



Patent- og
Varemærkestyrelsen

(12) Oversættelse af
europæisk patentskrift

-
- (51) Int.Cl.: **C 07 K 14/71 (2006.01)** **C 12 N 9/12 (2006.01)**
- (45) Oversættelsen bekendtgjort den: **2019-04-15**
- (80) Dato for Den Europæiske Patentmyndigheds bekendtgørelse om meddelelse af patentet: **2019-01-09**
- (86) Europæisk ansøgning nr.: **10829041.2**
- (86) Europæisk indleveringsdag: **2010-11-03**
- (87) Den europæiske ansøgnings publiceringsdag: **2012-09-12**
- (86) International ansøgning nr.: **US2010055329**
- (87) Internationalt publikationsnr.: **WO2011056894**
- (30) Prioritet: **2009-11-03 US 257567 P**
- (84) Designerede stater: **AL AT BE BG CH CY CZ DE DK EE ES FI FR GB GR HR HU IE IS IT LI LT LU LV MC MK MT NL NO PL PT RO RS SE SI SK SM TR**
- (73) Patenthaver: **City of Hope, 1500 East Duarte Road, Duarte, California 91010, USA**
- (72) Opfinder: **JENSEN, Michael C., 1500 East Duarte Road, Duarte, California 91010, USA**
- (74) Fuldmægtig i Danmark: **NORDIC PATENT SERVICE A/S, Bredgade 30, 1260 København K, Danmark**
- (54) Benævnelse: **TRUNKERET EPIDERMAL VÆKSTFAKTORRECEPTOR (EGFR) TIL TRUNKERET T-CELLEUDVÆLGELSE**
- (56) Fremdragne publikationer:
US-A1- 2004 026 363
US-A1- 2004 126 363
US-A1- 2005 053 608
US-B1- 6 790 614
X. WANG ET AL.: "A transgene-encoded cell surface polypeptide for selection, in vivo tracking, and ablation of engineered cells", BLOOD, vol. 118, no. 5, 4 August 2011 (2011-08-04), pages 1255-1263, XP55062819, ISSN: 0006-4971, DOI: 10.1182/blood-2011-02-337360
LI ET AL.: "Structural basis for inhibition of the epidermal growth factor receptor by cetuximab." CANCER CELL vol. 7, 2005, pages 301 - 311, XP002508255
CHAKRAVERTY ET AL.: "An inflammatory checkpoint regulates recruitment of graft-versus-host reactive T cells to peripheral tissues." JEM vol. 203, no. 8, 2006, pages 2021 - 2031, XP008158914
POWELL ET AL.: "Large-Scale Depletion of CD25+ Regulatory T Cells from Patient Leukapheresis Samples." J IMMUNOTHER vol. 28, no. 4, 2005, pages 403 - 411, XP002508255
DATABASE MEDLINE [Online] US NATIONAL LIBRARY OF MEDICINE (NLM), BETHESDA, MD, US; 29 January 1999 (1999-01-29), KIL S J ET AL: "A leucine-based determinant in the epidermal growth factor receptor juxtamembrane domain is required for the efficient transport of ligand-receptor complexes to lysosomes.", Database accession no. NLM9915853 & KIL S J ET AL: "A leucine-based determinant in the epidermal growth factor receptor juxtamembrane domain is required for the efficient transport of ligand-receptor complexes to

lysosomes.", THE JOURNAL OF BIOLOGICAL CHEMISTRY 29 JAN 1999, vol. 274, no. 5, 29 January 1999 (1999-01-29), pages 3141-3150, ISSN: 0021-9258

DESCRIPTION

TECHNICAL FIELD

[0001] The present products and methods relate to the fields of immunology and purification of genetically modified cells, specifically to a truncated receptor paired with a corresponding antibody, such as a polypeptide derived from human epidermal growth factor receptor (EGFR) paired with cetuximab, for use in cancer immunotherapy.

BACKGROUND

[0002] Immune cell products with homogenous expression of tumor targeting chimeric antigen receptors (CARs) are desirable for clinical evaluation of adoptive therapy strategies to eliminate the product-to-product variability of transgene expression otherwise intrinsic to transduction and other genetic modification procedures without subsequent selection. Immunotherapy using genetically redirected immune cells is an attractive approach for treating minimal residual disease in a variety of cancer patients. However, immunologic rejection of cell products expressing antibiotic selection proteins as part of the transduction strategy has impeded this strategy. A novel selection marker that is not expressed on human lymphocytes, does not contain endogenous signaling or trafficking function, and is recognized by a known, preferably commercially available, pharmaceutical grade antibody reagent that can be utilized for selection, *in vivo* tracking, and depletion of transduced cells would be a significant improvement in the art.

[0003] US6790614 relates to a method of identifying genetically modified cells using a mutated protein-tyrosine kinase receptor (PTKR), particularly a mutated epidermal growth factor receptor (EGFR) or mutated muscle specific kinase (MuSK) family member as selectable cell markers.

SUMMARY

[0004] The present invention provides a modified EGFR gene, which consists of a sequence which encodes a truncated EGFR consisting of the EGFR Domain III, the EGFR transmembrane domain and the EGFR Domain IV. The modified EGFR gene may be attached to a nucleotide sequence encoding only the GMCSFR alpha chain signal sequence. The amino acid sequence encoded by the modified EGFR gene may be at least 90% identical to, or consist of, SEQ ID NO: 3.

[0005] The present invention further provides a construct comprising the gene of the invention, wherein the modified EGFR gene is coupled with a nucleotide sequence encoding a chimeric

antigen receptor specific for a tumour associated antigen, wherein the nucleotide sequence encoding a chimeric antigen receptor is followed by a nucleotide sequence encoding a C-terminal 2A cleavable linker and the coding sequence for the modified EGFR gene.

[0006] The chimeric antigen receptor specific for a tumour associated antigen may be selected from CD19, CD20, and CD22, suitably it may be CD19. Suitably the construct may be CD19R-CD28gg-Zeta(CO)-T2A-EGFRt, and may comprise a nucleotide sequence encoding the amino acid sequence SEQ ID NO: 6.

[0007] The present invention also provides a genetically modified population of T cells transduced with the gene of the invention, wherein the gene is coupled to a gene encoding a tumour targeting chimeric antigen receptor (CAR), wherein the T-cells express inactive modified EGFR. Suitably the T cells may be for use in adoptive immunotherapy. The adoptive immunotherapy may be for use in treating cancer.

[0008] A non-immunogenic selection epitope compatible with immunomagnetic selection facilitates immunotherapy in cancer patients without undesirable immunologic rejection of cell products (i.e. as seen when expressing antibiotic selection proteins) may be generated by removing certain amino acid sequences of the protein. The non-immunogenic selection epitope is a gene encoding an endogenous cell-surface molecule that is truncated to retain an extracellular epitope recognized by a known antibody or functional fragment thereof, and to remove any signaling or trafficking domains and/or any extracellular domains unrecognized by the known antibody. The removal of the signaling or trafficking domains and/or any extracellular domains unrecognized by the known antibody renders the endogenous cell-surface molecule inert, which is a desired property for the molecule. The non-immunogenic selection epitope may also be used for as a selection tool or tracking marker.

[0009] Accordingly, the present invention provides a non-immunogenic selection epitope encoded by the gene or the construct of the invention. Suitably, the selection epitope may be for use in a use selected from:

1. (a) use as a non-immunogenic selection tool that is compatible with immunomagnetic selection;
2. (b) use as a tracking marker for in vivo T cell engraftment; and
3. (c) use as a suicide gene for transduced T cells that have immunotherapeutic potential, optionally for use as a suicide gene via cetuximab mediated complement and/or antibody dependent cell mediated cytotoxicity (ADCC) pathways.

[0010] Suitably the selection epitope may be compatible with immunomagnetic selection and facilitates immunotherapy in cancer patients without undesirable immunologic rejection of cell products.

[0011] Modified endogenous cell-surface molecules disclosed herein may be, but are not

limited to, any cell-surface related receptor, ligand, glycoprotein, cell adhesion molecule, antigen, integrin or cluster of differentiation (CD) that is modified as described herein. The modified endogenous cell-surface molecule is a truncated tyrosine kinase receptor. In one aspect, the truncated tyrosine kinase receptor is a member of the epidermal growth factor receptor family (e.g., ErbB1, ErbB2, ErbB3, ErbB4).

[0012] Epidermal growth factor receptor, also known as EGFR, ErbB1 and HER1, is a cell-surface receptor for members of the epidermal growth factor family of extracellular ligands. Alterations in EGFR activity have been implicated in certain cancers. In a first aspect, a gene encoding an EGFR polypeptide comprising human epidermal growth factor receptor (EGFR) that is constructed by removal of nucleic acid sequences that encode polypeptides including the membrane distal EGF-binding domain and the cytoplasmic signaling tail (a "truncated EGFR" or "EGFRt"), but retains the extracellular membrane proximal epitope recognized by an anti-EGFR antibody. Preferably, the antibody is a known, commercially available anti-EGFR monoclonal antibody, such as cetuximab, matuzumab, necitumumab or panitumumab.

[0013] Application of biotinylated-cetuximab to immunomagnetic selection in combination with anti-biotin microbeads successfully enriches T cells that have been lentivirally transduced with EGFRt-containing constructs from as low as 2% of the population to greater than 90% purity without observable toxicity to the cell preparation. Constitutive expression of this inert EGFRt molecule does not affect T cell phenotype or effector function as directed by the coordinately expressed chimeric antigen receptor (CAR), CD19R. Through flow cytometric analysis, EGFRt was successfully utilized as an *in vivo* tracking marker for T cell engraftment in mice. Furthermore, EGFRt was demonstrated to have suicide gene potential through Erbitux® mediated antibody dependent cellular cytotoxicity (ADCC) pathways. Thus, EGFRt may be used as a non-immunogenic selection tool, tracking marker, and suicide gene for transduced T cells that have immunotherapeutic potential. The EGFRt nucleic acid may also be detected by means well known in the art.

[0014] Methods of discovering and designing modified, truncated or altered endogenous cell-surface molecules which bind to antibodies, preferably commercially available antibodies, as described herein are disclosed. The methods include modeling the protein of interest and truncating functional portions, while leaving the antibody-binding portions intact. The resulting modified receptor or ligand can be sorted using a labeled antibody and then enriched such that the concentration of the modified receptor or ligand is increased.

[0015] A method of selecting transduced T cells comprising transducing T cells with a modified, truncated or altered endogenous cell-surface molecule gene sequence (e.g., truncated EGFR) and then applying an antibody that binds the modified ligand or receptor sequence to the transduced T cells is disclosed herein. If the modified receptor sequence is EGFRt, the antibody is preferably a biotinylated anti-EGFR monoclonal antibody. The T cells are then sorted by adding anti-biotin microbeads and selecting the T cells using immunomagnetic separation, adding fluorochrome-conjugated anti-biotin and selecting the T cells using Fluorescence Activated Cell Sorting, or any other reliable method of sorting the

cells. The modified ligand or receptor sequences, such as the EGFRt sequence, may be contained in a suitable transfer vehicle such as a lentiviral vector.

[0016] These and other embodiments are further explained in the drawing and detailed description herein.

BRIEF DESCRIPTION OF THE DRAWINGS

[0017]

Figure 1 is a molecular model of EGFR vs. EGFRt proteins based on the crystal structure files. The EGFR structure on the left shows a full-length EGFR with the structure of the four extracellular domains (Domains I-IV). The middle structure shows the truncated EGFR (EGFRt), which is missing Domain I, Domain II, the Juxatmembrane Domain, and the Tyrosine Kinase Domain as compared to an unmodified EGFR. The EGFRt on the right shows truncated structure bound to Eribitux® Fab, comprised of V_H-C_{H1} and V_L-C_L. The domains are separated with dotted lines.

Figure 2 illustrates the selection of EGFRt⁺ T cells using biotinylated cetuximab (referred to in the figure as Eribitux®). Figure 2a is a schematic of the cetuximab biotinylation and reformulation process. Figure 2b is a graph showing titration of biotinylated cetuximab. 10⁶ EGFR⁺ cells were stained with either 0µg (black), 1.45µg (red), 0.145µg (orange), 14.5ng (yellow), 1.45ng (green), 0.145ng (blue) or 14.5pg (purple) of biotinylated cetuximab followed by 0.5µg PE-conjugated streptavidin and analyzed by flow cytometry. 14.5ng or more of biotinylated cetuximab was deemed sufficient for future staining. Figure 2c depicts schematics of both the immunomagnetic (top) and the fluorescence activated cell sorting (bottom) EGFRt selection procedures.

Figure 2d shows immunomagnetic selection of various T cell lines lentivirally transduced with CAR and EGFRt containing constructs. Schematics of the CD19CAR-T2A-EGFRt (left) and CD19CAR-T2A-EGFRt-IMPDH2dm (right) constructs contained in lentiviral vectors are shown above the corresponding pre- and post-selection flow cytometric analyses for surface EGFRt expression. Codon optimized sequence portions of the CD19-specific, CD28 co-stimulatory CAR, followed by the self-cleavable T2A, EGFRt and IMPDH2dm selection markers are indicated, along with the Elongation Factor 1 promoter sequences (EF-1p), and the GCSFR alpha chain signal sequences (GCSFRss, which directs surface expression). Flow cytometric analysis of lentivirally transduced T cell lines that had been stained with a biotinylated-cetuximab antibody and PE-conjugated anti-biotin antibody (black histograms) was performed on both the input T cells (PRE SLXN) and the positive fraction obtained from AutoMACS™ (POS FRXN). Open histograms represent staining with PE-conjugated anti-biotin antibody alone, and the percent positive cells are indicated in each histogram. Selection of CD19CAR⁺EGFRt⁺ Line A occurred 3 days after transduction of T cell blasts. Selection of

CD19CAR⁺EGFRt⁺ Line B occurred after 3 REM stimulations of transduced CMVpp65-specific T_{CM}-derived cells. Selection of CD19CAR⁺EGFRt⁺ Line C occurred after 2 REM stimulations of transduced CD8⁺ T_{CM}-derived cells. Selection of CD19CAR⁺EGFRt⁺ Line D occurred after 1 REM stimulation of transduced T_{EM}-derived cells. Selection of CD19CAR⁺EGFRt⁺IMPDH2dm⁺ Line E occurred after 1 REM stimulation of transduced T_{CM}-derived cells.

Figure 3 shows that the EGFRt expressed on selected T cells is inert. In Figure 3a, EGFRt expressed on T cells is not phosphorylated upon co-incubation with EGF. Negative control T cells, CD19CAR⁺EGFRt⁺ Line A cells, or A431 cells were incubated for 5 minutes with or without either 100ng/mL EGF or cetuximab (referred to in the figure as Erbtx) and then lysed in the presence of phosphatase inhibitor. Lysates run on Western blots were then probed using antibodies specific for either β -actin, the cytoplasmic domain of EGFR, or the phosphorylated tyrosine at position 1068 of EGFR. Figure 3b shows that EGF does not bind to the surface of EGFRt expressing T cells. A431, Line A, and negative control T cells were stained with PE-conjugated anti-EGFR, or either biotinylated cetuximab or biotinylated EGF followed by PE-conjugated streptavidin (black histogram) versus PE-conjugated isotype control Ab or streptavidin alone (open histogram) by flow cytometry. Percent positive staining is indicated in each histogram.

Figure 4 illustrates that selected EGFRt⁺ CD19R⁺ T cells can be expanded with maintenance of effector phenotype. Figure 4a is a line graph showing expansion of EGFRt-selected T cells, Lines A-E, over 12 or more days after rapid expansion medium (REM) stimulation was initiated on the day of AutoMACS™ selection (day 0). (MACS is magnetic activated cell sorting.) Expansion of T cells in rapid expansion medium (REM) involved the incubation of 10⁶ T cells with 30 ng/mL anti-CD3 ϵ (OKT3; Ortho Biotech, Raritan, NJ), 5 x 10⁷ γ -irradiated PBMCs (3500 cGy), and 10⁷ γ -irradiated LCLs (8000 cGy) in 50 mL CM; with addition of 50U/mL rhIL-2 and 10ng/ml rhIL-15 (CellGenix) every 48 hours, beginning on day 1. T cells were re-stimulated in this manner every 14 days. Figure 4b shows histograms representing EGFRt-selected T cells (11 to 13 days after stimulation) that were phenotyped for surface EGFR (i.e., EGFRt, with biotinylated cetuximab), Fc (i.e., CAR), and T cell markers CD4 or CD8, (black histogram) vs. isotype control Ab (open histogram) by flow cytometry. Percent positive staining is indicated in each histogram. "N.D." indicates no data. Figure 4C are five line graphs, one for each of Lines A-E, of EGFRt-selected T cells (within 11 to 15 days after REM stimulation) incubated for 4 hours with ⁵¹Cr-labeled NS0, U251T, CD19t-expressing NS0, CMV pp65-expressing U251T, CD19-expressing Daudi or SupB15, or OKT3-expressing LCL cells as targets at the indicated E:T ratios. Chromium release was measured to determine cytotoxic activity. Figure 4d is a graph showing MPA resistance of the CD19CAR⁺EGFRt⁺IMPDH2dm⁺ Line E. Control T cells that do not express IMPDH2dm and EGFRt-selected IMPDH2dm-expressing Line E cells were cultured either with or without 1 μ M MPA and total cell numbers were monitored.

Figure 5 shows EGFRt expression can be used as a tracking marker for in vivo T cell engraftment. Day 36 bone marrow harvested from a control mouse or from a mouse that had

received 10^7 CD19CAR⁺EGFRt⁺ Line C at day 0 was stained using PerCP-conjugated anti-human CD45 and biotinylated cetuximab ("Bio-Erb") followed by PE-conjugated streptavidin. Quadrants were created based on isotype control staining, and percent positive staining in each quadrant is indicated in each histogram.

Figure 6 is a graph showing EGFRt expression targets T cells for cetuximab (referred to in the figure as Erbitux®) mediated ADCC. ⁵¹Cr-labeled Line A cells were pre-incubated either with or without up to 20µg/mL of cetuximab or the CD20-specific mAb Rituxan as a negative control prior to addition of human PBMC as effectors.

Figure 7 is the nucleotide (sense strand is SEQ ID NO: 1, antisense strand is SEQ ID NO: 2) and amino acid (SEQ ID NO: 3) sequences of GMCSFR alpha chain signal sequence linked to EGFRt. The GMCSFR alpha chain signal sequence, which directs surface expression, is encoded by nucleotides 1-66. EGFRt is encoded by nucleotides 67-1071.

Figure 8 is the nucleotide (sense strand is SEQ ID NO: 4, antisense strand is SEQ ID NO: 5) and amino acid (SEQ ID NO: 6) sequences of CD19R-CD28gg-Zeta(CO)-T2A-EGFRt. CD19R-CD28gg-Zeta(CO) is encoded by nucleotides 1-2040; T2A is encoded by nucleotides 2041-2112; GMCSFR is encoded by nucleotides 2113-2178; EGFRt is encoded by nucleotides 2179-3186.

Figure 9 is a graph showing CD19R-CD28gg-Zeta(CO)-T2A-EGFRt expression. Transduction of anti-CD3/anti-CD28 bead stimulated primary T cell blasts with the CD19R-CD28gg-Zeta(CO)-T2A-EGFRt_epHIV7 lentiviral vector (MOI = 3) results in surface detection of both the CAR (using a biotinylated anti-Fc Ab and streptavidin-PE) and the truncated EGFR molecule (using a biotinylated cetuximab Ab and streptavidin-PE) by flow cytometry on day 4. The white peak in each panel is non-transduced control T cell blasts.

Figure 10 is a schema showing a possible process flow for clinical trials for testing products of the present disclosure.

DETAILED DESCRIPTION

[0018] Certain embodiments of the invention are described in detail, using specific examples, sequences, and drawings.

[0019] Erbitux® is a registered trademark for the anti-EGFR monoclonal antibody cetuximab and is intended to independently include the trade name product formulation, the generic drug, and the active pharmaceutical ingredient(s) of the trade name product.

[0020] The term "genetic modification" means any process that adds, deletes, alters, or disrupts an endogenous nucleotide sequence and includes, but is not limited to viral mediated

gene transfer, liposome mediated transfer, transformation, transfection and transduction, e.g., viral mediated gene transfer such as the use of vectors based on DNA viruses such as lentivirus, adenovirus, retroviruses, adeno-associated virus and herpes virus.

[0021] The term "antibody" includes monoclonal antibodies, polyclonal antibodies, dimers, multimers, multispecific antibodies and antibody fragments that may be human, mouse, humanized, chimeric, or derived from another species. A "monoclonal antibody" is an antibody obtained from a population of substantially homogeneous antibodies that is being directed against a specific antigenic site.

[0022] "Variant" refers to polypeptides having amino acid sequences that differ to some extent from a native sequence polypeptide. Ordinarily, amino acid sequence variants will possess at least about 80% sequence identity, more preferably, at least about 90% homologous by sequence. The amino acid sequence variants may possess substitutions, deletions, and/or insertions at certain positions within the reference amino acid sequence.

[0023] "Percentage identity" or "percent identity" is defined as the percentage of residues in the amino acid sequence variant that are identical after best aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Methods and computer programs for the alignment are well known in the art. Such programs include GAP, BESTFIT, FASTA, BLAST or Align 2.

[0024] "Antibody-dependent cell-mediated cytotoxicity" and "ADCC" refer to a cell-mediated reaction in which nonspecific cytotoxic cells that express Fc receptors, such as natural killer cells, neutrophils, and macrophages, recognize bound antibody on a target cell and cause lysis of the target cell. ADCC activity may be assessed using methods, such as those described in U.S. Pat. No. 5,821,337.

[0025] "Effector cells" are leukocytes which express one or more constant region receptors and perform effector functions.

[0026] To "treat" a disease or a disorder, such as cancer, means to take either therapeutic measures or preventative measures to lessen or abate the disease or disorder. Such treatment includes prevention, alleviation of symptoms, diminishment or stabilization of scope, and/or remission.

[0027] The term "therapeutically effective amount" refers to an amount of a compound or molecule effective to treat a disease or disorder.

[0028] "Cancer" refers to cells undergoing uncontrolled cellular growth. Examples of cancer include colorectal cancer and head and neck cancer. A "chemotherapeutic agent" is a chemical compound useful in the treatment of cancer.

[0029] A "cytokine" is a protein released by one cell to act on another cell as an intercellular

mediator.

[0030] "Non-immunogenic" refers to a material that does not initiate, provoke or enhance an immune response where the immune response includes the adaptive and/or innate immune responses.

[0031] The term "gene" means the segment of DNA involved in producing a polypeptide chain; it includes regions preceding and following the coding region "leader and trailer" as well as intervening sequences (introns) between individual coding segments (exons). Some genes may be developed which lack, in whole or in part, introns. Some leader sequences may enhance translation of the nucleic acid into polypeptides.

[0032] The term "isolated" means that the material is removed from its original environment (e.g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or polypeptide, separated from some or all of the coexisting materials in the natural system, is isolated. Such polynucleotides could be part of a vector and/or such polynucleotides or polypeptides could be part of a composition, and still be isolated in that such vector or composition is not part of its natural environment.

[0033] As used herein, a "vector" may be any agent capable of delivering or maintaining nucleic acid in a host cell, and includes viral vectors (e.g. retroviral vectors, lentiviral vectors, adenoviral vectors, or adeno-associated viral vectors), plasmids, naked nucleic acids, nucleic acids complexed with polypeptide or other molecules and nucleic acids immobilized onto solid phase particles. The appropriate DNA sequence may be inserted into the vector by a variety of procedures. In general, the DNA sequence is inserted into an appropriate restriction endonuclease site(s) by procedures known in the art. Such procedures and others are deemed to be within the scope of those skilled in the art. Transcription of the DNA encoding the polypeptides of the present invention by higher eukaryotes is increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp that act on a promoter to increase its transcription. Examples including the SV40 enhancer on the late side of the replication origin bp 100 to 270, a cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers.

[0034] "Receptor" means a polypeptide that is capable of specific binding to a molecule. Whereas many receptors may typically operate on the surface of a cell, some receptors may bind ligands when located inside the cell (and prior to transport to the surface) or may reside predominantly intra-cellularly and bind ligand therein.

[0035] "Antibody or functional fragment thereof" means an immunoglobulin molecule that specifically binds to, or is immunologically reactive with a particular antigen or epitope, and includes both polyclonal and monoclonal antibodies. The term antibody includes genetically engineered or otherwise modified forms of immunoglobulins, such as intrabodies, peptibodies,

chimeric antibodies, fully human antibodies, humanized antibodies, and heteroconjugate antibodies (e.g., bispecific antibodies, diabodies, triabodies, and tetrabodies). The term functional antibody fragment includes antigen binding fragments of antibodies, including e.g., Fab', F(ab').sub.2, Fab, Fv, rIgG, and scFv fragments. The term scFv refers to a single chain Fv antibody in which the variable domains of the heavy chain and of the light chain of a traditional two chain antibody have been joined to form one chain.

[0036] In one embodiment, a gene encoding a modified EGFR gene, which consists of a sequence which encodes a truncated EGFR consisting of the EGFR Domain III, the EGFR transmembrane domain and the EGFR Domain IV, may be used as a non-immunogenic selection epitope compatible with immunomagnetic selection is provided. Such a non-immunogenic selection epitope may facilitate immunotherapy in cancer patients without undesirable immunologic rejection of cell products. The modified EGFR gene retains an extracellular epitope recognized by a known antibody or functional fragment thereof, and to remove any signaling or trafficking domains and/or any extracellular domains unrecognized by said known antibody. A modified endogenous cell surface molecule which lacks a signaling or trafficking domain and/or any extracellular domains unrecognized by said known antibody is rendered inert.

[0037] Modified endogenous cell-surface molecules disclosed herein are any non-immunogenic cell-surface related receptor, glycoprotein, cell adhesion molecule, antigen, integrin or cluster of differentiation (CD) that is modified as described herein. Modification of such cell-surface molecules is accomplished by keeping an epitope that is recognized by a known antibody or functional fragment thereof; and removing any signaling or trafficking domains and/or any extracellular domains unrecognized by a known antibody. Removal of the signaling or trafficking domains and/or any extracellular domains unrecognized by a known antibody renders the endogenous cell-surface molecule non-immunogenic and/or inert.

[0038] Examples of endogenous cell-surface molecules that may be modified or truncated include, but are not limited to EpCAM, VEGFR, integrins (e.g., integrins $\alpha v\beta 3$, $\alpha 4$, $\alpha IIb\beta 3$, $\alpha 4\beta 7$, $\alpha 5\beta 1$, $\alpha v\beta 3$, αv), TNF receptor superfamily (e.g., TRAIL-R1, TRAIL-R2), PDGF Receptor, interferon receptor, folate receptor, GPNMB, ICAM-1, HLA-DR, CEA, CA-125, MUC1, TAG-72, IL-6 receptor, 5T4, GD2, GD3, or clusters of differentiation (e.g., CD2, CD3, CD4, CD5, CD11, CD11a/LFA-1, CD15, CD18/ITGB2, CD19, CD20, CD22, CD23/IgE Receptor, CD25, CD28, CD30, CD33, CD38, CD40, CD41, CD44, CD51, CD52, CD62L, CD74, CD80, CD125, CD147/basigin, CD152/CTLA-4, CD154/CD40L, CD195/CCR5, CD319/SLAMF7).

[0039] Corresponding commercial antibodies that may be used to recognize a modified or truncated endogenous cell-surface molecule include, but are not limited to, 3F8, abagovomab, abciximab, adecatumumab, afutuzumab, alemtuzumab, altumomab pentetate, anatumomab mafenatox, apolizumab, arcitumomab, aselizumab, atlizumab (= tocilizumab), basiliximab, bectumomab, benralizumab, besilesomab, bivatuzumab mertansine, blinatumomab, brentuximab vedotin, cantuzumab mertansine, capromab pendetide, catumaxomab, CC49,

cedelizumab, celmoleukin, citatuzumab bogatox, clenoliximab, clivatuzumab tetraxetan, CNTO-95, conatumumab, dacetuzumab, daclizumab, daratumumab, detumomab, ecomeximab, edrecolomab, efalizumab, elotuzumab, enlimomab pegol, epitumomab cituxetan, epratuzumab, erlizumab, etaracizumab, fanolesomab, faralimomab, farletuzumab, galiximab, gavilimomab, gemtuzumab ozogamicin, glembatumumab vedotin, gomiliximab, ibalizumab, ibritumomab tiuxetan, igovomab, intetumumab, iratumumab, inolimomab, inotuzumab ozogamicin, ipilimumab, keliximab, labetuzumab, lintuzumab, lextatumumab, lucatumumab, lumiliximab, mapatumumab, maslimomab, milatuzumab, minretumomab, mitumomab, muromonab-CD3, naptumomab estafenatox, natalizumab, ocrelizumab, odulimomab, ofatumumab, olaratumab, oportuzumab monatox, oregovomab, otelixizumab, pentumomab, priliximab, PRO 140, rituximab, rovelizumab, ruplizumab, satumomab pendetide, sipilizumab, sontuzumab, tadocizumab, taplitumomab paptox, teneliximab, teplizumab, TGN1412, ticilimumab (= tremelimumab), tigatuzumab, tocilizumab (= atlizumab), toralizumab, tositumomab, tremelimumab, tucotuzumab, vedolizumab, veltuzumab, visilizumab, vitaxin, volociximab, votumomab, zanolimumab, ziralimumab, zolimomab aritox.

[0040] The modified endogenous cell-surface molecule may be encoded by a modified or truncated tyrosine kinase receptor gene. Examples of tyrosine kinase receptors that may be modified or truncated according to the embodiments described herein include, but are not limited to, members of the endothelial growth factor receptor family (EGFR/ErbB1/HER1; ErbB2/HER2/neu; ErbB3/HER3; ErbB4/HER4), hepatocyte growth factor receptor (HGFR/c-MET) and insulin-like growth factor receptor-1 (IGF-1R). According to some embodiments, modified tyrosine kinase receptors retain an extracellular epitope recognized by a known antibody or functional fragment thereof, and lack at least a tyrosine kinase domain. A modified tyrosine kinase receptor which lacks at least a tyrosine kinase domain renders the receptor inert.

[0041] Commercial antibodies that may be used to recognize a modified tyrosine kinase receptor include, but are not limited to AMG-102, AMG-479, B1B022OA-5D5, CP-751,871, IMC-A12, R1507, cetuximab, cixutumumab, ertumaxomab, figitumumab, matuzumab, necitumumab, panitumumab, pertuzumab, nimotuzumab, robatumumab, trastuzumab, zalutumumab.

[0042] In one embodiment, the modified endogenous cell surface molecule is a truncated EGFR (tEGFR). The tEGFR is missing Domain I, Domain II, the Juxtamembrane Domain and the Tyrosine Kinase Domain as compared to an unmodified EGFR (Figure 1).

[0043] A gene encoding a modified endogenous cell surface molecule may be used as a cell selection or enrichment marker for a genetically modified population of immune cells (e.g., T cells). The gene encoding a modified endogenous cell surface molecule may be coupled to a gene encoding a tumor targeting chimeric antigen receptor (CAR). These genes may be inserted into a vector to transduce the population of T cells to be genetically modified. After transduction, the cells that are successfully transduced and express the CAR and modified endogenous cell-surface molecule are enriched by any suitable purification method, such as

immunomagnetic purification with anti-biotin microbeads or fluorochrome-conjugated anti-biotin for fluorescence activated cell sorting, using a commercial antibody that recognizes the modified endogenous cell-surface molecule expressed by the transduced cell.

[0044] In another embodiment, a gene encoding a truncated human epidermal growth factor receptor (EGFRt) that lacks the membrane distal EGF-binding domain and the cytoplasmic signaling tail, but retains the extracellular membrane proximal epitope recognized by the FDA-approved anti-EGFR monoclonal antibody (mAb) cetuximab or another anti-EGFR antibody, is constructed and described herein. The EGFRt may be coupled with chimeric antigen receptors specific for a tumor associated antigen. The tumor associated antigen may be CD19, CD20, or CD22, or any other tumor associated antigen, but is preferably CD19 (CD19CAR). The tumor associated antigen is followed by a C-terminal 2A cleavable linker and the coding sequence for EGFRt. The biotinylated-cetuximab may be used in conjunction with commercially available anti-biotin microbeads for the purpose of immunomagnetic purification of the tumor associated antigen/CAR-expressing transductants. In the instance where the tumor associated antigen is CD19 the product is CD19CAR-expressing transductants. Alternatively, the biotinylated-cetuximab may be used in conjunction with Fluorochrome-conjugated anti-biotin for fluorescence activated cell sorting.

[0045] In another embodiment, a modified endogenous cell-surface molecule may be used as a marker for *in vivo* T cell engraftment. For example, when the modified endogenous cell-surface molecule is EGFRt, the EGFRt may be used to track the uptake of the T cells to which it is attached *in vivo* without affecting cellular function of the T cells or the cells to which the T cells are targeted, such as bone marrow cells in a transplant situation. The use of cetuximab conjugated to probes or reporter genes such as sr39TK may be used to improve the tracking potential of EGFRt-expressing cells to patients via PET imaging techniques.

[0046] In a separate embodiment, a modified endogenous cell-surface molecule may be used to induce cell suicide. For example, EGFRt may be used as a suicide gene via cetuximab mediated complement and/or antibody dependent cell mediated cytotoxicity (ADCC) pathways. The fact that cetuximab is a therapeutic FDA-approved antibody further facilitates the suicide gene potential of EGFRt in the clinical setting.

[0047] In other embodiments, the truncated epidermal growth factor receptor (EGFRt) selection epitope or other modified cell-surface molecule is attached to other sequences. One exemplar sequence is the GMCSFR alpha chain signal sequence, which directs surface expression, attached to EGFRt. GMCSFR is encoded by nucleotides 1-66 and EGFRt is encoded by nucleotides 67-1071 of SEQ ID NO: 1. See Figure 7. Also in Figure 7 is the antisense strand (SEQ ID NO: 2) and amino acid (SEQ ID NO: 3) sequences of GMCSFR alpha chain signal sequence linked to EGFRt. Another such sequence is a codon-optimized cDNA sequence encoding an anti-CD19 costimulatory chimeric antigen receptor (CD19R-CD28gg-Zeta(CO)), and a cleavable T2A linker. Cytotoxic T lymphocytes (CTLs) modified to express a CD19-specific chimeric antigen receptor (CAR) that signals via a cytoplasmic costimulatory (CD28) domain fused to the cytoplasmic CD3- ζ domain exhibits superior anti-

tumor potency that can be attributed to CD28-mediated survival and enhanced cytokine production. This construct may be further modified to incorporate a C-terminal 2A cleavable linker followed by the coding sequence for a truncated human EGFR (EGFRt) for the purpose of immunomagnetic purification of CAR-expressing transductants using cetuximab-biotin/anti-biotin microbeads. See the CD19R-CD28gg-Zeta(CO)-T2A-EGFRt sequence attached as Figure 8, SEQ ID NOS: 4 (nucleotide sense strand), 5 (nucleotide anti-sense strand), and 6 (protein). Lentivector transduction of primary human T cells with this codon-optimized cDNA directs the coordinated expression of the CAR and EGFRt (Fig. 9).

[0048] To eliminate variability between transgene expression products otherwise intrinsic to transduction procedures without subsequent selection, a non-immunogenic selection epitope, EGFRt, compatible with immunomagnetic selection using the CliniMACS device (Miltenyi Biotec, Bergisch Gladbach, Germany) was developed. For example, EGFRt is a truncated human epidermal growth factor receptor that lacks the membrane distal EGF-binding domain and the ectoplasmic signaling tail, but retains the extracellular membrane proximal epitope recognized by the commercial anti-EGFR mAb cetuximab. See Figure 1. Biotinylated-cetuximab is applied to immunomagnetic selection in combination with anti-biotin microbeads (Miltenyi). Human OKT3 blasts that had been lentivirally transduced with CD19R-CD28gg-Zeta(CO)-T2A-EGFRt were subjected to immunomagnetic selection using the Miltenyi AutoMACS device, and the frequency of EGFRt+CAR+ T cells was enriched from 22% (pre-selection) to 99% (post-selection) without observable toxicity to the cell preparation (Fig. 3). It is also possible that, instead of or in addition to immunomagnetic sorting, the EGFRt can be purified using fluorescence-based cell sorting techniques.

[0049] Due to the absence of the EGF-binding domains and intracellular signaling domains, EGFRt is inactive when expressed by T cells. Importantly, the EGFRt-selected T cells maintain their desired effector phenotype - including anti-tumor cytotoxic activity mediated by the chimeric antigen receptor that is coordinately expressed with the EGFRt - and remain amenable to established expansion protocols.

[0050] Overall, this EGFRt has various advantages for immunotherapeutic cell products compared to other selection markers that have been previously reported. Specifically, unlike truncated CD4 and CD19, it is not endogenously expressed by subpopulations of lymphocytes. Furthermore, in contrast to truncated CD34 and low affinity nerve growth factor receptor, it does not have any activity that might negatively affect the immune cell product (i.e., in terms of signaling or trafficking). Lastly, it alone can be bound/recognized by a known, preferably commercially available, pharmaceutical grade antibody reagent, i.e., cetuximab. Together, these attributes make EGFRt a superior selection marker for any transfection/transduction system that can be applied to the generation of cell products for adoptive immunotherapy. Thus, EGFRt is well suited to be used as a selection marker for lentivirally transduced T cells of immunotherapeutic relevance.

[0051] Also provided are methods for identifying new therapeutic cell products having the following criteria: a modified endogenous cell-surface molecule, ligand or receptor that is not,

as modified, endogenously expressed in the subject in which it is intended to be therapeutically utilized, does not have any immunoactivity or other functional activity that would hinder the functioning of the product or the subject into which the product is administered, and that it can be recognized by a known antibody.

[0052] The examples are set forth to aid in understanding the invention but are not intended to, and should not be construed to limit its scope in any way. The examples do not include detailed descriptions of conventional methods. Such methods are well known to those of ordinary skill in the art and are described in numerous publications.

Example 1: Generation of EGFRt and Immunomagnetic selection of EGFRt expressing T cells

Materials & Methods

Antibodies and Flow Cytometry

[0053] FITC-, PE- and PerCP-conjugated isotype controls, PerCP-conjugated anti-CD8, FITC conjugated anti-CD4, PE-conjugated anti-IFN γ , PerCP-conjugated anti-CD45 and PE-conjugated streptavidin were obtained from BD Biosciences (San Jose, CA). Biotinylated anti-Fc was purchased from Jackson ImmunoResearch Laboratories, Inc. (Westgrove, PA). PE-conjugated anti-Biotin was purchased from Miltenyi Biotec (Auburn, CA). Biotinylated EGF was purchased from Molecular Probes® Invitrogen (Carlsbad, CA). PE-conjugated anti-EGFR was purchased from Abcam Inc. (Cambridge, MA). All antibodies and biotin-EGF were used according to the manufacturer's instructions. Flow cytometric data acquisition was performed on a FACScalibur (BD Biosciences), and the percentage of cells in a region of analysis was calculated using FCS Express V3 (De Novo Software, Los Angeles, CA).

[0054] For generation of the biotinylated-cetuximab, 200mg of cetuximab (Erbix®) was buffer exchanged (19 hours) to PBS (D-PBS, pH 7.5 \pm 0.1) using a MidGee Hoop Cartridge (UFP-30-E-H42LA) with 527mL. The material at 2mg/mL was then modified at a 20:1 ratio using Sulfo-NHS-LC-Biotin in a reaction that was carried out for 1 hour at room temperature and then diafiltered to remove the excess biotin. The 200 mg of biotinylated cetuximab was then buffer exchanged (18 hours) to PBS (D-PBS, pH 7.5 \pm 0.1) using MidGee Hoop Cartridge (UFP-30-E-H42LA) with 533 mL. Glycerol was added to a final concentration of 20% and then the material was frozen in vials.

Cell lines

[0055] Unless otherwise indicated, all cell lines were maintained in RPMI 1640 (Irvine Scientific, Santa Ana, CA) supplemented with 2 mM L-glutamine (Irvine Scientific), 25 mM *N*-2-hydroxyethylpiperazine-*N'*-2-ethanesulfonic acid (HEPES, Irvine Scientific), 100 U/mL penicillin, 0.1 mg/mL streptomycin (Irvine Scientific), and 10% heat-inactivated fetal calf serum (FCS, Hyclone, Logan, UT), hereafter referred to as culture media (CM).

[0056] To generate T cells, human peripheral blood mononuclear cells (PBMC) were isolated by density gradient centrifugation over Ficoll-Paque (Pharmacia Biotech, Piscataway, NJ) from heparinized peripheral blood obtained from consented healthy donors participating on a City of Hope National Medical Center Internal Review Board-approved protocol. For generation of Line A, washed PBMC were stimulated with 25U/mL IL-2 and a 1:1 (cell:bead) ratio of Dynabeads® Human T expander CD3/CD28 (Invitrogen, Carlsbad, CA). For generation of the other lines, washed PBMC were first autoMACS™ depleted using anti-CD45RA beads (Miltenyi Biotec) per the manufacturer's protocol, and in some cases also depleted with PE-conjugated anti-CD4 (BD Biosciences) with anti-PE beads (Miltenyi Biotec). The resulting cells then underwent autoMACS™ positive selection using biotinylated DREG56 (anti-CD62L) and anti-biotin beads (Miltenyi Biotec) to produce purified CD62L⁺CD45RO⁺ T_{CM}. CD8⁺ cells were further selected in some cases using AutoMACS™ (Miltenyi Biotec) per the manufacturer's protocol. CMV-specific cells were generated by stimulating T cells with 5U/ml rhIL-2 (Chiron, Emeryville, CA) and autologous irradiated viral antigen presenting cells at a 4:1 (responder:stimulator) ratio once a week for three weeks, using 10% human serum instead of FCS to avoid non-specific stimulation. The viral antigen presenting cells were derived from PBMC that had been genetically modified to express CMVpp65 antigen.

[0057] PBMC were resuspended in nucleofection solution using the Human T cell Nucleofector kit (Amaxa Inc., Gaithersburg, MD), and 5×10^7 cells were aliquoted into 0.2-cm cuvettes containing 10µg HygroR-pp65_pEK (or pmaxGFP from Amaxa Inc., as a transfection control) in a final volume of 100 µL/cuvette, and electroporated using the Amaxa Nucleofector I (Amaxa Inc.), program U-14, after which cells were allowed to recover for 6 hours at 37°C prior to γ-irradiation (1200 cGy).

[0058] The CD19CAR-T2A-EGFRt_epHIV7 (pJ02104) and CD19CAR-T2A-EGFRt-T2A-IMPDH2dm_epHIV7 (pJ02111) lentiviral constructs contain a) the chimeric antigen receptor (CAR) sequences consisting of the V_H and V_L gene segments of the CD19-specific FmC63 mAb, an IgG1 hinge-C_{H2}-C_{H3}, the transmembrane and cytoplasmic signaling domains of the costimulatory molecule CD28, and the cytoplasmic domain of the CD3ζ chain[10]; b) the self-cleaving T2A sequence[11]; c) the truncated EGFR sequence (See Fig. 1); and d) the IMPDH2 double mutant that confers MPA-resistance, as indicated. Lentiviral transduction was carried out on T cells that were stimulated with either 30 ng/mL anti-CD3ε (OKT3; Ortho Biotech, Raritan, NJ) (i.e., for Line A) or human CD3/CD28Dynal beads at a 1:10 ratio (i.e., for Lines B, C, D and E) and 25U IL2/ml. Cells were cultured for up to 2 hours at 37°C on RetroNectin® (50ug/ml) coated plates prior to addition of the lentivirus at an MOI of 3 and 5µg/ml polybrene. After 4 hours, warm medium was added to triple to volume, and the cells were then washed

and plated in fresh media after 48 hours. AutoMACS™ sorting of EGFRt-expressing cells was carried out with biotinylated cetuximab and anti-biotin microbeads (Miltenyi Biotec) as per the manufacturer's instructions. Expansion of T cells in rapid expansion medium (REM) involved the incubation of 10^6 T cells with 30 ng/mL anti-CD3 ϵ (OKT3; Ortho Biotech, Raritan, NJ), 5×10^7 γ -irradiated PBMCs (3500 cGy), and 10^7 γ -irradiated LCLs (8000 cGy) in 50 mL CM; with addition of 50U/mL rIL-2 and 10ng/ml rIL-15 (CellGenix) every 48 hours, beginning on day 1. T cells were re-stimulated in this manner every 14 days.

[0059] EBV-transformed lymphoblastoid cell lines (LCLs) were made from PBMC as previously described [13]. LCL-OKT3 cells were generated by resuspending LCL in nucleofection solution using the Amaxa Nucleofector kit T, adding OKT3-2A-Hygromycin_pEK (pJ01609) plasmid at $5\mu\text{g}/10^7$ cells, and electroporating cells using the Amaxa Nucleofector I, program T-20. The resulting LCL - OKT3-2A-Hygro_pEK (cJ03987) were grown in CM containing 0.4mg/ml hygromycin. The mouse myeloma line NS0 (gift from Andrew Raubitschek, City of Hope National Medical Center, Duarte, CA) was resuspended in nucleofection solution using the Nucleofector kit T (Amaxa Inc., Gaithersburg, MD), CD19t-DHFRdm-2A-IL12_pEK (pJ01607) or GFP-IMP2H2dm-2A-IL15_pcDNA3.1(+) (pJ01043) plasmid was added at $5\mu\text{g}/5 \times 10^6$ cells, and cells were electroporated using the Amaxa Nucleofector I, program T-27. The resulting NS0 - CD19t-DHFRdm-2A-IL12_pEK (cJ03935) and NS0 - GFP:IMP2H2-IL15(IL2ss)_pcDNA3.1(+) (cJ02096) were grown in DMEM (Irvine Scientific, Santa Ana, CA) supplemented with 10% heat-inactivated FCS, 25mM HEPES, and 2 mM L-glutamine in the presence of either 0.05uM methotrexate (MTX) or 6 μM mycophenolic acid (MPA). The tumorigenic strain of U251, termed U251T, was a kind gift of Dr. Waldemar Debinski (Wake Forest, NC). U251T-pp65 were generated by lentiviral transduction of U251T with pp65-2A-eGFP-ffluc_epHIV7 (pJ01928) at an MOI of 1. The resulting U251T - pp65-2A-eGFP-ffluc_epHIV7 were then FACS sorted for the GFP⁺ population (cJ05058). The Daudi lymphoma line was purchased from ATCC and grown in media consisting of RPMI 1640 (Irvine Scientific), 2 mM L-Glutamine (Irvine Scientific), 10% heat-inactivated FCS (Hyclone). SupB15 acute lymphoblastic leukemia cells and A431 epidermoid carcinoma cells were purchased from ATCC.

Protein analysis

[0060] Cells (up to 10^7) were lysed with 80 μL of 1% Triton-X lysis buffer containing phosphatase inhibitor cocktail II (Sigma-Aldrich Corp., St. Louis, MO) (1:20 of inhibitor to buffer by volume). 50 μg of protein was loaded in each lane, and Western blots were probed with antibodies from the Phospho-EGF receptor antibody sampler kit (Cell Signaling Technology, Inc., Danvers, MA) followed by IRDye™ 680CW or 800CW conjugated goat anti-rabbit antibodies (LI-COR, Lincoln, NE), as well as the IRDye™ 800 conjugated anti-beta-Actin antibody (LI-COR) as per the manufacturers' instructions. Blots were imaged on the Odyssey Infrared Imaging System (LI-COR).

Chromium-release assays

[0061] The cytolytic activity of T cells was determined by 4-hour chromium-release assay (CRA), where effector cells were seeded into triplicate wells of V-bottom 96-well micro-plates containing 5×10^3 ^{51}Cr -labeled target cells ($\text{Na}_2^{51}\text{CrO}_4$; (5mCi/mL); Amersham Pharmacia, Piscataway, NJ) at various E:T ratios in 200 μL of CM and incubated for 4 hours at 5% CO_2 , 37°C . Plates were centrifuged, and 100 μL of supernatant was removed from each well to assess chromium release using a γ -counter (Packard Cobra II, Downer's Grove, IL). The percent specific lysis was calculated as follows: $100 \times (\text{experimental release} - \text{spontaneous release}) / (\text{maximum release} - \text{spontaneous release})$. Maximum release was determined by measuring the ^{51}Cr content of wells containing labeled targets lysed with 2% SDS.

[0062] Antibody dependent cell mediated cytotoxicity was determined by chromium release as above using 5×10^3 ^{51}Cr -labeled target cells that had been pre-incubated for 90 min with up to 10 $\mu\text{g}/\text{mL}$ of either cetuximab or rituximab (a CD20-specific mAb), washed and then co-incubated with 5×10^5 freshly isolated PBMC.

T cell engraftment and cetuximab mediated suicide in vivo

[0063] For T cell engraftment, six- to ten-week old NOD/Scid IL-2R γ C^{null} mice are injected i.v. on day 0 with 10^7 T cells (Line C). 2×10^7 irradiated (8000 rads) NS0 - GFP:IMPDH2-IL15(IL2ss)_pcDNA3.1(+) (cJ02096) cells are administered i.p. 3 times a week starting on day 0 to provide a systemic supply of human IL-15 *in vivo*. Bone marrow was harvested from euthanized animals and analyzed by flow cytometry. Antibody dependent cell mediated cytotoxicity assays are performed to determine the activity of cetuximab against EGFR⁺ T cells.

Results**Immunomagnetic selection of EGFRt expressing T cells**

[0064] A truncated human EGFR (EGFRt), which contains only the transmembrane domain and extracellular domains III and IV of the full length EGFR, was generated as a non-immunogenic selection epitope compatible with immunomagnetic selection. As shown in the Figure 1 molecular model, the EGFRt retains the ability to be bound by cetuximab, but not have any signaling capacity due to the absence of the intracellular domains. Furthermore, it

lacks the N-terminal domain required for EGF-binding.

[0065] To immunomagnetically select for EGFRt-expressing cells, biotinylated-cetuximab was generated (Fig. 2a, b) to be used in conjunction with commercially available anti-biotin microbeads and an AutoMACS™ separator (Miltenyi Biotec) (Fig. 2c). Lentiviral transduction of various T cell lines with EGFRt-containing constructs, where the EGFRt gene was separated from other genes of interest on either one or both ends with the self-cleaving T2A sequence, consistently resulted in surface detection of the EGFRt molecule on less than 40% of the cells (Fig. 2d). Surface detection may also be accomplished with a EGFRt-sr39TK fusion. Immunomagnetic selection allowed for recovery of EGFRt⁺ T cell populations with greater than 90% purity. T cell populations that underwent this transduction and selection procedure included anti-CD3/anti-CD28 bead stimulated T cell blasts (for Line A), central memory (CD45RO⁺CD62L⁺ T_{CM}) derived T cells (for Lines B, C and E), which in some cases were also pre-selected for CMV specificity (via the endogenous TCR; for Line B) or CD8 expression (for Line C), as well as effector memory (CD62L⁻ CD45RO⁺ T_{EM}) derived T cells (for line D). These data show that EGFRt can successfully be used as a selection marker for various sources of T cell transductants, even when the original transduction efficiency was as low as 2%.

Inactivity of EGFRt on selected T cells

[0066] To confirm that the EGFRt is inactive, Western immunoblot analyses for EGFR phosphorylation were carried out on the EGFRt-selected T cells after culture with either EGF or cetuximab. As expected, cetuximab did not induce EGFR phosphorylation above background even in the EGFR⁺ cell line A431 (Fig 3a). Furthermore, in contrast to that seen with the A431 cells, no phosphorylation was seen in lysates of Line A after co-incubation with EGF. Indeed, using biotinylated EGF, flow cytometric analysis confirmed that EGF cannot bind the EGFRt-selected T cells (Fig. 3b), as expected due to the truncation in its N-terminus. These EGFRt⁺ T cells were also not recognized by another anti-EGFR antibody distinct from cetuximab.

Maintenance of effector phenotype in expanded EGFRt⁺ CD19CAR⁺ T cells

[0067] Directly after AutoMACS™ separation, the selected T cells were expanded 30-fold or greater within 12 days after REM stimulation with OKT3, irradiated PBMC feeders and LCL, IL-2 and IL-15 (Fig. 4a). Flow cytometric analysis of the resulting expanded EGFRt⁺ T cells further confirmed that they express the CD19CAR and T cell markers such as CD8, TCR, CD3, perforin, granzyme, etc. (Fig. 4b). Furthermore, CD19CAR-directed cytotoxic activity of these EGFRt-selected lines is evident in chromium release assays using CD19-expressing tumor targets (Fig. 4c). A direct comparison of the CD19-specific reactivity of Line E versus its non-selected or 'parental' counterpart shows that there is enhanced CD19CAR-mediated

cytotoxicity upon EGFRt-selection. In addition, the CMV-specific T_{CM}-derived CD19CAR⁺EGFRt⁺ Line B cells also show cytotoxic activity through their endogenous T cell receptor against targets expressing CMV-pp65 antigen.

[0068] For the CD19CAR⁺EGFRt⁺IMPDH2dm⁺ Line E, the ability of the inosine monophosphate dehydrogenase 2 double mutant (IMPDH2dm) to confer resistance to the IMPDH2-inhibitor mycophenolic acid (MPA; a common immunosuppressant used to prevent rejection in organ transplantation) was also tested. Upon culture in 1 uM MPA, the survival and/or proliferation of Line E cells is not inhibited (Fig. 4d). This is in contrast to the inhibition seen with a control T cell line that lacks expression of the IMPDH2dn gene. These data provide further evidence that EGFRt-mediated selection results in the corresponding selection of the other genes present in the lentiviral construct used to transduce T cells.

Tracking of EGFRt⁺ T cells in vivo

[0069] To test the potential for detecting in vivo engrafted T cells, bone marrow cells collected from mice that had been engrafted with CD19CAR⁺EGFRt⁺ Line C was analyzed by flow cytometry using biotinylated cetuximab (Fig. 5). Control mice that did not receive T cells revealed that there was some cross-reaction of the cetuximab against murine EGFR. Thus, it was determined that successful detection of engrafted Line C cells required double staining for both human CD45 and EGFRt. Cells may also analyzed using immunohistochemistry to determine potential for screening biopsy material.

Cetuximab mediated cytotoxicity of EGFRt⁺ T cells

[0070] Because cetuximab is known to lyse EGFR-expressing cells via antibody dependent cell mediated cytotoxicity (ADCC), assays were performed to determine the ADCC activity of cetuximab against EGFRt⁺ T cells (Fig. 6). Using ⁵¹Cr-labeled Line A cells as targeted and freshly isolated human PBMC as effectors, cetuximab was found to significantly mediate chromium-release above that seen when using the CD20-specific humanized mAb Rituxan.

Example of therapeutic use of EGFRt⁺ T cells

[0071] Adult subjects with high-risk intermediate grade β -cell lymphomas who are candidates for an autologous myeloablative stem cell transplant procedure may receive post-transplant immunotherapy with adoptively transferred autologous Tcm-derived CD19R⁺ CD8⁺ EGFRt⁺ T cell grafts. A leukapheresis product collected from each patient undergoes selection of Tcm, transduction with clinical grade CD19CART2A-EGFRt_epHIV7, and then selection and

expansion of the EGFRt⁺ cells in a closed system. After the resulting cell products have undergone quality control testing (including sterility and tumor specific cytotoxicity tests), they are cryopreserved. Meanwhile, following leukapheresis, study participants commence with standard salvage chemotherapy, with mobilization for auto HSC collection with cytoreductive chemotherapy and G-CSF. Since the EGFRt-selected, CD19-specific T cells will also target normal CD20⁺ (CD19⁺) B cells, the B cell numbers can first be lowered using Rituximab™ to reduce the recipient's inflammatory response upon receiving the genetically modified CTL and also increase availability of infused T cells to immediately target lymphoma cells. Furthermore, Rituximab™ may blunt a humoral immune response against the genetically modified T cells. If Rituximab™ is not given as part of the Salvage/Priming chemotherapy regimen, research participants may receive a single intravenous infusion of Rituximab™ (chimeric anti-CD20 antibody) at 375 mg/m² within 4-weeks of the planned auto-HSCT procedure. Rituximab™ infusion would be carried out per standard practice including premedication with diphenhydramine and acetaminophen and hydrocortisone. On Day +2 or Day +3 after HSCT, the autologous cryopreserved CD19R⁺ CD8⁺ EGFRt⁺ T cell product will be transported, thawed and infused at the patient's bedside. Research participants can be pre-medicated at least 30 minutes prior to T cell infusion with 15mg/kg of acetaminophen P.O. (max. 650mg.) and diphenhydramine 0.5-1 mg/kg I.V. (max dose 50mg). Clinical and laboratory correlative follow-up studies can then be performed at the physician's discretion, and may include quantitative RT-PCR studies for the presence of CD19-expressing lymphoma cells and/or the adoptively transferred T cells; FDG-PET and/or CT scans; bone marrow examination for disease specific pathologic evaluation; lymph node biopsy; and/or long-term follow up per the guidelines set forth by the FDA's Biologic Response Modifiers Advisory Committee that apply to gene transfer studies. Figure 10 provides a possible schematic for clinical testing of the present products and methods.

[0072] The present invention is not to be limited in scope by the specific embodiments disclosed in the examples which are intended as illustrations of a few aspects of the invention.

REFERENCES

[0073]

1. 1. Berger, C, Flowers, ME, Warren, EH, and Riddell, SR (2006). Analysis of transgene-specific immune responses that limit the in vivo persistence of adoptively transferred HSV-TK-modified donor T cells after allogeneic hematopoietic cell transplantation. *Blood* 107: 2294-302.
2. 2. Tey, SK, Dotti, G, Rooney, CM, Heslop, HE, and Brenner, MK (2007). Inducible caspase 9 suicide gene to improve the safety of allodepleted T cells after haploidentical stem cell transplantation. *Biol Blood Marrow Transplant* 13: 913-24.
3. 3. Fehse, B, Richters, A, Putimtseva-Scharf, K, Klump, H, Li, Z, Ostertag, W, et al. (2000). CD34 splice variant: an attractive marker for selection of gene-modified cells.

Mol Ther 1: 448-56.

4. 4. Gaines, P, and Wojchowski, DM (1999). pIRES-CD4t, a dicistronic expression vector for MACS- or FACS-based selection of transfected cells. *Biotechniques* 26: 683-8.
5. 5. Fehse, B, Uhde, A, Fehse, N, Eckert, HG, Clausen, J, Ruger, R, et al. (1997). Selective immunoaffinity-based enrichment of CD34+ cells transduced with retroviral vectors containing an intracytoplasmatically truncated version of the human low-affinity nerve growth factor receptor (deltaLNGFR) gene. *Hum Gene Ther* 8: 1815-24.
6. 6. Lemoine, FM, Mesel-Lemoine, M, Cherai, M, Gallot, G, Vie, H, Leclercq, V, et al. (2004). Efficient transduction and selection of human T-lymphocytes with bicistronic Thy1/HSV1-TK retroviral vector produced by a human packaging cell line. *J Gene Med* 6: 374-86.
7. 7. Li, S, Schmitz, KR, Jeffrey, PD, Wiltzius, JJ, Kussie, P, and Ferguson, KM (2005). Structural basis for inhibition of the epidermal growth factor receptor by cetuximab. *Cancer Cell* 7: 301-11.
8. 8. Dawson, JP, Berger, MB, Lin, CC, Schlessinger, J, Lemmon, MA, and Ferguson, KM (2005). Epidermal growth factor receptor dimerization and activation require ligand-induced conformational changes in the dimer interface. *Mol Cell Biol* 25: 7734-42.
9. 9. Lange, C, Li, Z, Fang, L, Baum, C, and Fehse, B (2007). CD34 modulates the trafficking behavior of hematopoietic cells in vivo. *Stem Cells Dev* 16: 297-304.
10. 10. Kowolik, CM, Topp, MS, Gonzalez, S, Pfeiffer, T, Olivares, S, Gonzalez, N, et al. (2006). CD28 costimulation provided through a CD19-specific chimeric antigen receptor enhances in vivo persistence and antitumor efficacy of adoptively transferred T cells. *Cancer Res* 66: 10995-1004.
11. 11. Szymczak, AL, Workman, CJ, Wang, Y, Vignali, KM, Dilioglou, S, Vanin, EF, et al. (2004). Correction of multi-gene deficiency in vivo using a single 'self-cleaving' 2A peptide-based retroviral vector. *Nat Biotechnol* 22: 589-94.
12. 12. Yam, P, Jensen, M, Akkina, R, Anderson, J, Villacres, MC, Wu, J, et al. (2006). Ex vivo selection and expansion of cells based on expression of a mutated inosine monophosphate dehydrogenase 2 after HIV vector transduction: effects on lymphocytes, monocytes, and CD34+ stem cells. *Mol Ther* 14: 236-44.
13. 13. Pelloquin, F, Lamelin, JP, and Lenoir, GM (1986). Human B lymphocytes immortalization by Epstein-Barr virus in the presence of cyclosporin A. *In Vitro Cell Dev Biol* 22: 689-94.

SEQUENCE LISTING

[0074]

<110> JENSEN, Michael C

<120> TRUNCATED EPIDERMAL GROWTH FACTOR RECEPTOR (EGFRt) FOR
TRANSDUCED T CELL SELECTION

<130> 54435.8070.WO00

<140> PCT/US2010/055329

<141> 2010-11-03

<150> US 61/257,567

<151> 2009-11-03

<160> 6

<170> PatentIn version 3.5

<210> 1

<211> 1071

<212> DNA

<213> Homo sapiens

<400> 1

atgcttctcc	tggtgacaag	ccttctgctc	tgtgagttac	cacacccagc	attcctcctg	60
atcccacgca	aagtgtgtaa	cggaataggt	attggtgaat	ttaaagactc	actctccata	120
aatgctacga	atattaaaca	cttcaaaaac	tgcacctcca	tcagtggcga	tctccacatc	180
ctgccggtgg	catttagggg	tgactccttc	acacatactc	ctcctctgga	tccacaggaa	240
ctggatattc	tgaaaaccgt	aaaggaaatc	acagggtttt	tgctgattca	ggcttggcct	300
gaaaacagga	cggacctcca	tgcccttgag	aacctagaaa	tcatacgcg	caggaccaag	360
caacatggtc	agttttctct	tgcagtcgtc	agcctgaaca	taacatcctt	gggattacgc	420
tccctcaagg	agataagtga	tggagatgtg	ataatttcag	gaaacaaaaa	tttgtgctat	480
gcaaatacaa	taaaactggaa	aaaactgttt	gggacctccg	gtcagaaaac	caaaattata	540
agcaacagag	gtgaaaacag	ctgcaaggcc	acaggccagg	tctgccatgc	cttgtgctcc	600
cccgagggtc	gctggggccc	ggagcccagg	gactgctgtc	cttgccggaa	tgtcagccga	660
ggcaggggat	gcgtggacaa	gtgcaacctt	ctggagggtg	agccaaggga	gtttgtggag	720
aactctgagt	gcatacagtg	ccacccagag	tgacctgcctc	aggccatgaa	catcacctgc	780
acaggacggg	gaccagacaa	ctgtatccag	tgtgcccact	acattgacgg	ccccactgc	840
gtcaagacct	gcccggcagg	agtcatggga	gaaaacaaca	ccctggtctg	gaagtacgca	900
gacgccggcc	atgtgtgcca	cctgtgccat	ccaaactgca	cctacggatg	cactgggcca	960
ggtcttgaag	gctgtccaac	gaatgggcct	aagatcccgt	ccatcgccac	tgggatgggtg	1020
ggggccctcc	tcttgcctgt	ggtggtggcc	ctggggatcg	gcctcttcat	g	1071

<210> 2

<211> 1071

<212> DNA

<213> Homo sapiens

<400> 2

tacgaagagg	accactgttc	ggaagacgag	acactcaatg	gtgtgggtcg	taaggaggac	60
taggggtcgt	ttcacacatt	gccttatcca	taaccactta	aatttctgag	tgagaggtat	120

```

ttacgatgct tataatttgt gaagtttttg acgtggaggt agtcaccgct agaggtgtag      180
gacggccacc gtaaatcccc actgaggaag tgtgtatgag gaggagacct aggtgtcctt      240
gacctataag acttttgcca ttcccttttag tgtcccaaaa acgactaagt ccgaaccgga      300
cttttgtcct gcctggaggt acggaactc ttggatcttt agtatgcgcc gtcctggttc      360
gttgtaccag tcaaaagaga acgtcagcag tcggacttgt attgtaggaa ccctaatgcg      420
agggagtcc tctattcact acctctacac tattaagtc ctttgttttt aaacacgata      480
cgtttatgtt atttgacctt ttttgacaaa ccctggaggg cagtcttttg gttttaatat      540
tcgttgtctc cacttttgtc gacgttccgg tgtccgggcc agacggtacg gaacacgagg      600
gggctcccga cgaccccggg cctcgggtcc ctgacgcaga gaacggcctt acagtgcgct      660
ccgtccctta cgcacctgtt cacgttgga gacctccac tcggttccct caaacacctc      720
ttgagactca cgtatgtcac ggtgggtctc acggacggag tccggtactt gtagtggacg      780
tgtcctgccc ctggtctgtt gacataggtc acacgggtga tgtaactgcc gggggtgacg      840
cagttctgga cgggccgtcc tcagtaccct cttttgttgt gggaccagac cttcatgcgt      900
ctgcggccgg tacacacggt ggacacggtg ggtttgacgt ggatgcctac gtgaccgggt      960
ccagaacttc cgacaggttg cttaccggga ttctagggca ggtagcgggtg accctaccac     1020
ccccgggagg agaacgacga ccaccacgg gaccctagc cggagaagta c                     1071

```

<210> 3

<211> 357

<212> PRT

<213> Homo sapiens

<400> 3

```

Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
 1          5          10          15

Ala Phe Leu Leu Ile Pro Arg Lys Val Cys Asn Gly Ile Gly Ile Gly
 20          25          30

Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe
 35          40          45

Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala
 50          55          60

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

Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile
 85          90          95

Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu
100          105          110

Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala
115          120          125

Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu
130          135          140

Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr
145          150          155          160

```


Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys
165 170 175

Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly
180 185 190

Gln Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu
195 200 205

Pro Arg Asp Cys Val Ser Cys Arg Asn Val Ser Arg Gly Arg Glu Cys
210 215 220

Val Asp Lys Cys Asn Leu Leu Glu Gly Glu Pro Arg Glu Phe Val Glu
225 230 235 240

Asn Ser Glu Cys Ile Gln Cys His Pro Glu Cys Leu Pro Gln Ala Met
245 250 255

Asn Ile Thr Cys Thr Gly Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala
260 265 270

His Tyr Ile Asp Gly Pro His Cys Val Lys Thr Cys Pro Ala Gly Val
275 280 285

Met Gly Glu Asn Asn Thr Leu Val Trp Lys Tyr Ala Asp Ala Gly His
290 295 300

Val Cys His Leu Cys His Pro Asn Cys Thr Tyr Gly Cys Thr Gly Pro
305 310 315 320

Gly Leu Glu Gly Cys Pro Thr Asn Gly Pro Lys Ile Pro Ser Ile Ala
325 330 335

Thr Gly Met Val Gly Ala Leu Leu Leu Leu Val Val Ala Leu Gly
340 345 350

Ile Gly Leu Phe Met
355

<210> 4

<211> 3186

<212> DNA

<213> Homo sapiens

<400> 4

atgctgctgc tggtagaccag cctgctgctg tgcgagctgc cccaccccg ctttctgctg	60
atccccgaca tccagatgac ccagaccacc tccagcctga gcgccagcct gggcgaccgg	120
gtgaccatca gctgccgggc cagccaggac atcagcaagt acctgaactg gtatcagcag	180
aagcccgacg gcaccgtcaa gctgctgac taccacacca gccggctgca cagcggcgtg	240
cccagccggt tttagcggcag cggctccggc accgactaca gcctgaccat ctccaacctg	300
gaacaggaag atatcgccac ctacttttgc cagcagggca acacactgcc ctacaccttt	360
ggcggcggaa caaagctgga aatcaccggc agcacctccg gcagcggcaa gcctggcagc	420
ggcgagggca gcaccaaggg cgaggtgaag ctgcaggaaa gcggccctgg cctggtggcc	480

cccagccaga	gcctgagcgt	gacctgcacc	gtgagcggcg	tgagcctgcc	cgactacggc	540
gtgagctgga	tccggcagcc	ccccaggaag	ggcctggaat	ggctggggcgt	gatctggggc	600
agcgagacca	cctactacaa	cagcgccctg	aagagccggc	tgaccatcat	caaggacaac	660
agcaagagcc	agggtgttcct	gaagatgaac	agcctgcaga	ccgacgacac	cgccatctac	720
tactgcgcca	agcactacta	ctacggcggc	agctacgcca	tggactactg	gggccagggc	780
accagcgtga	ccgtgagcag	cgagagcaag	tacggccctc	cctgcccccc	ttgccctgcc	840
cccaggttcc	tgggcggacc	cagcgtgttc	ctgttcccc	ccaagcccaa	ggacaccctg	900
atgatcagcc	ggacccccga	ggtgacctgc	gtggtggtgg	acgtgagcca	ggaagatccc	960
gaggtccagt	tcaattggta	cgtggacggc	gtggaagtgc	acaacgccaa	gaccaagccc	1020
agagaggaac	agttcaacag	cacctaccgg	gtggtgtctg	tgctgaccgt	gctgcaccag	1080
gactggctga	acggcaaaga	atacaagtgc	aaggtgtcca	acaagggcct	gcccagcagc	1140
atcgaaga	ccatcagcaa	ggccaagggc	cagcctcgcg	agccccaggt	gtacaccctg	1200
cctccctccc	aggaagagat	gaccaagaac	caggtgtccc	tgacctgcct	ggtgaagggc	1260
SEQUENCE BREAK						
ttctacccca	gcgacatcgc	cgtggagtgg	gagagcaacg	gccagcctga	gaacaactac	1320
aagaccaccc	ctcccgtgct	ggacagcgac	ggcagcttct	tcctgtacag	ccggctgacc	1380
gtggacaaga	gccggtggca	ggaaggcaac	gtcttttagct	gcagcgtgat	gcacgagggc	1440
ctgcacaacc	actacaccca	gaagagcctg	agcctgtccc	tgggcaagat	gttctgggtg	1500
ctggtggtgg	tgggcggggg	gctggcctgc	tacagcctgc	tggtgacagt	ggccttcac	1560
atcttttggg	tgcggagcaa	gcggagcaga	ggcggccaca	gcgactacat	gaacatgacc	1620
cccagacggc	ctggccccac	ccggaagcac	taccagccct	acgccccacc	cagggacttt	1680
gccgcctacc	ggtccggcgg	agggcgggtg	aagttagca	gaagcgccga	cgccccctgc	1740
taccagcagg	gccagaatca	gctgtacaac	gagctgaacc	tgggcagaag	ggaagagtac	1800
gacgtcctgg	ataagcggag	aggccgggac	cctgagatgg	gcggcaagcc	tcggcggaag	1860
aacccccagg	aaggcctgta	taacgaactg	cagaaagaca	agatggccga	ggcctacagc	1920
gagatcggca	tgaagggcga	gcggagggcg	ggcaagggcc	acgacggcct	gtatcagggc	1980
ctgtccaccg	ccaccaagga	tacctacgac	gccctgcaca	tgaggccct	gcccccaagg	2040
ctcgagggcg	gcggagaggg	cagagggaagt	cttctaacat	gcggtgacgt	ggaggagaat	2100
cccgcccta	ggatgcttct	cctggtgaca	agccttctgc	tctgtgagtt	accacaccca	2160
gcattcctcc	tgatcccacg	caaagtgtgt	aacggaatag	gtattggtga	atttaaagac	2220
tcactctcca	taaagtctac	gaatattaaa	cacttcaaaa	actgcacctc	catcagtggc	2280
gatctccaca	tcctgccggg	ggcatttagg	ggtgactcct	tcacacatac	tcctcctctg	2340
gatccacagg	aactggatat	tctgaaaacc	gtaaaggaaa	tcacaggggt	tttgctgatt	2400
caggcttggc	ctgaaaacag	gacggacctc	catgcctttg	agaacctaga	aatcatacgc	2460
ggcaggacca	agcaacatgg	tcagttttct	cttgacgtcg	tcagcctgaa	cataacatcc	2520
ttgggattac	gctccctcaa	ggagataagt	gatggagatg	tgataatttc	aggaaacaaa	2580
aatttgctgt	atgcaaatac	aataaactgg	aaaaaactgt	ttgggacctc	cggtcagaaa	2640
acaaaatta	taagcaacag	agggtgaaac	agctgcaagg	ccacaggcca	ggtctgccat	2700
gccttgctgt	cccccgaggg	ctgctggggc	ccggagccca	gggactgcgt	ctcttgccgg	2760
aatgtcagcc	gaggcagggg	atgcgtggac	aagtgaacc	ttctggaggg	tgagccaagg	2820
qaqtttqtq	aqaaactctga	gtqcatacaq	tqccacccaq	aqtgccctqcc	tcaqqccatq	2880

```

aacatcacct gcacaggacg gggaccagac aactgtatcc agtgtgcca ctacattgac 2940
ggccccact gcgtcaagac ctgcccggca ggagtcattg gagaaaacaa caccctggtc 3000
tggaagtacg cagacgccgg ccatgtgtgc cacctgtgcc atccaaactg cacctacgga 3060
tgcactgggc caggtcttga aggctgtcca acgaatgggc ctaagatccc gtccatcgcc 3120
actgggatgg tgggggccct cctcttgctg ctggtggtgg ccctggggat cggcctcttc 3180

atgtga 3186

```

<210> 5

<211> 3186

<212> DNA

<213> Homo sapiens

<400> 5

```

tacgacgacg accactgggc ggacgacgac acgctcgacg gggtagggcg gaaagacgac 60
taggggctgt aggtctactg ggtctggtgg aggtcggact cgcggtcgga cccgctggcc 120
cactggtagt cgacggcccc gtcggtcctg tagtcgttca tggacttgac catagtcgtc 180
ttcgggctgc cgtggcagtt cgacgactag atggtgtggt cggccgacgt gtcgcccac 240
gggtcggcca aatcgccgct gccgaggccg tggctgatgt cggactggta gaggttgga 300
cttgtccttc tatagcgggt gatgaaaacg gtcgtcccgt tgtgtgacgg gatgtggaaa 360
ccgccgcctt gtttcgacct ttagtggccg tcgtggaggc cgtcgccgtt cggaccgtcg 420
ccgctcccgt cgtggttccc gctccacttc gacgtccttt cgcggggacc ggaccaccgg 480
gggtcggctc cggactcgca ctggacgtgg cactcgccgc actcggacgg gctgatgccg 540
cactcgacct aggccgtcgg ggggtccttc ccggacctta ccgaccgcga ctagaccccg 600
tcgctctggt ggatgatggt gtcgcgggac ttctcgccg actggtagta gttcctgttg 660
tcgttctcgg tccacaagga cttctacttg tcggacgtct ggctgctgtg gcggtagatg 720
atgacgcggt tcgtgatgat gatgccgccg tcgatcggtt acctgatgac cccggtcccc 780
tggtcgcact ggcactcgtc gctctcgttc atgccgggag ggacgggggg aacgggacgg 840
gggtcaagg acccgctcgg gtcgcacaag gacaaggggg ggttcgggtt cctgtgggac 900
tactagtcgg cctgggggct ccactggacg caccaccacc tgcactcggc cttcttaggg 960
ctccaggtca agttaacat gcacctgccg cacttcacg tgttgcggtt ctggttcggg 1020
tctctccttg tcaagttgtc gtggatggcc caccacagac acgactggca cgacgtggtc 1080
ctgaccgact tgccgtttct tatgttcacg ttccacaggt tgttcccggg cgggtcgtcg 1140
tagcttttct ggtagtcgtt ccggttcccc gtcggagcgc tcggggtcca catgtgggac 1200
ggagggaggg tccttctcta ctggttcttg gtccacaggg actggacgga ccacttccc 1260
aagatggggc cgctgtagcg gcacctcacc ctctcgttgc cggtcggact cttgttgatg 1320
ttctggtggg gagggcacga cctgtcgctg ccgtcgaaga aggacatgtc ggccgactgg 1380
cacctgttct cggccaccgt cttccgttg cagaaatcga cgtcgacta cgtgctccgg 1440
gacgtgttgg tgatgtgggt cttctcggac tcggacaggg acccgttcta caagaccac 1500
gaccaccacc acccgcccca cgaccggacg atgtcggacg accactgtca ccggaagtag 1560
tagaaaaccc acgcctcgtt cgcctcgtct ccgccggtgt cgctgatgta cttgtactgg 1620

```

```

-----

```

```

gggtctgccc gaccgggggtg ggcccttcgtg atggctcggga tgcgggggtgg gtccctgaaa 1680
cggcggatgg ccaggccgcc tcccgccac ttcaagtcgt ctctcgggct gcggggacgg 1740
atggctgtcc cggcttagt cgacatgttg ctgcacttg acccgcttct ccttctcatg 1800
ctgcaggacc tattgcctc tccggccctg ggactctacc cgcggttcgg agccgccttc 1860
ttgggggtcc ttccggacat attgcttgac gtctttctgt tctaccggct ccggatgtcg 1920
ctctagccgt acttcccgt cgccctccgc ccgttcccgg tgcctccgga catagtccc 1980
gacagggtggc ggtggttcct atggatgctg cgggacgtgt acgtccggga cgggggttcc 2040
gagctccgc cgctctccc gtctcttca gaagattgta cgccactgca cctcctctta 2100
gggcccggat cctacgaaga ggaccactgt tcggaagacg agacactcaa tgggtgtgggt 2160
cgtaaggagg actagggtgc gtttcacaca ttgccttct cataaccact taaatttctg 2220
agtgagaggt attacgatg cttataattt gtgaagtttt tgacgtggag gtagtcaccg 2280
ctagagggtg aggacggcca ccgtaaattc cactgagga agtgtgtatg aggaggagac 2340
ctagggtgcc ttgacctata agacttttgg catttccttt agtgtcccaa aaacgactaa 2400
gtccgaaccg gacttttgtc ctgcctggag gtacggaaac tcttgatct ttagtatgcg 2460
ccgtcctggt tcgttgatcc agtcaaaaga gaacgtcagc agtcggactt gtattgtagg 2520
aaccctaag cgagggagtt cctctattca ctacctctac actattaaag tcctttgttt 2580
ttaaacacga tacgtttatg ttatttgacc ttttttgaca aaccctggag gccagtcttt 2640
tggttttaat attcgttgtc tccacttttg tcgacgttcc ggtgtccggc ccagacggta 2700
cggaacacga gggggctccc gacgacccc ggccctcggg ccctgacgca gagaacggcc 2760
ttacagtcgg ctccgtccct tacgcacctg ttcacgttg aagacctccc actcggttcc 2820
ctcaaacacc tcttgagact cacgtatgtc acgggtgggtc tcacggacgg agtccggtag 2880
ttgtagtgga cgtgtcctgc ccctggctg ttgacatagg tcacacgggt gatgtaactg 2940
ccgggggtga cgcagttctg gacgggccgt cctcagtacc ctcttttggt gtgggaccag 3000
accttcatgc gtctgcggcc ggtacacacg gtggacacgg taggtttgac gtggatgcct 3060
acgtgacccg gtccagaact tccgacaggt tgcttaccgg gattctaggg caggtagcgg 3120
tgaccctacc acccccggga ggagaacgac gaccaccacc gggacccta gccggagaag 3180
tacact

```

<210> 6

<211> 1061

<212> PRT

<213> Homo sapiens

<400> 6

```

Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1      5      10      15

```

```

Ala Phe Leu Leu Ile Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser
20      25      30

```

```

Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser
35      40      45

```

```

Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly
50      55      60

```

```

Thr Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Glu Val

```

65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
Pro	Ser	Arg	Phe	Ser ₈₅	Gly	Ser	Gly	Ser	Gly ₉₀	Thr	Asp	Tyr	Ser	Leu ₉₅	Thr
Ile	Ser	Asn	Leu ₁₀₀	Glu	Gln	Glu	Asp	Ile ₁₀₅	Ala	Thr	Tyr	Phe	Cys ₁₁₀	Gln	Gln
Gly	Asn	Thr ₁₁₅	Leu	Pro	Tyr	Thr	Phe ₁₂₀	Gly	Gly	Gly	Thr	Lys ₁₂₅	Leu	Glu	Ile
Thr	Gly ₁₃₀	Ser	Thr	Ser	Gly	Ser ₁₃₅	Gly	Lys	Pro	Gly	Ser ₁₄₀	Gly	Glu	Gly	Ser
Thr ₁₄₅	Lys	Gly	Glu	Val	Lys ₁₅₀	Leu	Gln	Glu	Ser	Gly ₁₅₅	Pro	Gly	Leu	Val	Ala ₁₆₀
Pro	Ser	Gln	Ser	Leu ₁₆₅	Ser	Val	Thr	Cys	Thr ₁₇₀	Val	Ser	Gly	Val	Ser ₁₇₅	Leu
Pro	Asp	Tyr	Gly ₁₈₀	Val	Ser	Trp	Ile	Arg ₁₈₅	Gln	Pro	Pro	Arg	Lys ₁₉₀	Gly	Leu
Glu	Trp	Leu ₁₉₅	Gly	Val	Ile	Trp	Gly ₂₀₀	Ser	Glu	Thr	Thr	Tyr ₂₀₅	Tyr	Asn	Ser
Ala	Leu ₂₁₀	Lys	Ser	Arg	Leu	Thr ₂₁₅	Ile	Ile	Lys	Asp	Asn ₂₂₀	Ser	Lys	Ser	Gln
Val ₂₂₅	Phe	Leu	Lys	Met	Asn ₂₃₀	Ser	Leu	Gln	Thr	Asp ₂₃₅	Asp	Thr	Ala	Ile	Tyr ₂₄₀
Tyr	Cys	Ala	Lys	His ₂₄₅	Tyr	Tyr	Tyr	Gly	Gly ₂₅₀	Ser	Tyr	Ala	Met	Asp ₂₅₅	Tyr
Trp	Gly	Gln	Gly ₂₆₀	Thr	Ser	Val	Thr	Val ₂₆₅	Ser	Ser	Glu	Ser	Lys ₂₇₀	Tyr	Gly
Pro	Pro	Cys ₂₇₅	Pro	Pro	Cys	Pro	Ala ₂₈₀	Pro	Glu	Phe	Leu	Gly ₂₈₅	Gly	Pro	Ser
Val	Phe ₂₉₀	Leu	Phe	Pro	Pro	Lys ₂₉₅	Pro	Lys	Asp	Thr	Leu ₃₀₀	Met	Ile	Ser	Arg
Thr ₃₀₅	Pro	Glu	Val	Thr	Cys ₃₁₀	Val	Val	Val	Asp	Val ₃₁₅	Ser	Gln	Glu	Asp	Pro ₃₂₀
Glu	Val	Gln	Phe	Asn ₃₂₅	Trp	Tyr	Val	Asp	Gly ₃₃₀	Val	Glu	Val	His	Asn ₃₃₅	Ala
Lys	Thr	Lys	Pro ₃₄₀	Arg	Glu	Glu	Gln	Phe ₃₄₅	Asn	Ser	Thr	Tyr	Arg ₃₅₀	Val	Val
Ser	Val	Leu ₃₅₅	Thr	Val	Leu	His	Gln ₃₆₀	Asp	Trp	Leu	Asn	Gly ₃₆₅	Lys	Glu	Tyr
Lys	Cys ₃₇₀	Lys	Val	Ser	Asn	Lys ₃₇₅	Gly	Leu	Pro	Ser	Ser ₃₈₀	Ile	Glu	Lys	Thr
Ile ₃₈₅	Ser	Lys	Ala	Lys	Gly ₃₉₀	Gln	Pro	Arg	Glu	Pro ₃₉₅	Gln	Val	Tyr	Thr	Leu ₄₀₀

Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
 405 410 415
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 420 425 430
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 435 440 445
 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser
 450 455 460
 Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 465 470 475 480
 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 485 490 495
 Met Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
 500 505 510
 Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
 515 520 525
 Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
 530 535 540
 Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
 545 550 555 560
 Ala Ala Tyr Arg Ser Gly Gly Gly Arg Val Lys Phe Ser Arg Ser Ala
 565 570 575
 Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
 580 585 590
 Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
 595 600 605
 Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
 610 615 620
 Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
 625 630 635 640
 Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
 645 650 655
 Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
 660 665 670
 His Met Gln Ala Leu Pro Pro Arg Leu Glu Gly Gly Gly Glu Gly Arg
 675 680 685
 Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Arg
 690 695 700
 Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
 705 710 715 720

Ala Phe Leu Leu Ile Pro Arg Lys Val Cys Asn Gly Ile Gly Ile Gly
 725 730 735
 Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe
 740 745 750
 Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala
 755 760 765
 Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu
 770 775 780
 Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile
 785 790 795 800
 Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu
 805 810 815
 Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala
 820 825 830
 Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu
 835 840 845
 Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr
 850 855 860
 Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys
 865 870 875 880
 Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly
 885 890 895
 Gln Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu
 900 905 910
 Pro Arg Asp Cys Val Ser Cys Arg Asn Val Ser Arg Gly Arg Glu Cys
 915 920 925
 Val Asp Lys Cys Asn Leu Leu Glu Gly Glu Pro Arg Glu Phe Val Glu
 930 935 940
 Asn Ser Glu Cys Ile Gln Cys His Pro Glu Cys Leu Pro Gln Ala Met
 945 950 955 960
 Asn Ile Thr Cys Thr Gly Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala
 965 970 975
 His Tyr Ile Asp Gly Pro His Cys Val Lys Thr Cys Pro Ala Gly Val
 980 985 990
 Met Gly Glu Asn Asn Thr Leu Val Trp Lys Tyr Ala Asp Ala Gly His
 995 1000 1005
 Val Cys His Leu Cys His Pro Asn Cys Thr Tyr Gly Cys Thr Gly
 1010 1015 1020
 Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly Pro Lys Ile Pro Ser
 1025 1030 1035

Ile Ala Thr Gly Met Val Gly Ala Leu Leu Leu Leu Leu Val Val
 1040 1045 1050

Ala Leu Gly Ile Gly Leu Phe Met
 1055 1060

REFERENCES CITED IN THE DESCRIPTION

This list of references cited by the applicant is for the reader's convenience only. It does not form part of the European patent document. Even though great care has been taken in compiling the references, errors or omissions cannot be excluded and the EPO disclaims all liability in this regard.

Patent documents cited in the description

- [US6790614B \[0003\]](#)
- [US5821337A \[0024\]](#)
- [US2010055329W \[0074\]](#)
- [US61257567B \[0074\]](#)

Non-patent literature cited in the description

- **BERGER, CFLOWERS, MEWARREN, EHRIDDELL, SR**Analysis of transgene-specific immune responses that limit the in vivo persistence of adoptively transferred HSV-TK-modified donor T cells after allogeneic hematopoietic cell transplantationBlood, 2006, vol. 107, 2294-302 [\[0073\]](#)
- **TEY, SKDOTTI, GROONEY, CMHESLOP, HEBRENNER, MK**Inducible caspase 9 suicide gene to improve the safety of allodepleted T cells after haploidentical stem cell transplantationBiol Blood Marrow Transplant, 2007, vol. 13, 913-24 [\[0073\]](#)
- **FEHSE, BRICHTERS, APUTIMTSEVA-SCHARF, KKLUMP, HLI, ZOSTERTAG, W et al.**CD34 splice variant: an attractive marker for selection of gene-modified cellsMol Ther, 2000, vol. 1, 448-56 [\[0073\]](#)
- **GAINES, PWOJCHOWSKI, DM**pIRES-CD4t, a dicistronic expression vector for MACS- or FACS-based selection of transfected cellsBiotechniques, 1999, vol. 26, 683-8 [\[0073\]](#)
- **FEHSE, BUHDE, AFEHSE, NECKERT, HGCLAUSEN, JRUGER, R et al.**Selective

immunoaffinity-based enrichment of CD34+ cells transduced with retroviral vectors containing an intracytoplasmatically truncated version of the human low-affinity nerve growth factor receptor (deltaLNGFR) geneHum Gene Ther, 1997, vol. 8, 1815-24 [0073]

- **LEMOINE, FMMESEL-LEMOINE, MCHERAI, MGALLOT, GVIE, HLECLERCQ, V et al.**Efficient transduction and selection of human T-lymphocytes with bicistronic Thy1/HSV1-TK retroviral vector produced by a human packaging cell lineJ Gene Med, 2004, vol. 6, 374-86 [0073]
- **LI, SSCHMITZ, KRJEFFREY, PDWILTZIUS, JJKUSSIE, PFERGUSON, KM**Structural basis for inhibition of the epidermal growth factor receptor by cetuximabCancer Cell, 2005, vol. 7, 301-11 [0073]
- **DAWSON, JPBERGER, MBLIN, CCSCHLESSINGER, JLEMMON, MAFERGUSON, KM**Epidermal growth factor receptor dimerization and activation require ligand-induced conformational changes in the dimer interfaceMol Cell Biol, 2005, vol. 25, 7734-42 [0073]
- **LANGE, CLI, ZFANG, LBAUM, CFEHSE, BCD34** modulates the trafficking behavior of hematopoietic cells in vivoStem Cells Dev, 2007, vol. 16, 297-304 [0073]
- **KOWOLIK, CMTOPP, MSGONZALEZ, SPFEIFFER, TOLIVARES, SGONZALEZ, N et al.**CD28 costimulation provided through a CD19-specific chimeric antigen receptor enhances in vivo persistence and antitumor efficacy of adoptively transferred T cellsCancer Res, 2006, vol. 66, 10995-1004 [0073]
- **SZYMCZAK, ALWORKMAN, CJWANG, YVIGNALI, KMDILIOGLOU, SVANIN, EF et al.**Correction of multi-gene deficiency in vivo using a single 'self-cleaving' 2A peptide-based retroviral vectorNat Biotechnol, 2004, vol. 22, 589-94 [0073]
- **YAM, PJENSEN, MAKKINA, RANDERSON, JVILLACRES, MCWU, J et al.**Ex vivo selection and expansion of cells based on expression of a mutated inosine monophosphate dehydrogenase 2 after HIV vector transduction: effects on lymphocytes, monocytes, and CD34+ stem cellsMol Ther, 2006, vol. 14, 236-44 [0073]
- **PELLOQUIN, FLAMELIN, JPLENOIR, GM**Human B lymphocytes immortalization by Epstein-Barr virus in the presence of cyclosporin AIn Vitro Cell Dev Biol, 1986, vol. 22, 689-94 [0073]

Patentkrav

1. Modificeret EGFR-gen, der består af en sekvens, der koder for en trunke EGFR, der består af EGFR-domæne III, EGFR-transmembrandomæne og EGFR-domæne IV.
2. Gen ifølge krav 1, hvor det modificerede EGFR-gen er bundet til en nukleotidsekvens, 5 der kun koder for GMCSFR-alfa-kædesignalsekvensen.
3. Gen ifølge krav 1 eller krav 2, hvor aminosyresekvensen kodet for af det modificerede EGFR-gen er mindst 90 % identisk med SEQ ID NO: 3.
4. Gen ifølge et hvilket som helst af krav 1-3, hvor aminosyresekvensen kodet for af det modificerede EGFR-gen består af SEQ ID NO: 3.
- 10 5. Konstrukt, der omfatter genet ifølge et hvilket som helst af krav 1-4, hvor det modificerede EGFR-gen er koblet med en nukleotidsekvens, der koder for en kimærisk antigenreceptor, der er specifik for et tumor-associeret antigen, hvor nukleotidsekvensen, der koder for en kimærisk antigenreceptor, er efterfulgt af en nukleotidsekvens, der koder for en fraspaltelig C-terminal 2A-linker og kodningssekvensen for det modificerede EGFR-gen.
- 15 6. Konstrukt ifølge krav 5, hvor den kimæriske antigenreceptor, der er specifik for et tumor-associeret antigen er valgt fra CD19, CD20 og CD22.
7. Konstrukt ifølge krav 6, hvor det tumorassocierede antigen er CD19.
8. Konstrukt ifølge krav 5 eller krav 7, hvor konstruktet er CD19R-CD28gg-Zeta(CO)-T2A-EGFRt, og omfatter en nukleotidsekvens, der koder for aminosyresekvensen 20 SEQ ID NO: 6.
9. Genetisk modificeret population af T-celler transduceret med genet ifølge et hvilket som helst af krav 1-4, hvor genet er koblet til et a gen, der koder for en tumor-targetterende kimærisk antigenreceptor (CAR), hvor T-cellerne udtrykker inaktiv modificeret EGFR.
10. Population af T-celler ifølge krav 9, hvor T-cellerne er til anvendelse i adoptiv 25 immunterapi.
11. Population af T-celler til anvendelse ifølge krav 10, hvor adoptiv immunterapi er til anvendelse ved behandling af cancer.
12. Ikke-immunogen udvælgelsesepitop kodet for at genet ifølge et hvilket som helst af krav 1-4 eller konstruktet ifølge et hvilket som helst af krav 5-8.
- 30 13. Udvalgte epitop ifølge krav 12, hvor udvalgte epitopen er til anvendelse i en anvendelse valgt fra:
 - (a) anvendelse som et ikke-immunogent udvælgelsesredskab, der er foreneligt med immunmagnetisk udvælgelse;
 - (b) anvendelse som en sporingsmarkør for *in vivo* T-cellepodning; og

(c) anvendelse som et selvmordsgen til transducerede T-celler, der har immunterapeutisk potentiale, eventuelt til anvendelse som et selvmordsgen via cetuximabmedieret komplement og/eller antistofafhængig cellemedieret cytotoxicitets- (ADCC) baner.

14. Udvalgelsesepitop ifølge krav 12, hvor udvalgelsesepitopen er forenelig med
5 immunmagnetisk udvælgelse og fremmer immunterapi hos cancerpatienter uden uønsket immunologisk afstødning af celleprodukter.

DRAWINGS

Figure 1

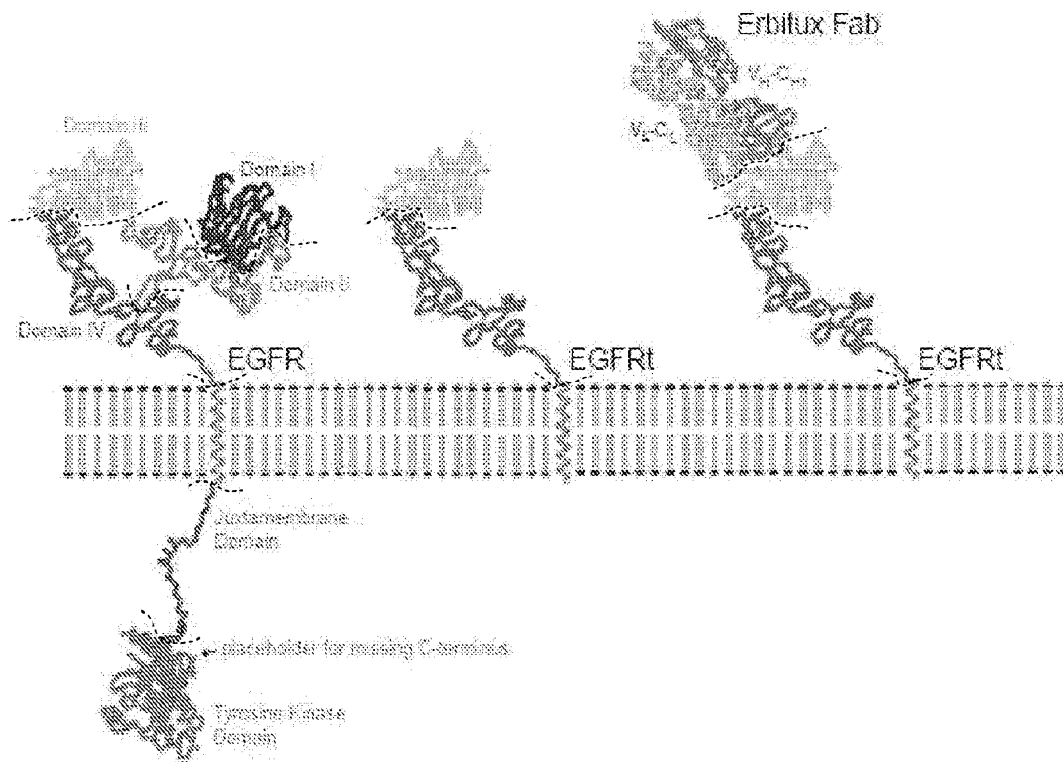


Figure 2A

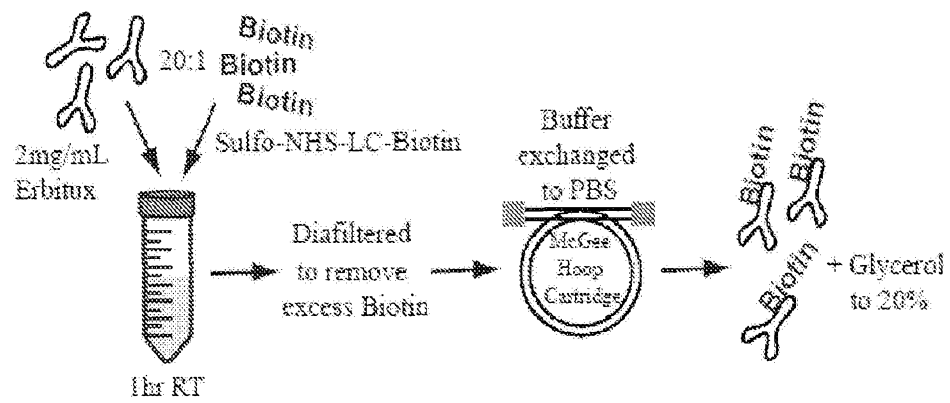


Figure 2B

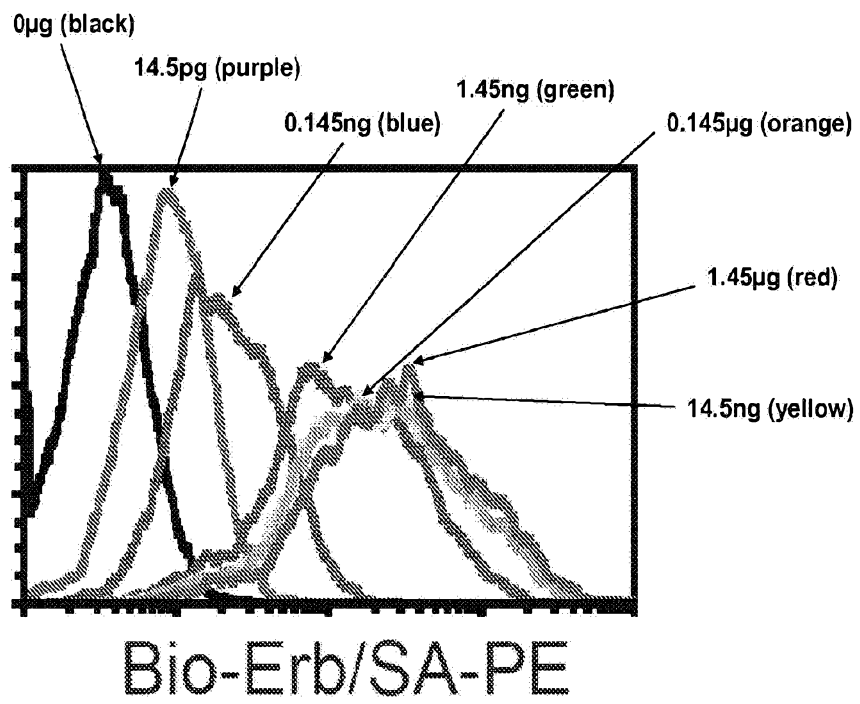


Figure 2C

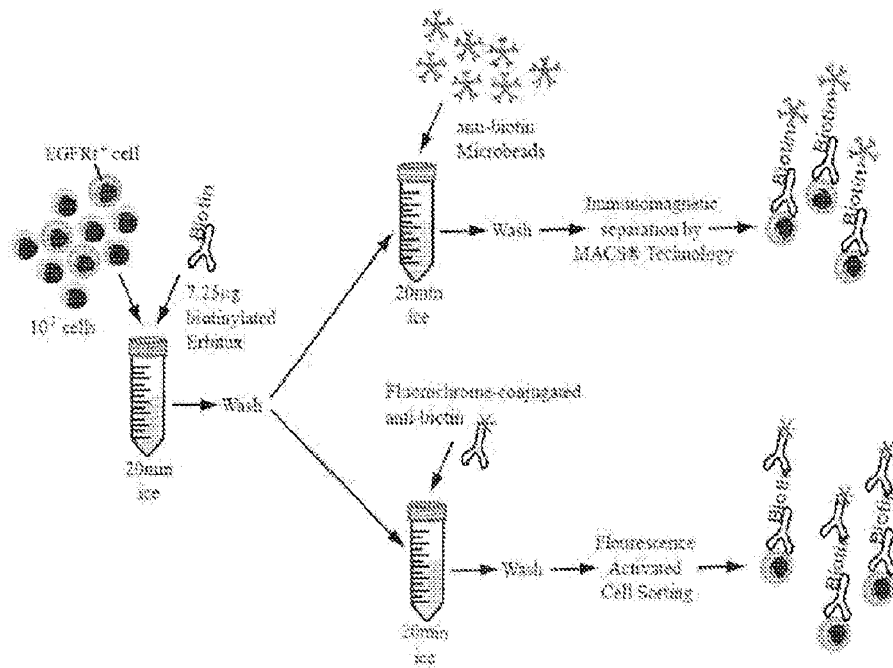


Figure 2D

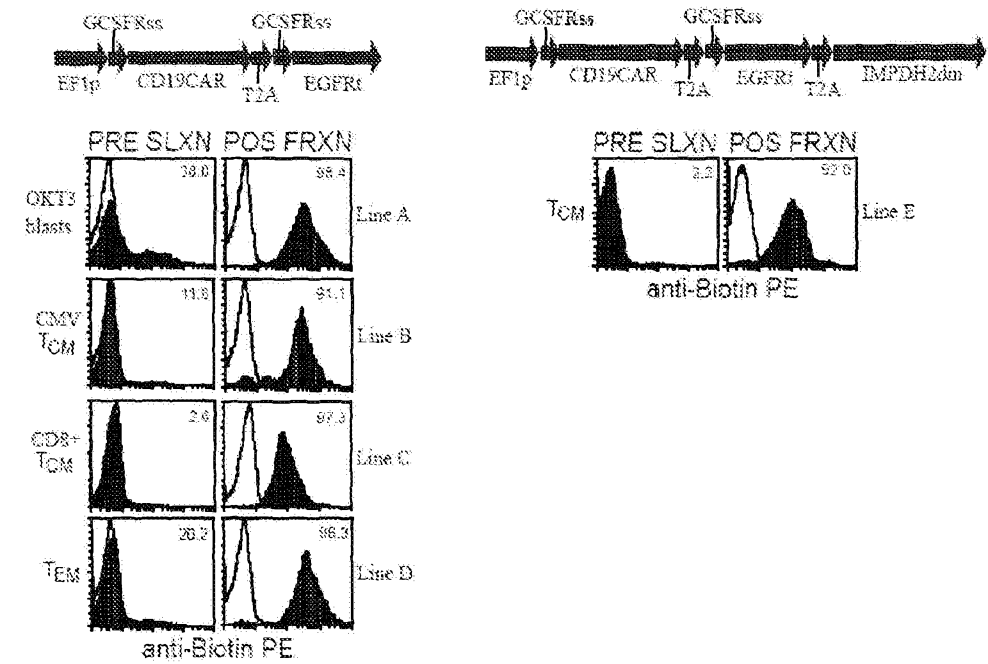


Figure 3A

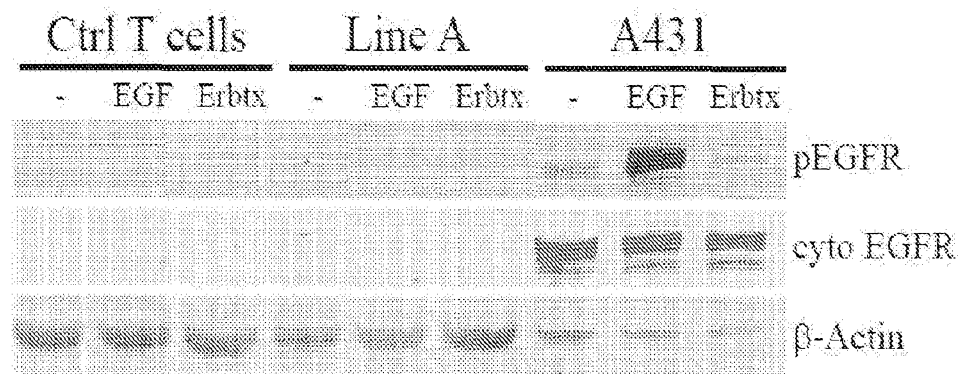


Figure 3B

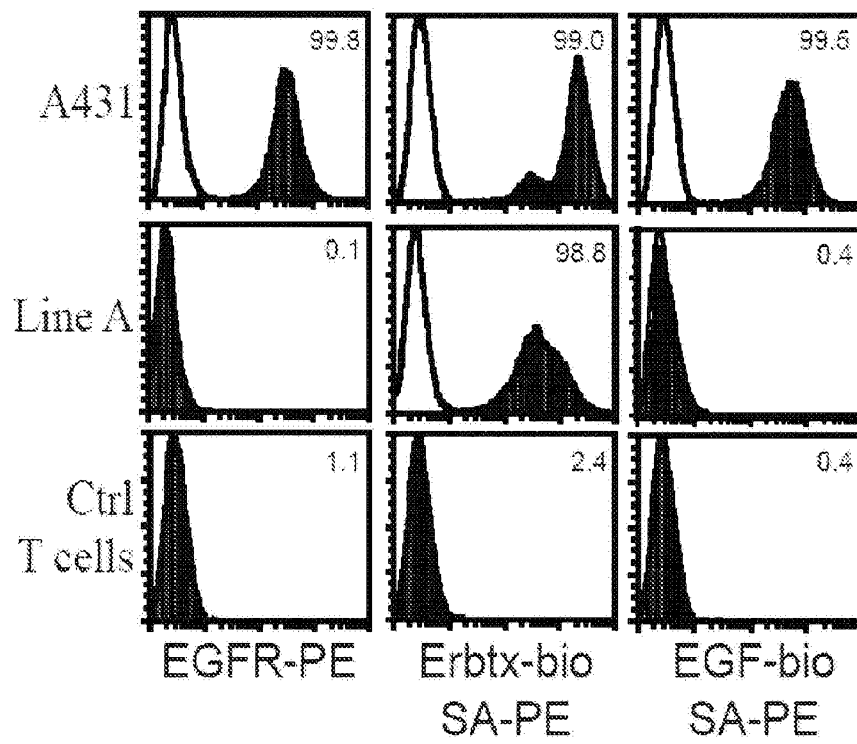


Figure 4A

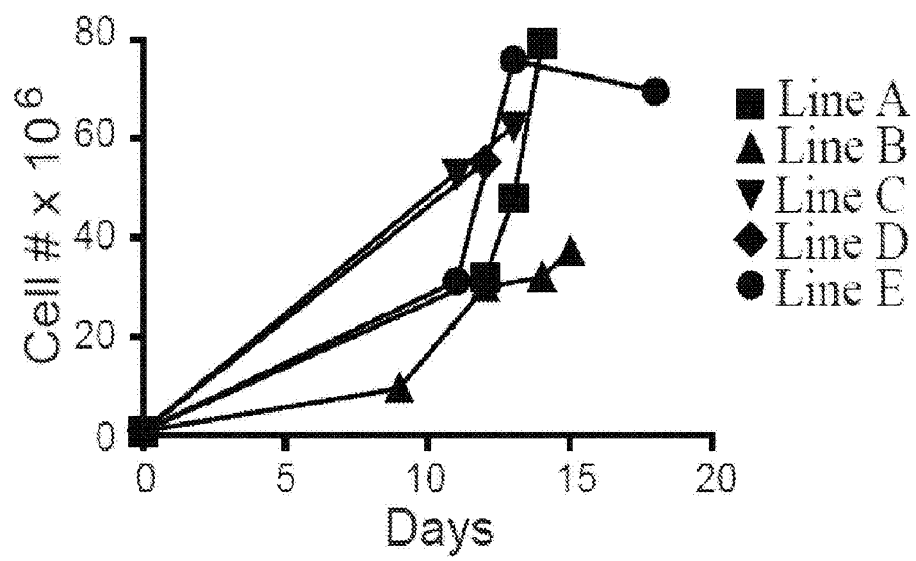


Figure 4B

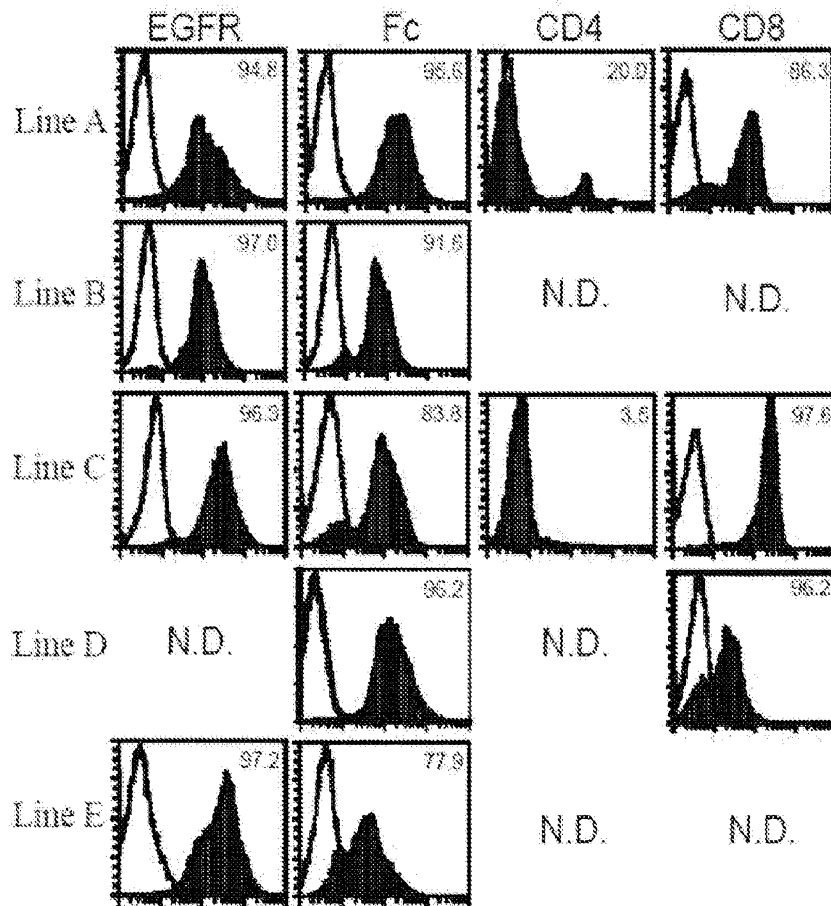


Figure 4C

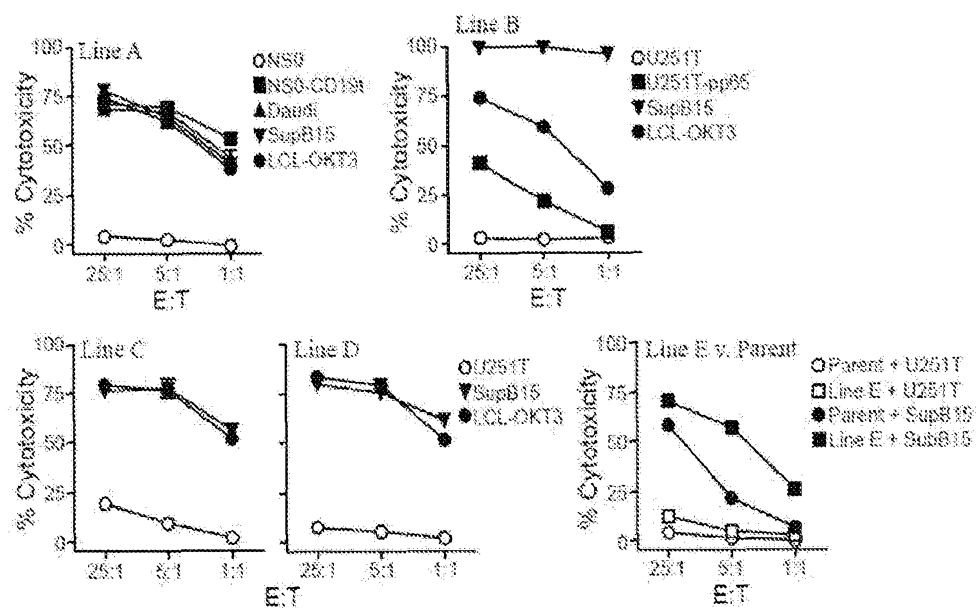


Figure 4D

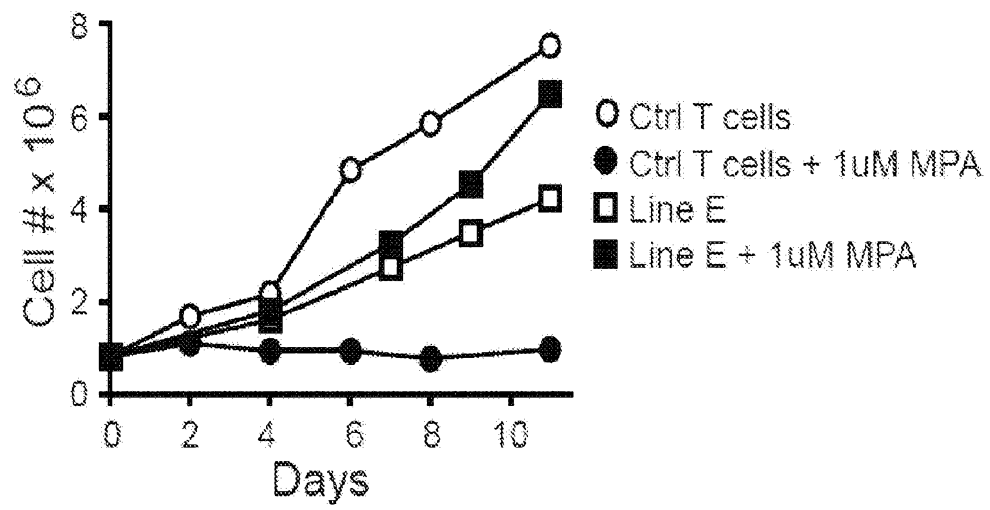


Figure 5

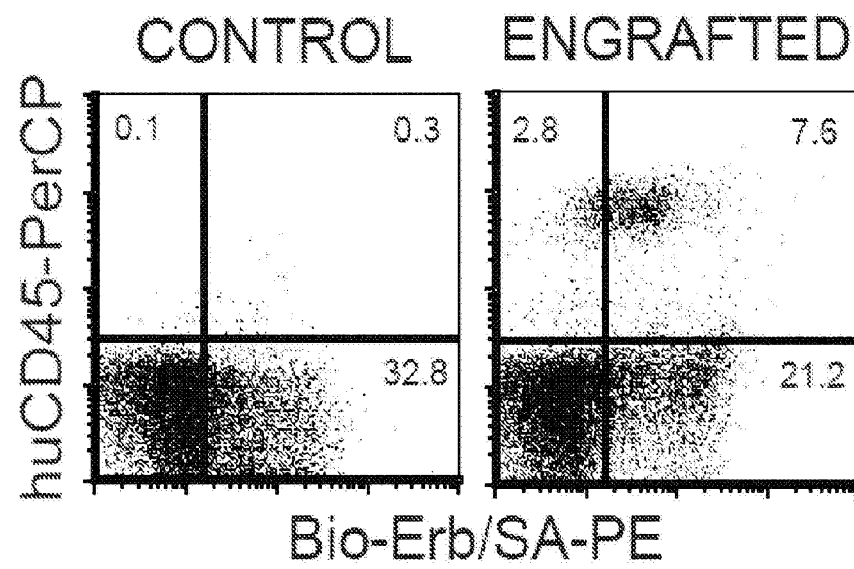


Figure 6

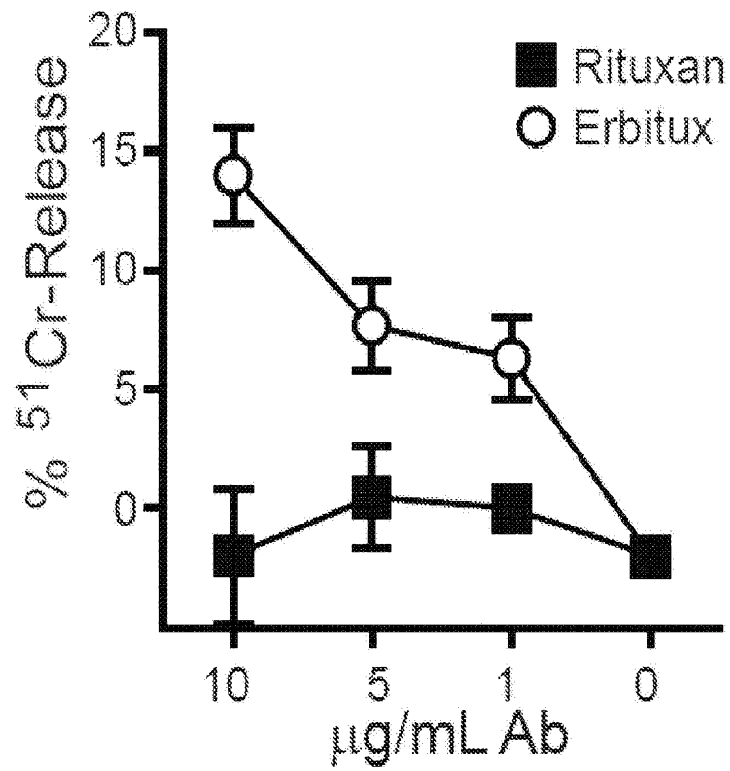


Figure 7

```

      M L L L V T S L L L C E L P H P A F L L
1  ATGCTTCTCC TGGTGACAAG CCTTCTGCTC TGTGAGTTAC CACACCCAGC ATTCTCTCTG
   TAGGAAGAGG ACCACTGTTT GGAAGACGAG ACACTCAATG GTGTGGGTCG TAAGGAGGAC
      I P R K V C N G I G I G E F K D S L S I
61 ATCCACGCA AAGTGTGTAA CGGAATAGGT ATTGGTGAAT TTAAAGACTC ACTCTCCATA
   TAGGGTGCCT TTCACACATT GCCTTATCCA TAACCACCTA AATTTCTGAG TGAGAGGTAT
      N A T N I K H F K N C T S I S G D L H I
121 AATGCTACGA ATATTAAACA CTTCAAAAAC TGCACCTCCA TCAGTGGCGA TCTCCACATC
   TTACGATGCT TATAATTTGT GAAGTTTTTG ACGTGGAGGT AGTCACCGCT AGAGGTGTAG
      L P V A F R G D S F T H T P P L D P Q E
181 CTGCCGGTGG CATTAGGGG TGACTCCTTC ACACATACTC CTCCTCTGGA TCCACAGGAA
   GACGCCACCC GTAAATCCCC ACTGAGGAAG TGTGTATGAG GAGGAGACCT AGGTGTCCCTT
      L D I L K T V K E I T G F L L I Q A W P
241 CTGGATATTC TGAAAACCGT AAAGGAAATC ACAGGGTTT TGCTGATTCA GGCTTGGCCT
   GACCTATAAG ACTTTTGGCA TTTCTTTAG TGTCCCAAAA ACGACTAAGT CCGAACCGGA
      E N R T D L H A F E N L E I I R G R T K
301 GAAAACAGGA CGGACCTCCA TGCCTTTGAG AACCTAGAAA TCATACCGCG CAGGACCAAG
   CTTTGTCTCT GCCTGGAGGT ACGGAAATC TTGGATCTTT AGTATGCGCC GTCCTGGTTC
      Q H G Q F S L A V V S L N I T S L G L R
361 CAACATGGTC AGTTTTCTCT TGCAGTCGTC AGCCTGAACA TAACATCCTT GGGATTACGC
   GTTGTACCAG TCAAAAGAGA ACGTCAGCAG TCGGACTTGT ATTGTAGGAA CCCTAATGCG
      S L K E I S D G D V I I S G N K N L C Y
421 TCCCTCAAGG AGATAAGTGA TGGAGATGTG ATAATTTTCTG GAAACAAAAA TTTGTGCTAT
   AGGGAGTTCC TCTATTCACT ACCTCTACAC TATTAAAGTC CTTTGTTTT AAACACGATA
      A N T I N W X K L F G T S G Q K T K I I
481 GCAAATACAA TAAACTGGAA AAAACTGTTT GGGACCTCCG GTCAGAAAAA CAAAATTATA
   CGTTTATGTT ATTTGACCTT TTTTGACAAA CCCTGGAGGC CAGTCTTTTG GTTTTAATAT
      S N R G E N S C K A T G Q V C H A L C S
541 AGCAACAGAG GTGAAAACAG CTGCAAGGCC ACAGGCCAGG TCTGCCATGC CTTGTGCTCC
   TCGTTGTCTC CACTTTTGTC GAGCTCCCG GAGTCCGGTCC AGACGGTACG GAACACGAGG
      P E G C W G P E P R D C V S C R N V S R
601 CCCGAGGGCT GCTGGGGCCC GGAGCCCAGG GACTGCGTCT CTTGCCGGA TGTGAGCCGA
   GGGCTCCCGA CGACCCCGGG CCTCGGTCC CTGACGCAGA GAACGGCCTT ACAGTCGGCT
      G R E C V D X C N L L E G E P R E F V E
661 GCGAGGGAAT GCGTGGACAA GTGCAACCTT CTGGAGGGTG AGCCAAGGGA GTTTGTGGAG
   CCGTCCCTTA CGCACCTGTT CACGTTGGAA GACCTCCAC TCGGTTCCCT CAAACACCTC
      N S E C I Q C H P E C L P Q A M N I T C
721 AACTCTGAGT GCATACAGTG CCACCCAGAG TGCCTGCCTC AGGCCATGAA CATCACCTGC
   TTGAGACTCA CGTATGTCAC GGTGGGTCTC ACGGACGGAG TCGGTACTT GTAGTGGACG
      T G R G P D N C I Q C A H Y I D G P H C
781 ACAGGACGGG GACCAGACAA CTGTATCCAG TGTGCCCCACT ACATTGACGG CCCCCACTGC
   TGTCTTGCCC CTGGTCTGTT GACATAGGTC ACACGGGTGA TGTAAGTCC GGGGGTGACG
      V K T C P A G V M G E N N T L V W K Y A
841 GTCAAGACCT GCCCGGCAGG AGTCATGGGA GAAAACAACA CCCTGGTCTG GAAGTACGCA
   CAGTTCTGGA CGGGCCGTCC TCAGTACCTT CTTTGTGTG GGGACCAGAC CTTTATGCGT
      D A G H V C H L C H P N C T Y G C T G P
901 GACGCCGGCC ATGTGTGCCA CCTGTGCCAT CCAAAGTGCA CCTACGGATG CACTGGGCCA
   CTGCGGCCGG TACACACGGT GGACACGGTA GGTTTGACGT GGATGCCTAC GTGACCCGGT
      G L E G C P T N G P K I P S I A T G M V
961 GGTCTTGAG GCTGTCCAAC GAATGGGCCT AAGATCCCGT CCATCGCCAC TGGGATGGTG
   CCAGAATTC CGACAGGTTG CTTACCCGGA TTCTAGGSCA GGATAGCGGT ACCCTACCAC
      G A L L L L L V V A L G I G L F M
1021 GGGGCCCTCC TCTTGCTGCT GGTGGTGCC CTGGGGATCG CCCTCTTCAT G
      CCCC GGAGG AGAACGACGA CCACCACCG GACCCCTAGC CGGAGAAGTA C

```

Figure 8 CD19R-CD28 η -Zeta(CO)-T2A-EGFRt

```

      M L L L V T S L L L C E L P H P A F L L
1  ATGCTGCTGC TGGTGACCAG CCTGCTGCTG TGGGAGCTGC CCCACCCCGC CTTTCCTGCTG
   TACGACGACG ACCACTGGTC GGACGACGAC ACGCTCGACG GGGTGGGGCG GAAAGACGAC
   I P D I Q M T Q T T S S L S A S L G D R
61 ATCCCGGACA TCCAGATGAC CCAGACCACC TCCAGCCTGA GCGCCAGCCT GGGCGACCGG
   TAGGGGCTGT AGGTCTACTG GGTCTGGTGG AGGTCCGACT CGCGGTCCGA CCCGCTGGCC
   V T I S C R A S Q D I S K Y L N W Y Q Q
121 GTGACCATCA GCT3CCGGGC CAGCCAGGAC ATCAGCAAGT ACCTGAAGTG GTATCAGCAG
   CACTGGTAGT CGACGGGCCG GTCGGTCCTG TAGTCGTTCA TGGACTTGAC CATAGTCGTC
   K P D G T V K L L I Y H T S R L H S S V
181 AAGCCCGACG GCACCGTCAA GCTGCTGATC TACCACACCA GCCGGCTGCA CAGCGGCGTG
   TTCGGGCTGC CGT3GCAGTT CGACGACTAG ATGGTGTGGT CGGCCGACGT GTCGCCGCAC
   P S R F S G S G S G T D Y S L T I S N L
241 CCCAGCCGGT TTAGCGGCAG CGGCTCCGSC ACCGACTACA GCCTGACCAT CTCCAACCTG
   GGGTCGGCCA AATCGCCGTC GCCGAGGCCG TGGCTGATGT CGGACTGGTA GAGGTGGAC
   E Q E D I A T Y F C Q Q G N T L P Y T F
301 GAACAGCCAG ATATCGCCAC CTACTTTTGC CAGCAGGGCA ACACACTGCC CTACACCTTT
   CTTGTCTCTC TATAGCGGTG GATGAAAACG GTCGTCCCGT TGTGTGACGG GATGTGGAAA
   G G G T K L E I T G S T S G S G K P S S
361 GGC GGCGGAA CAAAGCTGGA AATCACCGGC AGCACCTCCG GCAGCGGGCA GCCTGGCAGC
   CCGCCGCTT GTTTCGACCT TTAGTGGCCG TCGTGGAGGC CGTCGCCGTT CGGACCGTCG
   G E G S T K G E V K L Q E S G P G L V A
421 GGCGAGGGCA GCACCAAGGG CGAGGTGAAG CTGCAGGAAA GCGGCCCTGG CCTGGTGGCC
   CCGCTCCCGT CGT3GTCCG GCTCCACTTC GACGTCTTT CGCCGGGACC GGACCACCGG
   P S Q S L S V T C T V S G V S L P D Y G
481 CCCAGCCAGA GCTGAGCGT GACCTGCACC GTGAGCGGCG TGAGCCTGCC CGACTACGGC
   GGGTCGGTCT CGGACTCGCA CTGGACGTGG CACTCGCCGC ACTCGGACGG GCTGATGCCG
   V S W I R Q P P R K G L E W L G V I W G
541 GTGAGCTGGA TCCGGCAGCC CCCAGGGAAG GGCCTGGAAT GGTGGGGCGT GATCTGGGGC
   CACTCGACCT AGGCGGTCCG GGGGTCTTC CCGGACCTTA CCGACCCGCA CTAGACCCCG
   S E T T Y Y N S A L K S R L T I I K D N
601 AGCGAGACCA CTAATAACAA CAGCGCCCTG AAGAGCCGCG TGACCATCAT CAAGGACAAC
   TCGCTCTGCT GGATGATGTT GTCCGCGGAC TTCTCGGCCG ACTGGTAGTA GTTCTCTGTTG
   S K S Q V F L K M N S L Q T D D T A T Y
661 AGCAAGAGCC AGGTGTTCCT GAAGATGAAC AGCCTGCAGA CUGAGGACAC CGCATCTTAC
   TCGTTCTCGG TCCACAAGGA CTTCTACTTG TCGGACGTCT GGCTGCTGTG GCGGTAGATG
   Y C A K H Y Y Y G S S Y A M D Y W G Q G
721 TACTGCGCCA AGCACTACTA CTACGGCGGC AGCTACGCCA TGGAATACTG GGGCCAGGGC
   ATGACGCGGT TCGTGATGAT GATGCCGCGG TCGATGCGGT ACCTGATGAC CCCGGTCCCG
   T S V T V S S E S K Y G P P C P P C P A
781 ACCAGCGTGA CCGTGAACAG CGAGAGCAAG TACGGCCCTC CCTGCCCCCC TTGCCCTGCC
   TGGTCGCACT GGCACCTGTC GCTCTCGTTC ATGCCGGGAG GGACGGGGGG AACGGGACGG
   P E F L G G P S V F L F P P K P K D T L
841 CCCGAGTTCC TGG3CGGACC CAGCGTGTTC CTGTTCCCCC CCAAGCCCAA GGACACCTG
   GGGCTCAAGG ACCCGCCTGG GTCGCACAAG GACAAAGGGG GGTTCGGGTT CCTGTGGGAC
   M I S R T P E V T C V V V D V S Q E D P
901 ATGATCAGCC GGACCCCGCA GGTGACCTGC GTGGTGGTGG ACGTGAGCCA GGAAGATCCC
   TACTAGTCGG CCT3GGGGCT CCACGGGACG CACCACCACC TGCACTCGGT CCTTCAGGG
   E V Q F N W Y V D G V E V H N A K T K P
961 GAGGTCCAGT TCAATTGGTA CGTGGACGSC GTGGAAGTGC ACAACGCCAA GACCAAGCCC
   CTCCAGGTCA AGTTAACCAT GCACCTGCCG CACCTTCACG TGTGCGGTT CTGGTTCGGG

      R E E Q F N S T Y R V V S V L T V L H Q
1021 AGAGAGGAAC AGTTCAACAG CACCTACCAG GTGGTGTCTG TGCTGACCGT GCTGCACCAG
   TCTCTCTTG TCAAGTTGTC GTGGATGGCC CACCACAGAC ACGACTGGCA CGACGTGGTC
   D W L N G K E Y K C K V S N K G L P S S
1081 GACTGGCTGA ACGCCAAAGA ATACAAGTGC AAGGTGTCCA ACAAGGGCCT GCCCAGCAGC
   CTGACCGACT TGCCGTTTCT TATGTTACG TTCCACAGET TGTTCCCGA CCGGTCTCG

```

I E K T I S K A K G Q P R E P Q V Y T L
 1141 ATCGAAAAGA CCATCAGCAA GGCCAAGGGC CAGCCTCGCG AGCCCCAGGT GTACACCCCTG
 TAGCTTTTCT GGTACTCGIT CCGGTTCCTG CTCGGAGCGC TCGGGTCCA CATGTGGGAC
 P P S Q E E M T K N Q V S L T C L Y K G
 1201 CCTCCCTCCC AGGAAGAGAT GACCAAGAAC CAGGTGTCCC TGACCTGCCT GGTGAAGGGC
 GGAGGGAGGG TCCTTCTCTA CTGGTTCCTG STCCACAGGG ACTGGACGGA CCACTTCCCG
 F Y P S D I A V E W E S N G Q P E N N Y
 1261 TTCTACCCCA GCGACATCGC CGTGGAGTGG GAGAGCAACG GCCAGCCTGA GAACAACCTAC
 AAGATGGGGT CGCTGTAGCG GCACCTCACC CTCTCGTTGC CGGTGGGACT CTTGTGTATG
 K T T P P V L D S D G S F F L Y S R L T
 1321 AAGACCACCC CTCCTGTGCT GGACAGCGAC GGCAGCTTCT TCCTGTACAG CCGGCTGACC
 TTCTGGTGGG GAGGGCACGA CCTGTGCTG CCGTCGAAGA AGGACATGTC GGCCGACTGG
 V D K S R W Q E G N V F S C S V M H E A
 1381 GTGGACAAGA GCCGTGGCA GGAAGGCAAC STCTTTAGCT GCAGCGTGAT GCACGAGGCC
 CACCTGTTCT CGGCCACCGT CCTTCCGTTG CAGAAATCGA CGTCGCACTA CGTGCTCCGG
 L H N H Y T Q K S L S L S L G K M F W V
 1441 CTGCACAACC ACTACACCCA GAAGAGCCTG AGCCTGTCCC TGGGCAAGAT GTTCTGGGTG
 SACGTGTTGG TGATCTGGGT CTTCTCGGAC TCGGACAGGG ACCCSTTCTA CAAGACCCAC
 L V V V G G V L A C Y S L L V T V A F I
 1501 CTGGTGGTGG TGGGCGGGGT GCTGGCCTGC TACAGCCTGC TGGTGACAGT GGCCTTCATC
 GACCACCACC ACCCCGCCCA CGACCGGACG ATGTGCGGAC ACCACTGTCA CCGGAAGTAG
 I F W V R S K R S R G G H S D Y M N M T
 1561 ATCTTTTGGG TGGGAGCAA GCGGAGCAGA GCGGCCACA GCGACTACAT GAACATGACC
 TAGAAAACCC ACCCTCCTT CCCTCCTCT CCCTCCCTGT CCCTGATCTA CTTCTACTCG
 P R R P G P T R K H Y Q P Y A P P R D F
 1621 CCGAGACGGC CCGGCCCCAC CCGGAAGCAC TACCAGCCTT ACGCCCCACC CAGGGACTTT
 GGGTCTGCCG GACCGGGGTG GGCCTTCGTG ATGGTCGGGA TCGGSGGTGG GTCCCTGAAA
 A A Y R S G G G R V K F S R S A D A P A
 1681 GCGGCTTACC GGTCCGGCGG AGGGCGGGTG AAGTTCAGCA GAAGCGCCGA CGCCCTGCCC
 CCGCGGATGG CCAGCCCCGC TCCCGCCAC TTCAAGTCGT CTTCCGGGT GCGGGGACGG
 Y Q Q G Q N Q L Y N E L N L G R R E E Y
 1741 TACCAGCAGG GCCAGAATCA GCTGTACAAC GAGCTGAACC TGGGCAAGG GGAAGAGTAC
 ATGGTCGTCC CGGTCTTAGT CGACATGTTG CTGACTTGG ACCCTCTTC CTTCTCATG
 D V L D K R R G R D P E M G G K P R R K
 1801 GACGTCCTGG ATAAGCGGAG AGGCCGGGAC CCTGAGATGG GCGGCAAGCC TCGGCGGAAG
 CTGAGGAGCC TATTGCTTC TCGGCCCTG GACTCTACC CGCCSTTCGG AGCCGCTTC
 N P Q E G L Y N E L Q K D X M A E A Y S
 1861 AACCCCCAGG AAGGCTCTA TAACGAAGT CAGAAAGACA AGATGCGGA GGCCTACAGC
 TTGGGGGTCC TCCCGGACAT ATTGCTTGAC GTCTTCTGT TCTACGGGT CCGGATGTCG
 E I G M K G E R R R G K G H D G L Y Q G
 1921 GAGATCGGCA TGAAGGGCGA GCGGAGGCGG GCAAGGGCC ACGACGGCCT GTATCAGGGC
 CTCTAGCGGT ACTTCCCGCT CGCCTCCGCC CGGTCCCGG TGCTGCCGGA CATAGTCCCG
 L S T A T K D T Y D A L H M Q A L P P R
 1981 CTGTCCACCG CCACCAAGGA TACCTACGAC GCCCTGCACA TGCAGGCCCT GCGCCCAAGG
 SACAGGTGGC GGTGTTCCT ATGGATGCTG CGGGACGTGT ACGTCCGGGA CGGGGGTTC
 L E G G G E G R G S L L T C G D V E E N
 2041 CTCGAGGGCG GCGGAGAGG CAGAGGAAGT CTTCTAACAT CCGGTGACGT GGAGGAGAAT
 GAGTCCCGC CGCTCTCTCC GTCTCCTTCA GAAGATTGTA CGCCACTGCA CCTCCCTTA
 F G P R M L L L V T S L L L C E L P H P
 2101 CCGGCCCCTA GGATGCTTCT CTTGGTGACA AGCCTTCTGC TGTGTGAGTT ACCACACCCA
 GGGCCGGGAT CCTACGAAGA GGACACTGT TCGGAAGACG AGACACTCAA TGGTGTGGGT
 A F L L I P R K V C N G I G I G E F K D
 2161 GCATTCTTCC TGATCCACG CAAAGTGTGT AACGGAATAG GTATTGGTGA ATTTAAAGAC
 CGTAAGGAGG ACTAGGGTGC GTTTCACACA TTGCCTTATC CATAACCACT TAAATCTCTG
 S L S I N A T N I K H F K N C T S I S G
 2221 TCACTCTCCA TAAATGTAC GAATATTAAA CACTTCAAAA ACTGCACCTC CATCAGTGCC
 AGTGAGAGGT ATTACGATG CTTATAATTT GTGAAGTTTT TGACGTGGAG GTAGTCACCG
 D L H I L P V A F R G D S F T H T P P L
 2281 GATCTCCACA TCCTGCCGCT GGCATTTAGG GGTGACTCCT TCACACATAC TCCTCCTCTG
 CTAGAGGTGT AGGACGGCCA CCGTAAATCC CCACTGAGGA AGTGTGTATG AGGAGGAGAC
 D P Q E L D I L K T V K E I T G F L L I

2341 GATCCACAGG AACTGGATAT TCTGAAAACC GTAAAGGAAA TCACAGGGTT TTTGCTGATT
 CTAGGTGTCC TTGACCTATA AGACTTTTGG CATTTTCCTTT AGTGTCGCCAA AAACGACTAA
 Q A W P E N R T D L H A F E N L E I I R
 2401 CAGGCTTGGC CTGAAAACAG GACGGACCTC CATGCCTTTG AGAACCTAGA AATCATACGC
 GTCCGAACCG GACTTTTGTC CTGCCTGGAG GTACGGAAAC TCTTGGATCT TTAGTATGCG
 G R T K Q H G Q F S L A V V S L N I T S
 2461 GGCAGGACCA AGCAACATGG TCAGTTTCT CTTGCAGTCG TCAGCCTGAA CATAACATCC
 CCGTCCTGGT TCGTTGTACC AGTCAAAAGA GAACGTCAGC AGTCGGACTT GTATTGTAGG
 L G L R S L K E I S D G D V I I S G N K
 2521 TTGGGATTAC GCTCCCTCAA GGAGATAAGT GATGGAGATG TGATAATTTT AGGAAACAAA
 AACCTAATG CGAGGGAGTT CCTCTATTCA CTACCTCTAC ACTATTAAAG TCCTTTGTTT
 N L C Y A N T I N W K K L F G T S G Q K
 2581 AATTTGTGCT ATGCAAATAC AATAAACTGG AAAAACTGT TTGGGACCTC CGGTCAGAAA
 TTAACACGA TACGTTTATG TTATTTGACC TTTTITGACA AACCTGGAG GCCAGTCTTT
 T K I I S N R G E N S C K A T G Q V C H
 2641 ACCAAAATTA TAAGCAACAG AGGTGAAAAC AGCTGCAAGG CCACAGGCCA GGTCTGCCAT
 TGGTTTAAAT ATTGTTGTC TCCACTTTTG TCGACGTTCC GGTGTCCGGT CCAGACGGTA
 A L C S P E G C W G P E P R D C V S C R
 2701 GCCTTGTGCT CCCCCGAGGG CTGCTGGGGC CCGGAGCCCA GGGACTGCGT CTCITGGCCG
 CGGAACACGA GGGGGCTCCC GACGACCCG GGCCTCGGGT CCCTGACGCA GAGAACGGCC
 N V S R G R E C V D K C N L L E G E P R
 2761 AATGTCAGCC GAGGCAAGGA ATGCGTGGAC AAGTGCAACC TTCTGGAGGG TGAGCCAAGG
 TTACAGTCGG CTCGTCCTT TACGCACCTG TTCACGTTGG AAGACCTCCC ACTCGGTTCC
 E F V E N S E C I Q C H P E C L P Q A M
 2821 GAGTTTGTGG AGAACTCTGA GTGCATACAG TGCCACCCAG AGTGCCTGCC TCAGGCCATG
 CTCAAACACC TCTTGAGACT CACGTATGTC ACGGTGGGTC TCACGGACGG AGTCCGGTAC
 N I T C T G R G P D N C I Q C A H Y I D
 2881 AACATCACCT GCACAGSACG GGGACCAGAC AACTGTATCC AGTGTGCCCC CTACATTGAC
 TTGTAGTGA CGTGTCTGCT CCTTGGTCTG TTGACATAGG TCACACGGGT GATGTAAGTG
 G P H C V K T C P A G V M G E N N T L V
 2941 GGCCCCCACT GCGTCAAGAC CTGCCCCGCA GGAGTCATGG GAGAAAACAA CACCCTGGTC
 CCGGGGGTGA CGCAGTTCTG GACGGGCCGT CCTCAGTACC CTCTTTTGTG GTGGGACCAG
 W K Y A D A G H V C H L C H P N C T Y G
 3001 TGGAAGTACG CAGACGCGCG CCATGTGTGC CACCTGTGCC ATCCAACTG CACCTACGGA
 ACCTTCATGC GTCTGCGGCC GGTACACACG GTGGACACGG TAGGTTTGAC GTGGATGCCCT
 C T G P G L E G C P T N G P K I P S I A
 3061 TGCACTEGGC CAGGTCTTGA AGGCTGTCCA ACGAATGGGC CTAAGATCCC GTCCATCGCC
 ACGTGACCCG GTCCAGAACT TCCGACAGGT TGCTTACCCG GATTCTAGGG CAGGTAGCGG
 T G M V G A L L L L L V V A L G I G L F
 3121 ACTGGGATGG TGGGGGCCCT CCTCTGTCTG CTGGTGGTGG CCCTGGGGAT CGGCCTCTTC
 TGACCCTACC ACCCCCGGGA GGAGAACGAC GACCACCACC GGGACCCCTA GCCGGAGAAG
 M *
 3181 ATGTGA
 TAACT

Figure 9

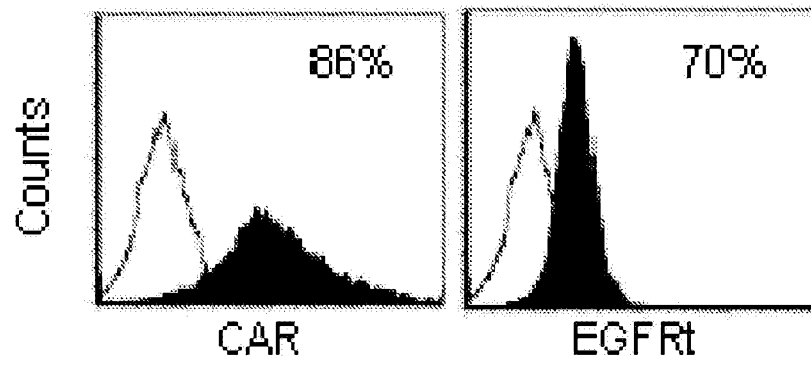


Figure 10

