMNMTPRRPG PTRKHYQPYA PPRDFAAYRS RVKFSRSADA PAYQQGQNQL
YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA
YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR

## FIG. 14I

Clone PP-26575 CAR DNA LxH (SEQ ID NO: 381)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATC
AACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCTTGGTAC
CAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGG
GTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG
CAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTTCGCCCACACTCCTTTCACTTTTGGC
GGAGGGACCAAGGTTGAGATCAAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGC
GAAGGTAGTACAAAGGGGCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGG
TCCTCGGTGAAGGTCTCCTGCAAGGCTTCTGGAGGCACCCTCAGCAGCCTGGCTATCAGCTGG
GTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAGGGGTCATCCCTATCTTGGGTCGG
GCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAGTCCACGAGCACA
GCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGGTGTACTACTGCGCCAGAACT
CCTGAATACTCCTCCAGCATATGGCACTATTACTACGGCATGGACGTATGGGGCCAGGGAACA
ACTGTCACCGTCTCCTCAGCCGCTGCCCTTGATAATGAAAAGTCAAACGGAACAATCATTCAC
GTGAAGGGCAAGCACCTCTGTCCGTCACCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTG
TTGGTCGTAGTGGGTGGAGTCCTCGCTTGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATC
TTCTGGGTTAGATCCAAAAGAAGCCGCCTGCTCCATAGCGATTACATGAATATGACTCCACGC
CGCCCTGGCCCCACAAGGAAACACTACCAGCCTTACGCACCACCTAGAGATTTCGCTGCCTAT
CGGAGCAGGGTGAAGTTTTCCAGATCTGCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAA
CTGTATAACGAGCTCAACCTGGGACGCAGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGA
CGGGACCCTGAGATGGGTGGCAAACCAAGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAG
CTGCAGAAGGATAAGATGGCTGAAGCCTATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGG
GGAAAAGGGCACGACGGTTTGTACCAGGGACTCAGCACTGCTACGAAGGATACTTATGACGCT
CTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 14J

Clone PP-26575 CAR LxH (SEQ ID NO: 382)

MALPVTALLL PLALLLHAAR PDIVMTQSPD SLAVSLGERA TINCKSSQSV
LYSSNNKNYL AWYQQKPGQP PKLLIYWAST RESGVPDRFS GSGSGTDFTL
TISSLQAEDV AVYYCQQFAH TPFTFGGGTK VEIKRGSTSG SGKPGSGEGS
TKGQVQLVQS GAEVKKPGSS VKVSCKASGG TLSSLAISWV RQAPGQGLEW
MGGVIPILGR ANYAQKFQGR VTITADESTS TAYMELSSLR SEDTAVYYCA
RTPEYSSSIW HYYYGMDVWG QGTTVTVSSA AALDNEKSNG TIIHVKGKHL
CPSPLFPGPS KPFWVLVVVG GVLACYSLLV TVAFIIFWVR SKRSRLLHSD
YMNMTPRRPG PTRKHYQPYA PPRDFAAYRS RVKFSRSADA PAYQQGQNQL
YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA
YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR

## FIG. 15A

Clone RD-26576 HC DNA (SEQ ID NO: 383)

CAGGTGCGGCTGGTGGAGTCTGGGGGGGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC
TGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATACACTGGGTCCGCCAGGCTCCAGGC
AAGGGGCTGGAGTGGGTGGCAGTTATAGGGTATGATGGACAGGAGAAATACTATGCAGACTCC
GTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAAGGGGCCGTTGCAGGAGCCGCCA
TACGCTTTTGGGATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA

## FIG. 15B

Clone RD-26576 HC (SEQ ID NO: 384). CDRs 1, 2, and 3 are underlined.

QVRLVESGGG VVQPGRSLRL SCAASGFTFS SYGIHWVRQA PGKGLEWVAV
IGYDGQEKYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKGP
LQEPPYAFGM DVWGQGTTVT VSS

## FIG. 15C

FTFSSYGIH (SEQ ID NO: 385) (HC CDR1)

VIGYDGQEKYYADSVKG (SEQ ID NO: 386) (HC CDR2)

VKGPLQEPPYAFGMDV (SEQ ID NO: 387) (HC CDR3)

## FIG. 15D

Clone RD-26576 LC DNA (SEQ ID NO: 388)

GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTC
TCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAG
GCTCCCAGGCTCCTCATCTATAGCGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGT
GGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCA
GTTTATTACTGTCAGCAGCACCACGTCTGGCCTCTCACTTTTGGCGGAGGGACCAAGGTTGAG
ATCAAACGG

## FIG. 15E

Clone RD-26576 LC (SEQ ID NO: 389). CDRs 1, 2, and 3 are underlined.

EIVMTQSPAT LSVSPGERAT LSCRASQSVS SNLAWYQQKP GQAPRLLIYS
ASTRATGIPA RFSGSGSGTE FTLTISSLQS EDFAVYYCQQ HHVWPLTFGG GTKVEIKR

## FIG. 15F

RASQSVSSNLA (SEQ ID NO: 390) (LC CDR1)

SASTRAT (SEQ ID NO: 391) (LC CDR2)

QQHHVWPLT (SEQ ID NO: 392) (LC CDR3)

## FIG. 15G

**Clone RD-26576 CAR DNA HxL (SEQ ID NO: 393)**

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
CAGGTGCGGCTGGTGGAGTCTGGGGGGGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC
TGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATACACTGGGTCCGCCAGGCTCCAGGC
AAGGGGCTGGAGTGGGTGGCAGTTATAGGGTATGATGGACAGGAGAAATACTATGCAGACTCC
GTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAAGGGGCCGTTGCAGGAGCCGCCA
TACGCTTTTGGGATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCAGGGTCTACA
TCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGAAATAGTGATGACGCAG
TCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAG
AGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATC
TATAGCGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACA
GAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAG
CACCACGTCTGGCCTCTCACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGGCCGCTGCC
CTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCA
CCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCT
TGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGC
CTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTAC
CAGCCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCT
GCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGC
AGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCA
AGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCC
TATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAG
GGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 15H

**Clone RD-26576 CAR HxL (SEQ ID NO: 394)**

MALPVTALLL PLALLLHAAR PQVRLVESGG GVVQPGRSLR LSCAASGFTF
SSYGIHWVRQ APGKGLEWVA VIGYDGQEKY YADSVKGRFT ISRDNSKNTL
YLQMNSLRAE DTAVYYCVKG PLQEPPYAFG MDVWGQGTTV TVSSGSTSGS
GKPGSGEGST KGEIVMTQSP ATLSVSPGER ATLSCRASQS VSSNLAWYQQ
KPGQAPRLLI YSASTRATGI PARFSGSGSG TEFTLTISSL QSEDFAVYYC
QQHHVWPLTF GGGTKVEIKR AAALDNEKSN GTIIHVKGKH LCPSPLFPGP
SKPFWVLVVV GGVLACYSLL VTVAFIIFWV RSKRSRLLHS DYMNMTPRRP
GPTRKHYQPY APPRDFAAYR SRVKFSRSAD APAYQQGQNQ LYNELNLGRR
EEYDVLDKRR GRDPEMGGKP RRKNPQEGLY NELQKDKMAE AYSEIGMKGE
RRRGKGHDGL YQGLSTATKD TYDALHMQAL PPR

## FIG. 15I

Clone RD-26576 CAR DNA LxH (SEQ ID NO: 395)

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTC
TCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAG
GCTCCCAGGCTCCTCATCTATAGCGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGT
GGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCA
GTTTATTACTGTCAGCAGCACCACGTCTGGCCTCTCACTTTTGGCGGAGGGACCAAGGTTGAG
ATCAAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGG
CAGGTGCGGCTGGTGGAGTCTGGGGGGGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC
TGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATACACTGGGTCCGCCAGGCTCCAGGC
AAGGGGCTGGAGTGGGTGGCAGTTATAGGGTATGATGGACAGGAGAAATACTATGCAGACTCC
GTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAAGGGGCCGTTGCAGGAGCCGCCA
TACGCTTTTGGGATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCAGCCGCTGCC
CTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCA
CCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCT
TGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGC
CTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTAC
CAGCCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCT
GCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGC
AGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCA
AGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCC
TATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAG
GGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

## FIG. 15J

Clone RD-26576 CAR LxH (SEQ ID NO: 396)

MALPVTALLL PLALLLHAAR PEIVMTQSPA TLSVSPGERA TLSCRASQSV
SSNLAWYQQK PGQAPRLLIY SASTRATGIP ARFSGSGSGT EFTLTISSLQ
SEDFAVYYCQ QHHVWPLTFG GGTKVEIKRG STSGSGKPGS GEGSTKGQVR
LVESGGGVVQ PGRSLRLSCA ASGFTFSSYG IHWVRQAPGK GLEWVAVIGY
DGQEKYYADS VKGRFTISRD NSKNTLYLQM NSLRAEDTAV YYCVKGPLQE
PPYAFGMDVW GQGTTVTVSS AAALDNEKSN GTIIHVKGKH LCPSPLFPGP
SKPFWVLVVV GGVLACYSLL VTVAFIIFWV RSKRSRLLHS DYMNMTPRRP
GPTRKHYQPY APPRDFAAYR SRVKFSRSAD APAYQQGQNQ LYNELNLGRR
EEYDVLDKRR GRDPEMGGKP RRKNPQEGLY NELQKDKMAE AYSEIGMKGE
RRRGKGHDGL YQGLSTATKD TYDALHMQAL PPR

## FIG. 16A

Clone RD-26578 HC DNA (SEQ ID NO: 397)

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC
TGTGCAGCGTCTGGATTCACCTTCAGTAGCCGTGGCATGCACTGGGTCCGCCAGGCTCCAGGC
AAGGGGCTGGAGTGGGTGGCAGTTATAGGGTATGATGGACAGGAGAAATACTATGCAGACTCC
GTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAAGGGGCCGTTGCAGGAGCCGCCA
TACGATTATGGAATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA

## FIG. 16B

Clone RD-26578 HC (SEQ ID NO: 398) CDRs 1, 2, and 3 are underlined.

QVQLVESGGG VVQPGRSLRL SCAASGFTFS SRGMHWVRQA PGKGLEWVAV
IGYDGQEKYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKGP
LQEPPYDYGM DVWGQGTTVT VSS

## FIG. 16C

FTFSSRGMH (SEQ ID NO: 399) (HC CDR1)

VIGYDGQEKYYADSVKG (SEQ ID NO: 400) (HC CDR2)

VKGPLQEPPYDYGMDV (SEQ ID NO: 401) (HC CDR3)

## FIG. 16D

Clone RD-26578 LC DNA (SEQ ID NO: 402)

GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTC
TCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAG
GCTCCCAGGCTCCTCATCTATAGCGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGT
GGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCA
GTTTATTACTGTCAGCAGCACCACGTCTGGCCTCTCACTTTTGGCGGAGGGACCAAGGTTGAG
ATCAAACGG

## FIG. 16E

Clone RD-26578 LC (SEQ ID NO: 403). CDRs 1, 2, and 3 are underlined.

EIVMTQSPAT LSVSPGERAT LSCRASQSVS SNLAWYQQKP GQAPRLLIYS
ASTRATGIPA RFSGSGSGTE FTLTISSLQS EDFAVYYCQQ HHVWPLTFGG GTKVEIKR

## FIG. 16F

RASQSVSSNLA (SEQ ID NO: 404) (LC CDR1)

SASTRAT (SEQ ID NO: 405) (LC CDR2)

QQHHVWPLT (SEQ ID NO: 406) (LC CDR3)

## FIG. 16G

**Clone RD-26578 CAR DNA HxL (SEQ ID NO: 407)**

ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC
TGTGCAGCGTCTGGATTCACCTTCAGTAGCCGTGGCATGCACTGGGTCCGCCAGGCTCCAGGC
AAGGGGCTGGAGTGGGTGGCAGTTATAGGGTATGATGGACAGGAGAAATACTATGCAGACTCC
GTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAAGGGGCCGTTGCAGGAGCCGCCA
TACGATTATGGAATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCAGGGTCTACA
TCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGGGAAATAGTGATGACGCAG
TCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAG
AGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATC
TATAGCGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACA
GAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAG
CACCACGTCTGGCCTCTCACTTTTGGCGGAGGGACCAAGGTTGAGATCAAACGGGCCGCTGCC
CTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCA
CCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCT
TGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGC
CTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTAC
CAGCCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCT
GCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGC
AGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCA
AGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCC
TATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAG
GGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

FIG. 16H

Clone RD-26578 CAR HxL (SEQ ID NO: 408)

MALPVTALLL PLALLLHAAR PQVQLVESGG GVVQPGRSLR LSCAASGFTF
SSRGMHWVRQ APGKGLEWVA VIGYDGQEKY YADSVKGRFT ISRDNSKNTL
YLQMNSLRAE DTAVYYCVKG PLQEPPYDYG MDVWGQGTTV TVSSGSTSGS
GKPGSGEGST KGEIVMTQSP ATLSVSPGER ATLSCRASQS VSSNLAWYQQ
KPGQAPRLLI YSASTRATGI PARFSGSGSG TEFTLTISSL QSEDFAVYYC
QQHHVWPLTF GGGTKVEIKR AAALDNEKSN GTIIHVKGKH LCPSPLFPGP
SKPFWVLVVV GGVLACYSLL VTVAFIIFWV RSKRSRLLHS DYMNMTPRRP
GPTRKHYQPY APPRDFAAYR SRVKFSRSAD APAYQQGQNQ LYNELNLGRR
EEYDVLDKRR GRDPEMGGKP RRKNPQEGLY NELQKDKMAE AYSEIGMKGE
RRRGKGHDGL YQGLSTATKD TYDALHMQAL PPR

FIG. 16I

Clone RD-26578 CAR DNA LxH (SEQ ID NO: 409)

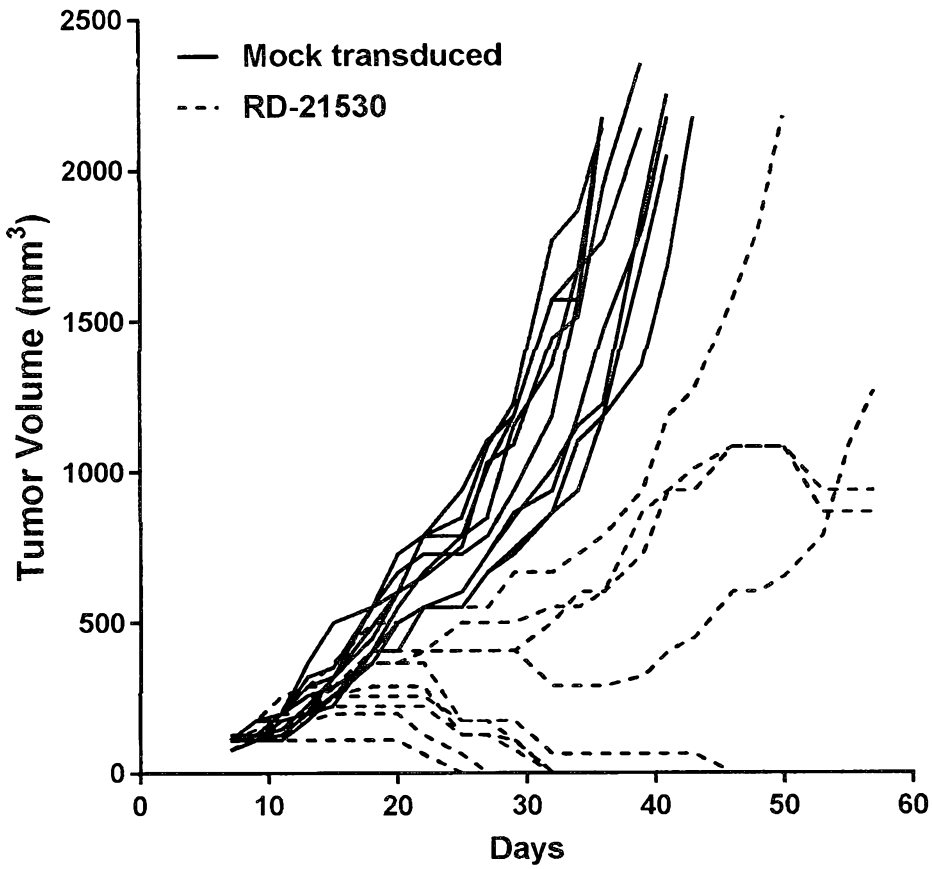
ATGGCACTCCCCGTAACTGCTCTGCTGCTGCCGTTGGCATTGCTCCTGCACGCCGCACGCCCG
GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTC
TCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGCCAG
GCTCCCAGGCTCCTCATCTATAGCGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGT
GGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCA
GTTTATTACTGTCAGCAGCACCACGTCTGGCCTCTCACTTTTGGCGGAGGGACCAAGGTTGAG
ATCAAACGGGGGTCTACATCCGGCTCCGGGAAGCCCGGAAGTGGCGAAGGTAGTACAAAGGGG
CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC
TGTGCAGCGTCTGGATTCACCTTCAGTAGCCGTGGCATGCACTGGGTCCGCCAGGCTCCAGGC
AAGGGGCTGGAGTGGGTGGCAGTTATAGGGTATGATGGACAGGAGAAATACTATGCAGACTCC
GTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAC
AGCCTGAGAGCCGAGGACACGGCGGTGTACTACTGCGTCAAGGGGCCGTTGCAGGAGCCGCCA
TACGATTATGGAATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCAGCCGCTGCC
CTTGATAATGAAAAGTCAAACGGAACAATCATTCACGTGAAGGGCAAGCACCTCTGTCCGTCA
CCCTTGTTCCCTGGTCCATCCAAGCCATTCTGGGTGTTGGTCGTAGTGGGTGGAGTCCTCGCT
TGTTACTCTCTGCTCGTCACCGTGGCTTTTATAATCTTCTGGGTTAGATCCAAAAGAAGCCGC
CTGCTCCATAGCGATTACATGAATATGACTCCACGCCGCCCTGGCCCCACAAGGAAACACTAC
CAGCCTTACGCACCACCTAGAGATTTCGCTGCCTATCGGAGCAGGGTGAAGTTTTCCAGATCT
GCAGATGCACCAGCGTATCAGCAGGGCCAGAACCAACTGTATAACGAGCTCAACCTGGGACGC
AGGGAAGAGTATGACGTTTTGGACAAGCGCAGAGGACGGGACCCTGAGATGGGTGGCAAACCA
AGACGAAAAAACCCCCAGGAGGGTCTCTATAATGAGCTGCAGAAGGATAAGATGGCTGAAGCC
TATTCTGAAATAGGCATGAAAGGAGAGCGGAGAAGGGGAAAAGGGCACGACGGTTTGTACCAG
GGACTCAGCACTGCTACGAAGGATACTTATGACGCTCTCCACATGCAAGCCCTGCCACCTAGG

FIG. 16J

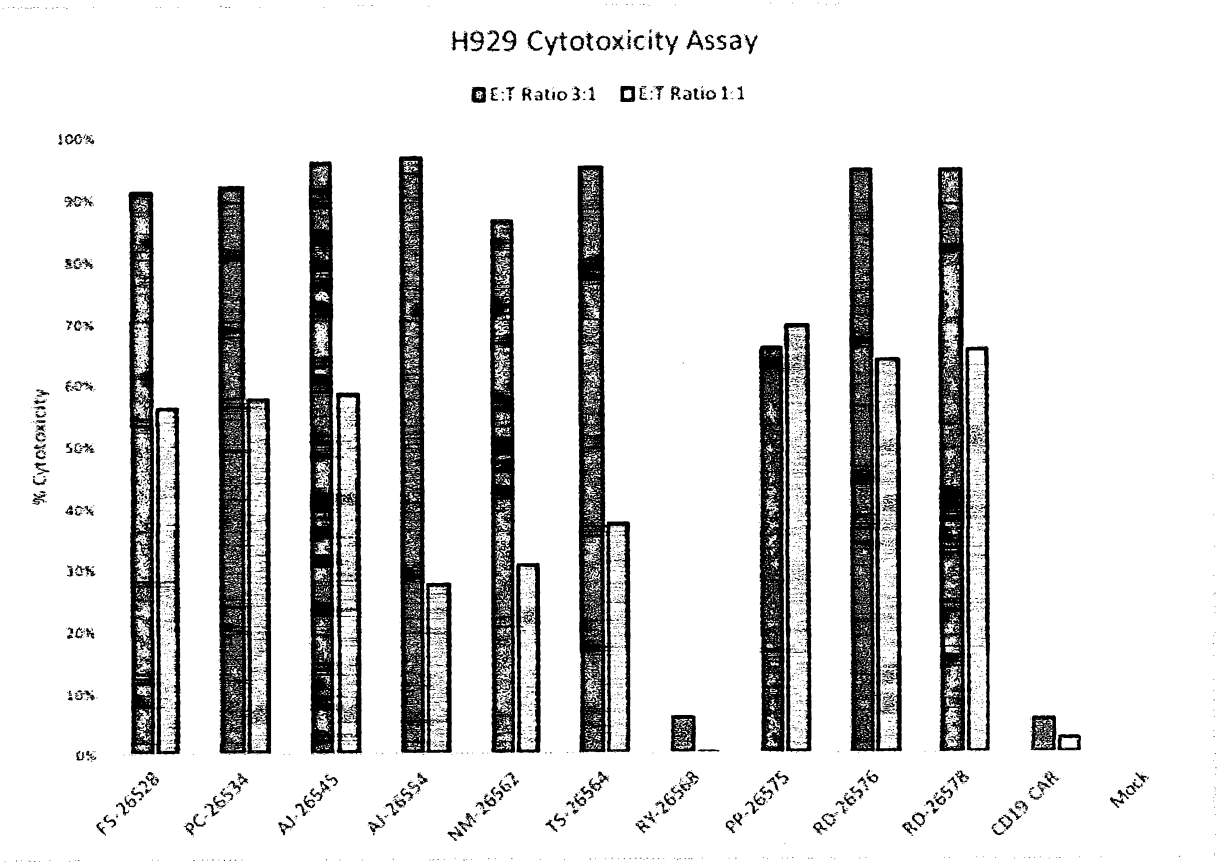
Clone RD-26578 CAR LxH (SEQ ID NO: 410)

MALPVTALLL PLALLLHAAR PEIVMTQSPA TLSVSPGERA TLSCRASQSV
SSNLAWYQQK PGQAPRLLIY SASTRATGIP ARFSGSGSGT EFTLTISSLQ
SEDFAVYYCQ QHHVWPLTFG GGTKVEIKRG STSGSGKPGS GEGSTKGQVQ
LVESGGGVVQ PGRSLRLSCA ASGFTFSSRG MHWVRQAPGK GLEWVAVIGY
DGQEKYYADS VKGRFTISRD NSKNTLYLQM NSLRAEDTAV YYCVKGPLQE
PPYDYGMDVW GQGTTVTVSS AAALDNEKSN GTIIHVKGKH LCPSPLFPGP
SKPFWVLVVV GGVLACYSLL VTVAFIIFWV RSKRSRLLHS DYMNMTPRRP
GPTRKHYQPY APPRDFAAYR SRVKFSRSAD APAYQQGQNQ LYNELNLGRR
EEYDVLDKRR GRDPEMGGKP RRKNPQEGLY NELQKDKMAE AYSEIGMKGE
RRRGKGHDGL YQGLSTATKD TYDALHMQAL PPR

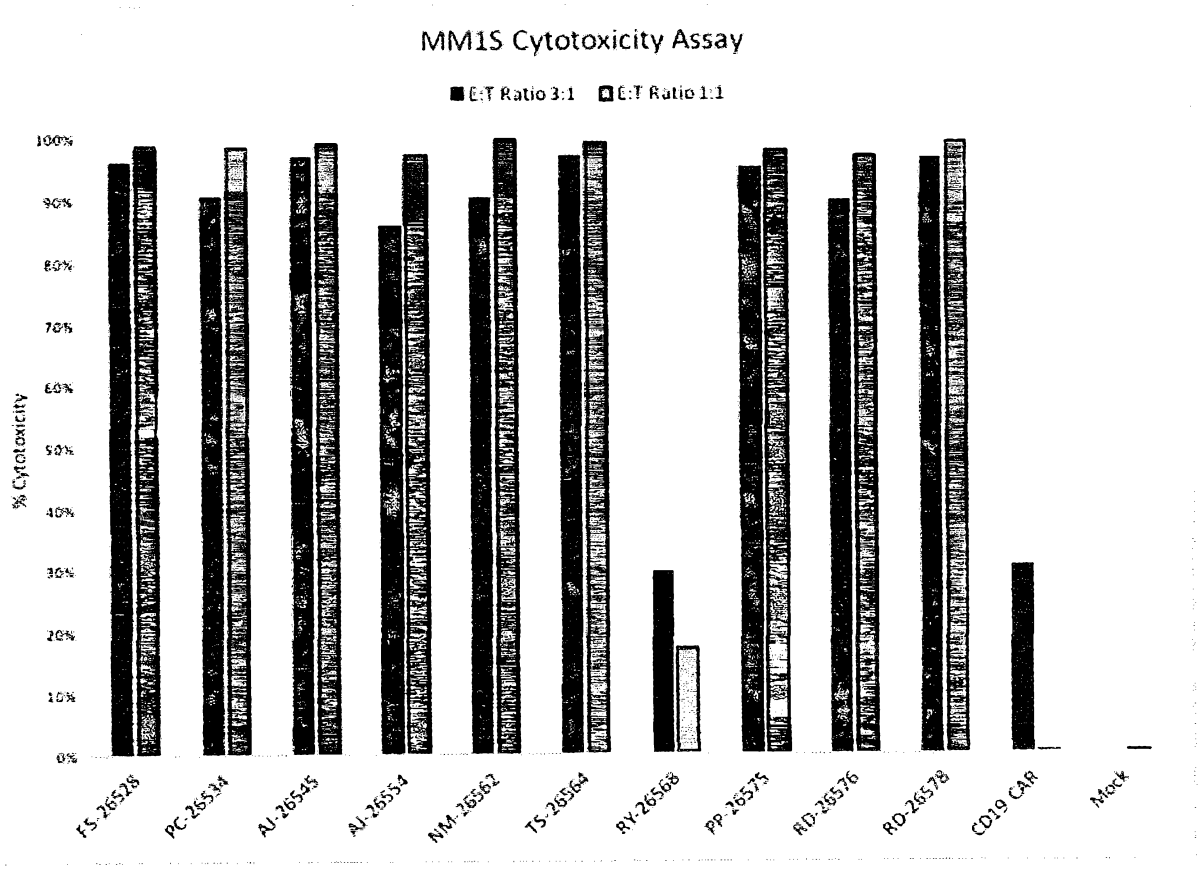
# FIG. 17


Mock transduced
RD-21530
Tumor Volume (mm3)
2500
2000
1500
1000
500
0
0
10
20
30
40
50
60
Days

# FIG. 18A


H929 Cytotoxicity Assay
E:T Ratio 3:1
E:T Ratio 1:1
% Cytotoxicity
100%
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
FS-26528
PC-26534
AJ-26545
AJ-26554
NM-26562
TS-26564
RY-26568
PP-26575
RD-26576
RD-26578
CD19 CAR
Mock

# FIG. 18B


MM1S Cytotoxicity Assay
E:T Ratio 3:1
E:T Ratio 1:1
% Cytotoxicity
100%
90%
80%
70%
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SEQUENCE LISTING

<110> KITE PHARMA, INC.

<120> BCMA BINDING MOLECULES AND METHODS OF USE THEREOF

<130> K-1030.02US

<140> 15/476,309
<141> 2017-03-31

<150> 62/317,334
<151> 2016-04-01

<160> 413

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VH FR1 peptide

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1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

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VH FR1 peptide

<400> 2
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
20 25

<210> 3
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR1 peptide

<400> 3
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
20 25

<210> 4
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR1 peptide

<400> 4
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
20 25

<210> 5
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<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
VH FR1 peptide

<400> 5
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
20 25

<210> 6
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VH FR1 peptide

<400> 6
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
20 25

<210> 7
<211> 25
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
VH FR1 peptide

<400> 7
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
20 25

<210> 8
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR1 peptide

<400> 8
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
20 25

<210> 9
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic VH CDR1 peptide

<400> 9
Gly Phe Thr Phe Ser Ser Tyr
1 5

<210> 10
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic VH CDR1 peptide

<400> 10
Gly Phe Thr Phe Ser Ser Tyr
1 5

<210> 11
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic VH CDR1 peptide

<400> 11
Gly Tyr Thr Phe Thr Ser Tyr
1 5

<210> 12
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR1 peptide

<400> 12
Gly Gly Ser Ile Ser Ser Ser Ser Tyr
1 5

<210> 13
<211> 7
<212> PRT
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VH CDR1 peptide

<400> 13
Gly Phe Thr Phe Ser Ser Tyr
1 5

<210> 14
<211> 7
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VH CDR1 peptide

<400> 14
Gly Phe Thr Phe Ser Ser Tyr
1 5

<210> 15
<211> 7
<212> PRT
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VH CDR1 peptide

<400> 15
Gly Gly Thr Phe Ser Ser Tyr
1 5

<210> 16
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR1 peptide

<400> 16
Gly Phe Thr Phe Ser Ser Tyr
1 5

<210> 17
<211> 17
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 17
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
1 5 10 15

Ser

<210> 18
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 18
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
1 5 10 15

Ala

<210> 19
<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 19
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
1 5 10 15

Gly

<210> 20
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 20
Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
1 5 10 15

Gly

<210> 21
<211> 17
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 21
Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
1 5 10 15

Ser

<210> 22
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 22
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
1 5 10 15

Ala

<210> 23
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 23
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
1 5 10 15

Gly

<210> 24
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 24
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
1 5 10 15

Ala

<210> 25
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR2 peptide

<400> 25
Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 26
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR2 peptide

<400> 26
Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 27
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR2 peptide

<400> 27
Ile Ile Asn Pro Gly Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 28
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR2 peptide

<400> 28
Ser Ile Ser Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 29
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR2 peptide

<400> 29
Thr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 30
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR2 peptide

<400> 30
Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 31
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR2 peptide

<400> 31
Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 32
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR2 peptide

<400> 32
Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 33
<211> 30
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
VH FR3 polypeptide

<400> 33
Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
20 25 30

<210> 34
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR3 polypeptide

<400> 34
Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
20 25 30

<210> 35
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR3 polypeptide

<400> 35
Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu
1 5 10 15

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

<210> 36
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR3 polypeptide

<400> 36
Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys
1 5 10 15

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
20 25 30

<210> 37
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR3 polypeptide

<400> 37
Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
20 25 30

<210> 38
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR3 polypeptide

<400> 38
Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
20 25 30

<210> 39
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR3 polypeptide

<400> 39

Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

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

<210> 40
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR3 polypeptide

<400> 40
Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
20 25 30

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

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3 peptide

<400> 41
Ala Arg Ala Glu Met Gly Ala Val Phe Asp Ile
1 5 10

<210> 42
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3 peptide

<400> 42
Ala Arg Asp Gly Thr Tyr Leu Gly Gly Leu Trp Tyr Phe Asp Leu
1 5 10 15

<210> 43
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3 peptide

<400> 43
Ala Arg Glu Ser Trp Pro Met Asp Val
1 5

<210> 44
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3 peptide

<400> 44
Ala Arg Gly Arg Gly Tyr Ala Thr Ser Leu Ala Phe Asp Ile
1 5 10

<210> 45
<211> 12
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3 peptide

<400> 45
Ala Arg Gly Ser Gln Glu His Leu Ile Phe Asp Tyr
1 5 10

<210> 46
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3 peptide

<400> 46
Ala Arg Thr Asp Phe Trp Ser Gly Ser Pro Pro Gly Leu Asp Tyr
1 5 10 15

<210> 47
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3 peptide

<400> 47
Ala Arg Thr Pro Glu Tyr Ser Ser Ser Ile Trp His Tyr Tyr Tyr Gly
1 5 10 15

Met Asp Val

<210> 48
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3 peptide

<400> 48
Val Lys Gly Pro Leu Gln Glu Pro Pro Tyr Asp Tyr Gly Met Asp Val
1 5 10 15

<210> 49
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR4 peptide

<400> 49
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
1 5 10

<210> 50
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR4 peptide

<400> 50
Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 51
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR4 peptide

<400> 51
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
1 5 10

<210> 52
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR4 peptide

<400> 52
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
1 5 10

<210> 53
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR4 peptide

<400> 53

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 54
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR4 peptide

<400> 54
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 55
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR4 peptide

<400> 55
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
1 5 10

<210> 56
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR4 peptide

<400> 56
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
1 5 10

<210> 57
<211> 354
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
VH polynucleotide

<400> 57
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggcggtgt actactgcgc aagagccgag 300

atgggagccg tattcgacat atggggtcag ggtacaatgg tcaccgtctc ctca 354

<210> 58
<211> 366
<212> DNA
<213> Artificial Sequence

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

<400> 58
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

ctgcaaatga acagcctgag agccgaggac acggcggtgt actactgcgc cagagacggt 300

acttatctag gtggtctctg gtacttcgac ttatggggga gaggtacctt ggtcaccgtc 360

tcctca 366

<210> 59
<211> 348
<212> DNA
<213> Artificial Sequence

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

<400> 59

caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 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 ccagggaaca actgtcaccg tctcctca 348

<210> 60
<211> 366
<212> DNA
<213> Artificial Sequence

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

<400> 60
cagctgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60

acctgcactg tctctggtgg ctccatcagc agtagtagtt actactgggg ctggatccgc 120

cagcccccag ggaaggggct ggagtggatt gggagtatct cctatagtgg gagcacctac 180

tacaacccgt ccctcaagag tcgagtcacc atatccgtag acacgtccaa gaaccagttc 240

tccctgaagc tgagttctgt gaccgccgca gacacggcgg tgtactactg cgccagaggc 300

aggggatatg caaccagctt agccttcgat atctggggtc agggtacaat ggtcaccgtc 360

tcctca 366

<210> 61
<211> 357
<212> DNA
<213> Artificial Sequence

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

<400> 61
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 ctcactgtat 240

ctgcaaatga acagcctgag agctgaggac acggcggtgt actactgcgc cagaggttct 300

caggagcacc tgattttcga ttattgggga cagggtacat tggtcaccgt ctcctca 357

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

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

<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

ctgcaaatga acagcctgag agccgaggac acggcggtgt actactgcgc cagaactgac 300

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tcctca 366

<210> 63
<211> 378
<212> DNA
<213> Artificial Sequence

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

<400> 63
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 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> 64
<211> 369
<212> DNA
<213> Artificial Sequence

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

<400> 64
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

ctgcaaatga acagcctgag agccgaggac acggcggtgt actactgcgt caaggggccg 300

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gtctcctca 369

<210> 65
<211> 118
<212> PRT
<213> Artificial Sequence

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

<400> 65
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> 66
<211> 122
<212> PRT
<213> Artificial Sequence

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

<400> 66
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> 67
<211> 116
<212> PRT
<213> Artificial Sequence

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

<400> 67
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> 68
<211> 122
<212> PRT
<213> Artificial Sequence

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

<400> 68
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> 69
<211> 119
<212> PRT
<213> Artificial Sequence

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

<400> 69
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> 70
<211> 122
<212> PRT
<213> Artificial Sequence

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

<400> 70
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> 71
<211> 126
<212> PRT
<213> Artificial Sequence

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

<400> 71
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> 72
<211> 123
<212> PRT
<213> Artificial Sequence

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

<400> 72
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> 73
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR1 peptide

<400> 73
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
20

<210> 74
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR1 peptide

<400> 74
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
20

<210> 75
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR1 peptide

<400> 75
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
20

<210> 76
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR1 peptide

<400> 76
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
20

<210> 77
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR1 peptide

<400> 77
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
20

<210> 78
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR1 peptide

<400> 78

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
20

<210> 79
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR1 peptide

<400> 79
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
20

<210> 80
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR1 peptide

<400> 80
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
20

<210> 81
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR1 peptide

<400> 81
Arg Ala Ser Gln Ser Val Ser Arg Tyr Leu Ala
1 5 10

<210> 82
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR1 peptide

<400> 82
Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp
1 5 10 15

<210> 83
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR1 peptide

<400> 83
Arg Ala Ser Gln Ser Val Ser Ser Asn Leu Ala
1 5 10

<210> 84
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR1 peptide

<400> 84
Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
1 5 10

<210> 85
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR1 peptide

<400> 85
Arg Ala Ser Gln Ser Val Ser Arg Tyr Leu Ala
1 5 10

<210> 86
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR1peptide

<400> 86
Arg Ala Ser Gln Gly Ile Ser Ser Trp Leu Ala
1 5 10

<210> 87
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR1 peptide

<400> 87
Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 88
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR1 peptide

<400> 88

Arg Ala Ser Gln Ser Val Ser Ser Asn Leu Ala
1 5 10

<210> 89
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR2 peptide

<400> 89
Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
1 5 10 15

<210> 90
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR2 peptide

<400> 90
Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr
1 5 10 15

<210> 91
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR2 peptide

<400> 91
Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
1 5 10 15

<210> 92
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
VL FR2 peptide

<400> 92
Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
1 5 10 15

<210> 93
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR2 peptide

<400> 93
Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
1 5 10 15

<210> 94
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR2 peptide

<400> 94
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
1 5 10 15

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

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR2 peptide

<400> 95
Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
1 5 10 15

<210> 96
<211> 15

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR2 peptide

<400> 96
Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
1 5 10 15

<210> 97
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR2 peptide

<400> 97
Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 98
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR2 peptide

<400> 98
Leu Gly Ser Asn Arg Ala Ser
1 5

<210> 99
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR2 peptide

<400> 99
Gly Ala Ser Thr Arg Ala Thr
1 5

<210> 100
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR2 peptide

<400> 100
Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 101
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR2 peptide

<400> 101
Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 102
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR2 peptide

<400> 102
Gly Ala Ser Ser Leu Gln Ser
1 5

<210> 103
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR2 peptide

<400> 103
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 104
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR2 peptide

<400> 104
Ser Ala Ser Thr Arg Ala Thr
1 5

<210> 105
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR3 polypeptide

<400> 105
Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
20 25 30

<210> 106
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR3 polypeptide

<400> 106
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys
20 25 30

<210> 107
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR3 polypeptide

<400> 107
Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys
20 25 30

<210> 108
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR3 polypeptide

<400> 108
Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
20 25 30

<210> 109
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR3 polypeptide

<400> 109
Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
20 25 30

<210> 110
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR3 polypeptide

<400> 110
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
20 25 30

<210> 111
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR3 polypeptide

<400> 111
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

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

<210> 112
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR3 polypeptide

<400> 112

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys
20 25 30

<210> 113
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR3 peptide

<400> 113
Gln Gln Arg Ile Ser Trp Pro Phe Thr
1 5

<210> 114
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR3 peptide

<400> 114
Met Gln Gly Leu Gly Leu Pro Leu Thr
1 5

<210> 115
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR3 peptide

<400> 115
Gln Gln Tyr Ala Ala Tyr Pro Thr
1 5

<210> 116
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR3 peptide

<400> 116
Gln Gln Arg His Val Trp Pro Pro Thr
1 5

<210> 117
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR3 peptide

<400> 117
Gln Gln Arg Phe Tyr Tyr Pro Trp Thr
1 5

<210> 118
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR3 peptide

<400> 118
Gln Gln Ile Tyr Thr Phe Pro Phe Thr
1 5

<210> 119
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR3 peptide

<400> 119
Gln Gln Phe Ala His Thr Pro Phe Thr
1 5

<210> 120
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR3 peptide

<400> 120
Gln Gln His His Val Trp Pro Leu Thr
1 5

<210> 121
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR4 peptide

<400> 121
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 122
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR4 peptide

<400> 122
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 123
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR4 peptide

<400> 123
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 124
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR4 peptide

<400> 124
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 125
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR4 peptide

<400> 125
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 126
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR4 peptide

<400> 126
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 127
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR4 peptide

<400> 127
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 128
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL FR4 peptide

<400> 128
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 129
<211> 321
<212> DNA
<213> Artificial Sequence

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

<400> 129
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 agaatctcct ggcctttcac ttttggcgga 300

gggaccaagg ttgagatcaa a 321

<210> 130
<211> 336
<212> DNA
<213> Artificial Sequence

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

<400> 130
gatattgtga tgactcagtc tccactctcc ctgcccgtca cccctggaga gccggcctcc 60

atctcctgca ggtctagtca gagcctcctg catagtaatg gatacaacta tttggattgg 120

tacctgcaga agccagggca gtctccacag ctcctgatct atttgggttc taatcgggcc 180

tccggggtcc ctgacaggtt cagtggcagt ggatcaggca cagattttac actgaaaatc 240

agcagagtgg aggctgagga tgttggggtt tattactgca tgcagggact cggcctccct 300

ctcacttttg gcggagggac caaggttgag atcaaa 336

<210> 131
<211> 318
<212> DNA
<213> Artificial Sequence

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

<400> 131
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> 132
<211> 321
<212> DNA
<213> Artificial Sequence

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

<400> 132
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 ggcctcctac ttttggcgga 300

gggaccaagg ttgagatcaa a 321

<210> 133
<211> 321
<212> DNA
<213> Artificial Sequence

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

<400> 133
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> 134
<211> 321
<212> DNA
<213> Artificial Sequence

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

<400> 134
gacatccagt tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60

atcacttgtc gggcgagtca gggtattagc agctggttag cctggtatca 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> 135
<211> 339
<212> DNA
<213> Artificial Sequence

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

<400> 135
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtgtttta tacagctcca acaataagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcagtt cgcccacact 300

cctttcactt ttggcggagg gaccaaggtt gagatcaaa 339

<210> 136
<211> 321
<212> DNA
<213> Artificial Sequence

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

<400> 136
gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc 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> 137
<211> 107
<212> PRT
<213> Artificial Sequence

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

<400> 137
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> 138
<211> 112
<212> PRT
<213> Artificial Sequence

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

<400> 138
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> 139
<211> 106
<212> PRT
<213> Artificial Sequence

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

<400> 139
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
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> 140
<211> 107
<212> PRT
<213> Artificial Sequence

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

<400> 140
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

<210> 141
<211> 107
<212> PRT
<213> Artificial Sequence

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

<400> 141
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> 142
<211> 107
<212> PRT
<213> Artificial Sequence

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

<400> 142
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> 143
<211> 113
<212> PRT
<213> Artificial Sequence

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

<400> 143
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> 144
<211> 107
<212> PRT
<213> Artificial Sequence

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

<400> 144
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

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

<210> 145
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR1 peptide

<220>
<221> MISC_FEATURE
<222> (2)..(3)
<223> May or may not be present

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Phe, Gly, Ile or Tyr

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Ser or Thr

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Phe or Ser

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Ser or Thr

<400> 145
Gly Gly Ser Xaa Xaa Xaa Xaa Ser Tyr
1 5

<210> 146
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR2 peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Ala, Gly, Ile, Ser, Thr or Val

<220>

<221> MOD_RES
<222> (3)..(3)
<223> Ile, Asn or Ser

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Gly, Pro, Ser or Tyr

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Asp, Gly, Ile or Ser

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Phe, Gly or Ser

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Gly, Ser or absent

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Asn, Ser or Thr

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Ala, Ile, Lys or Thr

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Asn, Ser or Tyr

<220>
<221> MOD_RES
<222> (12)..(12)
<223> Ala or Asn

<220>
<221> MOD_RES
<222> (13)..(13)
<223> Asp, Pro or Gln

<220>
<221> MOD_RES
<222> (14)..(14)

<223> Lys or Ser

<220>
<221> MOD_RES
<222> (15)..(15)
<223> Phe, Leu or Val

<220>
<221> MOD_RES
<222> (16)..(16)
<223> Lys or Gln

<220>
<221> MOD_RES
<222> (17)..(17)
<223> Gln or Ser

<400> 146
Xaa Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa

<210> 147
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3 peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Ala or Val

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Lys or Arg

<220>
<221> MOD_RES
<222> (3)..(3)
<223> Asp, Gly, Thr or absent

<220>

<221> MOD_RES
<222> (4)..(4)
<223> Ala, Asp, Gly, Pro, Arg, Ser or absent

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Glu, Phe, Gly, Leu, Gln, Thr or absent

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Glu, Met, Gln, Trp, Tyr or absent

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Ala, Glu, Leu, Ser or absent

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Gly, Pro, Ser, Thr or absent

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Gly, Pro, Ser or absent

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Ile, Leu, Pro, Tyr or absent

<220>
<221> MISC_FEATURE
<222> (11)..(12)
<223> May or may not be present

<220>
<221> MOD_RES
<222> (13)..(13)
<223> Glu, Tyr or absent

<220>
<221> MOD_RES
<222> (14)..(14)
<223> Asp, Gly, His, Pro, Ser, Trp, Tyr or absent

<220>
<221> MOD_RES
<222> (15)..(15)

<223> Ala, Gly, Leu, Trp or Tyr

<220>
<221> MOD_RES
<222> (16)..(16)
<223> Ala, Gly, Ile, Pro, Val or absent

<220>
<221> MOD_RES
<222> (17)..(17)
<223> Phe, Leu or Met

<220>
<221> MOD_RES
<222> (19)..(19)
<223> Ile, Leu, Val or Tyr

<400> 147
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp His Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Asp Xaa

<210> 148
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR1 peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Lys or Arg

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Ala or Ser

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Gly or Ser

<220>

<221> MOD_RES
<222> (6)..(6)
<223> Ile, Leu or Val

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Leu or Ser

<220>
<221> MOD_RES
<222> (8)..(8)
<223> His, Tyr or absent

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> May or may not be present

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Asn, Ser or absent

<220>
<221> MOD_RES
<222> (11)..(11)
<223> Gly, Asn or absent

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> May or may not be present

<220>
<221> MOD_RES
<222> (13)..(13)
<223> Lys, Tyr or absent

<220>
<221> MOD_RES
<222> (14)..(14)
<223> Asn, Arg or Ser

<220>
<221> MOD_RES
<222> (15)..(15)
<223> Asn, Trp or Tyr

<220>
<221> MOD_RES
<222> (17)..(17)

<223> Ala or Asp

<400> 148
Xaa Xaa Ser Gln Xaa Xaa Xaa Xaa Ser Xaa Xaa Asn Xaa Xaa Xaa Leu
1 5 10 15

Xaa

<210> 149
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR2 peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Asp, Gly, Leu, Ser or Trp

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Ala or Gly

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Asn, Ser or Thr

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Leu or Arg

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Ala, Glu or Gln

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Ser or Thr

<400> 149

Xaa Xaa Ser Xaa Xaa Xaa Xaa
1 5

<210> 150
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR3 peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Met or Gln

<220>
<221> MOD_RES
<222> (3)..(3)
<223> Phe, Gly, His, Ile, Arg or Tyr

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Ala, Phe, His, Ile, Leu or Tyr
<220>
<221> MOD_RES
<222> (5)..(5)
<223> Ala, Gly, His, Ser, Thr, Val or Tyr

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Phe, Leu, Thr, Trp or Tyr

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Phe, Leu, Pro or Trp

<400> 150
Xaa Gln Xaa Xaa Xaa Xaa Pro Xaa Thr
1 5

<210> 151
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR1 peptide

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Phe or Gly

<400> 151
Gly Xaa Thr Phe Ser Ser Tyr
1 5

<210> 152
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR1 peptide

<220>
<221> MISC_FEATURE
<222> (2)..(3)
<223> May or may not be present

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Phe, Gly or Ile

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Ser or Thr

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Phe or Ser

<400> 152
Gly Gly Ser Xaa Xaa Xaa Ser Ser Tyr
1 5

<210> 153

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

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR2 peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Ala, Gly, Ile, Thr or Val

<220>
<221> MOD_RES
<222> (3)..(3)
<223> Ile, Asn or Ser

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Gly, Pro, Ser or Tyr

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Asp, Gly, Ile or Ser

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Phe, Gly or Ser

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Gly or Ser

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Asn, Ser or Thr

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Ala, Ile, Lys or Thr

<220>
<221> MOD_RES
<222> (10)..(10)

<223> Asn, Ser or Tyr

<220>
<221> MOD_RES
<222> (13)..(13)
<223> Asp or Gln

<220>
<221> MOD_RES
<222> (14)..(14)
<223> Lys or Ser

<220>
<221> MOD_RES
<222> (15)..(15)
<223> Phe or Val

<220>
<221> MOD_RES
<222> (16)..(16)
<223> Lys or Gln

<400> 153
Xaa Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Ala Xaa Xaa Xaa Xaa
1 5 10 15

Gly

<210> 154
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR2 peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Ala, Thr or Val

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Gly, Ser or Tyr

<220>

<221> MOD_RES
<222> (5)..(5)
<223> Asp or Ser

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Gly or Ser

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Gly or Ser

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Asn, Ser or Thr

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Ile, Lys or Thr

<400> 154
Xaa Ile Ser Xaa Xaa Xaa Xaa Xaa Xaa Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 155
<211> 17
<212> PRT
<213> Artificial Sequence

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

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Gly or Ile

<220>
<221> MOD_RES
<222> (3)..(3)
<223> Ile or Asn

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Gly or Ile

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Phe or Gly

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Ser or Thr

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Ala or Thr

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Asn or Ser

<400> 155
Xaa Ile Xaa Pro Xaa Xaa Gly Xaa Xaa Xaa Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 156
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3 peptide

<220>
<221> MOD_RES
<222> (3)..(3)
<223> Asp, Gly, Thr or absent

<220>
<221> MOD_RES

<222> (4)..(4)
<223> Ala, Asp, Gly, Pro, Arg, Ser or absent

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Glu, Phe, Gly, Gln, Thr or absent

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Glu, Met, Trp, Tyr or absent

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Ala, Leu, Ser or absent

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Gly, Ser, Thr or absent

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Gly, Ser or absent

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Ile, Leu, Phe or absent

<220>
<221> MISC_FEATURE
<222> (11)..(12)
<223> May or may not be present

<220>
<221> MOD_RES
<222> (13)..(13)
<223> Glu, Tyr or absent

<220>
<221> MOD_RES
<222> (14)..(14)
<223> Gly, His, Pro, Ser, Trp, Tyr or absent

<220>
<221> MOD_RES
<222> (15)..(15)
<223> Ala, Gly, Leu, Trp or Tyr

<220>
<221> MOD_RES
<222> (16)..(16)
<223> Ala, Gly, Ile, Pro, Val or absent

<220>
<221> MOD_RES
<222> (17)..(17)
<223> Phe, Leu or Met

<220>
<221> MOD_RES
<222> (19)..(19)
<223> Ile, Leu, Val or Tyr

<400> 156
Ala Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp His Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Asp Xaa

<210> 157
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR1 peptide

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Gly or Ser

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Ile or Val

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Arg or Ser

<220>
<221> MOD_RES

<222> (9)..(9)
<223> Asn, Trp or Tyr

<400> 157
Arg Ala Ser Gln Xaa Xaa Ser Xaa Xaa Leu Ala
1 5 10

<210> 158
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR1 peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Lys or Arg

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Leu or Val

<220>
<221> MOD_RES
<222> (8)..(8)
<223> His or Tyr

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Asn or Ser

<220>
<221> MOD_RES
<222> (11)..(11)
<223> Gln or Asn

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> May or may not be present

<220>
<221> MOD_RES
<222> (13)..(13)
<223> Lys or Tyr

<220>
<221> MOD_RES
<222> (17)..(17)
<223> Ala or Asp

<400> 158
Xaa Ser Ser Gln Ser Xaa Leu Xaa Ser Xaa Xaa Asn Xaa Asn Tyr Leu
1 5 10 15

Xaa

<210> 159
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR2 peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Asp, Gly or Ser

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Asn or Thr

<400> 159
Xaa Ala Ser Xaa Arg Ala Thr
1 5

<210> 160
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR2 peptide

<220>
<221> MOD_RES

<222> (1)..(1)
<223> Asp, Gly or Ser

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Asn, Ser or Thr

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Leu or Arg

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Ala or Gln

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Ser or Thr

<400> 160
Xaa Ala Ser Xaa Xaa Xaa Xaa
1 5

<210> 161
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR2 peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Leu or Trp

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Ala or Gly

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Asn or Thr

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Ala or Glu

<400> 161
Xaa Xaa Ser Xaa Arg Xaa Ser
1 5

<210> 162
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VL CDR3 peptide

<220>
<221> MOD_RES
<222> (3)..(3)
<223> His, Ile, Arg or Tyr

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Ala, Phe, His, Ile or Tyr

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Ala, Ser, Thr, Val or Tyr

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Phe, Trp or Tyr

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Phe, Leu, Pro, Trp or absent

<400> 162
Gln Gln Xaa Xaa Xaa Xaa Pro Xaa Thr
1 5

<210> 163

<211> 184
<212> PRT
<213> Homo sapiens

<400> 163

```
Met Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser
1               5                  10                  15

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

Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser
        35                  40                  45

Val Lys Gly Thr Asn Ala Ile Leu Trp Thr Cys Leu Gly Leu Ser Leu
    50                  55                  60

Ile Ile Ser Leu Ala Val Phe Val Leu Met Phe Leu Leu Arg Lys Ile
65                  70                  75                  80

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

Leu Gly Met Ala Asn Ile Asp Leu Glu Lys Ser Arg Thr Gly Asp Glu
            100                 105                 110

Ile Ile Leu Pro Arg Gly Leu Glu Tyr Thr Val Glu Glu Cys Thr Cys
        115                 120                 125

Glu Asp Cys Ile Lys Ser Lys Pro Lys Val Asp Ser Asp His Cys Phe
    130                 135                 140

Pro Leu Pro Ala Met Glu Glu Gly Ala Thr Ile Leu Val Thr Thr Lys
145                 150                 155                 160

Thr Asn Asp Tyr Cys Lys Ser Leu Pro Ala Ala Leu Ser Ala Thr Glu
                165                 170                 175

Ile Glu Lys Ser Ile Ser Ala Arg
            180
```

<210> 164
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Signal Peptide

<400> 164
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccg 63

<210> 165
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Signal Peptide

<400> 165
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
20

<210> 166
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
CD28 Hinge Domain

<400> 166
cttgataatg aaaagtcaaa cggaacaatc attcacgtga agggcaagca cctctgtccg 60

tcacccttgt tccctggtcc atccaagcca 90

<210> 167
<211> 30
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
CD28 Hinge Domain

<400> 167
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
20 25 30

<210> 168
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
CD28 TM Domain

<400> 168
ttctgggtgt tggtcgtagt gggtggagtc ctcgcttgtt actctctgct cgtcaccgtg 60

gcttttataa tcttctgggt t 81

<210> 169
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
CD28 TM Domain

<400> 169
Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
1 5 10 15

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

<210> 170
<211> 123
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
CD28 Signaling Domain

<400> 170
agatccaaaa gaagccgcct gctccatagc gattacatga atatgactcc acgccgccct 60

ggccccacaa ggaaacacta ccagccttac gcaccaccta gagatttcgc tgcctatcgg 120

agc 123

<210> 171
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
CD28 Signaling Domain

<400> 171
Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
1 5 10 15

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

Pro Arg Asp Phe Ala Ala Tyr Arg Ser
35 40

<210> 172
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
CD3z Activation Domain

<400> 172
agggtgaagt tttccagatc tgcagatgca ccagcgtatc agcagggcca gaaccaactg 60

tataacgagc tcaacctggg acgcagggaa gagtatgacg ttttggacaa gcgcagagga 120

cgggaccctg agatgggtgg caaaccaaga cgaaaaaacc cccaggaggg tctctataat 180

gagctgcaga aggataagat ggctgaagcc tattctgaaa taggcatgaa aggagagcgg 240

agaaggggaa aagggcacga cggtttgtac cagggactca gcactgctac gaaggatact 300

tatgacgctc tccacatgca agccctgcca cctagg 336

<210> 173
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
CD3z Activation Domain

<400> 173
Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
1 5 10 15

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

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

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

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

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

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

<210> 174
<211> 18
<212> PRT
<213> Artificial Sequence

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

<400> 174
Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
1 5 10 15

Lys Gly

<210> 175
<211> 1437
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
FS-21495CARDNAHxL polynucleotide

<400> 175
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccggaggtgc agctgttgga gtctgggggga ggcttggtac agcctggggg gtccctgaga 120

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 catatggggt cagggtacaa tggtcaccgt ctcctcaggg 420

tctacatccg gctccgggaa gcccggaagt ggcgaaggta gtacaaaggg ggaaattgtg 480

ttgacacagt ctccagccac cctgtctttg tctccagggg aaagagccac cctctcctgc 540

agggccagtc agagtgttag caggtactta gcctggtacc aacagaaacc tggccaggct 600

cccaggctcc tcatctatga tgcatccaac agggccactg gcatcccagc caggttcagt 660

ggcagtgggt ctgggacaga cttcactctc accatcagca gcctagagcc tgaagatttt 720

gcagtttatt actgtcagca gagaatctcc tggcctttca cttttggcgg agggaccaag 780

gttgagatca aacgggccgc tgcccttgat aatgaaaagt caaacggaac aatcattcac 840

gtgaagggca agcacctctg tccgtcaccc ttgttccctg gtccatccaa gccattctgg 900

gtgttggtcg tagtgggtgg agtcctcgct tgttactctc tgctcgtcac cgtggctttt 960

ataatcttct gggttagatc 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

<210> 176
<211> 478
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
FS-21495CARHxL polypeptide

<400> 176
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
385 390 395 400

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
405 410 415

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
420 425 430

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
435 440 445

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
450 455 460

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
465 470 475

<210> 177
<211> 1437
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
FS-21495CARDNALxH polynucleotide

<400> 177
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccggaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg ggaaagagcc 120

accctctcct gcagggccag tcagagtgtt agcaggtact tagcctggta ccaacagaaa 180

cctggccagg ctcccaggct cctcatctat gatgcatcca acagggccac tggcatccca 240

gccaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagcctagag 300

cctgaagatt ttgcagttta ttactgtcag cagagaatct cctggccttt cacttttggc 360

ggagggacca aggttgagat caaacggggg tctacatccg gctccgggaa gcccggaagt 420

ggcgaaggta gtacaaaggg ggaggtgcag ctgttggagt ctgggggagg cttggtacag 480

cctgggggggt ccctgagact ctcctgtgca gcctctggat tcacctttag cagctatgcc 540

atgagctggg tccgccaggc tccagggaag gggctggagt gggtctcagc tattagtggt 600

agtggtggta gcacatacta cgcagactcc gtgaagggcc ggttcaccat ctccagagac 660

aattccaaga acacgctgta tctgcaaatg aacagcctga gagccgagga cacggcggtg 720

tactactgcg caagagccga gatgggagcc gtattcgaca tatggggtca gggtacaatg 780

gtcaccgtct cctcagccgc tgcccttgat aatgaaaagt caaacggaac aatcattcac 840

gtgaagggca agcacctctg tccgtcaccc ttgttccctg gtccatccaa gccattctgg 900

gtgttggtcg tagtgggtgg agtcctcgct tgttactctc tgctcgtcac cgtggctttt 960

ataatcttct gggttagatc 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

<210> 178
<211> 478

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
FS-21495CARLxH polypeptide

<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 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 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
225                 230                 235                 240

Tyr Tyr Cys Ala Arg Ala Glu Met Gly Ala Val Phe Asp Ile Trp Gly
                245                 250                 255

Gln Gly Thr Met Val Thr Val Ser Ser 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
```

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Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
385 390 395 400

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
405 410 415

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
420 425 430

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
435 440 445

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
450 455 460

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
465 470 475

<210> 179
<211> 1464
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
PC-21497CARDNAHxL polynucleotide

<400> 179
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtgc agctggtgga gtctgggggga 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 cgccagagac 360

ggtacttatc taggtggtct ctggtacttc gacttatggg ggagaggtac cttggtcacc 420

gtctcctcag ggtctacatc cggctccggg aagcccggaa gtggcgaagg tagtacaaag 480

ggggatattg tgatgactca gtctccactc tccctgcccg tcacccctgg agagccggcc 540

tccatctcct gcaggtctag tcagagcctc ctgcatagta atggatacaa ctatttggat 600

tggtacctgc agaagccagg gcagtctcca cagctcctga tctatttggg ttctaatcgg 660

gcctccgggg tccctgacag gttcagtggc agtggatcag gcacagattt tacactgaaa 720

atcagcagag tggaggctga ggatgttggg gtttattact gcatgcaggg actcggcctc 780

cctctcactt ttggcggagg gaccaaggtt gagatcaaac gggccgctgc ccttgataat 840

gaaaagtcaa acggaacaat cattcacgtg aagggcaagc acctctgtcc gtcacccttg 900

ttccctggtc catccaagcc attctgggtg ttggtcgtag 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 gagggtctct ataatgagct gcagaaggat 1320

aagatggctg aagcctattc tgaaataggc atgaaaggag agcggagaag gggaaaaggg 1380

cacgacggtt tgtaccaggg actcagcact gctacgaagg atacttatga cgctctccac 1440

atgcaagccc tgccacctag gtaa 1464

<210> 180
<211> 487
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
PC-21497CARHxL polypeptide

<400> 180
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 Asp Gly Thr Tyr Leu Gly Gly Leu Trp
        115                 120                 125

Tyr Phe Asp Leu Trp Gly Arg 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 Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro
                165                 170                 175

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

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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> 181
<211> 1464
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
PC-21497CARDNALxH polynucleotide

<400> 181
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccggatattg tgatgactca gtctccactc tccctgcccg tcacccctgg agagccggcc 120

tccatctcct gcaggtctag tcagagcctc ctgcatagta atggatacaa ctatttggat 180

tggtacctgc agaagccagg gcagtctcca cagctcctga tctatttggg ttctaatcgg 240

gcctccgggg tccctgacag gttcagtggc agtggatcag gcacagattt tacactgaaa 300

atcagcagag tggaggctga ggatgttggg gtttattact gcatgcaggg actcggcctc 360

cctctcactt ttggcggagg gaccaaggtt gagatcaaac gggggtctac atccggctcc 420

gggaagcccg gaagtggcga aggtagtaca aaggggcagg tgcagctggt 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 cggtgtacta ctgcgccaga gacggtactt atctaggtgg tctctggtac 780

ttcgacttat gggggagagg taccttggtc accgtctcct cagccgctgc ccttgataat 840

gaaaagtcaa acggaacaat cattcacgtg aagggcaagc acctctgtcc gtcacccttg 900

ttccctggtc catccaagcc attctgggtg ttggtcgtag 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 gagggtctct ataatgagct gcagaaggat 1320

aagatggctg aagcctattc tgaaataggc atgaaaggag agcggagaag gggaaaaggg 1380

cacgacggtt tgtaccaggg actcagcact gctacgaagg atacttatga cgctctccac 1440

atgcaagccc tgccacctag gtaa 1464

<210> 182
<211> 487
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
PC-21497CARHxL polypeptide

<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 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> 183
<211> 1428

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
AJ-21508CARDNAHxL polynucleotide

<400> 183
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtgc agctggtgca gtctggggct gaggtgaaga agcctggggc ctcagtgaag 120

gtttcctgca aggcatctgg atacaccttc accagctact atatgcactg ggtgcgacag 180

gcccctggac aagggcttga gtggatggga ataatcaacc ctggtggtgg tagcacaagc 240

tacgcacaga agttccaggg cagagtcacc atgaccaggg acacgtccac gagcacagtc 300

tacatggagc tgagcagcct gagatctgag gacacggcgg tgtactactg cgccagagag 360

agttggccaa tggacgtatg gggccaggga acaactgtca ccgtctcctc agggtctaca 420

tccggctccg ggaagcccgg aagtggcgaa ggtagtacaa agggggaaat agtgatgacg 480

cagtctccag ccaccctgtc tgtgtctcca ggggaaagag ccaccctctc ctgcagggcc 540

agtcagagtg ttagcagcaa cttagcctgg taccagcaga aacctggcca ggctcccagg 600

ctcctcatct atggtgcatc caccagggcc actggtatcc cagccaggtt cagtggcagt 660

gggtctggga cagagttcac tctcaccatc agcagcctgc agtctgaaga ttttgcagtt 720

tattactgtc agcagtacgc cgcctaccct acttttggcg gagggaccaa ggttgagatc 780

aaacgggccg ctgcccttga taatgaaaag tcaaacggaa caatcattca cgtgaagggc 840

aagcacctct gtccgtcacc cttgttccct ggtccatcca agccattctg ggtgttggtc 900

gtagtgggtg gagtcctcgc ttgttactct ctgctcgtca ccgtggcttt tataatcttc 960

tgggttagat ccaaaagaag ccgcctgctc catagcgatt acatgaatat gactccacgc 1020

cgccctggcc ccacaaggaa acactaccag ccttacgcac cacctagaga tttcgctgcc 1080

tatcggagca gggtgaagtt 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

<210> 184
<211> 475
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
AJ-21508CARHxL polypeptide

<400> 184

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
210 215 220

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val
225 230 235 240

Tyr Tyr Cys Gln Gln Tyr Ala Ala Tyr Pro Thr Phe Gly Gly Gly Thr
245 250 255

Lys Val Glu Ile Lys Arg 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

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> 185
<211> 1428
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
AJ-21508CARDNALxH polynucleotide

<400> 185
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccggaaatag tgatgacgca gtctccagcc accctgtctg tgtctccagg ggaaagagcc 120

accctctcct gcagggccag tcagagtgtt agcagcaact tagcctggta ccagcagaaa 180

cctggccagg ctcccaggct cctcatctat ggtgcatcca ccagggccac tggtatccca 240

gccaggttca 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 cagggacacg 660

tccacgagca cagtctacat ggagctgagc agcctgagat ctgaggacac ggcggtgtac 720

tactgcgcca gagagagttg gccaatggac gtatggggcc agggaacaac tgtcaccgtc 780

tcctcagccg ctgcccttga taatgaaaag tcaaacggaa caatcattca cgtgaagggc 840

aagcacctct gtccgtcacc cttgttccct ggtccatcca agccattctg ggtgttggtc 900

gtagtgggtg gagtcctcgc ttgttactct ctgctcgtca ccgtggcttt tataatcttc 960

tgggttagat ccaaaagaag ccgcctgctc catagcgatt acatgaatat gactccacgc 1020

cgccctggcc ccacaaggaa acactaccag ccttacgcac cacctagaga tttcgctgcc 1080

tatcggagca gggtgaagtt 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

<210> 186
<211> 475
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
AJ-21508CARLxH polypeptide

<400> 186
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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```
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
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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

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
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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> 187
<211> 1449
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
NM-21517CARDNAHxL polynucleotide

<400> 187
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcagctgc agctgcagga gtcgggccca ggactggtga 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 cggtgtacta ctgcgccaga 360

ggcaggggat atgcaaccag cttagccttc gatatctggg gtcagggtac aatggtcacc 420

gtctcctcag ggtctacatc cggctccggg aagcccggaa gtggcgaagg tagtacaaag 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 aggttgagat caaacgggcc gctgcccttg ataatgaaaa gtcaaacgga 840

acaatcattc acgtgaaggg caagcacctc tgtccgtcac ccttgttccc tggtccatcc 900

aagccattct gggtgttggt cgtagtgggt ggagtcctcg cttgttactc tctgctcgtc 960

accgtggctt ttataatctt ctgggttaga tccaaaagaa gccgcctgct ccatagcgat 1020

tacatgaata tgactccacg ccgccctggc cccacaagga aacactacca gccttacgca 1080

ccacctagag atttcgctgc ctatcggagc agggtgaagt 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

<210> 188
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
NM-21517CARHxL polypeptide

<400> 188
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
225 230 235 240

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
305 310 315 320

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> 189

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<211> 1449
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
NM-21517CARDNALxH polynucleotide

<400> 189
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

cctgaagatt ttgcagttta ttactgtcag cagagacacg tctggcctcc tacttttggc 360

ggagggacca aggttgagat caaacggggg tctacatccg gctccgggaa gcccggaagt 420

ggcgaaggta gtacaaaggg gcagctgcag ctgcaggagt cgggcccagg actggtgaag 480

ccttcggaga ccctgtccct cacctgcact gtctctggtg gctccatcag cagtagtagt 540

tactactggg gctggatccg ccagccccca gggaaggggc tggagtggat tgggagtatc 600

tcctatagtg ggagcaccta ctacaacccg tccctcaaga gtcgagtcac catatccgta 660

gacacgtcca agaaccagtt ctccctgaag ctgagttctg tgaccgccgc agacacggcg 720

gtgtactact gcgccagagg caggggatat gcaaccagct tagccttcga tatctggggt 780

cagggtacaa tggtcaccgt ctcctcagcc gctgcccttg ataatgaaaa gtcaaacgga 840

acaatcattc acgtgaaggg caagcacctc tgtccgtcac ccttgttccc tggtccatcc 900

aagccattct gggtgttggt cgtagtgggt ggagtcctcg cttgttactc tctgctcgtc 960

accgtggctt ttataatctt ctgggttaga tccaaaagaa gccgcctgct ccatagcgat 1020

tacatgaata tgactccacg ccgccctggc cccacaagga aacactacca gccttacgca 1080

ccacctagag atttcgctgc ctatcggagc agggtgaagt 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

<210> 190
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
NM-21517CARLxH polypeptide

<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 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

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> 191
<211> 1440
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
TS-21522CARDNAHxL polynucleotide

<400> 191
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccggaggtgc agctggtgga gtctgggggа ggcttggtac agcctggggg gtccctgaga 120

ctctcctgtg cagcctctgg attcaccttc agtagctata gcatgaactg ggtccgccag 180

gctccaggga aggggctgga gtgggtttca accattagta gtagtagtag taccatatac 240

tacgcagact ctgtgaaggg ccgattcacc atctccagag acaatgccaa gaactcactg 300

tatctgcaaa tgaacagcct gagagctgag gacacggcgg tgtactactg cgccagaggt 360

tctcaggagc acctgatttt cgattattgg ggacagggta cattggtcac cgtctcctca 420

gggtctacat ccggctccgg gaagcccgga agtggcgaag gtagtacaaa gggggaaatt 480

gtgttgacac agtctccagc caccctgtct ttgtctccag gggaaagagc caccctctcc 540

tgcagggcca gtcagagtgt tagcaggtac ttagcctggt accaacagaa acctggccag 600

gctcccaggc tcctcatcta tgatgcatcc aacagggcca ctggcatccc agccaggttc 660

agtggcagtg ggtctgggac agacttcact ctcaccatca gcagcctaga gcctgaagat 720

tttgcagttt attactgtca gcagagattc tactaccctt ggacttttgg cggagggacc 780

aaggttgaga tcaaacgggc 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 ccccacaagg 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> 192
<211> 479
<212> PRT
<213> Artificial Sequence

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

K-1030_02_SL_OAP1064

TS-21522CARHxL polypeptide

<400> 192

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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

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> 193
<211> 1440
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
TS-21522CARDNALxH polynucleotide

<400> 193
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccggaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg ggaaagagcc 120

accctctcct gcagggccag tcagagtgtt agcaggtact 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 aggttgagat caaacggggg tctacatccg gctccgggaa gcccggaagt 420

ggcgaaggta gtacaaaggg ggaggtgcag ctggtggagt ctgggggagg cttggtacag 480

cctgggggt ccctgagact ctcctgtgca 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 acagggtaca 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 ccccacaagg 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> 194
<211> 479
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
TS-21522CARLxH polypeptide

<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 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

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 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
```

K-1030_02_SL_OAP1064

<210> 195
<211> 1449
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
RY-21527CARDNAHxL polynucleotide

<400> 195
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtgc agctggtgga gtctgggggа 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

gtctcctcag ggtctacatc cggctccggg aagcccggaa gtggcgaagg tagtacaaag 480

ggggacatcc agttgaccca gtctccatct tccgtgtctg catctgtagg agacagagtc 540

accatcactt gtcgggcgag tcagggtatt agcagctggt tagcctggta tcagcagaaa 600

ccagggaaag cccctaagct cctgatctat ggtgcatcca gtttgcaaag tggggtccca 660

tcaaggttca gcggcagtgg atctgggaca gatttcactc tcaccatcag cagcctgcag 720

cctgaagatt ttgcaactta ttactgtcag cagatataca ccttcccttt cacttttggc 780

ggagggacca aggttgagat caaacgggcc gctgcccttg ataatgaaaa gtcaaacgga 840

acaatcattc acgtgaaggg caagcacctc tgtccgtcac ccttgttccc tggtccatcc 900

aagccattct gggtgttggt cgtagtgggt ggagtcctcg cttgttactc tctgctcgtc 960

accgtggctt ttataatctt ctgggttaga tccaaaagaa gccgcctgct ccatagcgat 1020

tacatgaata tgactccacg ccgccctggc cccacaagga aacactacca gccttacgca 1080

ccacctagag atttcgctgc ctatcggagc agggtgaagt 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

<210> 196
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
RY-21527CARHxL polypeptide

<400> 196

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> 197
<211> 1449
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
RY-21527CARDNALxH polynucleotide

<400> 197
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccggacatcc agttgaccca gtctccatct tccgtgtctg catctgtagg agacagagtc 120

accatcactt gtcgggcgag tcagggtatt agcagctggt tagcctggta tcagcagaaa 180

ccagggaaag cccctaagct cctgatctat ggtgcatcca gtttgcaaag tggggtccca 240

tcaaggttca gcggcagtgg atctgggaca gatttcactc tcaccatcag cagcctgcag 300

cctgaagatt ttgcaactta ttactgtcag cagatataca ccttcccttt cacttttggc 360

ggagggacca aggttgagat caaacggggg tctacatccg gctccgggaa gcccggaagt 420

ggcgaaggta gtacaaaggg gcaggtgcag ctggtggagt ctgggggagg cgtggtccag 480

cctgggaggt ccctgagact ctcctgtgca gcgtctggat tcaccttcag tagctatggc 540

atgcactggg tccgccaggc tccaggcaag gggctggagt gggtggcagt tatatcgtat 600

gatggaagta ataaatacta tgcagactcc gtgaagggcc gattcaccat ctccagagac 660

aattccaaga acacgctgta tctgcaaatg aacagcctga gagccgagga cacggcggtg 720

tactactgcg ccagaactga cttctggagc ggatcccctc caggcttaga ttactgggga 780

cagggtacat tggtcaccgt ctcctcagcc gctgcccttg ataatgaaaa gtcaaacgga 840

acaatcattc acgtgaaggg caagcacctc tgtccgtcac ccttgttccc tggtccatcc 900

aagccattct gggtgttggt cgtagtgggt ggagtcctcg cttgttactc tctgctcgtc 960

accgtggctt ttataatctt ctgggttaga tccaaaagaa gccgcctgct ccatagcgat 1020

tacatgaata tgactccacg ccgccctggc cccacaagga aacactacca gccttacgca 1080

ccacctagag atttcgctgc ctatcggagc agggtgaagt 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

<210> 198
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
RY-21527CARLxH polypeptide

<400> 198

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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

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                 160

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                 240

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> 199
<211> 1479
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
PP-21528CARDNAHxL polynucleotide

<400> 199
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtgc agctggtgca gtctggggct gaggtgaaga agcctgggtc ctcggtgaag 120

gtctcctgca aggcttctgg aggcaccttc agcagctatg ctatcagctg ggtgcgacag 180

gcccctggac aagggcttga 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 agggtctaca tccggctccg ggaagcccgg aagtggcgaa 480

ggtagtacaa agggggacat cgtgatgacc cagtctccag actccctggc tgtgtctctg 540

ggcgagaggg ccaccatcaa ctgcaagtcc agccagagtg ttttatacag ctccaacaat 600

aagaactact tagcttggta ccagcagaaa ccaggacagc ctcctaagct gctcatttac 660

tgggcatcta cccgggaatc cggggtccct gaccgattca gtggcagcgg gtctgggaca 720

gatttcactc tcaccatcag cagcctgcag gctgaagatg tggcagttta ttactgtcag 780

cagttcgccc acactccttt cacttttggc ggagggacca aggttgagat caaacgggcc 840

gctgcccttg ataatgaaaa gtcaaacgga acaatcattc acgtgaaggg caagcacctc 900

tgtccgtcac ccttgttccc tggtccatcc aagccattct gggtgttggt 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 agcagggcca gaaccaactg 1200

tataacgagc tcaacctggg acgcagggaa 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 agccctgcca cctaggtaa 1479

<210> 200
<211> 492
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
PP-21528CARHxL polypeptide

<400> 200
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 Ser Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu
145                 150                 155                 160

Gly Ser Thr Lys Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu
                165                 170                 175

Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln
            180                 185                 190

Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln
        195                 200                 205

Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr
    210                 215                 220

Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
225                 230                 235                 240
```

```
Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val
                245                 250                 255

Tyr Tyr Cys Gln Gln Phe Ala His Thr Pro Phe Thr Phe Gly Gly Gly
            260                 265                 270

Thr Lys Val Glu Ile Lys Arg 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                 320

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                 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
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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> 201
<211> 1479
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
PP-21528CARDNALxH polynucleotide

<400> 201
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccggacatcg tgatgaccca gtctccagac tccctggctg tgtctctggg cgagagggcc 120

accatcaact gcaagtccag ccagagtgtt ttatacagct ccaacaataa gaactactta 180

gcttggtacc agcagaaacc aggacagcct cctaagctgc tcatttactg ggcatctacc 240

cgggaatccg gggtccctga ccgattcagt ggcagcgggt ctgggacaga tttcactctc 300

accatcagca gcctgcaggc tgaagatgtg gcagtttatt 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 ctttggtaca gcaaactacg cacagaagtt ccagggcaga 660

gtcacgatta ccgcggacga atccacgagc acagcctaca tggagctgag cagcctgaga 720

tctgaggaca cggcggtgta ctactgcgcc agaactcctg aatactcctc cagcatatgg 780

cactattact acggcatgga cgtatggggc cagggaacaa ctgtcaccgt ctcctcagcc 840

gctgcccttg ataatgaaaa gtcaaacgga acaatcattc acgtgaaggg caagcacctc 900

tgtccgtcac ccttgttccc tggtccatcc aagccattct gggtgttggt 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 agcagggcca gaaccaactg 1200

tataacgagc tcaacctggg acgcagggaa 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 agccctgcca cctaggtaa 1479

<210> 202
<211> 492
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
PP-21528CARLxH polypeptide

<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 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                 240

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                 320

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                 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> 203
<211> 1452
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
RD-21530CARDNAHxL polynucleotide

<400> 203
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtgc agctggtgga gtctgggggа 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

aaggggggaaa tagtgatgac gcagtctcca gccaccctgt ctgtgtctcc aggggaaaga 540

gccaccctct cctgcagggc cagtcagagt gttagcagca acttagcctg gtaccagcag 600

aaacctggcc aggctcccag gctcctcatc tatagcgcat 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 cacccttgtt ccctggtcca 900

tccaagccat tctgggtgtt ggtcgtagtg ggtggagtcc tcgcttgtta ctctctgctc 960

gtcaccgtgg cttttataat 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 acgttttgga caagcgcaga ggacgggacc ctgagatggg tggcaaacca 1260

agacgaaaaa acccccagga gggtctctat aatgagctgc agaaggataa gatggctgaa 1320

gcctattctg aaataggcat gaaaggagag cggagaaggg gaaaagggca cgacggtttg 1380

taccagggac tcagcactgc tacgaaggat acttatgacg ctctccacat gcaagccctg 1440

ccacctaggt aa 1452

<210> 204
<211> 483
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
RD-21530CARHxL polypeptide

<400> 204
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> 205
<211> 1452
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
RD-21530CARDNALxH polynucleotide

<400> 205
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccggaaatag tgatgacgca gtctccagcc accctgtctg tgtctccagg ggaaagagcc 120

accctctcct gcagggccag tcagagtgtt agcagcaact tagcctggta ccagcagaaa 180

cctggccagg ctcccaggct cctcatctat agcgcatcca 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 ctggtggagt ctgggggagg cgtggtccag 480

cctgggaggt ccctgagact ctcctgtgca gcgtctggat tcaccttcag tagctatggc 540

atgcactggg tccgccaggc tccaggcaag gggctggagt gggtggcagt tatatcgtat 600

gatggaagta ataaatacta tgcagactcc gtgaagggcc gattcaccat ctccagagac 660

aattccaaga acacgctgta tctgcaaatg aacagcctga gagccgagga cacggcggtg 720

tactactgcg tcaaggggcc gttgcaggag ccgccatacg attatggaat ggacgtatgg 780

ggccagggaa caactgtcac cgtctcctca gccgctgccc ttgataatga aaagtcaaac 840

ggaacaatca ttcacgtgaa gggcaagcac ctctgtccgt caccttgtt ccctggtcca 900

tccaagccat tctgggtgtt ggtcgtagtg ggtggagtcc tcgcttgtta ctctctgctc 960

gtcaccgtgg cttttataat 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 acgttttgga caagcgcaga ggacgggacc ctgagatggg tggcaaacca 1260

agacgaaaaa acccccagga gggtctctat aatgagctgc agaaggataa gatggctgaa 1320

gcctattctg aaataggcat gaaaggagag cggagaaggg gaaaagggca cgacggtttg 1380

taccagggac tcagcactgc tacgaaggat acttatgacg ctctccacat gcaagccctg 1440

ccacctaggt aa 1452

<210> 206
<211> 483
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
RD-21530CARLxH polypeptide

<400> 206

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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                 160

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                 240

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

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> 207
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR1 peptide

<400> 207
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
20 25

<210> 208
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR1 peptide

<400> 208
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
20 25

<210> 209
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR1 peptide

<400> 209
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
20 25

<210> 210
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR1 peptide

<400> 210
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
20 25

<210> 211
<211> 26
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
VH FR1 peptide

<400> 211
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
20 25

<210> 212
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR1 peptide

<400> 212
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
20 25

<210> 213
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR1 peptide

<400> 213
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
20 25

<210> 214
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR1 peptide

<400> 214
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
20 25

<210> 215
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR1 peptide

<400> 215
Phe Thr Phe Ser Ser Tyr Ala Met Ser
1 5

<210> 216
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR1 peptide

<400> 216
Phe Thr Phe Ser Ser Tyr Gly Met His
1 5

<210> 217
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR1 peptide

<400> 217

Tyr Thr Phe Thr Ser Tyr Tyr Met His
1 5

<210> 218
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR1 peptide

<400> 218
Gly Ser Ile Ser Ser Ser Ser Tyr Tyr Trp Gly
1 5 10

<210> 219
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR1 peptide

<400> 219
Phe Thr Phe Ser Ser Tyr Ser Met Asn
1 5

<210> 220
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR1 peptide

<400> 220
Phe Thr Phe Ser Ser Tyr Gly Met His
1 5

<210> 221
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
VH CDR1 peptide

<400> 221
Gly Thr Phe Ser Ser Tyr Ala Ile Ser
1 5

<210> 222
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR1 peptide

<400> 222
Phe Thr Phe Ser Ser Tyr Gly Met His
1 5

<210> 223
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 223
Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
1 5 10

<210> 224
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 224
Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
1 5 10

<210> 225
<211> 14

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 225
Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
1 5 10

<210> 226
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 226
Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly
1 5 10

<210> 227
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 227
Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
1 5 10

<210> 228
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 228
Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
1 5 10

<210> 229
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 229
Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
1 5 10

<210> 230
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 230
Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
1 5 10

<210> 231
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 231
Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 232
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 232
Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 233
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 233
Ile Ile Asn Pro Gly Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 234
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 234
Ser Ile Ser Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 235
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 235
Thr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 236
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 236
Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 237
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 237
Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 238
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR2 peptide

<400> 238
Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 239
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR3 polypeptide

<400> 239
Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
20 25 30

<210> 240
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR3 polypeptide

<400> 240
Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
20 25 30

<210> 241
<211> 30

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR3 polypeptide

<400> 241
Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu
1 5 10 15

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

<210> 242
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR3 polypeptide

<400> 242
Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys
1 5 10 15

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
20 25 30

<210> 243
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR3 polypeptide

<400> 243
Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
20 25 30

<210> 244
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR3 polypeptide

<400> 244
Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
20 25 30

<210> 245
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR3 polypeptide

<400> 245
Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

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

<210> 246
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR3 polypeptide

<400> 246
Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
20 25 30

<210> 247
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3 peptide

<400> 247
Ala Arg Ala Glu Met Gly Ala Val Phe Asp Ile
1 5 10

<210> 248
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3 peptide

<400> 248
Ala Arg Asp Gly Thr Tyr Leu Gly Gly Leu Trp Tyr Phe Asp Leu
1 5 10 15

<210> 249
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3 peptide

<400> 249
Ala Arg Glu Ser Trp Pro Met Asp Val
1 5

<210> 250
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3 peptide

<400> 250
Ala Arg Gly Arg Gly Tyr Ala Thr Ser Leu Ala Phe Asp Ile
1 5 10

<210> 251
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3 peptide

<400> 251
Ala Arg Gly Ser Gln Glu His Leu Ile Phe Asp Tyr
1 5 10

<210> 252
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3 peptide

<400> 252
Ala Arg Thr Asp Phe Trp Ser Gly Ser Pro Pro Gly Leu Asp Tyr
1 5 10 15

<210> 253
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3 peptide

<400> 253
Ala Arg Thr Pro Glu Tyr Ser Ser Ser Ile Trp His Tyr Tyr Tyr Gly
1 5 10 15

Met Asp Val

<210> 254
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3 peptide

<400> 254
Val Lys Gly Pro Leu Gln Glu Pro Pro Tyr Asp Tyr Gly Met Asp Val
1 5 10 15

<210> 255
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR4 peptide

<400> 255
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
1 5 10

<210> 256
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR4 peptide

<400> 256
Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 257
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR4 peptide

<400> 257

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
1 5 10

<210> 258
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic VH FR4 peptide

<400> 258
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
1 5 10

<210> 259
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic VH FR4 peptide

<400> 259
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 260
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic VH FR4 peptide

<400> 260
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 261
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
VH FR4 peptide

<400> 261
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
1 5 10

<210> 262
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH FR4 peptide

<400> 262
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
1 5 10

<210> 263
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR1 peptide

<220>
<221> MISC_FEATURE
<222> (1)..(2)
<223> May or may not be present

<220>
<221> MOD_RES
<222> (3)..(3)
<223> Phe, Gly, Ile or Tyr

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Ser or Thr

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Phe or Ser

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Ser or Thr

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Ala, Gly, Ser or Tyr

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Ile, Met or Trp

<220>
<221> MOD_RES
<222> (11)..(11)
<223> Gly, His, Asn or Ser

<400> 263
Gly Ser Xaa Xaa Xaa Xaa Ser Tyr Xaa Xaa Xaa
1 5 10

<210> 264
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3 peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Ala or Val

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Lys or Arg

<220>
<221> MOD_RES
<222> (3)..(3)
<223> Asp, Gly or Thr

<220>
<221> MOD_RES

<222> (4)..(4)
<223> Asp, Gly, Pro or absent

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Phe, Leu, Thr or absent

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Pro, Gln, Arg, Trp, Tyr or absent

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Glu, Gly, Leu, Ser or absent

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Ala, Gly, Pro, Ser, Tyr or absent

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Ala, Glu, Gly, Pro, Gln, Ser or absent

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Glu, Leu, Met, Pro, Ser, Thr, Tyr or absent

<220>
<221> MOD_RES
<222> (11)..(11)
<223> Asp, Gly, His, Pro, Ser, Trp or absent

<220>
<221> MOD_RES
<222> (12)..(12)
<223> Ala, Gly, Ile, Leu, Tyr or absent

<220>
<221> MOD_RES
<222> (13)..(13)
<223> Ala, Gly, Ile, Val, Trp or absent

<220>
<221> MISC_FEATURE
<222> (14)..(16)
<223> May or may not be present

<220>
<221> MOD_RES
<222> (17)..(17)
<223> Trp, Tyr or absent

<220>
<221> MOD_RES
<222> (18)..(18)
<223> Pro, Gly or absent

<220>
<221> MOD_RES
<222> (19)..(19)
<223> Phe, Leu or Met

<220>
<221> MOD_RES
<222> (21)..(21)
<223> Ile, Leu, Val or Tyr

<400> 264
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa His Tyr Tyr
1 5 10 15

Xaa Xaa Xaa Asp Xaa
20

<210> 265
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR1 peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Phe, Gly or Tyr

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Ser or Thr

<220>
<221> MOD_RES

<222> (7)..(7)
<223> Ala, Gly, Ser or Tyr

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Ile or Met

<220>
<221> MOD_RES
<222> (9)..(9)
<223> His, Asn or Ser

<400> 265
Xaa Thr Phe Xaa Ser Tyr Xaa Xaa Xaa
1 5

<210> 266
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR1 peptide

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Ala, Gly or Ser

<220>
<221> MOD_RES
<222> (9)..(9)
<223> His, Asn or Ser

<400> 266
Phe Thr Phe Ser Ser Tyr Xaa Met Xaa
1 5

<210> 267
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
VH CDR3 peptide

<220>
<221> MOD_RES
<222> (3)..(3)
<223> Asp, Thr or absent

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Asp, Gly or absent

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Phe, Thr or absent

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Pro, Arg, Trp, Tyr or absent

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Glu, Gly, Leu, Ser or absent

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Ala, Gly, Ser, Tyr or absent

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Ala, Glu, Gly, Gln or Ser

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Glu, Leu, Met, Pro, Ser or Thr

<220>
<221> MOD_RES
<222> (11)..(11)
<223> Gly, His, Pro, Ser, Trp or absent

<220>
<221> MOD_RES
<222> (12)..(12)
<223> Ala, Gly, Ile, Leu, Tyr or absent

<220>

<221> MOD_RES
<222> (13)..(13)
<223> Ala, Ile, Val, Trp or absent

<220>
<221> MISC_FEATURE
<222> (14)..(16)
<223> May or may not be present

<220>
<221> MOD_RES
<222> (17)..(17)
<223> Trp, Tyr or absent

<220>
<221> MOD_RES
<222> (18)..(18)
<223> Pro, Gly or absent

<220>
<221> MOD_RES
<222> (19)..(19)
<223> Phe, Leu or Met

<220>
<221> MOD_RES
<222> (21)..(21)
<223> Ile, Leu, Val or Tyr

<400> 267
Ala Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa His Tyr Tyr
1 5 10 15

Xaa Xaa Xaa Asp Xaa
20

<210> 268
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
scFv G4s linker

<400> 268
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 269
<211> 288
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
CD8 DNA extracellular & transmembrane domain
polynucleotide

<400> 269
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> 270
<211> 97
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
CD8 AA extracellular & transmembrane domain
polypeptide

<400> 270
Ala Ala Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val Pro
1 5 10 15

Arg Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro
20 25 30

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
35 40 45

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
50 55 60

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
65 70 75 80

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg
85 90 95

Asn

<210> 271
<211> 354
<212> DNA
<213> Artificial Sequence

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

<400> 271
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac gactatgcca tggcatgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtgatg caggtgacag aacatactac 180

gcagactccg tgaggggccg gttcaccatc tccagagaca attccaagaa cacactgtat 240

ctgcaaatga acagcctgag agccgaggac acggcggtgt actactgcgc aagagccgag 300

atgggagccg tattcgacat atggggtcag ggtacaatgg tcaccgtctc ctca 354

<210> 272
<211> 118
<212> PRT
<213> Artificial Sequence

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

<400> 272
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 Asp Asp Tyr
20 25 30

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

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

Arg 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> 273
<211> 15
<212> PRT
<213> Artificial Sequence

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

<400> 273
Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met Ala
1 5 10 15

<210> 274
<211> 17
<212> PRT
<213> Artificial Sequence

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

<400> 274
Ala Ile Ser Asp Ala Gly Asp Arg Thr Tyr Tyr Ala Asp Ser Val Arg
1 5 10 15

Gly

<210> 275
<211> 11
<212> PRT
<213> Artificial Sequence

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

<400> 275
Ala Arg Ala Glu Met Gly Ala Val Phe Asp Ile
1 5 10

<210> 276
<211> 324
<212> DNA
<213> Artificial Sequence

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

<400> 276
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 agaatctcct ggcctttcac ttttggcgga 300

gggaccaagg ttgagatcaa acgg 324

<210> 277
<211> 108
<212> PRT
<213> Artificial Sequence

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

<400> 277
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 Arg
100 105

<210> 278
<211> 11
<212> PRT
<213> Artificial Sequence

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

<400> 278
Arg Ala Ser Gln Ser Val Ser Arg Tyr Leu Ala
1 5 10

<210> 279
<211> 7
<212> PRT
<213> Artificial Sequence

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

<400> 279
Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 280
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 280
Gln Gln Arg Ile Ser Trp Pro Phe Thr
1 5

<210> 281
<211> 1434
<212> DNA
<213> Artificial Sequence

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

<400> 281
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccggaggtgc agctgttgga gtctgggggа ggcttggtac agcctggggg gtccctgaga 120

ctctcctgtg cagcctctgg attcaccttt gacgactatg ccatggcatg ggtccgccag 180

gctccaggga aggggctgga gtgggtctca gctattagtg atgcaggtga cagaacatac 240

tacgcagact ccgtgagggg ccggttcacc atctccagag acaattccaa gaacacactg 300

tatctgcaaa tgaacagcct gagagccgag gacacggcgg tgtactactg cgcaagagcc 360

gagatgggag ccgtattcga catatggggt cagggtacaa tggtcaccgt ctcctcaggg 420

tctacatccg gctccgggaa gcccggaagt ggcgaaggta gtacaaaggg ggaaattgtg 480

ttgacacagt ctccagccac cctgtctttg tctccagggg aaagagccac cctctcctgc 540

agggccagtc agagtgttag caggtactta gcctggtacc aacagaaacc tggccaggct 600

cccaggctcc tcatctatga tgcatccaac agggccactg gcatcccagc caggttcagt 660

ggcagtgggt ctgggacaga cttcactctc accatcagca gcctagagcc tgaagatttt 720

gcagtttatt actgtcagca gagaatctcc tggcctttca cttttggcgg agggaccaag 780

gttgagatca aacgggccgc tgcccttgat aatgaaaagt caaacggaac aatcattcac 840

gtgaagggca agcacctctg tccgtcaccc ttgttccctg gtccatccaa gccattctgg 900

gtgttggtcg tagtgggtgg agtcctcgct tgttactctc tgctcgtcac cgtggctttt 960

ataatcttct gggttagatc 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 tagg 1434

<210> 282
<211> 478
<212> PRT
<213> Artificial Sequence

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

<400> 282

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 Asp Asp Tyr Ala Met Ala Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

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

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Tyr Ala Asp Ser Val Arg 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
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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
385 390 395 400

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
405 410 415

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
420 425 430

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
435 440 445

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
450 455 460

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
465 470 475

<210> 283
<211> 1434
<212> DNA
<213> Artificial Sequence

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

<400> 283
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccggaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg ggaaagagcc 120

accctctcct gcagggccag tcagagtgtt agcaggtact tagcctggta ccaacagaaa 180

cctggccagg ctcccaggct cctcatctat gatgcatcca acagggccac tggcatccca 240

gccaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagcctagag 300

cctgaagatt ttgcagttta ttactgtcag cagagaatct cctggccttt cacttttggc 360

ggagggacca aggttgagat caaacggggg tctacatccg gctccgggaa gcccggaagt 420

ggcgaaggta gtacaaaggg ggaggtgcag ctgttggagt ctgggggagg cttggtacag 480

cctgggggggt ccctgagact ctcctgtgca gcctctggat tcacctttga cgactatgcc 540

atggcatggg tccgccaggc tccagggaag gggctggagt gggtctcagc tattagtgat 600

gcaggtgaca gaacatacta cgcagactcc gtgaggggcc ggttcaccat ctccagagac 660

aattccaaga acacactgta tctgcaaatg aacagcctga gagccgagga cacggcggtg 720

tactactgcg caagagccga gatgggagcc gtattcgaca tatggggtca gggtacaatg 780

gtcaccgtct cctcagccgc tgcccttgat aatgaaaagt caaacggaac aatcattcac 840

gtgaagggca agcacctctg tccgtcaccc ttgttccctg gtccatccaa gccattctgg 900

gtgttggtcg tagtgggtgg agtcctcgct tgttactctc tgctcgtcac cgtggctttt 960

ataatcttct gggttagatc 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 tagg 1434

<210> 284
<211> 478
<212> PRT
<213> Artificial Sequence

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

<400> 284

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

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

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Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
                165                 170                 175

Asp Asp Tyr Ala Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
            180                 185                 190

Glu Trp Val Ser Ala Ile Ser Asp Ala Gly Asp Arg Thr Tyr Tyr Ala
        195                 200                 205

Asp Ser Val Arg 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                 240

Tyr Tyr Cys Ala Arg Ala Glu Met Gly Ala Val Phe Asp Ile Trp Gly
                245                 250                 255

Gln Gly Thr Met Val Thr Val Ser Ser 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
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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
385 390 395 400

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
405 410 415

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
420 425 430

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
435 440 445

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
450 455 460

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
465 470 475

<210> 285
<211> 366
<212> DNA
<213> Artificial Sequence

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

<400> 285
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctggatt caccttcagt gagcatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagct atatcttatg atggaaggaa taaacactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggcggtgt actactgcgc cagagacggt 300

acttatctag gtggtctctg gtacttcgac ttatggggga gaggtacctt ggtcaccgtc 360

tcctca 366

<210> 286
<211> 122
<212> PRT
<213> Artificial Sequence

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

<400> 286
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 Glu His
20 25 30

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

Ala Ala Ile Ser Tyr Asp Gly Arg Asn Lys His 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> 287
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 287
Phe Thr Phe Ser Glu His Gly Met His
1 5

<210> 288
<211> 17
<212> PRT
<213> Artificial Sequence

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

<400> 288
Ala Ile Ser Tyr Asp Gly Arg Asn Lys His Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 289
<211> 15
<212> PRT
<213> Artificial Sequence

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

<400> 289
Ala Arg Asp Gly Thr Tyr Leu Gly Gly Leu Trp Tyr Phe Asp Leu
1 5 10 15

<210> 290
<211> 339
<212> DNA
<213> Artificial Sequence

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

<400> 290
gatattgtga tgactcagtc tccactctcc ctgcccgtca cccctggaga gccggcctcc 60

atctcctgca ggtctagtca gagcctcctg catagtaatg gatacaacta tttggattgg 120

tacctgcaga agccagggca gtctccacag ctcctgatct atttgggttc taatcgggcc 180

tccggggtcc ctgacaggtt cagtggcagt ggatcaggca cagattttac actgaaaatc 240

agcagagtgg aggctgagga tgttggggtt tattactgca tgcagggact cggcctccct 300

ctcacttttg gcggagggac caaggttgag atcaaacgg 339

<210> 291
<211> 113
<212> PRT
<213> Artificial Sequence

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

<400> 291
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

Arg

<210> 292

<211> 16
<212> PRT
<213> Artificial Sequence

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

<400> 292
Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp
1 5 10 15

<210> 293
<211> 7
<212> PRT
<213> Artificial Sequence

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

<400> 293
Leu Gly Ser Asn Arg Ala Ser
1 5

<210> 294
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 294
Met Gln Gly Leu Gly Leu Pro Leu Thr
1 5

<210> 295
<211> 1461
<212> DNA
<213> Artificial Sequence

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

<400> 295
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtgc agctggtgga gtctggggga ggcgtggtcc agcctgggag gtccctgaga 120

ctctcctgtg cagcgtctgg attcaccttc agtgagcatg gcatgcactg ggtccgccag 180

gctccaggca aggggctgga gtgggtggca gctatatctt atgatggaag gaataaacac 240

tatgcagact ccgtgaaggg ccgattcacc atctccagag acaattccaa gaacacgctg 300

tatctgcaaa tgaacagcct gagagccgag gacacggcgg tgtactactg cgccagagac 360

ggtacttatc taggtggtct ctggtacttc gacttatggg ggagaggtac cttggtcacc 420

gtctcctcag ggtctacatc cggctccggg aagcccggaa gtggcgaagg tagtacaaag 480

ggggatattg tgatgactca gtctccactc tccctgcccg tcacccctgg agagccggcc 540

tccatctcct gcaggtctag tcagagcctc ctgcatagta atggatacaa ctatttggat 600

tggtacctgc agaagccagg gcagtctcca cagctcctga tctatttggg ttctaatcgg 660

gcctccgggg tccctgacag gttcagtggc agtggatcag gcacagattt tacactgaaa 720

atcagcagag tggaggctga ggatgttggg gtttattact gcatgcaggg actcggcctc 780

cctctcactt ttggcggagg gaccaaggtt gagatcaaac gggccgctgc ccttgataat 840

gaaaagtcaa acggaacaat cattcacgtg aagggcaagc acctctgtcc gtcacccttg 900

ttccctggtc catccaagcc attctgggtg ttggtcgtag 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 gagggtctct ataatgagct gcagaaggat 1320

aagatggctg aagcctattc tgaaataggc atgaaaggag agcggagaag gggaaaaggg 1380

cacgacggtt tgtaccaggg actcagcact gctacgaagg atacttatga cgctctccac 1440

atgcaagccc tgccacctag g 1461

<210> 296
<211> 487

<212> PRT
<213> Artificial Sequence

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

<400> 296

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 Glu His Gly Met His Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ala Ala Ile Ser Tyr Asp Gly Arg Asn Lys His
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 Asp Gly Thr Tyr Leu Gly Gly Leu Trp
115 120 125

Tyr Phe Asp Leu Trp Gly Arg 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 Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro
165 170 175

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> 297
<211> 1461
<212> DNA
<213> Artificial Sequence

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

<400> 297
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccggatattg tgatgactca gtctccactc tccctgcccg tcacccctgg agagccggcc 120

tccatctcct gcaggtctag tcagagcctc ctgcatagta atggatacaa ctatttggat 180

tggtacctgc agaagccagg gcagtctcca cagctcctga tctatttggg ttctaatcgg 240

gcctccgggg tccctgacag gttcagtggc agtggatcag gcacagattt tacactgaaa 300

atcagcagag tggaggctga ggatgttggg gtttattact gcatgcaggg actcggcctc 360

cctctcactt ttggcggagg gaccaaggtt gagatcaaac gggggtctac atccggctcc 420

gggaagcccg gaagtggcga aggtagtaca aaggggcagg tgcagctggt ggagtctggg 480

ggaggcgtgg tccagcctgg gaggtccctg agactctcct gtgcagcgtc tggattcacc 540

ttcagtgagc atggcatgca ctgggtccgc caggctccag gcaaggggct ggagtgggtg 600

gcagctatat cttatgatgg aaggaataaa cactatgcag actccgtgaa gggccgattc 660

accatctcca gagacaattc caagaacacg ctgtatctgc aaatgaacag cctgagagcc 720

gaggacacgg cggtgtacta ctgcgccaga gacggtactt atctaggtgg tctctggtac 780

ttcgacttat gggggagagg taccttggtc accgtctcct cagccgctgc ccttgataat 840

gaaaagtcaa acggaacaat cattcacgtg aagggcaagc acctctgtcc gtcacccttg 900

ttccctggtc catccaagcc attctgggtg ttggtcgtag 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 gagggtctct ataatgagct gcagaaggat 1320

aagatggctg aagcctattc tgaaataggc atgaaaggag agcggagaag gggaaaaggg 1380

cacgacggtt tgtaccaggg actcagcact gctacgaagg atacttatga cgctctccac 1440

atgcaagccc tgccacctag g 1461

<210> 298
<211> 487
<212> PRT
<213> Artificial Sequence

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

<400> 298
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 Glu His Gly Met His Trp Val Arg Gln Ala
180 185 190

Pro Gly Lys Gly Leu Glu Trp Val Ala Ala Ile Ser Tyr Asp Gly Arg
195 200 205

Asn Lys His 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> 299
<211> 348
<212> DNA
<213> Artificial Sequence

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

<400> 299
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaggg catctggata caccttcatg gagcactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggagta atcgggccta gtggtggtaa gacaagctac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc cagagagaat 300

tggccaatgg acgtatgggg ccagggaaca actgtcaccg tctcctca 348

<210> 300
<211> 116
<212> PRT
<213> Artificial Sequence

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

<400> 300
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 Arg Ala Ser Gly Tyr Thr Phe Met Glu His
20 25 30

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

Gly Val Ile Gly Pro Ser Gly Gly Lys 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> 301
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 301
Tyr Thr Phe Met Glu His Tyr Met His
1 5

<210> 302
<211> 17
<212> PRT
<213> Artificial Sequence

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

<400> 302

Val Ile Gly Pro Ser Gly Gly Lys Thr Ser Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 303
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 303
Ala Arg Glu Ser Trp Pro Met Asp Val
1 5

<210> 304
<211> 321
<212> DNA
<213> Artificial Sequence

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

<400> 304
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 agatcaaacg g 321

<210> 305
<211> 107
<212> PRT
<213> Artificial Sequence

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

polypeptide

<400> 305
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
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 Arg
100 105

<210> 306
<211> 11
<212> PRT
<213> Artificial Sequence

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

<400> 306
Arg Ala Ser Gln Ser Val Ser Ser Asn Leu Ala
1 5 10

<210> 307
<211> 7
<212> PRT
<213> Artificial Sequence

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

peptide

<400> 307
Gly Ala Ser Thr Arg Ala Thr
1 5

<210> 308
<211> 8
<212> PRT
<213> Artificial Sequence

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

<400> 308
Gln Gln Tyr Ala Ala Tyr Pro Thr
1 5

<210> 309
<211> 1425
<212> DNA
<213> Artificial Sequence

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

<400> 309
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtgc agctggtgca gtctggggct gaggtgaaga agcctggggc ctcagtgaag 120

gtttcctgca gggcatctgg atacaccttc atggagcact atatgcactg ggtgcgacag 180

gcccctggac aagggcttga gtggatggga gtaatcgggc ctagtggtgg taagacaagc 240

tacgcacaga agttccaggg cagagtcacc atgaccaggg acacgtccac gagcacagtc 300

tacatggagc tgagcagcct gagatctgag gacacggcgg tgtactactg cgccagagag 360

aattggccaa tggacgtatg gggccaggga acaactgtca ccgtctcctc agggtctaca 420

tccggctccg ggaagcccgg aagtggcgaa ggtagtacaa agggggaaat agtgatgacg 480

cagtctccag ccaccctgtc tgtgtctcca ggggaaagag ccaccctctc ctgcagggcc 540

agtcagagtg ttagcagcaa cttagcctgg taccagcaga aacctggcca ggctcccagg 600

ctcctcatct atggtgcatc caccagggcc actggtatcc cagccaggtt cagtggcagt 660

gggtctggga cagagttcac tctcaccatc agcagcctgc agtctgaaga ttttgcagtt 720

tattactgtc agcagtacgc cgcctaccct acttttggcg gagggaccaa ggttgagatc 780

aaacgggccg ctgcccttga taatgaaaag tcaaacggaa caatcattca cgtgaagggc 840

aagcacctct gtccgtcacc cttgttccct ggtccatcca agccattctg ggtgttggtc 900

gtagtgggtg gagtcctcgc ttgttactct ctgctcgtca ccgtggcttt tataatcttc 960

tgggttagat ccaaaagaag ccgcctgctc catagcgatt acatgaatat gactccacgc 1020

cgccctggcc ccacaaggaa acactaccag ccttacgcac cacctagaga tttcgctgcc 1080

tatcggagca gggtgaagtt 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 ctagg 1425

<210> 310
<211> 475
<212> PRT
<213> Artificial Sequence

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

<400> 310
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 Arg Ala Ser Gly Tyr
35 40 45

Thr Phe Met Glu His Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln
50 55 60

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Gly Leu Glu Trp Met Gly Val Ile Gly Pro Ser Gly Gly Lys 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
    210                 215                 220

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val
225                 230                 235                 240

Tyr Tyr Cys Gln Gln Tyr Ala Ala Tyr Pro Thr Phe Gly Gly Gly Thr
                245                 250                 255

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

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> 311
<211> 1425
<212> DNA
<213> Artificial Sequence

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

<400> 311
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccggaaatag tgatgacgca gtctccagcc accctgtctg tgtctccagg ggaaagagcc 120

accctctcct gcagggccag tcagagtgtt agcagcaact tagcctggta ccagcagaaa 180

cctggccagg ctcccaggct cctcatctat ggtgcatcca ccagggccac tggtatccca 240

gccaggttca 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 ctgcagggca tctggataca ccttcatgga gcactatatg 540

cactgggtgc gacaggcccc tggacaaggg cttgagtgga tgggagtaat cgggcctagt 600

ggtggtaaga caagctacgc acagaagttc cagggcagag tcaccatgac cagggacacg 660

tccacgagca cagtctacat ggagctgagc agcctgagat ctgaggacac ggcggtgtac 720

tactgcgcca gagagaattg gccaatggac gtatggggcc agggaacaac tgtcaccgtc 780

tcctcagccg ctgcccttga taatgaaaag tcaaacggaa caatcattca cgtgaagggc 840

aagcacctct gtccgtcacc cttgttccct ggtccatcca agccattctg ggtgttggtc 900

gtagtgggtg gagtcctcgc ttgttactct ctgctcgtca ccgtggcttt tataatcttc 960

tgggttagat ccaaaagaag ccgcctgctc catagcgatt acatgaatat gactccacgc 1020

cgccctggcc ccacaaggaa acactaccag ccttacgcac cacctagaga tttcgctgcc 1080

tatcggagca gggtgaagtt 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 ctagg 1425

<210> 312
<211> 475
<212> PRT
<213> Artificial Sequence

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

<400> 312

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 Arg Ala Ser Gly Tyr Thr Phe Met
165 170 175

Glu His Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
180 185 190

Trp Met Gly Val Ile Gly Pro Ser Gly Gly Lys 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

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> 313
<211> 348
<212> DNA
<213> Artificial Sequence

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

<400> 313
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacg gagcactata tgcactgggt gcgacaggcc 120

cctggacaaa ggcttgagtg gatgggagta atcgggccta gtggtggtaa gacaagctac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc cagagagagt 300

tggccaatgg acgtatgggg ccagggaaca actgtcaccg tctcctca 348

<210> 314
<211> 116
<212> PRT
<213> Artificial Sequence

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

<400> 314
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 Glu His
20 25 30

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

Gly Val Ile Gly Pro Ser Gly Gly Lys 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> 315
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 315
Tyr Thr Phe Thr Glu His Tyr Met His
1 5

<210> 316
<211> 17
<212> PRT
<213> Artificial Sequence

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

<400> 316
Val Ile Gly Pro Ser Gly Gly Lys Thr Ser Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 317
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 317
Ala Arg Glu Ser Trp Pro Met Asp Val
1 5

<210> 318
<211> 321
<212> DNA
<213> Artificial Sequence

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

<400> 318

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 agatcaaacg g 321

<210> 319
<211> 107
<212> PRT
<213> Artificial Sequence

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

<400> 319
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
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 Arg
100 105

<210> 320

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

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

<400> 320
Arg Ala Ser Gln Ser Val Ser Ser Asn Leu Ala
1 5 10

<210> 321
<211> 7
<212> PRT
<213> Artificial Sequence

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

<400> 321
Gly Ala Ser Thr Arg Ala Thr
1 5

<210> 322
<211> 8
<212> PRT
<213> Artificial Sequence

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

<400> 322
Gln Gln Tyr Ala Ala Tyr Pro Thr
1 5

<210> 323
<211> 1425
<212> DNA
<213> Artificial Sequence

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

<400> 323
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtgc agctggtgca gtctggggct gaggtgaaga agcctggggc ctcagtgaag 120

gtttcctgca aggcatctgg atacaccttc acggagcact atatgcactg ggtgcgacag 180

gcccctggac aaaggcttga gtggatggga gtaatcgggc ctagtggtgg taagacaagc 240

tacgcacaga agttccaggg cagagtcacc atgaccaggg acacgtccac gagcacagtc 300

tacatggagc tgagcagcct gagatctgag gacacggcgg tgtactactg cgccagagag 360

agttggccaa tggacgtatg gggccaggga acaactgtca ccgtctcctc agggtctaca 420

tccggctccg ggaagcccgg aagtggcgaa ggtagtacaa agggggaaat agtgatgacg 480

cagtctccag ccaccctgtc tgtgtctcca ggggaaagag ccaccctctc ctgcagggcc 540

agtcagagtg ttagcagcaa cttagcctgg taccagcaga aacctggcca ggctcccagg 600

ctcctcatct atggtgcatc caccagggcc actggtatcc cagccaggtt cagtggcagt 660

gggtctggga cagagttcac tctcaccatc agcagcctgc agtctgaaga ttttgcagtt 720

tattactgtc agcagtacgc cgcctaccct acttttggcg gagggaccaa ggttgagatc 780

aaacgggccg ctgcccttga taatgaaaag tcaaacggaa caatcattca cgtgaagggc 840

aagcacctct gtccgtcacc cttgttccct ggtccatcca agccattctg ggtgttggtc 900

gtagtgggtg gagtcctcgc ttgttactct ctgctcgtca ccgtggcttt tataatcttc 960

tgggttagat ccaaaagaag ccgcctgctc catagcgatt acatgaatat gactccacgc 1020

cgccctggcc ccacaaggaa acactaccag ccttacgcac cacctagaga tttcgctgcc 1080

tatcggagca gggtgaagtt 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 ctagg 1425

<210> 324
<211> 475
<212> PRT
<213> Artificial Sequence

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

<400> 324

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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 Glu His Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln
    50                  55                  60

Arg Leu Glu Trp Met Gly Val Ile Gly Pro Ser Gly Gly Lys 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
    210                 215                 220

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val
225                 230                 235                 240

Tyr Tyr Cys Gln Gln Tyr Ala Ala Tyr Pro Thr Phe Gly Gly Gly Thr
                245                 250                 255

Lys Val Glu Ile Lys Arg 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

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> 325
<211> 1425
<212> DNA
<213> Artificial Sequence

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

<400> 325
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccggaaatag tgatgacgca gtctccagcc accctgtctg tgtctccagg ggaaagagcc 120

accctctcct gcagggccag tcagagtgtt agcagcaact tagcctggta ccagcagaaa 180

cctggccagg ctcccaggct cctcatctat ggtgcatcca ccagggccac tggtatccca 240

gccaggttca 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 ccttcacgga gcactatatg 540

cactgggtgc gacaggcccc tggacaaagg cttgagtgga tgggagtaat cgggcctagt 600

ggtggtaaga caagctacgc acagaagttc cagggcagag tcaccatgac cagggacacg 660

tccacgagca cagtctacat ggagctgagc agcctgagat ctgaggacac ggcggtgtac 720

tactgcgcca gagagagttg gccaatggac gtatggggcc agggaacaac tgtcaccgtc 780

tcctcagccg ctgcccttga taatgaaaag tcaaacggaa caatcattca cgtgaagggc 840

aagcacctct gtccgtcacc cttgttccct ggtccatcca agccattctg ggtgttggtc 900

gtagtgggtg gagtcctcgc ttgttactct ctgctcgtca ccgtggcttt tataatcttc 960

tgggttagat ccaaaagaag ccgcctgctc catagcgatt acatgaatat gactccacgc 1020

cgccctggcc ccacaaggaa acactaccag ccttacgcac cacctagaga tttcgctgcc 1080

tatcggagca gggtgaagtt 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 ctagg 1425

<210> 326
<211> 475
<212> PRT
<213> Artificial Sequence

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

<400> 326
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

Glu His Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu
180 185 190

Trp Met Gly Val Ile Gly Pro Ser Gly Gly Lys 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

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> 327
<211> 366
<212> DNA
<213> Artificial Sequence

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

<400> 327
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60

acctgtactg tctctggtgg ctccatcggg agtggtggta gttactggag ctggatccgc 120

cagcacccag ggaagggcct ggagtggatt gggttgatct attacgatgg gagcacctac 180

tacaacccgt ccctcaagag tcgagttacc atatcagtag acacgtctaa gaaccagttc 240

tccctgaagc tgagttctgt gaccgccgca gacacggcgg tgtactactg cgccagaggc 300

aggggatatg agacttcttt agccttcgat atctggggtc agggtacaat ggtcaccgtc 360

tcctca 366

<210> 328
<211> 122
<212> PRT
<213> Artificial Sequence

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

<400> 328
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 Gly Ser Gly
20 25 30

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

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

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

<210> 329
<211> 11
<212> PRT
<213> Artificial Sequence

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

<400> 329
Gly Ser Ile Gly Ser Gly Gly Ser Tyr Trp Ser
1 5 10

<210> 330
<211> 16
<212> PRT
<213> Artificial Sequence

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

<400> 330
Leu Ile Tyr Tyr Asp Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 331
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 331
Ala Arg Gly Arg Gly Tyr Glu Thr Ser Leu Ala Phe Asp Ile
1 5 10

<210> 332
<211> 324
<212> DNA
<213> Artificial Sequence

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

<400> 332
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 ggcctcctac ttttggcgga 300

gggaccaagg ttgagatcaa acgg 324

<210> 333
<211> 108
<212> PRT
<213> Artificial Sequence

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

<400> 333
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 Arg
100 105

<210> 334
<211> 11
<212> PRT
<213> Artificial Sequence

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

<400> 334
Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
1 5 10

<210> 335
<211> 7
<212> PRT
<213> Artificial Sequence

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

<400> 335
Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 336
<211> 9
<212> PRT
<213> Artificial Sequence

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

peptide

<400> 336
Gln Gln Arg His Val Trp Pro Pro Thr
1 5

<210> 337
<211> 1446
<212> DNA
<213> Artificial Sequence

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

<400> 337
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtgc agctgcagga gtcgggccca ggactggtga agccttcaca gaccctgtcc 120

ctcacctgta ctgtctctgg tggctccatc gggagtggtg gtagttactg gagctggatc 180

cgccagcacc cagggaaggg cctggagtgg attgggttga tctattacga tgggagcacc 240

tactacaacc cgtccctcaa gagtcgagtt accatatcag tagacacgtc taagaaccag 300

ttctccctga agctgagttc tgtgaccgcc gcagacacgg cggtgtacta ctgcgccaga 360

ggcaggggat atgagacttc tttagccttc gatatctggg gtcagggtac aatggtcacc 420

gtctcctcag ggtctacatc cggctccggg aagcccggaa gtggcgaagg tagtacaaag 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 aggttgagat caaacgggcc gctgcccttg ataatgaaaa gtcaaacgga 840

acaatcattc acgtgaaggg caagcacctc tgtccgtcac ccttgttccc tggtccatcc 900

aagccattct gggtgttggt cgtagtgggt ggagtcctcg cttgttactc tctgctcgtc 960

accgtggctt ttataatctt ctgggttaga tccaaaagaa gccgcctgct ccatagcgat 1020

tacatgaata tgactccacg ccgccctggc cccacaagga aacactacca gccttacgca 1080

ccacctagag atttcgctgc ctatcggagc agggtgaagt 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

cctagg 1446

<210> 338
<211> 482
<212> PRT
<213> Artificial Sequence

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

<400> 338

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 Gly Ser Gly Gly Ser Tyr Trp Ser Trp Ile Arg Gln His Pro
50 55 60

Gly Lys Gly Leu Glu Trp Ile Gly Leu Ile Tyr Tyr Asp 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

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Thr Ala Val Tyr Tyr Cys Ala Arg Gly Arg Gly Tyr Glu 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                 240

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                 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> 339
<211> 1446
<212> DNA
<213> Artificial Sequence

<220>

K-1030_02_SL_OAP1064

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 339

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

cctgaagatt ttgcagttta ttactgtcag cagagacacg tctggcctcc tacttttggc 360

ggagggacca aggttgagat caaacggggg tctacatccg gctccgggaa gcccggaagt 420

ggcgaaggta gtacaaaggg gcaggtgcag ctgcaggagt cgggcccagg actggtgaag 480

ccttcacaga ccctgtccct cacctgtact gtctctggtg gctccatcgg gagtggtggt 540

agttactgga gctggatccg ccagcaccca gggaagggcc tggagtggat tgggttgatc 600

tattacgatg ggagcaccta ctacaacccg tccctcaaga gtcgagttac catatcagta 660

gacacgtcta agaaccagtt ctccctgaag ctgagttctg tgaccgccgc agacacggcg 720

gtgtactact gcgccagagg caggggatat gagacttctt tagccttcga tatctggggt 780

cagggtacaa tggtcaccgt ctcctcagcc gctgcccttg ataatgaaaa gtcaaacgga 840

acaatcattc acgtgaaggg caagcacctc tgtccgtcac ccttgttccc tggtccatcc 900

aagccattct gggtgttggt cgtagtgggt ggagtcctcg cttgttactc tctgctcgtc 960

accgtggctt ttataatctt ctgggttaga tccaaaagaa gccgcctgct ccatagcgat 1020

tacatgaata tgactccacg ccgccctggc cccacaagga aacactacca gccttacgca 1080

ccacctagag atttcgctgc ctatcggagc agggtgaagt 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

cctagg 1446

<210> 340
<211> 482
<212> PRT
<213> Artificial Sequence

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

<400> 340

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 Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
145 150 155 160

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Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile
                165                 170                 175

Gly Ser Gly Gly Ser Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys
            180                 185                 190

Gly Leu Glu Trp Ile Gly Leu Ile Tyr Tyr Asp 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

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 Glu 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> 341
<211> 357
<212> DNA
<213> Artificial Sequence

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

<400> 341
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctatagca tgaactgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtttcaacc attagtagta gtagtagtat catatactac 180

gcagactctg tgaagggccg attcaccatc tccagagaca atgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agctgaggac acggcggtgt actactgcgc cagaggttct 300

caggagcacc tgattttcga ttattgggga cagggtacat tggtcaccgt ctcctca 357

<210> 342
<211> 119
<212> PRT
<213> Artificial Sequence

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

<400> 342
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 Ile 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> 343
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 343
Phe Thr Phe Ser Ser Tyr Ser Met Asn
1 5

<210> 344
<211> 17
<212> PRT
<213> Artificial Sequence

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

<400> 344
Thr Ile Ser Ser Ser Ser Ser Ile Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 345
<211> 12
<212> PRT
<213> Artificial Sequence

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

<400> 345
Ala Arg Gly Ser Gln Glu His Leu Ile Phe Asp Tyr
1 5 10

<210> 346
<211> 324
<212> DNA
<213> Artificial Sequence

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

<400> 346
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 acgg 324

<210> 347
<211> 108
<212> PRT
<213> Artificial Sequence

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

<400> 347

| | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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 | Arg | | | | |
| | | | | 100 | | | | | 105 | | | | | | |

<210> 348
<211> 11
<212> PRT

<213> Artificial Sequence

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

<400> 348
Arg Ala Ser Gln Ser Val Ser Arg Tyr Leu Ala
1 5 10

<210> 349
<211> 7
<212> PRT
<213> Artificial Sequence

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

<400> 349
Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 350
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 350
Gln Gln Arg Phe Tyr Tyr Pro Trp Thr
1 5

<210> 351
<211> 1437
<212> DNA
<213> Artificial Sequence

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

<400> 351
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccggaggtgc agctggtgga gtctgggggga ggcttggtac agcctggggg gtccctgaga 120

ctctcctgtg cagcctctgg attcaccttc agtagctata gcatgaactg ggtccgccag 180

gctccaggga aggggctgga gtgggtttca accattagta gtagtagtag tatcatatac 240

tacgcagact ctgtgaaggg ccgattcacc atctccagag acaatgccaa gaactcactg 300

tatctgcaaa tgaacagcct gagagctgag gacacggcgg tgtactactg cgccagaggt 360

tctcaggagc acctgatttt cgattattgg ggacagggta cattggtcac cgtctcctca 420

gggtctacat ccggctccgg gaagcccgga agtggcgaag gtagtacaaa gggggaaatt 480

gtgttgacac agtctccagc caccctgtct ttgtctccag gggaaagagc caccctctcc 540

tgcagggcca gtcagagtgt tagcaggtac ttagcctggt accaacagaa acctggccag 600

gctcccaggc tcctcatcta tgatgcatcc aacagggcca ctggcatccc agccaggttc 660

agtggcagtg ggtctgggac agacttcact ctcaccatca gcagcctaga gcctgaagat 720

tttgcagttt attactgtca gcagagattc tactaccctt ggacttttgg cggagggacc 780

aaggttgaga tcaaacgggc 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 ccccacaagg 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 acctagg 1437

<210> 352
<211> 479
<212> PRT
<213> Artificial Sequence

<220>

K-1030_02_SL_OAP1064

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 352

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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 Ile 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
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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

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
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K-1030_02_SL_OAP1064

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> 353
<211> 1437
<212> DNA
<213> Artificial Sequence

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

<400> 353
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccggaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg ggaaagagcc 120

accctctcct gcagggccag tcagagtgtt agcaggtact 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 aggttgagat caaacggggg tctacatccg gctccgggaa gcccggaagt 420

ggcgaaggta gtacaaaggg ggaggtgcag ctggtggagt ctgggggagg cttggtacag 480

cctgggggggt ccctgagact ctcctgtgca gcctctggat tcaccttcag tagctatagc 540

atgaactggg tccgccaggc tccagggaag gggctggagt gggtttcaac cattagtagt 600

agtagtagta tcatatacta cgcagactct gtgaagggcc gattcaccat ctccagagac 660

aatgccaaga actcactgta tctgcaaatg aacagcctga gagctgagga cacggcggtg 720

tactactgcg ccagaggttc tcaggagcac ctgattttcg attattgggg acagggtaca 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 ccccacaagg 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 acctagg 1437

<210> 354
<211> 479
<212> PRT
<213> Artificial Sequence

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

<400> 354
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

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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

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 Ser Ile 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
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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> 355
<211> 366
<212> DNA
<213> Artificial Sequence

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

<400> 355
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctggatt caccttcggg agctatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atacattatg atggaagtgt tgaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagga cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggcggtgt actactgcgc cagaactgac 300

ttctggagcg gatcccctcc aagcttagat tactggggac agggtacatt ggtcaccgtc 360

tcctca 366

<210> 356
<211> 122
<212> PRT
<213> Artificial Sequence

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

<400> 356
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 Gly 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 His Tyr Asp Gly Ser Val Glu Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asp 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 Ser Leu Asp Tyr Trp
100 105 110

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

<210> 357
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 357
Phe Thr Phe Gly Ser Tyr Gly Met His
1 5

<210> 358
<211> 17
<212> PRT
<213> Artificial Sequence

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

<400> 358
Val Ile His Tyr Asp Gly Ser Val Glu Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 359
<211> 15
<212> PRT
<213> Artificial Sequence

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

<400> 359
Ala Arg Thr Asp Phe Trp Ser Gly Ser Pro Pro Ser Leu Asp Tyr
1 5 10 15

<210> 360
<211> 324
<212> DNA
<213> Artificial Sequence

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

<400> 360
gacatccagt tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60

atcacttgtc gggcgagtcg gggtattagc agctggttag cctggtatca 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 acgg 324

<210> 361
<211> 108
<212> PRT
<213> Artificial Sequence

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

<400> 361
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 Arg Gly Ile Ser Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

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 Arg
100 105

<210> 362
<211> 11
<212> PRT
<213> Artificial Sequence

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

<400> 362
Arg Ala Ser Arg Gly Ile Ser Ser Trp Leu Ala
1 5 10

<210> 363
<211> 7
<212> PRT
<213> Artificial Sequence

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

<400> 363
Gly Ala Ser Ser Leu Gln Ser
1 5

<210> 364
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 364
Gln Gln Ile Tyr Thr Phe Pro Phe Thr
1 5

<210> 365
<211> 1446
<212> DNA
<213> Artificial Sequence

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

<400> 365
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtgc agctggtgga gtctgggggа ggcgtggtcc agcctgggag gtccctgaga 120

ctctcctgtg cagcgtctgg attcaccttc gggagctatg gcatgcactg ggtccgccag 180

gctccaggca aggggctgga gtgggtggca gttatacatt atgatggaag tgttgaatac 240

tatgcagact ccgtgaaggg ccgattcacc atctccagag acaattccaa ggacacgctg 300

tatctgcaaa tgaacagcct gagagccgag gacacggcgg tgtactactg cgccagaact 360

gacttctgga gcggatcccc tccaagctta gattactggg gacagggtac attggtcacc 420

gtctcctcag ggtctacatc cggctccggg aagcccggaa gtggcgaagg tagtacaaag 480

ggggacatcc agttgaccca gtctccatct tccgtgtctg catctgtagg agacagagtc 540

accatcactt gtcgggcgag tcggggtatt agcagctggt tagcctggta tcagcagaaa 600

ccagggaaag cccctaagct cctgatctat ggtgcatcca gtttgcaaag tggggtccca 660

tcaaggttca gcggcagtgg atctgggaca gatttcactc tcaccatcag cagcctgcag 720

cctgaagatt ttgcaactta ttactgtcag cagatataca ccttcccttt cacttttggc 780

ggagggacca aggttgagat caaacgggcc gctgcccttg ataatgaaaa gtcaaacgga 840

acaatcattc acgtgaaggg caagcacctc tgtccgtcac ccttgttccc tggtccatcc 900

aagccattct gggtgttggt cgtagtgggt ggagtcctcg cttgttactc tctgctcgtc 960

accgtggctt ttataatctt ctgggttaga tccaaaagaa gccgcctgct ccatagcgat 1020

tacatgaata tgactccacg ccgccctggc cccacaagga aacactacca gccttacgca 1080

ccacctagag atttcgctgc ctatcggagc agggtgaagt 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

cctagg 1446

<210> 366
<211> 482
<212> PRT
<213> Artificial Sequence

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

<400> 366
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 Gly Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ala Val Ile His Tyr Asp Gly Ser Val Glu 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 Asp 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

Ser 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 Arg 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> 367
<211> 1446
<212> DNA
<213> Artificial Sequence

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

<400> 367
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccggacatcc agttgaccca gtctccatct tccgtgtctg catctgtagg agacagagtc 120

accatcactt gtcgggcgag tcggggtatt agcagctggt tagcctggta tcagcagaaa 180

ccagggaaag cccctaagct cctgatctat ggtgcatcca gtttgcaaag tggggtccca 240

tcaaggttca gcggcagtgg atctgggaca gatttcactc tcaccatcag cagcctgcag 300

cctgaagatt ttgcaactta ttactgtcag cagatataca ccttcccttt cacttttggc 360

ggagggacca aggttgagat caaacggggg tctacatccg gctccgggaa gcccggaagt 420

ggcgaaggta gtacaaaggg gcaggtgcag ctggtggagt ctgggggagg cgtggtccag 480

cctgggaggt ccctgagact ctcctgtgca gcgtctggat tcaccttcgg gagctatggc 540

atgcactggg tccgccaggc tccaggcaag gggctggagt gggtggcagt tatacattat 600

gatggaagtg ttgaatacta tgcagactcc gtgaagggcc gattcaccat ctccagagac 660

aattccaagg acacgctgta tctgcaaatg aacagcctga gagccgagga cacggcggtg 720

tactactgcg ccagaactga cttctggagc ggatcccctc caagcttaga ttactgggga 780

cagggtacat tggtcaccgt ctcctcagcc gctgcccttg ataatgaaaa gtcaaacgga 840

acaatcattc acgtgaaggg caagcacctc tgtccgtcac ccttgttccc tggtccatcc 900

aagccattct gggtgttggt cgtagtgggt ggagtcctcg cttgttactc tctgctcgtc 960

accgtggctt ttataatctt ctgggttaga tccaaaagaa gccgcctgct ccatagcgat 1020

tacatgaata tgactccacg ccgccctggc cccacaagga aacactacca gccttacgca 1080

ccacctagag atttcgctgc ctatcggagc agggtgaagt 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

cctagg 1446

<210> 368
<211> 482
<212> PRT
<213> Artificial Sequence

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

<400> 368

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 Arg
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

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

145 150 155 160

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
165 170 175

Gly Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
180 185 190

Glu Trp Val Ala Val Ile His Tyr Asp Gly Ser Val Glu Tyr Tyr Ala
195 200 205

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asp
210 215 220

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
225 230 235 240

Tyr Tyr Cys Ala Arg Thr Asp Phe Trp Ser Gly Ser Pro Pro Ser 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> 369
<211> 378
<212> DNA
<213> Artificial Sequence

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

<400> 369
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccctcagc agcctggcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg gtcatcccta tcttgggtcg ggcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggacg agtccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc cagaactcct 300

gaatactcct ccagcatatg gcactattac tacggcatgg acgtatgggg ccagggaaca 360

actgtcaccg tctcctca 378

<210> 370
<211> 126
<212> PRT
<213> Artificial Sequence

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

<400> 370

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 Leu Ser Ser Leu
20 25 30

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

Gly Gly Val Ile Pro Ile Leu Gly Arg 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> 371
<211> 9

<212> PRT
<213> Artificial Sequence

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

<400> 371
Gly Thr Leu Ser Ser Leu Ala Ile Ser
1 5

<210> 372
<211> 17
<212> PRT
<213> Artificial Sequence

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

<400> 372
Gly Val Ile Pro Ile Leu Gly Arg Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 373
<211> 19
<212> PRT
<213> Artificial Sequence

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

<400> 373
Ala Arg Thr Pro Glu Tyr Ser Ser Ser Ile Trp His Tyr Tyr Tyr Gly
1 5 10 15

Met Asp Val

<210> 374
<211> 342
<212> DNA
<213> Artificial Sequence

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

<400> 374
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtgtttta tacagctcca acaataagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcagtt cgcccacact 300

cctttcactt ttggcggagg gaccaaggtt gagatcaaac gg 342

<210> 375
<211> 114
<212> PRT
<213> Artificial Sequence

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

<400> 375
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 Arg

<210> 376
<211> 17
<212> PRT
<213> Artificial Sequence

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

<400> 376
Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 377
<211> 7
<212> PRT
<213> Artificial Sequence

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

<400> 377
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 378
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 378
Gln Gln Phe Ala His Thr Pro Phe Thr

1 5

<210> 379
<211> 1476
<212> DNA
<213> Artificial Sequence

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

<400> 379
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtgc agctggtgca gtctggggct gaggtgaaga agcctgggtc ctcggtgaag 120

gtctcctgca aggcttctgg aggcaccctc agcagcctgg ctatcagctg ggtgcgacag 180

gcccctggac aagggcttga gtggatggga ggggtcatcc ctatcttggg tcgggcaaac 240

tacgcacaga agttccaggg cagagtcacg attaccgcgg acgagtccac gagcacagcc 300

tacatggagc tgagcagcct gagatctgag gacacggcgg tgtactactg cgccagaact 360

cctgaatact cctccagcat atggcactat tactacggca tggacgtatg gggccaggga 420

acaactgtca ccgtctcctc agggtctaca tccggctccg ggaagcccgg aagtggcgaa 480

ggtagtacaa agggggacat cgtgatgacc cagtctccag actccctggc tgtgtctctg 540

ggcgagaggg ccaccatcaa ctgcaagtcc agccagagtg ttttatacag ctccaacaat 600

aagaactact tagcttggta ccagcagaaa ccaggacagc ctcctaagct gctcatttac 660

tgggcatcta cccgggaatc cggggtccct gaccgattca gtggcagcgg gtctgggaca 720

gatttcactc tcaccatcag cagcctgcag gctgaagatg tggcagttta ttactgtcag 780

cagttcgccc acactccttt cacttttggc ggagggacca aggttgagat caaacgggcc 840

gctgcccttg ataatgaaaa gtcaaacgga acaatcattc acgtgaaggg caagcacctc 900

tgtccgtcac ccttgttccc tggtccatcc aagccattct gggtgttggt 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 agcagggcca gaaccaactg 1200

tataacgagc tcaacctggg acgcagggaa 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 agccctgcca cctagg 1476

<210> 380
<211> 492
<212> PRT
<213> Artificial Sequence

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

<400> 380
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 Leu Ser Ser Leu Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln
50 55 60

Gly Leu Glu Trp Met Gly Gly Val Ile Pro Ile Leu Gly Arg 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 Ser Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu
145                 150                 155                 160

Gly Ser Thr Lys Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu
                165                 170                 175

Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln
            180                 185                 190

Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln
        195                 200                 205

Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr
    210                 215                 220

Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
225                 230                 235                 240

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val
                245                 250                 255

Tyr Tyr Cys Gln Gln Phe Ala His Thr Pro Phe Thr Phe Gly Gly Gly
            260                 265                 270

Thr Lys Val Glu Ile Lys Arg 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                 320

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                 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> 381
<211> 1476
<212> DNA
<213> Artificial Sequence

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

<400> 381

K-1030_02_SL_OAP1064

atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccggacatcg tgatgaccca gtctccagac tccctggctg tgtctctggg cgagagggcc 120

accatcaact gcaagtccag ccagagtgtt ttatacagct ccaacaataa gaactactta 180

gcttggtacc agcagaaacc aggacagcct cctaagctgc tcatttactg ggcatctacc 240

cgggaatccg gggtccctga ccgattcagt ggcagcgggt ctgggacaga tttcactctc 300

accatcagca gcctgcaggc tgaagatgtg gcagtttatt actgtcagca gttcgcccac 360

actcctttca cttttggcgg agggaccaag gttgagatca aacgggggtc tacatccggc 420

tccgggaagc ccggaagtgg cgaaggtagt acaaaggggc aggtgcagct ggtgcagtct 480

ggggctgagg tgaagaagcc tgggtcctcg gtgaaggtct cctgcaaggc ttctggaggc 540

accctcagca gcctggctat cagctgggtg cgacaggccc ctggacaagg gcttgagtgg 600

atgggagggg tcatccctat cttgggtcgg gcaaactacg cacagaagtt ccagggcaga 660

gtcacgatta ccgcggacga gtccacgagc acagcctaca tggagctgag cagcctgaga 720

tctgaggaca cggcggtgta ctactgcgcc agaactcctg aatactcctc cagcatatgg 780

cactattact acggcatgga cgtatggggc cagggaacaa ctgtcaccgt ctcctcagcc 840

gctgcccttg ataatgaaaa gtcaaacgga acaatcattc acgtgaaggg caagcacctc 900

tgtccgtcac ccttgttccc tggtccatcc aagccattct gggtgttggt 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 agcagggcca gaaccaactg 1200

tataacgagc tcaacctggg acgcagggaa 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 agccctgcca cctagg 1476

<210> 382

<211> 492
<212> PRT
<213> Artificial Sequence

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

<400> 382

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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 Leu Ser Ser Leu Ala Ile Ser Trp Val Arg Gln
180 185 190

Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Gly Val Ile Pro Ile Leu
195 200 205

Gly Arg 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
225 230 235 240

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
305 310 315 320

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
385 390 395 400

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> 383
<211> 369
<212> DNA
<213> Artificial Sequence

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

<400> 383
caggtgcggc tggtggagtc tgggggggggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctggatt caccttcagt agctatggca tacactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atagggtatg atggacagga gaaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggcggtgt actactgcgt caaggggccg 300

ttgcaggagc cgccatacgc ttttgggatg gacgtatggg gccagggaac aactgtcacc 360

gtctcctca 369

<210> 384
<211> 123
<212> PRT
<213> Artificial Sequence

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

<400> 384
Gln Val Arg 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 Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Gly Tyr Asp Gly Gln Glu 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 Ala Phe Gly Met Asp Val
100 105 110

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

<210> 385
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 385
Phe Thr Phe Ser Ser Tyr Gly Ile His
1 5

<210> 386
<211> 17
<212> PRT
<213> Artificial Sequence

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

<400> 386
Val Ile Gly Tyr Asp Gly Gln Glu Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 387
<211> 16
<212> PRT
<213> Artificial Sequence

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

<400> 387
Val Lys Gly Pro Leu Gln Glu Pro Pro Tyr Ala Phe Gly Met Asp Val
1 5 10 15

<210> 388
<211> 324
<212> DNA
<213> Artificial Sequence

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

<400> 388
gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc 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 acgg 324

<210> 389
<211> 108
<212> PRT
<213> Artificial Sequence

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

<400> 389
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

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

<210> 390
<211> 11
<212> PRT
<213> Artificial Sequence

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

<400> 390
Arg Ala Ser Gln Ser Val Ser Ser Asn Leu Ala
1 5 10

<210> 391
<211> 7
<212> PRT
<213> Artificial Sequence

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

<400> 391
Ser Ala Ser Thr Arg Ala Thr
1 5

<210> 392
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 392
Gln Gln His His Val Trp Pro Leu Thr
1 5

<210> 393
<211> 1449
<212> DNA
<213> Artificial Sequence

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

<400> 393
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtgc ggctggtgga gtctgggggg ggcgtggtcc agcctgggag gtccctgaga 120

ctctcctgtg cagcgtctgg attcaccttc agtagctatg gcatacactg ggtccgccag 180

gctccaggca aggggctgga gtgggtggca gttatagggt atgatggaca ggagaaatac 240

tatgcagact ccgtgaaggg ccgattcacc atctccagag acaattccaa gaacacgctg 300

tatctgcaaa tgaacagcct gagagccgag gacacggcgg tgtactactg cgtcaagggg 360

ccgttgcagg agccgccata cgcttttggg atggacgtat ggggccaggg aacaactgtc 420

accgtctcct cagggtctac atccggctcc gggaagcccg gaagtggcga aggtagtaca 480

aaggggggaaa tagtgatgac gcagtctcca gccaccctgt ctgtgtctcc aggggaaaga 540

gccaccctct cctgcagggc cagtcagagt gttagcagca acttagcctg gtaccagcag 600

aaacctggcc aggctcccag gctcctcatc tatagcgcat 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 caccttgtt ccctggtcca 900

tccaagccat tctgggtgtt ggtcgtagtg ggtggagtcc tcgcttgtta ctctctgctc 960

gtcaccgtgg cttttataat 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 acgttttgga caagcgcaga ggacgggacc ctgagatggg tggcaaacca 1260

agacgaaaaa acccccagga gggtctctat aatgagctgc agaaggataa gatggctgaa 1320

gcctattctg aaataggcat gaaaggagag cggagaaggg gaaaagggca cgacggtttg 1380

taccagggac tcagcactgc tacgaaggat acttatgacg ctctccacat gcaagccctg 1440

ccacctagg 1449

<210> 394
<211> 483
<212> PRT
<213> Artificial Sequence

<220>

K-1030_02_SL_OAP1064

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 394

```
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 Arg 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 Ile His Trp Val Arg Gln Ala Pro Gly Lys
    50                  55                  60

Gly Leu Glu Trp Val Ala Val Ile Gly Tyr Asp Gly Gln Glu 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 Ala
        115                 120                 125

Phe 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> 395
<211> 1449
<212> DNA
<213> Artificial Sequence

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

<400> 395
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccggaaatag tgatgacgca gtctccagcc accctgtctg tgtctccagg ggaaagagcc 120

accctctcct gcagggccag tcagagtgtt agcagcaact tagcctggta ccagcagaaa 180

cctggccagg ctcccaggct cctcatctat agcgcatcca 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 gcaggtgcgg ctggtggagt ctgggggggg cgtggtccag 480

cctgggaggt ccctgagact ctcctgtgca gcgtctggat tcaccttcag tagctatggc 540

atacactggg tccgccaggc tccaggcaag gggctggagt gggtggcagt tatagggtat 600

gatggacagg agaaatacta tgcagactcc gtgaagggcc gattcaccat ctccagagac 660

aattccaaga acacgctgta tctgcaaatg aacagcctga gagccgagga cacggcggtg 720

tactactgcg tcaaggggcc gttgcaggag ccgccatacg cttttgggat ggacgtatgg 780

ggccagggaa caactgtcac cgtctcctca gccgctgccc ttgataatga aaagtcaaac 840

ggaacaatca ttcacgtgaa gggcaagcac ctctgtccgt caccttgtt ccctggtcca 900

tccaagccat tctgggtgtt ggtcgtagtg ggtggagtcc tcgcttgtta ctctctgctc 960

gtcaccgtgg cttttataat 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 acgttttgga caagcgcaga ggacgggacc ctgagatggg tggcaaacca 1260

agacgaaaaa acccccagga gggtctctat aatgagctgc agaaggataa gatggctgaa 1320

gcctattctg aaataggcat gaaaggagag cggagaaggg gaaaagggca cgacggtttg 1380

taccagggac tcagcactgc tacgaaggat acttatgacg ctctccacat gcaagccctg 1440

ccacctagg 1449

<210> 396
<211> 483
<212> PRT
<213> Artificial Sequence

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

<400> 396
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 Arg Leu Val Glu Ser Gly Gly Gly Val Val Gln
145 150 155 160

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
165 170 175

Ser Ser Tyr Gly Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
180 185 190

Glu Trp Val Ala Val Ile Gly Tyr Asp Gly Gln Glu 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
225 230 235 240

Tyr Tyr Cys Val Lys Gly Pro Leu Gln Glu Pro Pro Tyr Ala Phe 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

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> 397
<211> 369
<212> DNA
<213> Artificial Sequence

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

<400> 397
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctggatt caccttcagt agccgtggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atagggtatg atggacagga gaaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggcggtgt actactgcgt caaggggccg 300

ttgcaggagc cgccatacga ttatggaatg gacgtatggg gccagggaac aactgtcacc 360

gtctcctca 369

<210> 398
<211> 123
<212> PRT
<213> Artificial Sequence

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

<400> 398
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 Arg
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 Gly Tyr Asp Gly Gln Glu 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> 399
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 399
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Phe Thr Phe Ser Ser Arg Gly Met His
1               5
```

<210> 400
<211> 17
<212> PRT
<213> Artificial Sequence

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

<400> 400
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Val Ile Gly Tyr Asp Gly Gln Glu Lys Tyr Tyr Ala Asp Ser Val Lys
1               5                   10                  15
```

Gly

<210> 401
<211> 16
<212> PRT
<213> Artificial Sequence

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

<400> 401
Val Lys Gly Pro Leu Gln Glu Pro Pro Tyr Asp Tyr Gly Met Asp Val
1 5 10 15

<210> 402
<211> 324
<212> DNA
<213> Artificial Sequence

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

<400> 402
gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc 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 acgg 324

<210> 403
<211> 108
<212> PRT
<213> Artificial Sequence

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

<400> 403
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

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

<210> 404
<211> 11
<212> PRT
<213> Artificial Sequence

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

<400> 404
Arg Ala Ser Gln Ser Val Ser Ser Asn Leu Ala
1 5 10

<210> 405
<211> 7
<212> PRT
<213> Artificial Sequence

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

<400> 405
Ser Ala Ser Thr Arg Ala Thr
1 5

<210> 406
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 406
Gln Gln His His Val Trp Pro Leu Thr
1 5

<210> 407
<211> 1449
<212> DNA
<213> Artificial Sequence

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

<400> 407
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtgc agctggtgga gtctgggggа ggcgtggtcc agcctgggag gtccctgaga 120

ctctcctgtg cagcgtctgg attcaccttc agtagccgtg gcatgcactg ggtccgccag 180

gctccaggca aggggctgga gtgggtggca gttatagggt atgatggaca ggagaaatac 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

aaggggggaaa tagtgatgac gcagtctcca gccaccctgt ctgtgtctcc aggggaaaga 540

gccaccctct cctgcagggc cagtcagagt gttagcagca acttagcctg gtaccagcag 600

aaacctggcc aggctcccag gctcctcatc tatagcgcat 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 cacccttgtt ccctggtcca 900

tccaagccat tctgggtgtt ggtcgtagtg ggtggagtcc tcgcttgtta ctctctgctc 960

gtcaccgtgg cttttataat 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 acgttttgga caagcgcaga ggacgggacc ctgagatggg tggcaaacca 1260

agacgaaaaa acccccagga gggtctctat aatgagctgc agaaggataa gatggctgaa 1320

gcctattctg aaataggcat gaaaggagag cggagaaggg gaaaagggca cgacggtttg 1380

taccagggac tcagcactgc tacgaaggat acttatgacg ctctccacat gcaagccctg 1440

ccacctagg 1449

<210> 408
<211> 483
<212> PRT
<213> Artificial Sequence

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

<400> 408
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 Arg Gly Met His Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

```
Gly Leu Glu Trp Val Ala Val Ile Gly Tyr Asp Gly Gln Glu 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> 409
<211> 1449
<212> DNA
<213> Artificial Sequence

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

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gcctattctg aaataggcat gaaaggagag cggagaaggg gaaaagggca cgacggtttg 1380

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<211> 483
<212> PRT
<213> Artificial Sequence

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

<400> 410

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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

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His Val Trp Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
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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                 160

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
                165                 170                 175

Ser Ser Arg Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
            180                 185                 190

Glu Trp Val Ala Val Ile Gly Tyr Asp Gly Gln Glu 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                 240

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
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Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
305                 310                 315                 320
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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
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Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
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Pro Pro Arg

<210> 411
<211> 20
<212> PRT
<213> Artificial Sequence

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

peptide

<400> 411
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Gly Gly Gly Ser
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<210> 412
<211> 112
<212> PRT
<213> Homo sapiens

<400> 412
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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
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<210> 413
<211> 6762
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic polynucleotide

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ccacgttcgc cggctttccc cgtcaagctc taaatcgggg gctcccttta gggttccgat 180

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ggggatgtgc tgcaaggcga ttaagttggg taacgccagg gttttcccag tcacgacgtt 600

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