

Chimeric Antigen Receptors

FIELD OF THE INVENTION

The present invention relates to chimeric antigen receptors (CARs) comprising low-affinity nerve growth factor receptor (LNGFR) based spacers.

BACKGROUND TO THE INVENTION

Immunotherapy based on adoptive transfer of immune cells (e.g., T cells) into a patient can play an important role in treating disease, in particular cancer. Among many different types of immunotherapeutic agents, one of the most promising therapeutic methods involves the use of chimeric antigen receptors (CARs). CARs are genetically engineered receptors that are designed to target a specific antigen such as a tumor antigen (Sadelain et al., *Cancer Discovery*. 2013. 3(4):388-98). For example, T cells are transduced with CARs such that T cells expressing CARs kill tumors via the target antigen.

CARs comprise an extracellular ligand binding domain, most commonly a single chain variable fragment of a monoclonal antibody (scFv) linked to intracellular signaling components, most commonly CD3 ζ alone or combined with one or more costimulatory domains. A spacer is often added between the extracellular antigen-binding domain and the transmembrane moiety to optimize the interaction with the target.

Most commonly, the constant immunoglobulin IgG1 hinge-CH2-CH3 Fc domain is used as a spacer domain. This spacer is used to select and track cells expressing the CAR. However, the IgG1 spacer may also bind to surface IgG Fc gamma receptors expressed on innate immune cells, like macrophages and natural killer cells (Hombach et al, *Gene Ther* 2000, Jun;7(12):1067-75). This binding activates both the engineered T cells and the innate immune cells independent of the specificity of the CAR binding domain leading to an unwanted, off-target, immune response.

There is a need for CARs that do not generate off-target immune responses and are not prematurely cleared by the host immune system. There is also a need for CARs comprising spacer units that facilitate selection of cells genetically engineered to express CARs. The present invention addresses these needs.

SUMMARY OF THE INVENTION

According to a first aspect of the present invention there is provided a chimeric antigen receptor (CAR) comprising an extracellular spacer, which comprises at least part of the extracellular domain of the human low affinity nerve growth factor receptor (LNGFR) or a derivative thereof.

The CAR may comprise at least a fragment of the extracellular domain of the human low affinity nerve growth factor receptor (LNGFR) or a derivative thereof.

Preferably at least part of the LNGFR is suitable for facilitating immunoselection of cells transduced with said CAR.

Preferably the spacer lacks the intracellular domain of LNGFR.

Preferably the extracellular spacer comprises the first three TNFR-Cys domains of LNGFR or fragments or derivatives thereof.

In one embodiment the spacer comprises all four TNFR-Cys domains of LNGFR or fragments or derivatives thereof.

In another embodiment the spacer comprises the fourth TNFR-Cys domain (TNFR-Cys 4) but wherein the following amino acids are removed from said domain: NHVDPCLPCTVCEDTERQLRECTRW. Preferably the NHVDPCLPCTVCEDTERQLRECTRW sequence is replaced with the following amino acid sequence ARA.

In another embodiment, the spacer comprises the serine /threonine-rich stalk of LNGFR.

In another embodiment, the spacer lacks the serine /threonine-rich stalk of LNGFR.

The spacer may comprise a sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5 or SEQ ID NO:7 or a sequence at least 80, 85, 90, 95, 96, 97, 98 or 99% identical thereto.

In another embodiment, the spacer may consist of a sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5 or SEQ ID NO:7 or a sequence at least 80, 85, 90, 95, 96, 97, 98 or 99% identical thereto.

SEQ ID NO:1, SEQ ID NO:3 and SEQ ID NO:5 are preferred spacer elements.

According to an aspect of the present invention there is provided a chimeric antigen receptor (CAR) comprising

- (i) an antigen-specific targeting domain;
- (ii) an extracellular spacer domain as defined herein;
- (iii) a transmembrane domain;
- (iv) optionally at least one costimulatory domain; and
- (v) an intracellular signaling domain.

Preferably the antigen-specific targeting domain comprises an antibody or fragment thereof, more preferably a single chain variable fragment.

Preferably the antigen-specific targeting domain targets a tumour antigen. Examples of such antigens include CD44, CD19, CD20, CD22, CD23, CD123, CS-1, ROR1, mesothelin, c-Met, PSMA, Her2, GD-2, CEA, MAGE A3 TCR.

Preferably the tumour antigen is isoform 6 of CD44 (CD44v6).

Examples of transmembrane domains include a transmembrane domain of a zeta chain of a T cell receptor complex, CD28 and CD8a.

Examples of costimulatory domains include a costimulating domain from CD28, CD137 (4-1BB), CD134 (OX40), Dap10, CD27, CD2, CD5, ICAM-1, LFA-1, Lck, TNFR-I, TNFR-II, Fas, CD30 and CD40.

Examples of intracellular signaling domains include human CD3 zeta chain, FcγRIII, FcεRI, a cytoplasmic tail of a Fc receptor and an immunoreceptor tyrosine-based activation motif (ITAM) bearing cytoplasmic receptors.

In a preferred embodiment, the antigen-specific targeting domain of the CAR targets CD44v6, the transmembrane domain of the CAR comprises a transmembrane domain of CD28, the intracellular signaling domain of the CAR comprises an intracellular signaling domain of human CD3 zeta chain and the costimulatory domain of the CAR comprises a CD28 endo-costimulating domain.

In another aspect of the present invention there is provided a polynucleotide encoding a CAR of the invention and as defined herein.

Preferably the polynucleotide encodes a spacer domain that comprises the sequence of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 or SEQ ID NO:8, or a sequence at least 80, 85, 90, 95, 96, 97, 98 or 99% identical thereto.

In one embodiment, the polynucleotide encodes a spacer domain that consists of the sequence of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 or SEQ ID NO:8, or a sequence at least 80, 85, 90, 95, 96, 97, 98 or 99% identical thereto.

In another aspect of the present invention there is provided a vector comprising the polynucleotide of the invention.

In one embodiment, the vector is a viral vector.

In another aspect of the present invention there is provided a cell comprising a CAR, a polynucleotide, or a vector of the present invention. Preferably the cell is a T-cell.

In another aspect of the present invention there is provided a pharmaceutical composition comprising the cell of the invention.

In another aspect of the present invention there is provided a CAR, a polynucleotide, a vector or a cell of the invention for use in therapy, preferably cancer therapy.

In another aspect of the present invention there is provided a CAR of the present invention wherein the antigen-specific targeting domain targets CD44v6 for use in treating tumours that express CD44.

In another aspect of the present invention there is provided a method of treatment comprising administering a CAR, a polynucleotide, a vector or a cell of the invention to a subject in need of the same.

Exemplary CARs are shown in Figures 10 to 17.

DESCRIPTION OF THE DRAWINGS

Figure 1. Rationale of generating different LNGFR-spaced CD44v6-CAR.28z constructs. **A.** Scheme explaining the limitations of CAR T cells carrying the IgG1 CH2CH3 spacer. **B.** Structure of the extracellular portion of the low-affinity nerve growth factor receptor (LNGFR) and of the 4 new CAR constructs that have been generated. The CD44v6-CAR.28z carrying the wild-type or the mutated IgG1 CH2CH3 spacer (mCH2CH3) are also included. CHW: CD44v6-CAR.28z carrying the wild-type CH2CH3 spacer. CHM:

CD44v6-CAR.28z carrying the mutated CH2CH3 spacer. NWL: CD44v6-CAR.28z carrying the LNGFR wild-type long spacer (including the 4 TNFR-Cys domains and the stalk). NWS: CD44v6-CAR.28z carrying the LNGFR wild-type short spacer (including only the 4 TNFR-Cys domains). NML: CD44v6-CAR.28z carrying the LNGFR mutated long spacer (including the 4 TNFR-Cys domains with a deletion in the fourth domain and the stalk). NMS: CD44v6-CAR.28z carrying the LNGFR mutated short spacer (including the 4 TNFR-Cys domains with a deletion in the fourth domain and the stalk). Curly brackets indicate the spacer length expressed in amino acids. Grey: scFv. White: co-stimulatory domain CD28; Black: CD3 ζ .

Figure 2. LNGFR-spaced CD44v6-CAR.28z T cells can be sorted with anti-LNGFR mAbs, efficiently expand *in vitro* and maintain an early-differentiated phenotype. T cells were activated with CD3/CD28-beads, transduced with retroviral vectors (RVs) encoding for the different LNGFR-spaced CD44v6.CAR28z and cultured with IL-7/IL-15. **A.** CAR identification on the T-cell surface using the LNGFR-specific mAb C40-1457 (upper plots). CAR identification on the T-cell surface using the LNGFR-specific mAb ME20.4 (lower plots) **B.** Left: T cells expressing the different LNGFR-spaced CD44v6-CAR.28z after sorting with the C40-1457 mAb and anti-PE beads. Right: expansion kinetics of sorted CH2CH3-spaced and LNGFR-spaced CD44v6-CAR.28z T cells expressed as fold increase. **C.** Functional differentiation phenotype of the different LNGFR-spaced CD44v6-CAR.28z 15 days after activation. CD45RA⁺/CD62L⁺ memory stem T cells, CD45RA⁻/CD62L⁺ central memory T cells, CD45RA⁻/CD62L⁻ effector memory T cells, CD45RA⁺/CD62L⁻ effector memory T cells RA. Plots and graph are representative of n=4 independent experiments.

Figure 3. LNGFR-spaced CD44v6-CAR.28z T cells specifically recognize CD44v6+ve tumor cells *in vitro*. **A.** After sorting, the different LNGFR-spaced CD44v6-CAR.28z T cells (NWL, NWS, NML, NMS), CH2CH3-spaced CD44v6-CAR T cells (CHW, CHM) and T cells carrying an irrelevant CAR were cultured with CD44v6+ve MM1.S myeloma cells, CD44v6+ve THP-1 leukemia cells or CD44v6-ve BV-173 lymphoblastoid cells at different E: T ratios. After 4 days, residual tumor cells were counted and analyzed by FACS. The elimination index (see Example Methods) by CD44v6-CAR.28z T cells at different E:T ratio is shown. **B.** CD44v6-CAR.28z T cells were loaded with the CFSE dye and stimulated with irradiated tumor cell lines at the E:T ratio 1:5. After 6 days, the proliferation of T cells was analyzed by FACS expressed as CFSE-diluting cells. Graphs and plots are representative of n=4 independent experiments.

Figure 4. LNGFR-spaced CD44v6-CAR.28z T cells lack FcRg-mediated recognition. **A.** After sorting, the different LNGFR-spaced CD44v6-CAR.28z T cells (NWL, NWS, NML, NMS), CH2CH3-spaced CD44v6-CAR T cells (CHW, CHM) and T cells carrying an

irrelevant CAR from n=4 healthy donors were cultured with CD44v6+ve/FcRg+ve THP-1 leukemia cells or CD44v6-ve/FcRg+ve HL-60 leukemia cells at different E: T ratios. After 4 days, residual tumor cells were counted and analyzed by FACS. The elimination index (see Example Methods) by CD44v6-CAR.28z T cells at different E:T ratios is shown. **B.** CD44v6-CAR.28z T cells were loaded with the CFSE dye and stimulated with irradiated THP1, HL60 or CD44v6-ve/FcRg-ve BV-173 lymphoblastoid cells. After 6 days, the proliferation of T cells was analyzed by FACS and expressed as CFSE-diluting cells. Graph and plots are representative of n=4 independent experiments.

Figure 5. LNGFR-spaced CD44v6-CAR.28z are not stimulated *via* soluble NGF. **A.** After 24hrs exposure to human recombinant NGF at different concentrations, LNGFR+ve PC-12 neuronal cells were analyzed for dendrite formation by optic microscopy. **B.** After sorting, the different LNGFR-spaced CD44v6-CAR.28z T cells (NWL, NWS, NML, NMS) and CH2CH3-spaced CD44v6-CAR.28z T cells (CHW, CHM) were loaded with the CFSE dye and exposed to different NGF concentrations. After 4 days, the proliferation of T cells was analyzed by FACS and expressed as CFSE-diluting cells. CFSE dilution after co-culture with CD44v6+ve MM1.S myeloma cells or CD44v6-ve BV-173 lymphoblastoid cells is shown for comparison. Picture and plots are representative of n=2 independent experiments. Graphs depict mean $\pm$ SD from the two experiments.

Figure 6. LNGFR-spaced CD44v6-CAR.28z T cells better expand, persist and mediate superior antileukemia effects in a minimal-residual disease model. NSG mice were infused with CD44v6+ve THP-1 leukemia cells and, after 3 days, treated with the different LNGFR-spaced CD44v6-CAR.28z T cells (NWL, NWS, NML, NMS), CH2CH3-spaced CD44v6-CAR T cells (CHW) or with T cells expressing an irrelevant CAR (CTR), all sorted to >95% purity. **A.** Representative plots (left) and all-inclusive graph (right) showing circulating CD44v6-CAR.28z T cells from each mouse three days after infusion. The differently spaced CD44v6-CAR.28z were tracked by FACS after staining with an anti-IgG polyclonal antibody (CTR and CHW) or the LNGFR-specific mAb, C40-1457 mAb. **B.** Kinetics of CD44v6-CAR.28z T-cell expansion and persistence over time. **C.** THP1-infiltrated liver weight of treated mice at sacrifice (7 weeks). Dashed zone depicts the range of normal liver weight from age/sex-matched normal NSG mice. Results from a one-way ANOVA test are shown when statistically significant (*P<0.05, **P<0.01, ***P<0.001).

Figure 7. LNGFR-spaced CD44v6-CAR.28z T cells better expand, persist and mediate superior antimyeloma effects in a well-established disease model. NSG mice were infused with CD44v6+ve MM1.S cells and, after 5 weeks, treated with different LNGFR-spaced CD44v6-CAR.28z T cells (NWL, NWS, NMS), CH2CH3-spaced CD44v6-CAR.28z T

cells (CHW) or with T cells expressing an irrelevant CAR (CTR), all sorted to >95% purity. **A.** All-inclusive graph (right) showing circulating CD44v6-CAR.28z T cells from each mouse three days after infusion. The differently spaced CD44v6-CAR28.z were tracked by FACS after staining with an anti-IgG polyclonal antibody (CTR and CHW) or the LNGFR-specific mAb C40-1457 mAb. **B.** Kaplan-Meyer survival curves of treated mice. Results from a Log-Rank test comparing the different conditions are shown (ns: non-significant, *P<0.05, ***P<0.001).

Figure 7 BIS. LNGFR-spaced CD44v6-CAR.28z T cells mediate superior antimyeloma effects in a well-established disease model. NSG mice were infused with CD44v6+ MM1.S cells expressing luciferase and, after 26 days, treated with LNGFR-spaced CD44v6-CAR.28z T cells (NMS), CH2CH3-spaced CD44v6-CAR.28z T cells (CHW) or with T cells expressing an irrelevant CAR (CTR), all sorted to >95% purity. **A.** The circulating amount of tumor cells was evaluated as relative light units (RLU) at the indicated time points. **B.** Kaplan-Meyer survival curves of treated mice. Results from a Log-Rank test comparing the different conditions are shown (**P<0.01).

Figure 8. Sequence of human LNGFR.

Figure 9. Sequence of CD44v6CAR.28z. The SCFV, CH2CH3, CD28 and zeta chain sequences are shown.

Figure 10. Exemplary sequence of a CD44v6CAR.28z with spacer LNGFR wild-type long (NWL) (SEQ ID NO:21)

Figure 11. Exemplary sequence of a CD44v6-CAR28z with spacer LNGFR wild-type short (NWS) (SEQ ID NO:22)

Figure 12. Exemplary sequence of a CD44v6-CAR28z with spacer LNGFR mutated long (NML) (SEQ ID NO:23)

Figure 13. Exemplary sequence of a CD44v6-CAR28z with spacer LNGFR mutated short (NMS) (SEQ ID NO:24)

Figure 14. Exemplary sequence of a CD44v6CAR.28z with spacer LNGFR wild-type long (NWL) (SEQ ID NO:25)

Figure 15. Exemplary sequence of a CD44v6-CAR28z with spacer LNGFR wild-type short (NWS) (SEQ ID NO:26)

Figure 16. Exemplary sequence of a CD44v6-CAR28z with spacer LNGFR mutated long (NML) (SEQ ID NO:27)

Figure 17. Exemplary sequence of a CD44v6-CAR28z with spacer LNGFR mutated short (NMS) (SEQ ID NO:28)

Figure 18. Sequence of CD44v6-4GS2-CAR28z, with spacer LNGFR wild-type long (NWL) (SEQ ID NO:32)

Figure 19. Sequence of CD44v6-4GS2-CAR28z, with spacer LNGFR wild-type short (NWS) (SEQ ID NO:33)

Figure 20. Sequence of CD44v6-4GS2-CAR28z with spacer LNGFR mutated long (NML) (SEQ ID NO:34)

Figure 21. Sequence of CD44v6-4GS2-CAR28z with spacer LNGFR mutated short (NMS) (SEQ ID NO:35)

Figure 22. Generation of different LNGFR-spaced CARs. Structure of the extracellular portion of the low-affinity nerve growth factor receptor (LNGFR) and of the different CAR constructs targeting CD19 and CEA, which have been generated. The CD19/CEA-CAR.28z carrying the wild-type IgG1 CH2CH3 spacer (CH2CH3) are also included. NWL: CD19/CEA-CAR.28z carrying the LNGFR wild-type long spacer (including the 4 TNFR-Cys domains and the stalk). NMS: CD19/CEA-CAR.28z carrying the LNGFR mutated short spacer (including the 4 TNFR-Cys domains with a deletion in the fourth domain). Curly brackets indicate the spacer length expressed in amino acids. Grey: scFv.

Figure 23. LNGFR-spaced CD19/CEA-CAR.28z T cells can be stained by the anti-LNGFR mAb. T cells were activated with CD3/CD28-beads, transduced with retroviral vectors (RVs) encoding for the different LNGFR-spaced CD19/CEA.CAR28z, cultured with IL-7/IL-15 and selected with the C40-1457 mAb and anti-PE beads. As positive control, CD44v6-4GS2.CAR28z T cells were produced in the same conditions. CAR identification on the T-cell surface using the LNGFR-specific mAb C40-1457 is shown.

Figure 24. LNGFR-spaced CD19/CEA-CAR.28z T cells specifically recognize antigen-expressing tumor cells *in vitro*. A. After sorting, the different LNGFR-spaced CD19/CEA/CD44v6-4GS2-CAR.28z T cells (NWL, NMS), and the CH2CH3-spaced CD19/CEA-CAR T cells (CHW), were cultured with ALL-CM and HL60 leukemia cells, BV-173 lymphoblastoid cells and BXP3C carcinoma cells at a 1:10 E:T ratio. After 4 days, residual tumor cells were counted and analyzed by FACS. The elimination index (see

Example Methods) by the different CAR.28z T cells is shown. **B.** Supernatants of the co-cultures described in A, were harvested after 24 hours and analyzed for cytokine production with the CBA assay (Biolegend). Release of IFN γ , IL-2, and TNF α upon recognition of target cells is shown.

Figure 25. LNGFR-spaced CD19-CAR.28z T cells mediate antileukemia effects. NSG mice were infused with CD19+ ALL-CM leukemia cells and, after 3 days, treated with the different LNGFR-spaced CD19-CAR.28z T cells (19 NWL and 19 NMS). T cells expressing the unrelated CD44v6-4GS2-CAR.28z (v6 NWL and v6 NMS), are infused as control. All CAR T cells were sorted to >95% purity before infusion. The plot shows the presence of ALL-CM tumor cells in the bone marrow (BM) of each mouse at the sacrifice. The tumor cells were tracked by FACS after staining with an anti-hCD45 and an anti-hCD19 mAb. Results from a T test are shown when statistically significant (*P<0.05, **P<0.01, ***P<0.001).

Figure 26. Polynucleotide sequence of CD44v6-4GS2-CAR28z, with spacer LNGFR wild-type long (NWL) (SEQ ID NO:37)

Figure 27. Polynucleotide sequence of CD44v6-4GS2-CAR28z, with spacer LNGFR wild-type short (NWS) (SEQ ID NO:38)

Figure 28. Polynucleotide sequence of CD44v6-4GS2-CAR28z with spacer LNGFR mutated long (NML) (SEQ ID NO:39)

Figure 29. Polynucleotide sequence of CD44v6-4GS2-CAR28z with spacer LNGFR mutated short (NMS) (SEQ ID NO:40)

DETAILED DESCRIPTION OF THE INVENTION

Various preferred features and embodiments of the present invention will now be described by way of non-limiting examples.

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of chemistry, biochemistry, molecular biology, microbiology and immunology, which are within the capabilities of a person of ordinary skill in the art. Such techniques are explained in the literature. See, for example, Sambrook, J., Fritsch, E.F., and Maniatis, T. (1989) *Molecular Cloning: A Laboratory Manual*, 2nd Edition, Cold Spring Harbor Laboratory Press; Ausubel, F.M. *et al.* (1995 and periodic supplements) *Current Protocols in Molecular Biology*, Ch. 9, 13 and 16, John Wiley & Sons; Roe, B., Crabtree, J., and Kahn, A. (1996) *DNA Isolation and Sequencing: Essential Techniques*, John Wiley & Sons; Polak, J.M., and

McGee, J.O'D. (1990) *In Situ Hybridization: Principles and Practice*, Oxford University Press; Gait, M.J. (1984) *Oligonucleotide Synthesis: A Practical Approach*, IRL Press; and Lilley, D.M., and Dahlberg, J.E. (1992) *Methods in Enzymology: DNA Structures Part A: Synthesis and Physical Analysis of DNA*, Academic Press. Each of these general texts is herein incorporated by reference.

Chimeric Antigen Receptors

"Chimeric antigen receptor" or "CAR" or "CARs" as used herein refers to engineered receptors which can confer an antigen specificity onto cells (for example T cells such as naive T cells, central memory T cells, effector memory T cells or combinations thereof). CARs are also known as artificial T-cell receptors, chimeric T-cell receptors or chimeric immunoreceptors. Preferably the CARs of the invention comprise an antigen-specific targeting region, an extracellular domain, a transmembrane domain, optionally one or more co-stimulatory domains, and an intracellular signaling domain.

Antigen-specific targeting domain

The antigen-specific targeting domain provides the CAR with the ability to bind to the target antigen of interest. The antigen-specific targeting domain preferably targets an antigen of clinical interest against which it would be desirable to trigger an effector immune response that results in tumor killing.

The antigen-specific targeting domain may be any protein or peptide that possesses the ability to specifically recognize and bind to a biological molecule (e.g., a cell surface receptor or tumor protein, or a component thereof). The antigen-specific targeting domain includes any naturally occurring, synthetic, semi-synthetic, or recombinantly produced binding partner for a biological molecule of interest.

Illustrative antigen-specific targeting domains include antibodies or antibody fragments or derivatives, extracellular domains of receptors, ligands for cell surface molecules/receptors, or receptor binding domains thereof, and tumor binding proteins.

In a preferred embodiment, the antigen-specific targeting domain is, or is derived from, an antibody. An antibody-derived targeting domain can be a fragment of an antibody or a genetically engineered product of one or more fragments of the antibody, which fragment is involved in binding with the antigen. Examples include a variable region (Fv), a complementarity determining region (CDR), a Fab, a single chain antibody (scFv), a heavy chain variable region (VH), a light chain variable region (VL) and a camelid antibody (VHH).

In a preferred embodiment, the binding domain is a single chain antibody (scFv). The scFv may be murine, human or humanized scFv.

"Complementarity determining region" or "CDR" with regard to an antibody or antigen-binding fragment thereof refers to a highly variable loop in the variable region of the heavy chain or the light chain of an antibody. CDRs can interact with the antigen conformation and largely determine binding to the antigen (although some framework regions are known to be involved in binding). The heavy chain variable region and the light chain variable region each contain 3 CDRs.

"Heavy chain variable region" or "VH" refers to the fragment of the heavy chain of an antibody that contains three CDRs interposed between flanking stretches known as framework regions, which are more highly conserved than the CDRs and form a scaffold to support the CDRs.

"Light chain variable region" or "VL" refers to the fragment of the light chain of an antibody that contains three CDRs interposed between framework regions.

"Fv" refers to the smallest fragment of an antibody to bear the complete antigen binding site. An Fv fragment consists of the variable region of a single light chain bound to the variable region of a single heavy chain.

"Single-chain Fv antibody" or "scFv" refers to an engineered antibody consisting of a light chain variable region and a heavy chain variable region connected to one another directly or via a peptide linker sequence.

Antibodies that specifically bind a tumor cell surface molecule can be prepared using methods well known in the art. Such methods include phage display, methods to generate human or humanized antibodies, or methods using a transgenic animal or plant engineered to produce human antibodies. Phage display libraries of partially or fully synthetic antibodies are available and can be screened for an antibody or fragment thereof that can bind to the target molecule. Phage display libraries of human antibodies are also available. Once identified, the amino acid sequence or polynucleotide sequence coding for the antibody can be isolated and/or determined.

Examples of antigens which may be targeted by the CAR of the invention include but are not limited to antigens expressed on cancer cells and antigens expressed on cells associated with various hematologic diseases, autoimmune diseases, inflammatory diseases and infectious diseases.

With respect to targeting domains that target cancer antigens, the selection of the targeting domain will depend on the type of cancer to be treated, and may target tumor antigens. A tumor sample from a subject may be characterized for the presence of certain biomarkers or cell surface markers. For example, breast cancer cells from a subject may be positive or negative for each of Her2Neu, Estrogen receptor, and/or the Progesterone receptor. A tumor antigen or cell surface molecule is selected that is found on the individual subject's tumor cells. Preferably the antigen-specific targeting domain targets a cell surface molecule that is found on tumor cells and is not substantially found on normal tissues, or restricted in its expression to non-vital normal tissues.

Further antigens specific for cancer which may be targeted by the CAR of the invention include but are not limited to any one or more of carcinoembryonic antigen (CEA), prostate specific antigen, PSMA, Her2/neu, estrogen receptor, progesterone receptor, ephrinB2, ROR1, mesothelin, c-Met, GD-2, and MAGE A3 TCR, 4-1BB, 5T4, adenocarcinoma antigen, alpha-fetoprotein, BAFF, B-lymphoma cell, C242 antigen, CA-125, carbonic anhydrase 9 (CA-IX), CCR4, CD152, CD200, CD22, CD19, CD22, CD123, CD221, CD23 (IgE receptor), CD28, CD30 (TNFRSF8), CD33, CD4, CD40, CD44, CD44 v6, CD51, CD52, CD56, CD74, CD80, CS-1, CEA, CNT0888, CTLA-4, DR5, EGFR, EpCAM, CD3, FAP, fibronectin extra domain-B, folate receptor 1, GD2, GD3 ganglioside, glycoprotein 75, GPNMB, HGF, human scatter factor receptor kinase, IGF-1 receptor, IGF-I, IgG1, L1-CAM, IL-13, IL-6, insulin-like growth factor I receptor, integrin $\alpha 5 \beta 1$, integrin $\alpha v \beta 3$, MORAb-009, MS4A1, MUC1, mucin CanAg, N-glycolylneuraminic acid, NPC-1C, PDGF-R α , PDL192, phosphatidylserine, prostatic carcinoma cells, RANKL, RON, SCH 900105, SDC1, SLAMF7, TAG-72, tenascin C, TGF beta 2, TGF- β , TRAIL-R1, TRAIL-R2, tumor antigen CTAA16.88, VEGF-A, VEGFR-1, VEGFR2 or vimentin.

Antigens specific for inflammatory diseases which may be targeted by the CAR of the invention include but are not limited to any one or more of AOC3 (VAP-1), CAM-3001, CCL11 (eotaxin-1), CD125, CD147 (basigin), CD154 (CD40L), CD2, CD20, CD23 (IgE receptor), CD25 (a chain of IL-2 receptor), CD3, CD4, CD5, IFN- α , IFN- γ , IgE, IgE Fc region, IL-1, IL-12, IL-23, IL-13, IL-17, IL-17A, IL-22, IL-4, IL-5, IL-5, IL-6, IL-6 receptor, integrin $\alpha 4$, integrin $\alpha 4 \beta 7$, Lama glama, LFA-1 (CD11a), MEDI-528, myostatin, OX-40, rhuMAb $\beta 7$, sclerostin, SOST, TGF $\beta 1$, TNF- α or VEGF-A.

Antigens specific for neuronal disorders which may be targeted by the CAR of the invention include but are not limited to any one or more of beta amyloid or MABT5102A.

Antigens specific for diabetes which may be targeted by the CAR of the invention include but are not limited to any one or more of L-1 β or CD3. Other antigens specific for diabetes or other metabolic disorders will be apparent to those of skill in the art.

Antigens specific for cardiovascular diseases which may be targeted by the CARs of the invention include but are not limited to any one or more of C5, cardiac myosin, CD41 (integrin α -IIb), fibrin II, beta chain, ITGB2 (CD18) and sphingosine-1-phosphate.

Preferably, the antigen-specific binding domain specifically binds to a tumor antigen. In a specific embodiment, the polynucleotide codes for a single chain Fv that specifically binds CD44v6.

An exemplary antigen-specific targeting domain is a CD44v6-specific single-chain fragment (scFv) such as described in Casucci M et al, *Blood*, 2013, Nov 14;122(20):3461-72. Such a sequence is shown below:

CD44v6-specific single-chain fragment (scFv)

MEAPAQLLFLLLLWLPD TTGEIVLTQSPATLSLSPGERATLSCSASSSINYIYWLQQKPGQAP
RILYLTSLNLSGVPARFSGSGSGTDFTLTISSELPEDFAVYYCLQWSSNPLTFGGGTKEIK
RGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYDMSW
VRQAPGKGLEWSTISSGGSYTYYLDSIKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCA
RQGLDYWGRGTLTVSS (SEQ ID NO: 17)

In one embodiment, the CD44v6-specific single-chain fragment comprises at least 85, 90, 95, 97, 98 or 99% identity to SEQ ID NO: 17.

In a further preferred embodiment, the light chain variable region and the heavy chain variable region of the CD44v6-specific single chain fragment are connected to one another via a peptide linker having the following sequence GGGGSGGGGS (4GS2). Such CD44v6-specific single chain fragment (CD44v6-4GS2) has the following sequence:

MEAPAQLLFLLLLWLPD TTGEIVLTQSPATLSLSPGERATLSCSASSSINYIYWLQQKPGQAP
RILYLTSLNLSGVPARFSGSGSGTDFTLTISSELPEDFAVYYCLQWSSNPLTFGGGTKEIK
RGGGSGGGGSEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEW
VSTISSGGSYTYYLDSIKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCARQGLDYWGRGT
LTVSS (SEQ ID NO: 31)

Co-stimulatory domain

The CAR of the invention may also comprise one or more co-stimulatory domains. This domain may enhance cell proliferation, cell survival and development of memory cells.

Each co-stimulatory domain comprises the co-stimulatory domain of any one or more of, for example, members of the TNFR super family, CD28, CD137 (4-1BB), CD134 (OX40), Dap1O, CD27, CD2, CD5, ICAM-1, LFA-1, Lck, TNFR-1, TNFR-II, Fas, CD30, CD40 or combinations thereof. Co-stimulatory domains from other proteins may also be used with the CAR of the invention. Additional co-stimulatory domains will be apparent to those of skill in the art.

In one embodiment the transmembrane and costimulatory domain are both derived from CD28. In one embodiment the transmembrane and intracellular costimulatory domain comprise the sequence below:

Transmembrane and intracellular portion of the human CD28 (UNIPROT: P10747, CD28_HUMAN, position 153-220)

FWLVVVGGVLACYSLLVTVAFIIFWVRSKRSLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRS (SEQ ID NO:18)

In one embodiment the transmembrane and intracellular signaling domain comprises at least 85, 90, 95, 97, 98 or 99% identity to SEQ ID NO: 18.

In one embodiment the transmembrane domain of CD28 comprises the sequence FWLVVVGGVLACYSLLVTVAFIIFWV (SEQ ID NO: 29).

In one embodiment the intracellular costimulatory domain of CD28 comprises the sequence RSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRS (SEQ ID NO: 30).

Intracellular signaling domain

The CAR of the invention may also comprise an intracellular signaling domain. This domain may be cytoplasmic and may transduce the effector function signal and direct the cell to perform its specialized function. Examples of intracellular signaling domains include, but are not limited to, ζ chain of the T-cell receptor or any of its homologs (e.g., η chain, Fc ϵ R1 γ and β chains, MB1 (Ig α) chain, B29 (Ig β) chain, etc.), CD3 polypeptides (Δ , δ and ϵ), syk family tyrosine kinases (Syk, ZAP 70, etc.), src family tyrosine kinases (Lck, Fyn, Lyn, etc.) and other molecules involved in T-cell transduction, such as CD2, CD5 and CD28. The intracellular signaling domain may be human CD3 zeta chain, Fc γ RIII, Fc ϵ RI, cytoplasmic tails of Fc receptors, immunoreceptor tyrosine-based activation motif (ITAM) bearing cytoplasmic receptors or combinations thereof.

Preferable, the intracellular signaling domain comprises the intracellular signaling domain of human CD3 zeta chain.

In one embodiment the intracellular signaling domain of human CD3 zeta chain comprises the following sequence:

UNIPROT: P20963, CD3Z_HUMAN, position 31-143

RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPKRRKNPQEG
LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR (SEQ
ID NO:20)

In one embodiment, the intracellular signaling domain comprises at least 85, 90, 95, 97, 98 or 99% identity to SEQ ID NO: 20.

Additional intracellular signaling domains will be apparent to those of skill in the art and may be used in connection with alternate embodiments of the invention.

Transmembrane domain

The CAR of the invention may also comprise a transmembrane domain. The transmembrane domain may comprise the transmembrane sequence from any protein which has a transmembrane domain, including any of the type I, type II or type III transmembrane proteins. The transmembrane domain of the CAR of the invention may also comprise an artificial hydrophobic sequence. The transmembrane domains of the CARs of the invention may be selected so as not to dimerize. Additional transmembrane domains will be apparent to those of skill in the art. Examples of transmembrane (TM) regions used in CAR constructs are: 1) The CD28 TM region (Pule et al, *Mol Ther*, 2005, Nov;12(5):933-41; Brentjens et al, *CCR*, 2007, Sep 15;13(18 Pt 1):5426-35; Casucci et al, *Blood*, 2013, Nov 14;122(20):3461-72.); 2) The OX40 TM region (Pule et al, *Mol Ther*, 2005, Nov;12(5):933-41); 3) The 41BB TM region (Brentjens et al, *CCR*, 2007, Sep 15;13(18 Pt 1):5426-35); 4) The CD3 zeta TM region (Pule et al, *Mol Ther*, 2005, Nov;12(5):933-41; Savoldo B, *Blood*, 2009, Jun 18;113(25):6392-402.); 5) The CD8a TM region (Maher et al, *Nat Biotechnol*, 2002, Jan;20(1):70-5.; Imai C, *Leukemia*, 2004, Apr;18(4):676-84; Brentjens et al, *CCR*, 2007, Sep 15;13(18 Pt 1):5426-35; Milone et al, *Mol Ther*, 2009, Aug;17(8):1453-64.).

In one embodiment the transmembrane and intracellular signaling domain are both derived from CD28. In one embodiment the transmembrane and intracellular signaling domain comprise the sequence below:

Transmembrane and intracellular portion of the human CD28 (UNIPROT: P10747, CD28_HUMAN, position 153-220)

FWWLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTRKHYQPYAPPR
DFAAYRS (SEQ ID NO:18)

In one embodiment the transmembrane and intracellular signaling domain comprises at least 85, 90, 95, 97, 98 or 99% identity to SEQ ID NO: 18.

Spacer domain - Low Affinity Nerve Growth Factor (LNGFR)

The CAR of the invention comprises an extracellular spacer domain. The extracellular spacer domain is attached to the antigen-specific targeting region and the transmembrane domain.

The CAR of the present invention comprises an extracellular spacer which comprises at least part of the extracellular domain of human low affinity nerve growth factor (LNGFR) or a derivative thereof.

LNGFR is not expressed on the majority of human hematopoietic cells, thus allowing quantitative analysis of transduced gene expression by immunofluorescence, with single cell resolution. Thus, fluorescence activated cell sorter analysis of expression of LNGFR may be performed in transduced cells to study gene expression. Further details on analysis using LNGFR may be found in Mavilio 1994, Blood 83, 1988-1997.

A sequence of human LNGFR is shown in Figure 8 (SEQ ID NO:14).

The present invention in one embodiment makes use of a truncated LNGFR (also known as ΔLNGFR). Preferably the LNGFR used in the present invention is truncated in its intracytoplasmic domain. Such a truncation is described in Mavilio 1994.

Thus, preferably the LNGFR spacer of the present invention comprises at least part of the extracellular domain or a derivative thereof but lacks the intracellular domain of LNGFR. The extracellular domain may comprise amino acids 29-250 of LNGFR or a derivative thereof.

Extracellular domain of the human LNGFR (UNIPROT # P08138, TNFR16_HUMAN, position 29-250)

KEACPTGLYTHSGECCKACNLGEGVAQPCGANQTVCEPCLDSVTFSDVVSATEPCKPCTE
CVGLQSMSAPCVEADDAVCRCAYGYYQDETTGRCEACRVCEAGSGLVFSCQDKQNTVCE
ECPDGTYSDEANHVDPCLPCTVCEDTERQLRECTRWADAECEEIPGRWITRSTPPEGSDS
TAPSTQEPEAPPEQDLIASTVAGVTTVMGSSQPVVTRGTTDN (SEQ ID NO: 19)

Preferably the LNGFR lacks the signal peptide.

In one embodiment, the spacer comprises at least part of a protein having at least 85, 90, 95, 96, 97, 98 or 99% identity to the extracellular domain of LNGFR (e.g., SEQ ID NO:19). In

one embodiment, the spacer comprises at least part of a protein having at least 85, 90, 95, 96, 97, 98 or 99% identity to amino acids 29-250 of the LNGFR protein.

LNGFR comprises 4 TNFR-Cys domains (TNFR-Cys 1, TNFR-Cys 2, TNFR-Cys 3 and TNFR-Cys 4). Sequences of the domains are exemplified below:

TNFR-Cys 1, SEQ ID NO: 9

ACPTGLYTHSGECCKACNLGEGVAQPCGANQTV

TNFR-Cys 2, SEQ ID NO: 10

PCLDSVTFSDVVSATEPCKPCTECVGLQSMSAPCVEADDAVC

TNFR-Cys 3, SEQ ID NO: 11

RCAYGYYQDETTGRCEACRVCEAGSGLVFSCQDKQNTVC

TNFR-Cys 4, SEQ ID NO: 12

ECPDGTYSDEANHVDPCLPCTVCEDTERQLRECTRWADAEC

In one embodiment, the spacer comprises TNFR-Cys 1, 2 and 3 domains or fragments or derivatives thereof. In another embodiment, the spacer comprises the TNFR-Cys 1, 2, 3 and 4 domains or fragments or derivatives thereof.

In one embodiment the spacer comprises a sequence having at least 80, 85, 90, 95, 96, 97, 98, 99% identity or 100% identity to TNFR-Cys 1 (SEQ ID NO: 9), a sequence having at least 80, 85, 90, 95, 96, 97, 98, 99% identity or 100% identity to TNFR-Cys 2 (SEQ ID NO: 10), or a sequence having at least 80, 85, 90, 95, 96, 97, 98, 99% identity or 100% identity to TNFR-Cys 3 (SEQ ID NO: 11). The spacer may further comprise a sequence having at least 80, 85, 90, 95, 96, 97, 98, 99% identity or 100% identity to TNFR-Cys 4 (SEQ ID NO: 12).

Rather than comprise the full TNFR-Cys 4 domain, the spacer may comprise a TNFR-Cys 4 domain with the following amino acids deleted from said domain:

NHVDPLPCTVCEDTERQLRECTRW. In one embodiment, the

NHVDPLPCTVCEDTERQLRECTRW amino acids are replaced with the following amino acid ARA.

In one embodiment the spacer lacks the LNGFR serine/threonine-rich stalk. In another embodiment the spacer comprises the LNGFR serine/threonine-rich stalk.

The spacer may comprise or consist of a sequence of SEQ ID NO:1 or a sequence having at least 85 %, 90%, 95%, 96%, 97%, 98% or 99% identity to SEQ ID NO:1.

The spacer may comprise or consist of a sequence of SEQ ID NO:3 or a sequence having at least 85 %, 90%, 95%, 96%, 97%, 98% or 99% identity to SEQ ID NO:3.

The spacer may comprise or consist of a sequence of SEQ ID NO:5 or a sequence having at least 85 %, 90%, 95%, 96%, 97%, 98% or 99% identity to SEQ ID NO:5.

The spacer may comprise or consist of a sequence of SEQ ID NO:1 or a sequence having at least 85 %, 90%, 95%, 96%, 97%, 98% or 99% identity to SEQ ID NO:7.

The spacer may confer properties to the CAR such that it allows for immunoselection of cells, preferably T-cells, expressing said CAR.

The CAR of the present invention (comprising the spacer referred to herein) preferably enables T-cells expressing the CAR to proliferate in the presence of cells expressing the antigen for which the CAR is designed.

The CAR of the present invention (comprising the spacer referred to herein) preferably enables T-cells expressing the CAR to mediate therapeutically significant anti-cancer effects against a cancer that the CAR is designed to target.

The CAR of the present invention (comprising the spacer referred to herein) is preferably suitable for facilitating immunoselection of cells transduced with said CAR.

The CAR of the present invention comprising the LNGFR-based spacer avoids activation of unwanted and potentially toxic off-target immune responses and allows CAR-expressing T cells to persist in vivo without being prematurely cleared by the host immune system.

As mentioned below, the present invention also encompasses the use of variants, derivatives, homologues and fragments of the spacer elements described herein.

Derivatives and fragments

In addition to the specific proteins, peptides and nucleotides mentioned herein, the present invention also encompasses the use of derivatives and fragments thereof.

The term “derivative” as used herein, in relation to proteins or polypeptides of the present invention includes any substitution of, variation of, modification of, replacement of, deletion of and/or addition of one (or more) amino acid residues from or to the sequence providing that the resultant protein or polypeptide retains the desired function.

Typically, amino acid substitutions may be made, for example from 1, 2 or 3 to 10 or 20 substitutions provided that the modified sequence retains the required activity or ability. Amino acid substitutions may include the use of non-naturally occurring analogues.

Proteins or peptides used in the present invention may also have deletions, insertions or substitutions of amino acid residues which produce a silent change and result in a functionally equivalent protein. Deliberate amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues as long as the endogenous function is retained. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include asparagine, glutamine, serine, threonine and tyrosine.

Conservative substitutions may be made, for example according to the table below. Amino acids in the same block in the second column and preferably in the same line in the third column may be substituted for each other:

ALIPHATIC	Non-polar	G A P
		I L V
	Polar - uncharged	C S T M
		N Q
AROMATIC	Polar - charged	D E
		K R H
		F W Y

The derivative may be a homolog. The term “homologue” as used herein means an entity having a certain homology with the wild type amino acid sequence and the wild type nucleotide sequence. The term “homology” can be equated with “identity”.

A homologous sequence may include an amino acid sequence which may be at least 50%, 55%, 65%, 75%, 85% or 90% identical, preferably at least 95% or 97% or 99% identical to the subject sequence. Typically, the homologues will comprise the same active sites etc. as the subject amino acid sequence. Although homology can also be considered in terms of similarity (i.e. amino acid residues having similar chemical properties/functions), in the

context of the present invention it is preferred to express homology in terms of sequence identity.

A homologous sequence may include a nucleotide sequence which may be at least 50%, 55%, 65%, 75%, 85% or 90% identical, preferably at least 95% or 97% or 99% identical to the subject sequence. Although homology can also be considered in terms of similarity, in the context of the present invention it is preferred to express homology in terms of sequence identity.

Homology comparisons can be conducted by eye or, more usually, with the aid of readily available sequence comparison programs. These commercially available computer programs can calculate percentage homology or identity between two or more sequences.

Percentage homology may be calculated over contiguous sequences, i.e. one sequence is aligned with the other sequence and each amino acid in one sequence is directly compared with the corresponding amino acid in the other sequence, one residue at a time. This is called an "ungapped" alignment. Typically, such ungapped alignments are performed only over a relatively short number of residues.

Although this is a very simple and consistent method, it fails to take into consideration that, for example, in an otherwise identical pair of sequences, one insertion or deletion in the nucleotide sequence may cause the following codons to be put out of alignment, thus potentially resulting in a large reduction in percent homology when a global alignment is performed. Consequently, most sequence comparison methods are designed to produce optimal alignments that take into consideration possible insertions and deletions without penalising unduly the overall homology score. This is achieved by inserting "gaps" in the sequence alignment to try to maximise local homology.

However, these more complex methods assign "gap penalties" to each gap that occurs in the alignment so that, for the same number of identical amino acids, a sequence alignment with as few gaps as possible, reflecting higher relatedness between the two compared sequences, will achieve a higher score than one with many gaps. "Affine gap costs" are typically used that charge a relatively high cost for the existence of a gap and a smaller penalty for each subsequent residue in the gap. This is the most commonly used gap scoring system. High gap penalties will of course produce optimised alignments with fewer gaps. Most alignment programs allow the gap penalties to be modified. However, it is preferred to use the default values when using such software for sequence comparisons. For example when using the GCG Wisconsin Bestfit package the default gap penalty for amino acid sequences is -12 for a gap and -4 for each extension.

Calculation of maximum percentage homology therefore firstly requires the production of an optimal alignment, taking into consideration gap penalties. A suitable computer program for carrying out such an alignment is the GCG Wisconsin Bestfit package (University of Wisconsin, U.S.A.; Devereux *et al.* (1984) *Nucleic Acids Res.* 12: 387). Examples of other software that can perform sequence comparisons include, but are not limited to, the BLAST package (see Ausubel *et al.* (1999) *ibid* – Ch. 18), FASTA (Atschul *et al.* (1990) *J. Mol. Biol.* 403-410) and the GENWORKS suite of comparison tools. Both BLAST and FASTA are available for offline and online searching (see Ausubel *et al.* (1999) *ibid*, pages 7-58 to 7-60). However, for some applications, it is preferred to use the GCG Bestfit program. Another tool, called BLAST 2 Sequences is also available for comparing protein and nucleotide sequences (see *FEMS Microbiol. Lett.* (1999) 174: 247-50; *FEMS Microbiol. Lett.* (1999) 177: 187-8).

Although the final percentage homology can be measured in terms of identity, the alignment process itself is typically not based on an all-or-nothing pair comparison. Instead, a scaled similarity score matrix is generally used that assigns scores to each pairwise comparison based on chemical similarity or evolutionary distance. An example of such a matrix commonly used is the BLOSUM62 matrix – the default matrix for the BLAST suite of programs. GCG Wisconsin programs generally use either the public default values or a custom symbol comparison table if supplied (see the user manual for further details). For some applications, it is preferred to use the public default values for the GCG package, or in the case of other software, the default matrix, such as BLOSUM62.

Once the software has produced an optimal alignment, it is possible to calculate percentage homology, preferably percentage sequence identity. The software typically does this as part of the sequence comparison and generates a numerical result.

Fragments typically refer to a selected region of the polypeptide or polynucleotide that is of interest functionally. "Fragment" thus refers to an amino acid sequence that is a portion of a full length polypeptide or a nucleic acid sequence that is a portion of a full-length polynucleotide. Since fragments are of interest functionally e.g., retain the desired functionality, they will therefore exclude e.g. a single amino acid or a single nucleic acid.

Such derivatives and fragments may be prepared using standard recombinant DNA techniques such as site-directed mutagenesis. Where insertions are to be made, synthetic DNA encoding the insertion together with 5' and 3' flanking regions corresponding to the naturally-occurring sequence either side of the insertion site may be made. The flanking regions will contain convenient restriction sites corresponding to sites in the naturally-

occurring sequence so that the sequence may be cut with the appropriate enzyme(s) and the synthetic DNA ligated into the cut. The DNA is then expressed in accordance with the invention to make the encoded protein. These methods are only illustrative of the numerous standard techniques known in the art for manipulation of DNA sequences and other known techniques may also be used.

Polynucleotides

Polynucleotides of the invention may comprise DNA or RNA. They may be single-stranded or double-stranded. It will be understood by a skilled person that numerous different polynucleotides can encode the same polypeptide as a result of the degeneracy of the genetic code. In addition, it is to be understood that the skilled person may, using routine techniques, make nucleotide substitutions that do not affect the polypeptide sequence encoded by the polynucleotides of the invention to reflect the codon usage of any particular host organism in which the polypeptides of the invention are to be expressed.

The polynucleotides may be modified by any method available in the art. Such modifications may be carried out in order to enhance the *in vivo* activity or lifespan of the polynucleotides of the invention.

Polynucleotides such as DNA polynucleotides may be produced recombinantly, synthetically or by any means available to those of skill in the art. They may also be cloned by standard techniques.

Longer polynucleotides will generally be produced using recombinant means, for example using polymerase chain reaction (PCR) cloning techniques. This will involve making a pair of primers (e.g. of about 15 to 30 nucleotides) flanking the target sequence which it is desired to clone, bringing the primers into contact with mRNA or cDNA obtained from an animal or human cell, performing a polymerase chain reaction under conditions which bring about amplification of the desired region, isolating the amplified fragment (e.g. by purifying the reaction mixture with an agarose gel) and recovering the amplified DNA. The primers may be designed to contain suitable restriction enzyme recognition sites so that the amplified DNA can be cloned into a suitable vector.

Codon optimisation

The polynucleotides used in the present invention may be codon-optimised. Codon optimisation has previously been described in WO 1999/41397 and WO 2001/79518. Different cells differ in their usage of particular codons. This codon bias corresponds to a bias in the relative abundance of particular tRNAs in the cell type. By altering the codons in

the sequence so that they are tailored to match with the relative abundance of corresponding tRNAs, it is possible to increase expression. By the same token, it is possible to decrease expression by deliberately choosing codons for which the corresponding tRNAs are known to be rare in the particular cell type. Thus, an additional degree of translational control is available.

Vectors

A vector is a tool that allows or facilitates the transfer of an entity from one environment to another. In accordance with the present invention, and by way of example, some vectors used in recombinant nucleic acid techniques allow entities, such as a segment of nucleic acid (e.g. a heterologous DNA segment, such as a heterologous cDNA segment), to be transferred into a target cell. Vectors may be non-viral or viral. Examples of vectors used in recombinant nucleic acid techniques include, but are not limited to, plasmids, mRNA molecules (e.g. *in vitro* transcribed mRNAs), chromosomes, artificial chromosomes and viruses. The vector may also be, for example, a naked nucleic acid (e.g. DNA). In its simplest form, the vector may itself be a nucleotide of interest.

The vectors used in the invention may be, for example, plasmid, mRNA or virus vectors and may include a promoter for the expression of a polynucleotide and optionally a regulator of the promoter.

Vectors comprising polynucleotides of the invention may be introduced into cells using a variety of techniques known in the art, such as transformation and transduction. Several techniques are known in the art, for example infection with recombinant viral vectors, such as retroviral, lentiviral, adenoviral, adeno-associated viral, baculoviral and herpes simplex viral vectors; direct injection of nucleic acids and biolistic transformation.

Non-viral delivery systems include but are not limited to DNA transfection methods. Here, transfection includes a process using a non-viral vector to deliver a gene to a target cell.

Typical transfection methods include electroporation, DNA biolistics, lipid-mediated transfection, compacted DNA-mediated transfection, liposomes, immunoliposomes, lipofectin, cationic agent-mediated transfection, cationic facial amphiphiles (CFAs) (*Nat. Biotechnol.* (1996) 14: 556) and combinations thereof.

Retroviral vectors

In one embodiment, the vector used in the present invention is a retrovirus-based vector which has been genetically engineered so that it cannot replicate and produce progeny

infectious virus particles once the virus has entered the target cell. There are many retroviruses that are widely used for delivery of genes both in tissue culture conditions and in living organisms. Examples include and are not limited to murine leukemia virus (MLV), human immunodeficiency virus (HIV-1), equine infectious anaemia virus (EIAV), mouse mammary tumour virus (MMTV), Rous sarcoma virus (RSV), Fujinami sarcoma virus (FuSV), Moloney murine leukemia virus (Mo-MLV), FBR murine osteosarcoma virus (FBR MSV), Moloney murine sarcoma virus (Mo-MSV), Abelson murine leukemia virus (A-MLV), Avian myelocytomatosis virus-29 (MC29), and Avian erythroblastosis virus (AEV) and all other *retroviridae* including lentiviruses. A detailed list of retroviruses may be found in Coffin *et al.*, 1997, "retroviruses", Cold Spring Harbour Laboratory Press Eds: JM Coffin, SM Hughes, HE Varmus pp 758-763.

The basic structure of a retrovirus genome is a 5' LTR and a 3' LTR, between or within which are located a packaging signal to enable the genome to be packaged, a primer binding site, integration sites to enable integration into a host cell genome and *gag*, *pol* and *env* genes encoding the packaging components - these are polypeptides required for the assembly of viral particles. More complex retroviruses have additional features, such as *rev* and RRE sequences in HIV, which enable the efficient export of RNA transcripts of the integrated provirus from the nucleus to the cytoplasm of an infected target cell.

In the provirus, these genes are flanked at both ends by regions called long terminal repeats (LTRs). The LTRs are responsible for proviral integration, and transcription. LTRs also serve as enhancer-promoter sequences and can control the expression of the viral genes. Encapsidation of the retroviral RNAs occurs by virtue of a *psi* sequence located at the 5' end of the viral genome.

The LTRs themselves are identical sequences that can be divided into three elements, which are called U3, R and U5. U3 is derived from the sequence unique to the 3' end of the RNA. R is derived from a sequence repeated at both ends of the RNA and U5 is derived from the sequence unique to the 5' end of the RNA. The sizes of the three elements can vary considerably among different retroviruses.

In a defective retroviral vector genome *gag*, *pol* and *env* may be absent or not functional. The R regions at both ends of the RNA are repeated sequences. U5 and U3 represent unique sequences at the 5' and 3' ends of the RNA genome respectively.

More preferably, the viral vector is a targeted vector, that is it has a tissue tropism which is altered compared to the native virus, so that the vector is targeted to particular cells. This

may be achieved by modifying the retroviral Env protein. Preferably the envelope protein is a non-toxic envelope or an envelope which may be produced in non-toxic amounts within the primary target cell, such as for example a MMLV amphotropic envelope or a modified amphotropic envelope.

Preferably the envelope is one which allows transduction of human cells. Examples of suitable *env* genes include, but are not limited to, VSV-G, a MLV amphotropic *env* such as the 4070A *env*, the RD114 feline leukaemia virus *env* or haemagglutinin (HA) from an influenza virus. The Env protein may be one which is capable of binding to a receptor on a limited number of human cell types and may be an engineered envelope containing targeting moieties. The *env* and *gag-pol* coding sequences are transcribed from a promoter and optionally an enhancer active in the chosen packaging cell line and the transcription unit is terminated by a polyadenylation signal. For example, if the packaging cell is a human cell, a suitable promoter-enhancer combination is that from the human cytomegalovirus major immediate early (hCMV-MIE) gene and a polyadenylation signal from SV40 virus may be used. Other suitable promoters and polyadenylation signals are known in the art.

MLV

Preferably, the retroviral vector used in the present invention is an Murine Leukemia Virus (MLV) vector. Retroviral vectors derived from the amphotropic Moloney murine leukemia virus (MLV-A) are commonly used in clinical protocols worldwide. These viruses use cell surface phosphate transporter receptors for entry and then permanently integrate into proliferating cell chromosomes. The genes are then maintained for the lifetime of the cell. Gene activity on MLV based constructs are easy to control and can be effective over a long time. Clinical trials conducted with these MLV -based systems have shown them to be well tolerated with no adverse side effects.

An example of an MLV vector for use in the present invention is a vector derived from SFCMM-3, which carries both the suicide gene HSV-tk and the marker gene Δ LNGFR (Verzeletti 98, Human Gene Therapy 9:2243). The original vector used in the preparation of SFCMM-3 is LXS_N (Miller et al. Improved retroviral vectors for gene transfer and expression. BioTechniques 7:980-990, 1989) (Genebank accession #28248). LXS_N vector was modified by the insertion of the HSV-tk gene into the unique Hpa I site ("blunt cut"), removal of the neo gene by digestion with Hind III and Nae I, and insertion of the cDNA encoding Δ LNGFR in this site.

Lentiviral vector

In one embodiment, the vector of the present invention may be a lentiviral vector. Lentivirus vectors are part of a larger group of retroviral vectors. A detailed list of lentiviruses may be found in Coffin *et al* ("Retroviruses" 1997 Cold Spring Harbour Laboratory Press Eds: JM Coffin, SM Hughes, HE Varmus pp 758-763). In brief, lentiviruses can be divided into primate and non-primate groups. Examples of primate lentiviruses include but are not limited to: the human immunodeficiency virus (HIV), the causative agent of human acquired-immunodeficiency syndrome (AIDS), and the simian immunodeficiency virus (SIV). The non-primate lentiviral group includes the prototype "slow virus" visna/maedi virus (VMV), as well as the related caprine arthritis-encephalitis virus (CAEV), equine infectious anaemia virus (EIAV) and the more recently described feline immunodeficiency virus (FIV) and bovine immunodeficiency virus (BIV).

A distinction between the lentivirus family and other types of retroviruses is that lentiviruses have the capability to infect both dividing and non-dividing cells. In contrast, other retroviruses - such as MLV - are unable to infect non-dividing or slowly dividing cells such as those that make up, for example, muscle, brain, lung and liver tissue. As lentiviruses are able to transduce terminally differentiated/primary cells, the use of a lentiviral screening strategy allows library selection in a primary target non-dividing or slowly dividing host cell.

Adenovirus vectors

In another embodiment, the vector of the present invention may be an adenovirus vector. The adenovirus is a double-stranded, linear DNA virus that does not go through an RNA intermediate. There are over 50 different human serotypes of adenovirus divided into 6 subgroups based on the genetic sequence homology. The natural target of adenovirus is the respiratory and gastrointestinal epithelia, generally giving rise to only mild symptoms. Serotypes 2 and 5 (with 95% sequence homology) are most commonly used in adenoviral vector systems and are normally associated with upper respiratory tract infections in the young.

Adenoviruses are nonenveloped, regular icosahedrons. A typical adenovirus comprises a 140nm encapsidated DNA virus. The icosahedral symmetry of the virus is composed of 152 capsomeres: 240 hexons and 12 pentons. The core of the particle contains the 36kb linear duplex DNA which is covalently associated at the 5' ends with the Terminal Protein (TP)

which acts as a primer for DNA replication. The DNA has inverted terminal repeats (ITR) and the length of these varies with the serotype.

The adenovirus is a double stranded DNA nonenveloped virus that is capable of *in vivo* and *in vitro* transduction of a broad range of cell types of human and non-human origin. These cells include respiratory airway epithelial cells, hepatocytes, muscle cells, cardiac myocytes, synoviocytes, primary mammary epithelial cells and post-mitotically terminally differentiated cells such as neurons.

Adenoviral vectors are also capable of transducing non dividing cells. This is very important for diseases, such as cystic fibrosis, in which the affected cells in the lung epithelium, have a slow turnover rate. In fact, several trials are underway utilising adenovirus-mediated transfer of cystic fibrosis transporter (CFTR) into the lungs of afflicted adult cystic fibrosis patients.

Adenoviruses have been used as vectors for gene therapy and for expression of heterologous genes. The large (36 kilobase) genome can accommodate up to 8kb of foreign insert DNA and is able to replicate efficiently in complementing cell lines to produce very high titres of up to 10^{12} . Adenovirus is thus one of the best systems to study the expression of genes in primary non-replicative cells.

The expression of viral or foreign genes from the adenovirus genome does not require a replicating cell. Adenoviral vectors enter cells by receptor mediated endocytosis. Once inside the cell, adenovirus vectors rarely integrate into the host chromosome. Instead, it functions episomally (independently from the host genome) as a linear genome in the host nucleus. Hence the use of recombinant adenovirus alleviates the problems associated with random integration into the host genome.

Pox viral vectors

Pox viral vectors may be used in accordance with the present invention, as large fragments of DNA are easily cloned into their genome and recombinant attenuated vaccinia variants have been described (Meyer, *et al.*, 1991; Smith and Moss, 1983).

Examples of pox viral vectors include but are not limited to leporipoxvirus: Upton, *et al.*, 1986, (Shope fibroma virus); capripoxvirus: Gershon, *et al.*, 1989, (Kenya sheep-1); orthopoxvirus: Weir, *et al.*, 1983, (vaccinia); Esposito, *et al.*, 1984, (monkeypox and variola virus); Hruby, *et al.*, 1983, (vaccinia); Kilpatrick, *et al.*, 1985, (Yaba monkey tumour virus);

avipoxvirus: Binns, et al., (1988) (fowlpox); Boyle, et al., 1987, (fowlpox); Schnitzlein, et al., 1988, (fowlpox, quailpox); entomopox (Lytvyn, et al., 1992).

Poxvirus vectors are used extensively as expression vehicles for genes of interest in eukaryotic cells. Their ease of cloning and propagation in a variety of host cells has led, in particular, to the widespread use of poxvirus vectors for expression of foreign protein and as delivery vehicles for vaccine antigens.

Vaccinia viral vectors

The vector of the present invention may be a vaccinia virus vector such as MVA or NYVAC. Most preferred is the vaccinia strain modified virus ankara (MVA) or a strain derived therefrom. Alternatives to vaccinia vectors include avipox vectors such as fowlpox or canarypox known as ALVAC and strains derived therefrom which can infect and express recombinant proteins in human cells but are unable to replicate.

Cells

The invention also provides genetically engineered cells which comprise and stably express the CAR of the invention.

The antigen-specific targeting domains may be capable of specifically binding, in an MHC unrestricted manner, an antigen which is not normally bound by a T-cell receptor in that manner. In one embodiment, the antigen-specific targeting regions comprise target-specific antibodies or functional equivalents or fragments or derivatives thereof. The antigen-specific antibody may be the Fab fragment of the antibody or the single chain variable fragment (scFv) of the antibody.

Genetically engineered cells which may comprise and express the CARs of the invention include, but are not limited to, T-cells, naive T cells, stem cell memory T cells, central memory T cells, effector memory T cells, natural killer cells, hematopoietic stem cells and/or cells capable of giving rise to therapeutically relevant progeny. In an embodiment, the genetically engineered cells are autologous cells. By way of example, individual T-cells of the invention may be CD4+/CD8-, CD4-/CD8+, CD4-/CD8- or CD4+/CD8+. The T-cells may be a mixed population of CD4+/CD8- and CD4-/CD8+ cells or a population of a single clone.

Genetically modified cells may be produced by stably transfecting cells with DNA encoding the CAR of the invention.

Various methods produce stable transfectants which express the CARs of the invention. In one embodiment, a method of stably transfecting and re-directing cells is by electroporation using naked DNA. By using naked DNA, the time required to produce redirected cells may be significantly reduced. Additional methods to genetically engineer cells using naked DNA encoding the CAR of the invention include but are not limited to chemical transformation methods (e.g., using calcium phosphate, dendrimers, liposomes and/or cationic polymers), non-chemical transformation methods (e.g., electroporation, optical transformation, gene electrotransfer and/or hydrodynamic delivery) and/or particle-based methods (e.g., impalefection, using a gene gun and/or magnetofection). The transfected cells demonstrating presence of a single integrated un-rearranged vector and expression of the CAR may be expanded ex vivo. In one embodiment, the cells selected for ex vivo expansion are CD8+ and demonstrate the capacity to specifically recognize and lyse antigen-specific target cells.

Viral transduction methods may also be used to generate redirected cells which express the CAR of the invention.

Stimulation of the T-cells by an antigen under proper conditions results in proliferation (expansion) of the cells and/or production of IL-2. The cells comprising the CAR of the invention will expand in number in response to the binding of one or more antigens to the antigen-specific targeting regions of the CAR. The invention also provides a method of making and expanding cells expressing a CAR. The method may comprise transfecting or transducing the cells with the vector expressing the CAR after stimulating the cells with: 1) polyclonal stimuli such as cell-free scaffolds, preferably optimally-sized beads, containing at least an activating polipeptide, preferably an antibody, specific for CD3 and an activating polipeptide, preferably an antibody, specific for CD28; 2) tumor cells expressing the target antigen; 3) natural artificial antigen presenting cells, and culturing them with cytokines including IL-2, IL-7, IL-15, IL-21 alone or in combination.

Therapeutic methods and pharmaceutical compositions

There are provided herein methods for treating a disease associated with the antigen targeted by the CAR of the invention in a subject in need thereof. The method comprises administering an effective amount of the CAR, polynucleotide or vector encoding the CAR, or a cell expressing said CAR so as to treat the disease associated with the antigen in the subject.

There is also provided a pharmaceutical composition comprising a CAR of the invention. The CAR of the invention in the composition may be any one or more of a polynucleotide

encoding the CAR, a vector encoding the CAR, a protein comprising the CAR or genetically modified cells comprising the CAR.

A pharmaceutical composition is a composition that comprises or consists of a therapeutically effective amount of a pharmaceutically active agent. It preferably includes a pharmaceutically acceptable carrier, diluent or excipient (including combinations thereof). Acceptable carriers or diluents for therapeutic use are well known in the pharmaceutical art, and are described, for example, in Remington's Pharmaceutical Sciences, Mack Publishing Co. (A. R. Gennaro edit. 1985). The choice of pharmaceutical carrier, excipient or diluent can be selected with regard to the intended route of administration and standard pharmaceutical practice. The pharmaceutical compositions may comprise as - or in addition to - the carrier, excipient or diluent any suitable binder(s), lubricant(s), suspending agent(s), coating agent(s) or solubilising agent(s).

Examples of pharmaceutically acceptable carriers include, for example, water, salt solutions, alcohol, silicone, waxes, petroleum jelly, vegetable oils, polyethylene glycols, propylene glycol, liposomes, sugars, gelatin, lactose, amylose, magnesium stearate, talc, surfactants, silicic acid, viscous paraffin, perfume oil, fatty acid monoglycerides and diglycerides, petroethral fatty acid esters, hydroxymethyl-cellulose, polyvinylpyrrolidone, and the like.

EXAMPLES

Example 1 - Methods

Generation of LNGFR-spaced CD44v6-CAR.28z constructs

The sequences of the LNGFR-based spacers were derived from the extracellular portion of the low-affinity nerve growth factor receptor (LNGFR), excluding the signal peptide (P08138, TNFR16_HUMAN). The wild-type long (NWL) design contains both the four TNFR cysteine-rich domains and the serine/threonine-rich stalk. The wild-type short (NWS) design comprises only the four TNFR cysteine-rich domains. The mutated long (NML) design contains the four TNFR cysteine-rich domains, the serine/threonine-rich stalk and includes a specific modification in the fourth domain to avoid binding to NGF (Yan et al, *J Biol Chem*, 1991, Jun 25;266(18):12099-104). The mutated short (NMS) design contains only the four TNFR cysteine-rich domains including the specific modification in the fourth domain. The spacers were synthesized by GENEART, flanked by specific restriction sites (BamH1 and PflMI) to allow the cloning into our original CD44v6-specific, second-generation CAR construct (Figure 9; SEQ ID NO: 15) in place of the IgG1 CH2CH3 spacer. All the constructs

have been codon-optimized for expression in humans. All the constructs were expressed into SFG-RV backbones (a splicing MoMLV-based retroviral vector commonly used (Riviere et al, *PNAS*, 1995, Jul 18;92(15):6733-7)).

Spacer LNGFR wild-type long (NWL):

Protein sequence (SEQ ID NO:1)

KEACPTGLYTHSGECCACNLGEGVAQPCGANQTVCEPCLDSVTFSDVVSATEPCKPCTECVGLQSMSAPCWEADDAVCRC
AYGYYQDETTGRCEACRVCEAGSGLVFSCQDKQNTVCEECPDGTYSDEANHVDPCLPCTVCEDTERQLRECTRWADAECEE
IPGRWITRSTPPEGSDSTAPSTQEPEAPPEQDLIASTVAGVVTVMGSSQPVVTRGTTDN.

Nucleotide sequence (SEQ ID NO:2):

AAAGAGGCCTGCCCCACCGGCCTGTACACCCACAGCGGAGAGTGCTGCAAGGCCTGCAACCTGGGAGAGGGCGTGCC
CAGCCTTGCGGCGCCAATCAGACCGTGTGCGAGCCCTGCCTGGACAGCGTGACCTTCAGCGACGTGGTGTCCGCCACC
GAGCCCTGCAAGCCTTGACCCGAGTGTGTGGGCCTGCAGAGCATGAGCGCCCCCTGCGTGGAAGCCGACGACGCCGT
GTGTAGATGCGCCTACGGCTACTACCAGGACGAGACAACCGGCAGATGCGAGGCCTGTAGAGTGTGCGAGGCCGGCA
GCGGCCTGGTGTTCAGTTGTCAAGACAAGCAGAATACCGTGTGTGAAAGAGTGCCCCGACGGCACCTACAGCGACGAGG
CCAACCACGTGGACCCCTGCCTGCCCTGCACTGTGTGCGAGGACACCGAGCGGCAGCTGCGCGAGTGCAAGATGGG
CCGACGCCGAGTGCGAAGAGATCCCCGGCAGATGGATCACCAGAAGCACCCCCCTGAGGGCAGCGACAGCACCGCCC
CTAGCACCCAGGAACCTGAGGCCCTCCCGAGCAGGACCTGATCGCCTCTACAGTGGCCGGCGTGGTGACAACCGTGAT
GGGCAGCTCTCAGCCCGTGGTGACACGGGGCACCCAGACAAT.

Spacer LNGFR wild-type short (NWS):

Protein sequence (SEQ ID NO:3):

KEACPTGLYTHSGECCACNLGEGVAQPCGANQTVCEPCLDSVTFSDVVSATEPCKPCTECVGLQSMSAPCWEADDAVCRC
AYGYYQDETTGRCEACRVCEAGSGLVFSCQDKQNTVCEECPDGTYSDEANHVDPCLPCTVCEDTERQLRECTRWADAECEE
 .

Nucleotide sequence (SEQ ID NO:4):

AAAGAGGCCTGCCCCACCGGCCTGTACACCCACAGCGGAGAGTGCTGCAAGGCCTGCAACCTGGGAGAGGGCGTGCC
CAGCCTTGCGGCGCCAATCAGACCGTGTGCGAGCCCTGCCTGGACAGCGTGACCTTCAGCGACGTGGTGTCCGCCACC
GAGCCCTGCAAGCCTTGACCCGAGTGTGTGGGCCTGCAGAGCATGAGCGCCCCCTGCGTGGAAGCCGACGACGCCGT
GTGTAGATGCGCCTACGGCTACTACCAGGACGAGACAACCGGCAGATGCGAGGCCTGTAGAGTGTGCGAGGCCGGCA
GCGGCCTGGTGTTCAGTTGTCAAGACAAGCAGAACACCGTGTGTGAAAGAGTGCCCCGACGGCACCTACAGCGACGAGG
CCAACCACGTGGACCCCTGCCTGCCCTGCACTGTGTGCGAGGACACCGAGCGGCAGCTGCGCGAGTGCAAGATGGG
CCGACGCCGAGTGCGAGGAA.

Spacer LNGFR mutated long (NML):

Protein sequence (SEQ ID NO:5):

KEACPTGLYTHSGECCACNLGEGVAQPCGANQTVCEPCLDSVTFSDVVSATEPCKPCTECVGLQSMSAPCVEADDAVCRC
AYGYQDETTGRCEACRVCEAGSGLVFSCQDKQNTVCEECPDGTYSDAARAADAECEEIPGRWITRSTPPEGSDSTAPSTQ
EPEAPPEQDLIASTVAGVTTVMGSSQPVVTRGTTDN.

Nucleotide sequence (SEQ ID NO:6):

AAAGAGGCCTGCCCCACCGGCCTGTACACCCACAGCGGAGAGTGCTGCAAGGCCTGCAACCTGGGAGAGGGCGTGCC
CAGCCTTGCGGCGCCAATCAGACCGTGTGCGAGCCCTGCCTGGACAGCGTGACCTTCAGCGACGTGGTGTCGCCACC
GAGCCCTGCAAGCCTTGACCGAGTGTGTGGGCCTGCAGAGCATGAGCGCCCCCTGCGTGGAAGCCGACGACGCCGT
GTGTAGATGCGCCTACGGCTACTACCAGGACGAGACAACCGGCAGATGCGAGGCCTGTAGAGTGTGCGAGGCCGCA
GCGGCCTGGTGTTCAAGTGTCAAGACAAGCAGAATACCGTGTGTGAAGAGTGCCCCGACGGCACCTACAGCGACGAAG
 CCGCCAGAGCCGCGGACGCGGAGTGCGAAGAGATCCCCGGCAGATGGATCACCAGAAGACCCCCCTGAGGGCAGCG
 ACAGCACCGCCCTAGCACCCAGGAACCTGAGGCCCTCCCGAGCAGGACCTGATCGCCTCTACAGTGGCCGGCGTGGT
GACAACCGTGATGGGCAGCTCTCAGCCCGTGGTGACACGGGGCACCACCGACAAT.

Spacer LNGFR mutated short (NMS):

Protein sequence (SEQ ID NO:7):

KEACPTGLYTHSGECCACNLGEGVAQPCGANQTVCEPCLDSVTFSDVVSATEPCKPCTECVGLQSMSAPCVEADDAVCRC
AYGYQDETTGRCEACRVCEAGSGLVFSCQDKQNTVCEECPDGTYSDAARAADAECEE.

Nucleotide sequence (SEQ ID NO:8):

AAAGAGGCCTGCCCCACCGGCCTGTACACCCACAGCGGAGAGTGCTGCAAGGCCTGCAACCTGGGAGAGGGCGTGCC
CAGCCTTGCGGCGCCAATCAGACCGTGTGCGAGCCCTGCCTGGACAGCGTGACCTTCAGCGACGTGGTGTCGCCACC
GAGCCCTGCAAGCCTTGACCGAGTGTGTGGGCCTGCAGAGCATGAGCGCCCCCTGCGTGGAAGCCGACGACGCCGT
GTGTAGATGCGCCTACGGCTACTACCAGGACGAGACAACCGGCAGATGCGAGGCCTGTAGAGTGTGCGAGGCCGCA
GCGGCCTGGTGTTCAAGTGTCAAGACAAGCAGAACACCGTGTGTGAAGAGTGCCCCGACGGCACCTACAGCGACGAGG
 CCGCCCGGGCGCGGACGCGGAGTGCGAGGAA.

Legend:

Underlined: TNFR cysteine-rich domain number 1.

Bold: TNFR cysteine-rich domain number 2.

Bold and underlined: TNFR cysteine-rich domain number 3.

Italics: TNFR cysteine-rich domain number 4.

Italics and underlined: Serine/Threonine rich stalk

Transduction and culture conditions.

T cells were activated with cell-sized CD3/CD28-beads (ClinExVivo, Invitrogen) plus IL-7/IL-

15 (5 ng/ml, Peprotech) and RV-transduced by two rounds of spinoculation at day 2 and 3 after stimulation. At day 6, beads were removed and T cells cultured in RPMI 1640 (Gibco-Brl) 10% FBS (BioWhittaker) in the presence of IL-7 and IL-15. Surface expression of CH2CH3-spaced, CD44v6-specific CAR constructs (CHW and CHM) was detected with mAbs specific for the IgG1 CH2CH3 spacer (Jackson Laboratories), while surface expression of LNGFR-spaced CD44v6-specific CAR constructs (NWL, NWS, NML and NMS) was analysed using LNGFR-specific mAbs from BD Bioscience (Clone: C40-14579) or from Miltenyi (Clone: ME20.4). Between day 9 and day 15 from activation, CH2CH3-spaced CD44v6-CAR.28z T cells were FACS-sorted using the polyclonal IgG1 CH2CH3-specific mAbs, while LNGFR-spaced CD44v6-CAR.28z T cells were stained with the PE-conjugated, LNGFR-specific mAb C40-14579 and sorted with columns using anti-PE paramagnetic beads (Miltenyi). Post-sorting T-cell expansion has been expressed as fold increase: T-cell number at day x/ T-cell number after sorting.

In vitro assays to analyze specific recognition.

In co-culture assays, CAR-sorted T cells were cultured with target cells at different E:T ratios. After 4 days, surviving cells were counted and analysed by FACS. T cells transduced with an irrelevant CAR (CD19) were always used as control. Elimination index was calculated as follows: $1 - (\text{number of residual target cells in presence of CD44v6.CAR28z+ T cells}) / (\text{number of residual target cells in presence of CTR.CAR28z+ T cells})$. In CFSE-diluting assays, CAR-sorted T cells were loaded with CFSE and stimulated with irradiated (10'000 rad) tumor cells at the E:S ratio of 1:5 or with biologically active concentrations of NGF. After 6 days, T-cell proliferation was measured by FACS by analyzing the percentage of cells that have diluted the CFSE dye.

Xenograft models of antitumor efficacy

Experimental protocols were approved by the Institutional Animal Care and Use Committee (IACUC). For the minimal-residual disease model, NSG mice (Jackson) were infused i.v. with $1,5 \times 10^6$ THP1 leukemia cells/mouse. Three days after, mice were treated i.v with 5×10^6 sorted LNGFR-spaced CD44v6-CAR.28z T cells, CH2CH3-spaced CD44v6-CAR.28z T cells or T cells carrying an irrelevant CAR (CD19). T-cell engraftment was monitored weekly by bleeding and FACS analysis. After 7 weeks, mice were sacrificed and their liver analyzed by histopathology and FACS for the presence of THP-1 cells. For the well-established disease model, NSG mice were infused i.v. with 2×10^6 MM1.S myeloma cells/mouse. Five weeks after, mice were treated i.v with 5×10^6 sorted LNGFR-spaced CD44v6-CAR.28z T cells, CH2CH3-spaced CD44v6-CAR.28z T cells or T cells carrying an irrelevant CAR (CD19). T-cell engraftment and myeloma progression were monitored weekly by bleeding and FACS

analysis (myeloma cells will be discerned from T cells according to the different human CD45/CD3 phenotype). When circulating MM1.S cells exceeded the 30 cells/ μ l and/or mice manifested clear signs of tumor-related suffering (paralysis or >10% weight loss), mice were euthanized.

Flow cytometry.

For FACS analysis, we used FITC-, PE-, PerCP-, PE-Cy7-, APC-, APC-Cy7 and Pacific Blue-conjugated antibodies directed to human CD44v6, CD4 (e-Bioscience), CD123, CD19, CD14, CD3, CD8, CD45RA, CD62L, CXCR4, CD127, CD33, CD38, CD45, LNGFR, mouse CD45, 7AAD (BD Biosciences) and IgG1 CH2CH3 (Jackson laboratories). Cells (2×10^5) were incubated with antibodies for 15 minutes at 4 °C and washed with PBS 1% FBS. Samples were run through a FACS Canto II flow cytometer (BD Biosciences), and data were analysed with the Flow Jo software (Tree star Inc). Relative Fluorescence Intensity (RFI) was calculated as follows: mean fluorescence intensity of the sample / mean fluorescence intensity of the corresponding isotype control.

Example 2 - Generation of LNGFR-spaced CD44v6-CAR.28z constructs.

We recently constructed a CD44v6-specific CAR based on the CD3 ζ chain combined with a CD28 endo-costimulatory domain (Casucci et al, *Blood* 2013, Nov 14;122(20):3461-72). In the extracellular spacer region of this CAR, an IgG1 CH2CH3 spacer was inserted for better targeting of the CD44v6 antigen and for allowing the selection and *in vivo* tracking of transduced T cells. A serious drawback of CH2CH3-spaced CARs is however their interaction with Fc γ receptors (Fc γ Rs) (Hombach et al, *Gene Ther* 2000, Jun;7(12):1067-75), potentially leading to non-specific targeting of cells expressing these receptors (e.g. monocytes/macrophages) and/or the *in vivo* clearance of transduced T cells (**Figure 1A**). To circumvent this problem, we substituted the original CH2CH3 spacer with different extracellular domains from the low-affinity nerve growth factor receptor (LNGFR). A truncated version of the LNGFR lacking intracellular signalling components has already been used in the clinic for gene marking of T cells (Bonini et al, *Nat Med*, 2003, Apr;9(4):367-9; Ciceri et al, *Lancet Oncol*, 2009, May;10(5):489-500). The extracellular portion of the LNGFR is composed of 4 TNFR cysteine-rich regions and a serine/threonine-rich stalk (**Figure 1B**). First of all, we generated two CD44v6-CAR.28z constructs: one spaced with the entire extracellular portion of the LNGFR (LNGFR wild type long or NWL) and the other with only the 4 TNFR cysteine-rich regions (LNGFR wild-type short or NWS). To exclude the possibility of antigen-independent activation of LNGFR-spaced construct *via* the natural ligand NGF, we generated two additional CD44v6-CAR.28z constructs carrying a specific

deletion of the fourth TNFR cysteine-rich domain, which is known to abrogate NGF signaling (Yan et al, *J Biol Chem*, 1991, Jun 25;266(18):12099-104), creating a LNGFR-mutated long isoform or NML and a LNGFR-mutated short isoform or NMS, respectively. As a control, we also generated a CD44v6-CAR.28z construct including a mutated version of the original CH2CH3 spacer (CHM), which is unable to recognize the Fc γ RI (Hombach et al, *Gene Ther* 2000, Jun;7(12):1067-75). Remarkably, both the Fc γ RII and the Fc γ RIII can use residues besides this common set, suggesting that this mutation does not completely abrogate the binding (Shields et al, *J Biol Chem*, 2001, Mar 2;276(9):6591-604. Armour et al, *Mol Immunol*, 2003, Dec;40(9):585-93).

Example 3 - The LNGFR-spaced CD44v6-CAR.28z constructs can be used to select and track transduced T cells

The different LNGFR-spaced CD44v6-CAR.28z constructs were cloned into retroviral vectors (RV) for transducing primary T cells. For transduction, T cells were activated with CD3/CD28-beads plus IL-7/IL-15, according to a protocol that better preserves their functional phenotype (Kaneko et al, *Blood*, 2009, Jan 29;113(5):1006-15. Bondanza et al, *Blood* 2011, Jun 16;117(24):6469-78. Cieri et al, *Blood*, 2013, Jan 24;121(4):573-84). After transduction, all constructs could be identified on the T-cell surface using the anti-LNGFR mAb C40-1457 (**Figure 2A**), indicating that they were correctly processed, mounted on the cell membrane and, most importantly, recognized by anti-NGFR mAbs. As a consequence, the different LNGFR-spaced CD44v6-CAR.28z T cells could be sorted with immunomagnetic beads (**Figure 2B**). At a closer look, we found that only the NWL-spaced isoform bound another anti-LNGFR mAb, ME20.4, suggesting that conformational changes dictated by LNGFR spacers of different lengths may control the accessibility of the ME20.4 epitope. Importantly, the expansion kinetics of the different LNGFR-spaced cells was similar to that of CH2CH3-spaced CD44v6-CAR.28z T cells (**Figure 2B**), ruling out a potential proliferative advantage induced by extracellular LNGFR sequences mounted on a CAR. At the end of the culture the resulting population was enriched for early-differentiated T cells (**Figure 2C**), indicating no interference with the functional differentiation path of bead-activated T cells in the presence of IL-7/IL-15.

Example 4 - LNGFR-spaced CD44v6-CAR.28z T cells retain CD44v6-specific recognition, while losing non-specific recognition mediated by the interaction with Fc γ Rs.

To verify the preservation of CD44v6-specific recognition after substituting the original CH2CH3 spacer with LNGFR spacers, LNGFR-spaced CD44v6-CAR.28z T cells were

tested in co-culture experiments with CD44v6-expressing tumor cells. Similarly to the CH2CH3-spaced, LNGFR-spaced CD44v6-CAR.28z T cells efficiently eliminated CD44v6+ve (MM1S and THP-1 cell lines), but not CD44v6-ve (BV173 cell lines) tumor cells (**Figure 3A**). Moreover, CD44v6-specific recognition was associated with vigorous T-cell expansion (**Figure 3B**), suggesting the full preservation of their therapeutic potential of LNGFR-spaced CD44v6-CAR.28z T cells. Therefore, LNGFR-spaced CARs according to the present invention result to be effective against tumor models expressing the specific antigen they are targeted to.

To demonstrate lack of non-specific recognition mediated by the interaction with FcR γ , LNGFR-spaced CD44v6-CAR.28z T-cells were co-cultured with CD44v6+ve/FcR γ s+ve THP1 leukemia cells or with CD44v6-ve/FcR γ s+ve HL-60 leukemia cells. In this system, while the CH2CH3-spaced CD44v6-CAR.28z T cells eliminated both CD44v6+ve THP1 and CD44v6-ve HL-60 cells, LNGFR-spaced CD44v6-CAR.28z CAR T cells specifically eliminated CD44v6+ve THP-1, but not CD44v6-ve HL-60 cells (**Figure 4A**). Correspondingly, LNGFR-spaced CD44v6-CAR.28z CAR T cells proliferated in response to CD44v6+ve THP-1, but not to CD44v6-ve HL-60 cells (**Figure 4B**). In both systems, the behaviour of the LNGFR-spaced cells was superimposable to that of mutated CH2CH3-spaced CD44v6-CAR.28z CAR T cells, demonstrating abrogation of FcR γ -mediated effects.

Therefore, because of the absence of the constant immunoglobulin IgG1 hinge-CH2-CH3 Fc domain as spacer, CARs containing a LNGFR-derived spacer according to the present invention do not bind to IgG Fc gamma receptors thus avoiding activation of unwanted and potentially toxic off-target immune response. Accordingly, LNGFR-spaced CARs are safer than those containing IgG hinge-CH2-CH3.

Finally, to rule out antigen-independent stimulation *via* soluble NGF, LNGFR-spaced CD44v6-CAR.28z T cells were cultured *in vitro* with NGF. Even at supra-physiological NGF concentrations, known to force the differentiation of the LNGFR-expressing neuronal cell line PC12 (**Figure 5A**), the LNGFR-spaced CD44v6-CAR.28z CAR T cells were not induced to proliferate (**Figure 5B**), indicating the absence of signaling *via* soluble NGF.

Example 5 - LNGFR-spaced CD44v6-CAR.28z T cells better persist in vivo and mediate superior antitumor effects

After demonstrating effective and specific recognition *in vitro*, LNGFR-spaced CD44v6-CAR.28z T cells were challenged for antitumor activity *in vivo*, first in a minimal-residual disease and then in a well-established disease (WED) model. In the first model, NSG mice were infused with THP-1 leukemia cells and after three days treated with CH2CH3-spaced

or the different LNGFR-spaced CD44v6-CAR.28z T cells. The different LNGFR-spaced CD44v6-CAR.28z T cells better expanded (**Figure 6A**) and persisted (**Figure 6B**) than CH2CH3-spaced CD44v6-CAR.28z T cells. Accordingly, LNGFR-spaced CD44v6-CAR.28z T cells appear to mediate superior antitumor effects, as demonstrated by better normalization of THP1-infiltrated liver weight compared to mice infused with CH2CH3-spaced CD44v6-CAR.28z T cells (**Figure 6C**). In the second well-established disease model, NSG mice were infused with CD44v6-expressing MM1.S myeloma cells, and after 5 weeks, when the tumor had already colonized the bone marrow, treated with CH2CH3-spaced or the different LNGFR-spaced CD44v6-CAR.28z T cells. CD44v6-CAR.28z T cells carrying the NML isoform were not included. In this more stringent model, while CH2CH3-spaced CD44v6-CAR.28z T cells barely engrafted and did not mediate any significant antitumor effect, the different LNGFR-spaced CD44v6-CAR.28z T cells expanded (**Figure 7A**), persisted and resulted in striking antitumor activity (**Figure 7B**).

The ability of LNGFR-spaced CD44v6-CAR.28z T cells mediate superior antitumor activity was further confirmed by the use of a well-established myeloma model with CD44v6+ MM1.S cells expressing a secreted luciferase. The presence of this luciferase allows to monitor day-by-day the amount of circulating MM1.S tumor cells in mice treated with the CH2CH3-spaced (v6 CHW) or with NMS LNGFR-spaced (v6 NMS) CD44v6-CAR.28z T cells. In this challenging model, while CH2CH3-spaced CD44v6-CAR.28z T cells showed the same antitumor activity of the unrelated CAR T cells (CTR), the NMS-spaced CD44v6-CAR.28z T cells are able to keep under control the number of circulating tumor cells up to 21 days (Figure 7BIS A) and to significantly prolong overall survival (Figure 7BIS B).

Example 6 - Methods

Generation of LNGFR-spaced CD19-CAR.28z and CEA-CAR.28z constructs

A strategy similar to that described in the example 1, was used to generate CD19-specific and CEA-specific CAR constructs (Figure 22). The following constructs have been generated:

CD19-CAR.28z: carrying a CD19 specific targeting domain, CD3 ζ chain combined with a CD28 endo-costimulatory domain and the wild-type IgG1 CH2CH3 spacer (CH2CH3)

NWL: CD19-CAR.28z carrying the LNGFR wild-type long spacer (including the 4 TNFR-Cys domains and the stalk)

NMS: CD19 -CAR.28z carrying the LNGFR mutated short spacer (including the 4 TNFR-Cys domains with a deletion in the fourth domain)

CEA-CAR.28z: carrying a CEA specific targeting domain, CD3 ζ chain combined with a CD28 endo-costimulatory domain and the wild-type IgG1 CH2CH3 spacer (CH2CH3)

NWL: CEA-CAR.28z carrying the LNGFR wild-type long spacer (including the 4 TNFR-Cys domains and the stalk)

NMS: CEA-CAR.28z carrying the LNGFR mutated short spacer (including the 4 TNFR-Cys domains with a deletion in the fourth domain)

Transduction and culture conditions.

T cells were activated with cell-sized CD3/CD28-beads (ClinExVivo, Invitrogen) plus IL-7/IL-15 (5 ng/ml, Peprotech) and RV-transduced by two rounds of spinoculation at day 2 and 3 after stimulation. At day 6, beads were removed and T cells cultured in RPMI 1640 (Gibco-Brl) 10% FBS (BioWhittaker) in the presence of IL-7 and IL-15. Surface expression of CH2CH3-spaced, CD19 and CEA-specific CAR constructs (CHW) was detected with mAbs specific for the IgG1 CH2CH3 spacer (Jackson Laboratories), while surface expression of LNGFR-spaced CAR constructs (NWL and NMS) was analysed using LNGFR-specific mAbs from BD Bioscience (Clone: C40-14579). Between day 9 and day 15 from activation, CH2CH3-spaced CAR.28z T cells were FACS-sorted using the polyclonal IgG1 CH2CH3-specific mAbs, while LNGFR-spaced CAR.28z T cells were stained with the PE-conjugated, LNGFR-specific mAb C40-14579 and sorted with columns using anti-PE paramagnetic beads (Miltenyi).

In vitro assays to analyze specific recognition.

In co-culture assays, CAR-sorted T cells were cultured with target cells at a 1:10 E:T ratio. After 4 days, surviving cells were counted and analysed by FACS. Elimination index was calculated as follows: $1 - (\text{number of residual target cells in presence of CD44v6-4GS2.CAR28z+ T cells, CD19.CAR28z+ T cells and CEA.CAR28z+ T cells}) / (\text{number of residual target cells in presence of CTR.CAR28z+ T cells})$. Supernatant of the co-cultures were harvested after 24 hour of incubation and analyzed for cytokine production (IFN γ , IL-2 and TNF α) with the CBA assay (BD Biolegend).

Xenograft models of antitumor efficacy

For the minimal-residual disease model, NSG mice (Jackson) were infused i.v. with 1.5×10^6 ALL-CM leukemia cells/mouse. Three days after, mice were treated i.v with 5×10^6 sorted

LNGFR-spaced (NWL, NMS) CD19-CAR.28z or CD44v6-4GS2.CAR.28z T cells. T-cell engraftment was monitored weekly by bleeding and FACS analysis. After 7 weeks, mice were sacrificed and their bone marrow (BM) analyzed by FACS for the presence of ALL-CM cells with an anti-hCD45 and an anti-hCD19 mAb.

Example 7 - The LNGFR-spaced -CAR.28z constructs can be used to select and track transduced T cells

The different LNGFR-spaced CAR.28z constructs were cloned into retroviral vectors (RV) for transducing primary T cells. For transduction, T cells were activated with CD3/CD28-beads plus IL-7/IL-15, according to a protocol that better preserves their functional phenotype (Kaneko et al, *Blood*, 2009, Jan 29;113(5):1006-15. Bondanza et al, *Blood* 2011, Jun 16;117(24):6469-78. Cieri et al, *Blood*, 2013, Jan 24;121(4):573-84). After transduction, T cells could be sorted with immunomagnetic beads (**Figure 23**) indicating that, as shown with CARs targeted to CD44v6 antigen, the LNGFR-derived spacers were correctly processed and mounted on the cell membrane, also in the context of two other CARs specific for the CD19 and the CEA antigens.

Example 8 - LNGFR-spaced CD19-CAR.28z T cells, CEA-CAR.28z T and CD44v6-4GS2.CAR.28z T cells retain antigen-specific recognition, while losing non-specific recognition mediated by the interaction with Fc γ Rs.

To verify the preservation of CD19 and CEA-specific recognition after substituting the original CH2CH3 spacer with LNGFR spacers, LNGFR-spaced CD19-CAR.28z and CEA-CAR.28z T cells were tested in co-culture experiments with antigen-expressing tumor cells. Similarly to the CH2CH3-spaced, LNGFR-spaced CD19-CAR.28z, CEA-CAR.28z T cells and CD44v6-4GS2.CAR.28z T cells efficiently eliminated CD19+, CEA+ and CD44v6+ tumor cells respectively, sparing antigen negative tumor cells (**Figure 24 A**). In particular, LNGFR-spaced CD19-CAR.28z CAR T cells specifically eliminated CD19+ ALL-CM and BV-173 cells, but not CD19- HL-60 and BXPC3 cells (Figure 24A). Similarly, LNGFR-spaced CEA-CAR.28z T cells specifically eliminated CEA+ BXPC3 cells, but not CEA- HL-60, ALL-CM and BV-173 cells (Figure 24 A) and CD44v6-4GS2.CAR.28z T cells specifically eliminated CD44v6+ BXPC3 cells, but not CD44v6- ALL-CM, BV173 and HL-60 cells (Figure 24 A) . Comparable results were obtained when antigen-specific cytokine release (IFN γ , IL2 and TNF α) was evaluated (Figure 24 B).

CARs containing LNGFR as spacer according to the present invention, result to retain specificity and antitumor effect with different antigen specific targeting domains.

To demonstrate lack of non-specific recognition mediated by the interaction with FcR γ , LNGFR-spaced CD19-CAR.28z T-cells, CEA-CAR.28z T-cells and CD44v6-4GS2.CAR.28z T cells were co-cultured with FcR γ s+, CD19- CEA- HL-60 cells. In this system, only the CH2CH3-spaced CD19-CAR.28z and CEA-CAR.28z T cells are able to eliminate the HL-60 target cells, thus confirming that the use of LNGFR-based spacer avoid activation of unwanted innate immune response.

Example 12 - LNGFR-spaced CD19-CAR.28z T cells mediate antitumor effects in vivo

After demonstrating effective and specific recognition *in vitro*, LNGFR-spaced CD19-CAR.28z T cells were challenged for antitumor activity *in vivo*, in a minimal-residual disease model. NSG mice were infused with ALL-CM leukemia cells and after three days treated with the different LNGFR-spaced (NWL and NMS) CD19-CAR.28z T cells. In this case, LNGFR-spaced (NWL and NMS) CD44v6-4GS2.CAR.28z T cells were used as negative control since the ALL-CM leukemia cells do not express the CD44v6 antigen (Figure 25). Both LNGFR-spaced CD19-CAR.28z T cells appear to mediate antitumor effects, as demonstrated by lower concentration of ALL-CM cells infiltrating the bone marrow, compared to mice infused with CD44v6-CAR.28z T cells (Figure 25).

All publications mentioned in the above specification are herein incorporated by reference. Various modifications and variations of the described CARS, polynucleotides, vectors, cells and compositions of the present invention will be apparent to those skilled in the art without departing from the scope and spirit of the present invention. Although the present invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention, which are obvious to those skilled in biochemistry and biotechnology or related fields, are intended to be within the scope of the following claims.