(12) STANDARD PATENT (11) Application No. **AU 2014351557 B2**
(19) AUSTRALIAN PATENT OFFICE

(54) Title
Cell

(51) International Patent Classification(s)
C12N 5/0783 (2010.01) ***C07K 14/725*** (2006.01)
A61K 39/00 (2006.01) ***C07K 16/28*** (2006.01)
C07K 14/705 (2006.01) ***C07K 16/30*** (2006.01)

(21) Application No: **2014351557** (22) Date of Filing: **2014.11.21**

(87) WIPO No: **WO15/075469**

(30) Priority Data

(31) Number	(32) Date	(33) Country
1410934.2	**2014.06.19**	**GB**
1320573.7	**2013.11.21**	**GB**

(43) Publication Date: **2015.05.28**
(44) Accepted Journal Date: **2019.04.18**

(71) Applicant(s)
UCL Business PLC

(72) Inventor(s)
Pule, Martin;Kong, Khai;Cordoba, Shaun

(74) Agent / Attorney
Pairman IP, P.O. Box 33252, Christchurch, 8244, NZ

(56) Related Art
E. LANITIS ET AL, "Chimeric Antigen Receptor T Cells with Dissociated Signaling Domains Exhibit Focused Antitumor Activity with Reduced Potential for Toxicity In Vivo", CANCER IMMUNOLOGY RESEARCH, 2013, 1(1):43-53

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
28 May 2015 (28.05.2015)

WIPO | PCT

(10) International Publication Number
WO 2015/075469 A1

(51) International Patent Classification:
A61K 39/00 (2006.01) *C07K 16/28* (2006.01)
C07K 14/725 (2006.01) *C07K 16/30* (2006.01)
C07K 14/705 (2006.01) *C12N 5/0783* (2010.01)

(21) International Application Number:
PCT/GB2014/053452

(22) International Filing Date:
21 November 2014 (21.11.2014)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
1320573.7 21 November 2013 (21.11.2013) GB
1410934.2 19 June 2014 (19.06.2014) GB

(71) Applicant: **UCL BUSINESS PLC** [GB/GB]; The Network Building, 97 Tottenham Court Road, London W1T 4TP (GB).

(72) Inventors: **PULÉ, Martin**; c/o UCL Business PLC, The Network Building, 97 Tottenham Court Road, London W1T 4TP (GB). **KONG, Khai**; c/o UCL Business PLC, The Network Building, 97 Tottenham Court Road, London W1T 4TP (GB). **CORDOBA, Shaun**; c/o UCL Business PLC, The Network Building, 97 Tottenham Court Road, London W1T 4TP (GB).

(74) Agent: **HOLLIDAY, Louise**; D Young & Co LLP, 120 Holborn, London, EC1N 2DY (GB).

(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JP, KE, KG, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Published:

— *with international search report (Art. 21(3))*

— *with sequence listing part of description (Rule 5.2(a))*

WO 2015/075469 A1

(54) **Title**: CELL

(57) **Abstract**: The present invention provides a cell which co-expresses a first chimeric antigen receptor (CAR) and second CAR at the cell surface, each CAR comprising: (i) an antigen-binding domain; (ii) a spacer (iii) a trans-membrane domain; and (iv) an endodomain wherein the antigen binding domains of the first and second CARs bind to different antigens, wherein the spacer of the first CAR is different to the spacer of the second CAR and wherein one of the first or second CARs is an activating CAR comprising an activating endodomain and the other CAR is an inhibitory CAR comprising a ligation-off inhibitory endodomain.

CELL

FIELD OF THE INVENTION

The present invention relates to a cell which comprises more than one chimeric antigen receptor (CAR). The cell may be capable of specifically recognising a target cell, due to a differential pattern of expression (or non-expression) of two or more antigens by the target cell.

BACKGROUND TO THE INVENTION

A number of immunotherapeutic agents have been described for use in cancer treatment, including therapeutic monoclonal antibodies (mAbs), immunoconjugated mAbs, radioconjugated mAbs and bi-specific T-cell engagers.

Typically these immunotherapeutic agents target a single antigen: for instance, Rituximab targets CD20; Myelotarg targets CD33; and Alemtuzumab targets CD52.

However, it is relatively rare for the presence (or absence) of a single antigen effectively to describe a cancer, which can lead to a lack of specificity.

Most cancers cannot be differentiated from normal tissues on the basis of a single antigen. Hence, considerable "on-target off-tumour" toxicity occurs whereby normal tissues are damaged by the therapy. For instance, whilst targeting CD20 to treat B-cell lymphomas with Rituximab, the entire normal B-cell compartment is depleted, whilst targeting CD52 to treat chronic lymphocytic leukaemia, the entire lymphoid compartment is depleted, whilst targeting CD33 to treat acute myeloid leukaemia, the entire myeloid compartment is damaged etc.
The predicted problem of "on-target off-tumour" toxicity has been borne out by clinical trials. For example, an approach targeting ERBB2 caused death to a patient with colon cancer metastatic to the lungs and liver. ERBB2 is over-expressed in colon caner in some patients, but it is also expressed on several normal tissues, including heart and normal vasculature.

For some cancers, targeting the presence of two cancer antigens may be more selective and therefore effective than targeting one. For example, B-chronic lymphocytic leukaemia (B-CLL) is a common leukaemia which is currently treated by targeting CD19. This treats the lymphoma but also depletes the entire B-cell compartment such that the treatment has a considerable toxic effect. B-CLL has an unusual phenotype in that CD5 and CD19 are co-

expressed. By targeting only cells which express CD5 and CD19, it would be possible to considerably reduce on-target off-tumour toxicity.

There is thus a need for immunotherapeutic agents which are capable of more targeting to reflect the complex pattern of marker expression that is associated with many cancers.

Chimeric Antigen Receptors (CARs)

Chimeric antigen receptors are proteins which graft the specificity of a monoclonal antibody (mAb) to the effector function of a T-cell. Their usual form is that of a type I transmembrane domain protein with an antigen recognizing amino terminus, a spacer, a transmembrane domain all connected to a compound endodomain which transmits T-cell survival and activation signals (see Figure 1A).

The most common form of these molecules are fusions of single-chain variable fragments (scFv) derived from monoclonal antibodies which recognize a target antigen, fused via a spacer and a trans-membrane domain to a signaling endodomain. Such molecules result in activation of the T-cell in response to recognition by the scFv of its target. When T cells express such a CAR, they recognize and kill target cells that express the target antigen. Several CARs have been developed against tumour associated antigens, and adoptive transfer approaches using such CAR-expressing T cells are currently in clinical trial for the treatment of various cancers.

However, the use of CAR-expressing T cells is also associated with on-target, off tumour toxicity. For example, a CAR-based approach targeting carboxy anyhydrase-IX (CAIX) to treat renal cell carcinoma resulted in liver toxicity which is thought to be caused by the specific attack on bile duct epithelial cells (Lamers et al (2013) Mol. Ther. 21:904-912).

Dual targeting CAR approaches

In order to address the problem of "on target, off tumour" toxicity, CAR T cells have been developed with dual antigen specificty. In the "dual targeting" approach, two complementary CARs are co-expressed in the same T-cell population, each directed to a distant tumour target and engineered to provide complementary signals.

Wlikie et al (2012 J Clin Immunol 32:1059-1070) describe a dual targeting approach in which ErbB2- and MUC1-specific CARs are co-expressed. The ErbB2-specific CAR provided the CD3ζ signal only and the MUC1-specific CAR provided the CD28 co-stimulatory signal only.

It was found that complementary signalling occurred in the presence of both antigens, leading to IL-2 production. However, IL-2 production was modest when compared to control CAR-engineered T cells in which signaling is delivered by a fused CD28+CD3ζ endodomain.

A similar approach was described by Kloss et al (2013 Nature Biotechnol. 31:71-75) in which a CD-19 specific CAR was used which provides a CD3ζ-mediated activation signal in combination with a chimeric co-stimulatory receptor specific for PSMA. With this 'co-CAR' design, the CAR T-cell receives an activation signal when it encounters a target cell with one antigen, and a co-stimulatory signal when it encounters a target cell with the other antigen, and only receives both activatory and co-stimulatory signals upon encountering target cells bearing both antigens.

This represents an early attempt at restricting CAR activity to only a target cell bearing two antigens. This approach however is limited: although CAR T-cell activity will be greatest against targets expressing both antigens, CAR T-cells will still kill targets expressing only antigen recognized by the activatory CAR; further, co-stimulation results in prolonged effects on T-cells which last long after release of target cell. Hence, activity against single-antigen positive T-cells equal to that against double-positives might be possible for example in a situation where single-positive tissues are adjacent to, or in a migratory path from double positive tumour.

There is thus a need for improved CAR-based therapeutic approaches with reduced on-target off-tumour toxicity where T-cell activation is wholly restricted to target cells which express both antigens.

DESCRIPTION OF THE FIGURES

Figure 1: (a) Generalized architecture of a CAR: A binding domain recognizes antigen; the spacer elevates the binding domain from the cell surface; the trans-membrane domain anchors the protein to the membrane and the endodomain transmits signals. (b) to (d): Different generations and permutations of CAR endodomains: (b) initial designs transmitted ITAM signals alone through FcεR1-γ or CD3ζ endodomain, while later designs transmitted additional (c) one or (d) two co-stimulatory signals in cis.

Figure 2: Schematic diagram illustrating the invention

The invention relates to engineering T-cells to respond to logical rules of target cell antigen expression. This is best illustrated with an imaginary FACS scatter-plot. Target cell

populations express both, either or neither of antigens "A" and "B". Different target populations (marked in red) are killed by T-cells transduced with a pair of CARs connected by different gates. With OR gated receptors, both single-positive and double-positive cells will be killed. With AND gated receptors, only double-positive target cells are killed. With AND NOT gating, double-positive targets are preserved while single-positive targets

Figure 3: Creation of target cell populations
SupT1 cells were used as target cells. These cells were transduced to express either CD19, CD33 or both CD19 and CD33. Target cells were stained with appropriate antibodies and analysed by flow cytometry.

Figure 4: Cassette design for an OR gate
A single open reading frame provides both CARs with an in-frame FMD-2A sequence resulting in two proteins. Signal1 is a signal peptide derived from IgG1 (but can be any effective signal peptide). scFv1 is the single-chain variable segment which recognizes CD19 (but can be a scFv or peptide loop or ligand or in fact any domain which recognizes any desired arbitrary target). STK is the CD8 stalk but may be any suitable extracellular domain. CD28tm is the CD28 trans-membrane domain but can by any stable type I protein transmembrane domain and CD3Z is the CD3 Zeta endodomain but can be any endodomain which contains ITAMs. Signal2 is a signal peptide derived from CD8 but can be any effective signal peptide which is different in DNA sequence from signal1. scFv recognizes CD33 but as for scFv1 is arbitrary. HC2CH3 is the hinge-CH2-CH3 of human IgG1 but can be any extracellular domain which does not cross-pair with the spacer used in the first CAR. CD28tm' and CD3Z' code for the same protein sequence as CD28tm and CD3Z but are codon-wobbled to prevent homologous recombination.

Figure 5: Schematic representation of the chimeric antigen receptors (CARs) for an OR gate
Stimulatory CARs were constructed consisting of either an N-terminal A) anti-CD19 scFv domain followed by the extracellular hinge region of human CD8 or B) anti-CD33 scFv domain followed by the extracellular hinge, CH2 and CH3 (containing a pvaa mutation to reduce FcR binding) region of human IgG1. Both receptors contain a human CD28 transmembrane domain and a human CD3 Zeta (CD247) intracellular domain. "S" depicts the presence of disulphide bonds.

Figure 6: Expression data showing co-expression of both CARs on the surface of one T-cell.

Figure 7: Functional analysis of the OR gate

Effector cells (5x10^4 cells) expressing the OR gate construct were co-incubated with a varying number of target cells and IL-2 was analysed after 16 hours by ELISA. The graph displays the average maximum IL-2 secretion from a chemical stimulation (PMA and Ionomycin) of the effector cells alone and the average background IL-2 from effector cells without any stimulus from three replicates.

Figure 8: Cartoon showing both versions of the cassette used to express both AND gates
Activating and inhibiting CARs were co-expressed once again using a FMD-2A sequence. Signal1 is a signal peptide derived from IgG1 (but can be any effective signal peptide). scFv1 is the single-chain variable segment which recognizes CD19 (but can be a scFv or peptide loop or ligand or in fact any domain which recognizes any desired arbitrary target). STK is the CD8 stalk but may be any non-bulky extracellular domain. CD28tm is the CD28 trans-membrane domain but can by any stable type I protein transmembrane domain and CD3Z is the CD3 Zeta endodomain but can be any endodomain which contains ITAMs. Signal2 is a signal peptide derived from CD8 but can be any effective signal peptide which is different in DNA sequence from signal1. scFv recognizes CD33 but as for scFv1 is arbitrary. HC2CH3 is the hinge-CH2-CH3 of human IgG1 but can be any bulky extracellular domain. CD45 and CD148 are the transmembrane and endodomains of CD45 and CD148 respectively but can be derived from any of this class of protein.

Figure 9: Schematic representation of the protein structure of chimeric antigen receptors (CARs) for the AND gates
The stimulatory CAR consisting of an N-terminal anti-CD19 scFv domain followed by the extracellular stalk region of human CD8, human CD28 transmembrane domain and human CD3 Zeta (CD247) intracellular domain. Two inhibitory CARs were tested. These consist of an N-terminal anti-CD33 scFv domain followed by the extracellular hinge, CH2 and CH3 (containing a pvaa mutation to reduce FcR binding) region of human IgG1 followed by the transmembrane and intracellular domain of either human CD148 or CD45. “S” depicts the presence of disulphide bonds.

Figure 10: Co-expression of activation and inhibitory CARs
BW5147 cells were used as effector cells and were transduced to express both the activation anti-CD19 CAR and one of the inhibitory anti-CD33 CARs. Effector cells were stained with CD19-mouse-Fc and CD33-rabbit-Fc and with appropriate secondary antibodies and analysed by flow cytometry.

Figure 11: Functional analysis of the AND gates

Effector cells (5x10^4 cells) expressing activation anti-CD19 CAR and the inhibitory anti-CD33 CAR with the A) CD148 or B) CXD45 intracellular domain were co- incubated with a varying number of target cells and IL-2 was analysed after 16hours by ELISA. The graph displays the maximum IL-2 secretion from a chemical stimulation (PMA and Ionomycin) of the effector cells alone and the background IL-2 from effector cells without any stimulus from three replicates.

Figure 12: Cartoon showing three versions of the cassette used to generate the AND NOT gate

Activating and inhibiting CARs were co-expressed once again using a FMD-2A sequence. Signal1 is a signal peptide derived from IgG1 (but can be any effective signal peptide). scFv1 is the single-chain variable segment which recognizes CD19 (but can be a scFv or peptide loop or ligand or in fact any domain which recognizes any desired arbitrary target). STK is the human CD8 stalk but may be any non-bulky extracellular domain. CD28tm is the CD28 trans-membrane domain but can by any stable type I protein transmembrane domain and CD3Z is the CD3 Zeta endodomain but can be any endodomain which contains ITAMs. Signal2 is a signal peptide derived from CD8 but can be any effective signal peptide which is different in DNA sequence from signal1. scFv recognizes CD33 but as for scFv1 is arbitrary. muSTK is the mouse CD8 stalk but can be any spacer which co-localises but does not cross-pair with that of the activating CAR. dPTPN6 is the phosphatase domain of PTPN6. LAIR1 is the transmembrane and endodomain of LAIR1. 2Aw is a codon-wobbled version of the FMD-2A sequence. SH2-CD148 is the SH2 domain of PTPN6 fused with the phosphatase domain of CD148.

Figure 13: Schematic representation of the chimeric antigen receptors (CARs) for the NOT AND gates

A) A stimulatory CAR consisting of an N-terminal anti-CD19 scFv domain followed by the stalk region of human CD8, human CD28 transmembrane domain and human CD247 intracellular domain. B) An inhibitory CAR consisting of an N-terminal anti-CD33 scFv domain followed by the stalk region of mouse CD8, transmembrane region of mouse CD8 and the phosphatase domain of PTPN6. C) an inhibitory CAR consisting of an N-terminal anti-CD33 scFv domain followed by the stalk region of mouse CD8 and the transmembrane and intracellular segments of LAIR1. D) An inhibitory CAR identical to previous CAR except it is co-expressed with a fusion protein of the PTPN6 SH2 domain and the CD148 phosphatase domain.

Figure 14: Functional analysis of the NOT AND gate

Effector cells (5x10^4 cells) expressing the A) full length SHP-1 or B) truncated form of SHP-1 were co- incubated with a varying number of target cells and IL-2 was analysed after 16 hours by ELISA. The graph displays the average maximum IL-2 secretion from a chemical stimulation (PMA and Ionomycin) of the effector cells alone and the average background IL-2 from effector cells without any stimulus from three replicates.

Figure 15: Amino acid sequence of an OR gate

Figure 16: Amino acid sequence of a CD148 and a CD145 based AND gate

Figure 17: Amino acid sequence of two AND NOT gates

Figure 18: Dissection of AND gate function
A. The prototype AND gate is illustrated on the right and its function in response to CD19, CD33 single and CD19, CD33 double positive targets is shown on the left. **B.** The scFvs are swapped so the activating endodomain is triggered by CD33 and the inhibitory endodomain is activated by CD19. This AND gate remains functional despite this scFv swap. **C.** The CD8 mouse stalk replaced Fc in the spacer of the inhibitory CAR. With this modification, the gate fails to respond to either CD19 single positive or CD19, CD33 double positive targets.

Figure 19: Expression of target antigens on artificial target cells
A. Shows flow cytometry scatter plots CD19 vs CD33 of the original set of artificial target cells derived from SupT1 cells. From left to right: double negative SupT1 cells, SupT1 cells positive for CD19, positive for CD33 and positive for both CD19 and CD33. **B**. Shows flow cytometry scatter plots CD19 vs GD2 of the artificial target cells generated to test the CD19 AND GD2 gate: From left to right: negative SupT1 cells, SupT1 cells expressing CD19, SupT1 cells transduced with GD2 and GM3 synthase vectors which become GD2 positive and SupT1 cells transduced with CD19 as well as GD2 and GM3 synthase which are positive for both GD2 and CD19. **C**. Shows flow cytometry scatter plots of CD19 vs EGFRvIII of the artificial targets generated to test the CD19 AND EGFRvIII gate. From left to right: negative SupT1 cells, SupT1 cells expressing CD19, SupT1 cells transduced with EGFRvIII and SupT1 cells transduced with both CD19 and EGFRvIII. **D**. Shows flow cytometry scatter plots of CD19 vs CD5 of the artificial targets generated to test the CD19 AND CD5 gate. From left to right: negative 293T cells, 293T cells transduced with CD19, 293T cells transduced with CD5, 293T cells transduced with both CD5 and CD19 vectors.

Figure 20: Generalizability of the AND gate

A. Cartoon of AND gate modified so the second CAR's specificity is changed from the original specificity of CD33, to generate 3 new CARs: CD19 AND GD2, CD19 AND EGFRvIII, CD19 AND CD5. **B.** CD19 AND GD2 AND gate: Left: expression of AND gate is shown recombinant CD19-Fc staining (x-axis) for the CD19 CAR, versus anti-human-Fc staining (Y-axis) for the GD2 CAR. Right: function in response to single positive and double positive targets. **C.** CD19 AND EGFRvIII AND gate: Left: expression of AND gate is shown recombinant CD19-Fc staining (x-axis) for the CD19 CAR, versus anti-human-Fc staining (Y-axis) for the EGFRvIII CAR. Right: function in response to single positive and double positive targets. **D.** CD19 AND CD5 AND gate: Left: expression of AND gate is shown recombinant CD19-Fc staining (x-axis) for the CD19 CAR, versus anti-human-Fc staining (Y-axis) for the CD5 CAR. Right: function in response to single positive and double positive targets.

Figure 21: Function of the AND NOT gates

Function of the three implementations of an AND NOT gate is shown. A cartoon of the gates tested is shown to the right, and function in response to single positive and double positive targets is shown to the left. **A.** PTPN6 based AND NOT gate whereby the first CAR recognizes CD19, has a human CD8 stalk spacer and an ITAM containing activating endodomain; is co-expressed with a second CAR that recognizes CD33, has a mouse CD8 stalk spacer and has an endodomain comprising of a PTPN6 phosphatase domain. **B.** ITIM based AND NOT gate is identical to the PTPN6 gate, except the endodomain is replaced by the endodomain from LAIR1. **C.** CD148 boosted AND NOT gate is identical to the ITIM based gate except an additional fusion between the PTPN6 SH2 and the endodomain of CD148 is expressed. All three gates work as expected with activation in response to CD19 but not in response to CD19 and CD33 together.

Figure 22: Dissection of PTPN6 based AND NOT gate function

The original PTPN6 based AND NOT gate is compared with several controls to demonstrate the model. A cartoon of the gates tested is shown to the right, and function in response to single positive and double positive targets is shown to the left. **A.** Original AND NOT gate whereby the first CAR recognizes CD19, has a human CD8 stalk spacer and an ITAM containing activating endodomain; is co-expressed with a second CAR recognizes CD33, has a mouse CD8 stalk spacer and has an endodomain comprising of a PTPN6 phosphatase domain. **B**. AND NOT gate modified so the mouse CD8 stalk spacer is replaced with an Fc spacer. **C** AND NOT gate modified so that the PTPN6 phosphatase domain is replaced with the endodomain from CD148. Original AND NOT gate (**A.**) functions as expected triggering in response to CD19, but not in response to both CD19 and CD33.

The gate in **B.** triggers both in response to CD19 along or CD19 and CD33 together. The gate in **C.** does not trigger in response to one or both targets.

Figure 23: Dissection of LAIR1 based AND NOT gate
Functional activity against CD19 positive, CD33 positive and CD19, CD33 double-positive targets is shown. **A**. Structure and activity of the original ITIM based AND NOT gate. This gate is composed of two CARs: the first recognizes CD19, has a human CD8 stalk spacer and an ITAM containing endodomain; the second CAR recognizes CD33, has a mouse CD8 stalk spacer and an ITIM containing endodomain. **B** Structure and activity of the control ITIM based gate where the mouse CD8 stalk spacer has been replaced by an Fc domain. This gate is composed of two CARs: the first recognizes CD19, has a human CD8 stalk spacer and an ITAM containing endodomain; the second CAR recognizes CD33, has an Fc spacer and an ITIM containing endodomain. Both gates respond to CD19 single positive targets, while only the original gate is inactive in response to CD19 and CD33 double positive targets.

Figure 24: Kinetic segregation model of CAR logic gates
Model of kinetic segregation and behaviour of AND gate, NOT AND gate and controls. CARs recognize either CD19 or CD33. The immunological synapse can be imagined between the blue line, which represents the target cell membrane and the red line, which represents the T-cell membrane. '45' is the native CD45 protein present on T-cells. 'H8' is a CAR ectodomain with human CD8 stalk as the spacer. 'Fc' is a CAR ectodomain with human HCH2CH3 as the spacer. 'M8' is a CAR ectodomain with murine CD8 stalk as the spacer. '19' represents CD19 on the target cell surface. '33' represents CD33 on the target cell surface. The symbol '⊕' represents an activating endodomain containing ITAMS. The symbol '⊖' represents a phosphatase with slow kinetics - a 'ligation on' endodomain such as one comprising of the catalytic domain of PTPN6 or an ITIM. The symbol '∅' represents a phosphatase with fast kinetics - a 'ligation off' endodomain such as the endodomain of CD45 or CD148. This symbol is enlarged in the figure to emphasize its potent activity.
(a) Shows the postulated behaviour of the functional AND gate which comprises of a pair of CARs whereby the first CAR recognizes CD19, has a human CD8 stalk spacer and an activating endodomain; and the second CAR recognizes CD33, has an Fc spacer and a CD148 endodomain;
(b) Shows the postulated behaviour of the control AND gate. Here, the first CAR recognizes CD19, has a human CD8 stalk spacer and an activating endodomain; and the second CAR recognizes CD33, but has a mouse CD8 stalk spacer and a CD148 endodomain;

(c) Shows the behaviour of a functional AND NOT gate which comprises of a pair of CARs whereby the first CAR recognizes CD19, has a human CD8 stalk spacer and an activating endodomain; and the second CAR recognizes CD33, has a mouse CD8 stalk spacer and a PTPN6 endodomain;

(d) Shows the postulated behaviour of the control AND NOT gate which comprises of a pair of CARs whereby the first CAR recognizes CD19, has a human CD8 stalk spacer and an activating endodomain; and the second CAR recognizes CD33, but has an Fc spacer and a PTPN6 endodomain;

In the first column, target cells are both CD19 and CD33 negative. In the second column, targets are CD19 negative and CD33 positive. In the third column, target cells are CD19 positive and CD33 negative. In the fourth column, target cells are positive for both CD19 and CD33.

Figure 25: Design of APRIL-based CARs.

The CAR design was modified so that the scFv was replaced with a modified form of A proliferation-inducing ligand (APRIL), which interacts with interacts with BCMA, TACI and proteoglycans, to act as an antigen binding domain: APRIL was truncated so that the proteoglycan binding amino-terminus is absent. A signal peptide was then attached to truncated APRIL amino-terminus to direct the protein to the cell surface. Three CARs were generated with this APRIL based binding domain: A. In the first CAR, the human CD8 stalk domain was used as a spacer domain. B. In the second CAR, the hinge from IgG1 was used as a spacer domain. C. In the third CAR, the hinge, CH2 and CH3 domains of human IgG1 modified with the pva/a mutations described by Hombach et al (2010 Gene Ther. 17:1206-1213) to reduce Fc Receptor binding was used as a spacer (henceforth referred as Fc-pvaa). In all CARs, these spacers were connected to the CD28 transmembrane domain and then to a tripartite endodomain containing a fusion of the CD28, OX40 and the CD3-Zeta endodomain (Pule et al, Molecular therapy, 2005: Volume 12; Issue 5; Pages 933-41).

Figure 26: Annotated Amino acid sequence of the above three APRIL-CARS

A: Shows the annotated amino acid sequence of the CD8 stalk APRIL CAR; B: Shows the annotated amino acid sequence of the APRIL IgG1 hinge based CAR; C: Shows the annotated amino acid sequence of the APRIL Fc-pvaa based CAR.

Figure 27: Expression and ligand binding of different APRIL based CARs

A. The receptors were co-expressed with a marker gene truncated CD34 in a retroviral gene vector. Expression of the marker gene on transduced cells allows confirmation of transduction. B. T-cells were transduced with APRIL based CARs with either the CD8 stalk

spacer, IgG1 hinge or Fc spacer. To test whether these receptors could be stably expressed on the cell surface, T-cells were then stained with anti-APRIL-biotin/Streptavidin APC and anti-CD34. Flow-cytometric analysis was performed. APRIL was equally detected on the cell surface in the three CARs suggesting they are equally stably expressed. C. Next, the capacity of the CARs to recognize TACI and BCMA was determined. The transduced T-cells were stained with either recombinant BCMA or TACI fused to mouse IgG2a Fc fusion along with an anti-mouse secondary and anti-CD34. All three receptor formats showed binding to both BCMA and TACI. A surprising finding was that binding to BCMA seemed greater than to TACI. A further surprising finding was that although all three CARs were equally expressed, the CD8 stalk and IgG1 hinge CARs appeared better at recognizing BCMA and TACI than that with the Fc spacer.

Figure 28: Function of the different CAR constructs.

Functional assays were performed with the three different APRIL based CARs. Normal donor peripheral blood T-cells either non-transduced (NT), or transduced to express the different CARs. Transduction was performed using equal titer supernatant. These T-cells were then CD56 depleted to remove non-specific NK activity and used as effectors. SupT1 cells either non-transduced (NT), or transduced to express BCMA or TACI were used as targets. Data shown is mean and standard deviation from 5 independent experiments. A. Specific killing of BCMA and TACI expressing T-cells was determined using Chromium release. B. Interferon-μ release was also determined. Targets and effectors were co-cultured at a ratio of 1:1. After 24 hours, Interferon-μ in the supernatant was assayed by ELISA. C. Proliferation / survival of CAR T-cells were also determined by counting number of CAR T-cells in the same co-culture incubated for a further 6 days. All 3 CARs direct responses against BCMA and TACI expressing targets. The responses to BCMA were greater than for TACI.

Figure 29: AND gate functionality in primary cells

PBMCs were isolated from blood and stimulated using PHA and IL-2. Two days later the cells were transduced on retronectin coated plates with retro virus containing the CD19:CD33 AND gate construct. On day 5 the expression level of the two CARs translated by the AND gate construct was evaluated via flow cytometry and the cells were depleted of CD56+ cells (predominantly NK cells). On day 6 the PBMCs were placed in a co-culture with target cells at a 1:2 effector to target cell ratio. On day 8 the supernatant was collected and analysed for IFN-gamma secretion via ELISA.

Figure 30: A selection / hierarchy of possible spacer domains of increasing size is shown. The ectodomain of CD3-Zeta is suggested as the shortest possible spacer, followed by the (b) the IgG1 hinge. (c) murine or human CD8 stalk and the CD28 ectodomains are considered intermediate in size and co-segregate. (d) The hinge, CH2 and CH3 domain of IgG1 is bigger and bulkier, and (e) the hinge, CH2, CH3 and CH4 domain of IgM is bigger still. Given the properties of the target molecules, and the epitope of the binding domains on said target molecules, it is possible to use this hierarchy of spacers to create a CAR signaling system which either co-segregates or segregates apart upon synapse formation.

Figure 31: Design rules for building logic gated CAR T-cells.
OR, AND NOT and AND gated CARs are shown in cartoon format with the target cell on top, and the T-cell at the bottom with the synapse in the middle. Target cells express arbitrary target antigens A, and B.
T-cells express two CARs which comprise of anti-A and anti-B recognition domains, spacers and endodomains. An OR gate requires (1) spacers simply which allow antigen recognition and CAR activation, and (2) both CARs to have activatory endodomains; An AND NOT gate requires (1) spacers which result in co-segregation of both CARs upon recognition of both antigens and (2) one CAR with an activatory endodomain, and the other whose endodomain comprises or recruits a weak phosphatase; An AND gate requires (1) spacers which result in segregation of both CARs into different parts of the immunological synapse upon recognition of both antigens and (2) one CAR with an activatory endodomain, and the other whose endodomain comprises of a potent phosphatase.

SUMMARY OF ASPECTS OF THE INVENTION

The present inventors have developed a panel of "logic-gated" chimeric antigen receptor pairs which, when expressed by a cell, such as a T cell, are capable of detecting a particular pattern of expression of at least two target antigens. If the at least two target antigens are arbitrarily denoted as antigen A and antigen B, the three possible options are as follows:

"OR GATE" – T cell triggers when either antigen A or antigen B is present on the target cell
"AND GATE" – T cell triggers only when both antigens A and B are present on the target cell
"AND NOT GATE" – T cell triggers if antigen A is present alone on the target cell, but not if both antigens A and B are present on the target cell

Engineered T cells expressing these CAR combinations can be tailored to be exquisitely specific for cancer cells, based on their particular expression (or lack of expression) of two or more markers.

Thus in a first aspect, the present invention provides a cell which co-expresses a first chimeric antigen receptor (CAR) and second CAR at the cell surface, each CAR comprising:

(i) an antigen-binding domain;

(ii) a spacer

(iii) a trans-membrane domain; and

(iv) an intracellular T cell signaling domain (endodomain)

wherein the antigen binding domains of the first and second CARs bind to different antigens, and wherein the spacer of the first CAR is different to the spacer of the second CAR, such that the first and second CARs do not form heterodimers, and wherein

one of the first or second CARs is an activating CAR comprising an activating intracellular T cell signaling domain and the other CAR is an inhibitory CAR comprising a "ligation-off" (as defined herein) inhibitory intracellular T cell signaling domain.

The cell may be an immune effector cell, such as a T-cell or natural killer (NK) cell. Features mentioned herein in connection with a T cell apply equally to other immune effector cells, such as NK cells.

The spacer of the first CAR may have a different length and/or charge and/or shape and/or configuration and/or glycosylation to the spacer of the second CAR, such that when the first CAR and the second CAR bind their respective target antigens, the first CAR and second CAR become spatially separated on the T cell. Ligation of the first and second CARs to their respective antigens causes them to be compartmentalized together or separately in the immunological synapse resulting in control of activation. This may be understood when one considers the kinetic separation model of T-cell activation (see below).

The first spacer or the second spacer may comprise a CD8 stalk and the other spacer may comprise the hinge, CH2 and CH3 domain of an IgG1.

In the present invention, which relates to the "AND" gate, one of the first or second CARs is an activating CAR comprising an activating endodomain, and the other CAR is a "ligation-off" inhibitory CAR comprising an inhibitory endodomain. The ligation-off inhibitory CAR inhibits T-cell activation by the activating CAR in the absence of inhibitory CAR ligation, but does not significantly inhibit T-cell activation by the activating CAR when the inhibitory CAR is ligated.

Since the spacer of the first CAR has a different length and/or charge and/or shape and/or configuration and/or glycosylation from the spacer of the second CAR, when both CARs are ligated they segregate. This causes the inhibitory CAR to be spatially separated from the activating CAR, so that T cell activation can occur. T cell activation therefore only occurs in response to a target cell bearing both cognate antigens.

The inhibitory endodomain may comprise all or part of the endodomain from a receptor-like tyrosine phosphatase, such as CD148 or CD45.

The antigen-binding domain of the first CAR may bind CD5 and the antigen-binding domain of the second CAR may bind CD19. This is of use in targeting chronic lymphocytic leukaemia (CLL). This disease can be treated by targeting CD19 alone, but at the cost of depleting the entire B-cell compartment. CLL cells are unusual in that they co-express CD5 and CD19. Targeting this pair of antigens with an AND gate will increase specificity and reduce toxicity.

In a second aspect, the present invention provides a nucleic acid sequence encoding both the first and second chimeric antigen receptors (CARs) as defined in the first aspect of the invention.

The nucleic acid sequence according may have the following structure:AgB1-spacer1-TM1-endo1-coexpr-AgB2-spacer2-TM2-endo2

in which
AgB1 is a nucleic acid sequence encoding the antigen-binding domain of the first CAR;
spacer 1 is a nucleic acid sequence encoding the spacer of the first CAR;
TM1 is a a nucleic acid sequence encoding the transmembrane domain of the first CAR;
endo 1 is a nucleic acid sequence encoding the endodomain of the first CAR;
coexpr is a nucleic acid sequence allowing co-expression of two CARs (e.g. a cleavage site);
AgB2 is a nucleic acid sequence encoding the antigen-binding domain of the second CAR;
spacer 2 is a nucleic acid sequence encoding the spacer of the second CAR;
TM2 is a a nucleic acid sequence encoding the transmembrane domain of the second CAR;
endo 2 is a nucleic acid sequence encoding the endodomain of the second CAR;
which nucleic acid sequence, when expressed in a T cell, encodes a polypeptide which is cleaved at the cleavage site such that the first and second CARs are co-expressed at the T cell surface.

The nucleic acid sequence allowing co-expression of two CARs may encode a self-cleaving peptide or a sequence which allows alternative means of co-expressing two CARs such as an internal ribosome entry sequence or a 2nd promoter or other such means whereby one skilled in the art can express two proteins from the same vector.

Alternative codons may be used in regions of sequence encoding the same or similar amino acid sequences, in order to avoid homologous recombination.

In a third aspect, the present invention provides a kit which comprises

(i) a first nucleic acid sequence encoding the first chimeric antigen receptor (CAR) as defined in the first aspect of the invention, which nucleic acid sequence has the following structure:

AgB1-spacer1-TM1-endo1

in which

AgB1 is a nucleic acid sequence encoding the antigen-binding domain of the first CAR;
spacer 1 is a nucleic acid sequence encoding the spacer of the first CAR;
TM1 is a a nucleic acid sequence encoding the transmembrane domain of the first CAR;
endo 1 is a nucleic acid sequence encoding the endodomain of the first CAR; and

(ii) a second nucleic acid sequence encoding the second chimeric antigen receptor (CAR) as defined in the first aspect of the invention, which nucleic acid sequence has the following structure:

AgB2-spacer2-TM2-endo2

AgB2 is a nucleic acid sequence encoding the antigen-binding domain of the second CAR;
spacer 2 is a nucleic acid sequence encoding the spacer of the second CAR;
TM2 is a a nucleic acid sequence encoding the transmembrane domain of the second CAR;
endo 2 is a nucleic acid sequence encoding the endodomain of the second CAR.

In a fourth aspect, the present invention provides a kit comprising: a first vector which comprises the first nucleic acid sequence as defined above; and a second vector which comprises the first nucleic acid sequence as defined above.

The vectors may be plasmid vectors, retroviral vectors or transposon vectors. The vectors may be lentiviral vectors.

In a fifth aspect, the present invention provides a vector comprising a nucleic acid sequence according to the second aspect of the invention. The vector may be a lentiviral vector.

The vector may be a plasmid vector, a retroviral vector or a transposon vector.

In a sixth aspect, the present invention involves co-expressing more than two CARs in such a fashion that a complex pattern of more than two antigens can be recognized on the target cell.

In a seventh aspect, the present invention provides a method for making a T cell according to the first aspect of the invention, which comprises the step of introducing one or more nucleic acid sequence (s) encoding the first and second CARs; or one or more vector(s) as defined above into a T cell.

The T cell may be from a sample isolated from a patient, a related or unrelated haematopoietic transplant donor, a completely unconnected donor, from cord blood, differentiated from an embryonic cell line, differentiated from an inducible progenitor cell line, or derived from a transformed T cell line.

In an eighth aspect, the present invention provides a pharmaceutical composition comprising a plurality of T cells according to the first aspect of the invention.

In a ninth aspect, the present invention provides a method for treating and/or preventing a disease, which comprises the step of administering a pharmaceutical composition according to the eighth aspect of the invention to a subject.

The method may comprise the following steps:

(i) isolation of a T cell as listed above.

(ii) transduction or transfection of the T cells with one or more nucleic acid sequence(s) encoding the first and second CAR or one or more vector(s) comprising such nucleic acid sequence(s); and

(iii) administering the T cells from (ii) to the subject.

The disease may be a cancer.

In a tenth aspect, the present invention provides a pharmaceutical composition according to the eighth aspect of the invention for use in treating and/or preventing a disease.

The disease may be a cancer.

In an eleventh aspect, the present invention provides use of a T cell according to the first aspect of the invention in the manufacture of a medicament for treating and/or preventing a disease.

The disease may be a cancer.

The present invention also provides a nucleic acid sequence which comprises:
a) a first nucleotide sequence encoding a first chimeric antigen receptor (CAR);
b) a second nucleotide sequence encoding a second CAR;
c) a sequence encoding a self-cleaving peptide positioned between the first and second nucleotide sequences, such that the two CARs are expressed as separate entities.

Alternative codons may be used in one or more portion(s) of the first and second nucleotide sequences in regions which encode the same or similar amino acid sequence(s).

The present invention also provides a vector and a cell comprising such a nucleic acid.

The kinetic-segregation based AND gate of the present invention offers a significant technical advantage to the previously described "co-CAR", i.e. the dual targeting approach in which two antigens are recognized by two CARs which supply either an activating or a co-stimulating signal to the T-cell.

With the co-CAR approach, although greatest activity might be expected against target cells bearing both antigens, considerable activity against tissues bearing only antigen recognized by the activating CAR can be expected. This activity can be expected to be at least that of a first-generation CAR. First generation CARs have resulted in considerable toxicity: for instance biliary toxicity was observed in clinical testing of a first generation CAR recognizing Carbonic anhydrase IX which was unexpectedly expressed on biliary epithelium (Rotterdam ref). Notably, terminally differentiated effectors do not require or respond to co-stimulatory signals, so any terminally differentiated CAR T-cells would act maximally despite the absence of a co-stimulatory CAR signal.

Further, co-stimulatory signals lead to long-lasting effects on the T-cell population. These effects long outlast the T-cell / target synapse interaction. Consequently, CAR T-cells which

become fully activated within the tumour and migrate could have maximally potent activity against single-antigen bearing normal tissues. This "spill-over" effect may be most pronounced in tissues within, near or which drain from the tumour. In fact, strategies based on the concept of the activity of a first generation CAR being enhanced by co-stimulatory signals engaged not CAR activation but through a distinct receptor, have been proposed and tested (Rossig, Blood. 2002 Mar 15;99(6):2009-16.).

The co-CAR approach hence can be expected to result at best to a reduction but not abolition of toxicity towards single antigen expressing normal tissue. The present invention uses kinetic segregation at the immunological synapse formed between the T-cell / target cell to regulate T-cell triggering itself. Consequently tight absolute control of triggering in the absence of the second antigen is achieved. Hence the totality of T-cell activation is restricted to target cells expressing both antigens, the AND gate should function irrespective of the effector cell type or differentiation state, and no "spill-over" effect AND gate T-cell activation is possible.

FURTHER ASPECTS OF THE INVENTION

The present invention also relates to the aspects listed in the following numbered paragraphs:

1. A T cell which co-expresses a first chimeric antigen receptor (CAR) and second CAR at the cell surface, each CAR comprising:

(i) an antigen-binding domain;

(ii) a spacer

(iii) a trans-membrane domain; and

(iv) an endodomain

wherein the antigen binding domains of the first and second CARs bind to different antigens, wherein the spacer of the first CAR is different to the spacer of the second CAR and wherein one of the first or second CARs is an activating CAR comprising an activating endodomain and the other CAR is either an activating CAR comprising an activating endodomain or an inhibitory CAR comprising a ligation-on or ligation-off inhibitory endodomain.

2. A T cell according to paragraph 1, wherein the spacer of the first CAR has a different length and/or charge and/or size and/or configuration and/or glycosylation of the spacer of the second CAR, such that when the first CAR and the second CAR bind their respective

target antigens, the first CAR and second CAR become spatially separated on the T cell membrane.

3. A T cell according to paragraph 2, wherein either the first spacer or the second spacer comprises a CD8 stalk and the other spacer comprises the hinge, CH2 and CH3 domain of IgG1.

4. A T cell according to paragraph 1, wherein both the first and second CARs are activating CARs.

5. A T cell according to paragraph 4, wherein one CAR binds CD19 and the other CAR binds CD20.

6. A T cell according to paragraph 2 or 3, wherein one of the first or second CARs is an activating CAR comprising an activating endodomain, and the other CAR is an inhibitory CAR comprising a ligation-off inhibitory endodomain, which inhibitory CAR inhibits T-cell activation by the activating CAR in the absence of inhibitory CAR ligation, but does not significantly inhibit T-cell activation by the activating CAR when the inhibitory CAR is ligated.

7. A T cell according to paragraph 6, wherein the inhibitory endodomain comprises all or part of the endodomain from CD148 or CD45.

8. A T cell according to paragraph 6 or 7, wherein the antigen-binding domain of the first CAR binds CD5 and the antigen-binding domain of the second CAR binds CD19.

9. A T cell according to paragraph 1 wherein the first and second spacers are sufficiently different so as to prevent cross-pairing of the first and second CARs but are sufficiently similar to result in co-localisation of the first and second CARs following ligation.

10. A T cell according to paragraph 9, wherein one of the first or second CARs in an activating CAR comprising an activating endodomain, and the other CAR is an inhibitory CAR comprising a ligation-on inhibitory endodomain, which inhibitory CAR does not significantly inhibit T-cell activation by the activating CAR in the absence of inhibitory CAR ligation, but inhibits T-cell activation by the activating CAR when the inhibitory CAR is ligated.

11. A T cell according to paragraph 10, wherein the ligation-on inhibitory endodomain comprises at least part of a phosphatase.

12. A T cell according to paragraph 11, wherein the ligation-on inhibitory endodomain comprises all or part of PTPN6.

13. A T cell according to paragraph 10, wherein the ligation-on inhibitory endodomain comprises at least one ITIM domain.

14. A T cell according to paragraph 13, wherein activity of the ligation-on inhibitory endodomain is enhanced by co-expression of a PTPN6-CD45 or –CD148 fusion protein.

15. A T cell according to any of paragraphs 10 to 14, wherein the CAR comprising the activating endodomain comprises an antigen-binding domain which binds CD33 and the CAR which comprises the ligation-on inhibitory endodomain comprises an antigen-binding domain which binds CD34.

16. A T cell which comprises more than two CARs as defined in the preceding paragraphs such that it is specifically stimulated by a cell, such as a T cell, bearing a distinct pattern of more than two antigens.

17. A nucleic acid sequence encoding both the first and second chimeric antigen receptors (CARs) as defined in any of paragraphs 1 to 16.

18. A nucleic acid sequence according to paragraph 17, which has the following structure:

AgB1-spacer1-TM1-endo1-coexpr-AbB2-spacer2-TM2-endo2

in which
AgB1 is a nucleic acid sequence encoding the antigen-binding domain of the first CAR;
spacer 1 is a nucleic acid sequence encoding the spacer of the first CAR;
TM1 is a a nucleic acid sequence encoding the transmembrane domain of the first CAR;
endo 1 is a nucleic acid sequence encoding the endodomain of the first CAR;
coexpr is a nucleic acid sequence enabling co-expression of both CARs
AgB2 is a nucleic acid sequence encoding the antigen-binding domain of the second CAR;
spacer 2 is a nucleic acid sequence encoding the spacer of the second CAR;

TM2 is a a nucleic acid sequence encoding the transmembrane domain of the second CAR;
endo 2 is a nucleic acid sequence encoding the endodomain of the second CAR;
which nucleic acid sequence, when expressed in a T cell, encodes a polypeptide which is cleaved at the cleavage site such that the first and second CARs are co-expressed at the T cell surface.

19. A nucleic acid sequence according to paragraph 18, wherein coexpr encodes a sequence comprising a self-cleaving peptide.

20. A nucleic acid sequence according to paragraph 18 or 19, wherein alternative codons are used in regions of sequence encoding the same or similar amino acid sequences, in order to avoid homologous recombination.

21. A kit which comprises

(i) a first nucleic acid sequence encoding the first chimeric antigen receptor (CAR) as defined in any of paragraphs 1 to 16, which nucleic acid sequence has the following structure:

AgB1-spacer1-TM1-endo1
in which
AgB1 is a nucleic acid sequence encoding the antigen-binding domain of the first CAR;
spacer 1 is a nucleic acid sequence encoding the spacer of the first CAR;
TM1 is a nucleic acid sequence encoding the transmembrane domain of the first CAR;
endo 1 is a nucleic acid sequence encoding the endodomain of the first CAR; and

(ii) a second nucleic acid sequence encoding the second chimeric antigen receptor (CAR) as defined in any of paragraphs 1 to 16, which nucleic acid sequence has the following structure:

AgB2-spacer2-TM2-endo2
AgB2 is a nucleic acid sequence encoding the antigen-binding domain of the second CAR;
spacer 2 is a nucleic acid sequence encoding the spacer of the second CAR;
TM2 is a a nucleic acid sequence encoding the transmembrane domain of the second CAR;
endo 2 is a nucleic acid sequence encoding the endodomain of the second CAR.

22. A kit comprising: a first vector which comprises the first nucleic acid sequence as defined in paragraph 21; and a second vector which comprises the first nucleic acid sequence as defined in paragraph 21.

23. A kit according to paragraph 22, wherein the vectors are integrating viral vectors or transposons.

24. A vector comprising a nucleic acid sequence according to any of paragraphs 17 to 20.

25. A retroviral vector or a lentiviral vector or a transposon according to paragraph 24.

26. A method for making a T cell according to any of paragraphs 1 to 16, which comprises the step of introducing: a nucleic acid sequence according to any of paragraphs 17 to 20; a first nucleic acid sequence and a second nucleic acid sequence as defined in paragraph 21; and/or a first vector and a second vector as defined in paragraph 22 or a vector according to paragraph 24 or 25, into a T cell.

27. A method according to paragraph 24, wherein the T cell is from a sample isolated from a subject.

28. A pharmaceutical composition comprising a plurality of T cells according to any of paragraphs 1 to 16.

29. A method for treating and/or preventing a disease, which comprises the step of administering a pharmaceutical composition according to paragraph 28 to a subject.

30. A method according to paragraph 29, which comprises the following steps:

(i) isolation of a T cell-containing sample from a subject;

(ii) transduction or transfection of the T cells with: a nucleic acid sequence according to any of paragraphs 17 to 20; a first nucleic acid sequence and a second nucleic acid sequence as defined in paragraph 21; a first vector and a second vector as defined in paragraph 22 or 23 or a vector according to paragraph 24 or 25; and

(iii) administering the T cells from (ii) to a the subject.

31. A method according to paragraph 29 or 30, wherein the disease is a cancer.

32. A pharmaceutical composition according to paragraph 28 for use in treating and/or preventing a disease.

33. The use of a T cell according to any of paragraphs 1 to 16 in the manufacture of a medicament for treating and/or preventing a disease.

DETAILED DESCRIPTION

CHIMERIC ANTIGEN RECEPTORS (CARs)

CARs, which are shown schematically in Figure 1, are chimeric type I trans-membrane proteins which connect an extracellular antigen-recognizing domain (binder) to an intracellular signalling domain (endodomain). The binder is typically a single-chain variable fragment (scFv) derived from a monoclonal antibody (mAb), but it can be based on other formats which comprise an antibody-like antigen binding site. A spacer domain is usually necessary to isolate the binder from the membrane and to allow it a suitable orientation. A common spacer domain used is the Fc of IgG1. More compact spacers can suffice e.g. the stalk from CD8α and even just the IgG1 hinge alone, depending on the antigen. A trans-membrane domain anchors the protein in the cell membrane and connects the spacer to the endodomain.

Early CAR designs had endodomains derived from the intracellular parts of either the γ chain of the FcεR1 or CD3ζ. Consequently, these first generation receptors transmitted immunological signal 1, which was sufficient to trigger T-cell killing of cognate target cells but failed to fully activate the T-cell to proliferate and survive. To overcome this limitation, compound endodomains have been constructed: fusion of the intracellular part of a T-cell co-stimulatory molecule to that of CD3ζ results in second generation receptors which can transmit an activating and co-stimulatory signal simultaneously after antigen recognition. The co-stimulatory domain most commonly used is that of CD28. This supplies the most potent co-stimulatory signal - namely immunological signal 2, which triggers T-cell proliferation. Some receptors have also been described which include TNF receptor family endodomains, such as the closely related OX40 and 41BB which transmit survival signals. Even more potent third generation CARs have now been described which have endodomains capable of transmitting activation, proliferation and survival signals.

CAR-encoding nucleic acids may be transferred to T cells using, for example, retroviral vectors. Lentiviral vectors may be employed. In this way, a large number of cancer-specific T cells can be generated for adoptive cell transfer. When the CAR binds the target-antigen, this results in the transmission of an activating signal to the T-cell it is expressed on. Thus

the CAR directs the specificity and cytotoxicity of the T cell towards tumour cells expressing the targeted antigen.

The first aspect of the invention relates to a T-cell which co-expresses a first CAR and a second CAR such that a T-cell can recognize a desired pattern of expression on target cells in the manner of a logic gate as detailed in the truth tables: table 1, 2 and 3.

Both the first and second (and optionally subsequent) CARs comprise:
(i) an antigen-binding domain;
(ii) a spacer;
(iii) a transmembrane domain; and
(iii) an intracellular domain.

Table 1: Truth Table for CAR OR GATE

Antigen A	*Antigen B*	*Response*
Absent	Absent	No activation
Absent	Present	Activation
Present	Absent	Activation
Present	Present	Activation

Table 2: Truth Table for CAR AND GATE

Antigen A	*Antigen B*	*Response*
Absent	Absent	No activation
Absent	Present	No Activation
Present	Absent	No Activation
Present	Present	Activation

Table 3: Truth Table for CAR AND NOT GATE

Antigen A	*Antigen B*	*Response*
Absent	Absent	No activation
Absent	Present	No Activation
Present	Absent	Activation
Present	Present	No Activation

The first and second CAR of the T cell of the present invention may be produced as a polypeptide comprising both CARs, together with a cleavage site.

SEQ ID No. 1 to 5 give examples of such polypeptides, which each comprise two CARs. The CAR may therefore comprise one or other part of the following amino acid sequences, which corresponds to a single CAR.

SEQ ID No 1 is a CAR OR gate which recognizes CD19 OR CD33
SEQ ID No 2 Is a CAR AND gate which recognizes CD19 AND CD33 using a CD148 phosphatase
SEQ ID No 3 Is an alternative implementation of the CAR AND GATE which recognizes CD19 AND CD33 which uses a CD45 phosphatase
SEQ ID No 4 Is a CAR AND NOT GATE which recognizes CD19 AND NOT CD33 based on PTPN6 phosphatase
SEQ ID No 5 Is an alternative implementation of the CAR AND NOT gate which recognizes CD19 AND NOT CD33 and is based on an ITIM containing endodomain from LAIR1
SEQ ID No 6. Is a further alternative implementation of the CAR AND NOT gate which recognizes CD19 AND NOT CD33 and recruits a PTPN6-CD148 fusion protein to an ITIM containing endodomain.

SEQ ID No. 1

MSLPVTALLLPLALLLHAARPDIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPD
GTVKLLIYHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTK
LEITKAGGGGSGGGGSGGGGSGGGGSEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYG
VSWIRQPPRKGLEWLGVIWGSETTYYNSALKSRLTIIKDNSKSQVFLKMNSLQTDDTAIYYC
AKHYYYGGSYAMDYWGQGTSVTVSSDPTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGG
AVHTRGLDFACDIFWVLVVVGGVLACYSLLVTVAFIIFWVRRVKFSRSADAPAYQQGQNQL
YNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGE
RRRGKGHDGLYQGLSTATKDTYDALHMQALPPRRAEGRGSLLTCGDVEENPGPMAVPTQ
VLGLLLLWLTDARCDIQMTQSPSSLSASVGDRVTITCRASEDIYFNLVWYQQKPGKAPKLLI
YDTNRLADGVPSRFSGSGSGTQYTLTISSLQPEDFATYYCQHYKNYPLTFGQGTKLEIKRS
GGGGSGGGGSGGGGSGGGGSRSEVQLVESGGGLVQPGGSLRLSCAASGFTLSNYGMH
WIRQAPGKGLEWVSSISLNGGSTYYRDSVKGRFTISRDNAKSTLYLQMNSLRAEDTAVYYC
AAQDAYTGGYFDYWGQGTLVTVSSMDPAEPKSPDKTHTCPPCPAPPVAGPSVFLFPPKPK
DTLMIARTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL
HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK

GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE
ALHNHYTQKSLSLSPGKKDPKFWVLVVVGGVLACYSLLVTVAFIIFWVRSRVKFSRSADAPA
YQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEA
YSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

SEQ ID No. 2
MSLPVTALLLPLALLLHAARPDIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPD
GTVKLLIYHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTK
LEITKAGGGGSGGGGSGGGGSGGGGSEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYG
VSWIRQPPRKGLEWLGVIWGSETTYYNSALKSRLTIIKDNSKSQVFLKMNSLQTDDTAIYYC
AKHYYYGGSYAMDYWGQGTSVTVSSDPTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGG
AVHTRGLDFACDIFWVLVVVGGVLACYSLLVTVAFIIFWVRRVKFSRSADAPAYQQGQNQL
YNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGE
RRRGKGHDGLYQGLSTATKDTYDALHMQALPPRRAEGRGSLLTCGDVEENPGPMAVPTQ
VLGLLLLWLTDARCDIQMTQSPSSLSASVGDRVTITCRASEDIYFNLVWYQQKPGKAPKLLI
YDTNRLADGVPSRFSGSGSGTQYTLTISSLQPEDFATYYCQHYKNYPLTFGQGTKLEIKRS
GGGGSGGGGSGGGGSGGGGSRSEVQLVESGGGLVQPGGSLRLSCAASGFTLSNYGMH
WIRQAPGKGLEWVSSISLNGGSTYYRDSVKGRFTISRDNAKSTLYLQMNSLRAEDTAVYYC
AAQDAYTGGYFDYWGQGTLVTVSSMDPAEPKSPDKTHTCPPCPAPPVAGPSVFLFPPKPK
DTLMIARTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL
HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE
ALHNHYTQKSLSLSPGKKDPKAVFGCIFGALVIVTVGGFIFWRKKRKDAKNNEVSFSQIKPK
KSKLIRVENFEAYFKKQQADSNCGFAEEYEDLKLVGISQPKYAAELAENRGKNRYNNVLPY
DISRVKLSVQTHSTDDYINANYMPGYHSKKDFIATQGPLPNTLKDFWRMVWEKNVYAIIMLT
KCVEQGRTKCEEYWPSKQAQDYGDITVAMTSEIVLPEWTIRDFTVKNIQTSESHPLRQFHF
TSWPDHGVPDTTDLLINFRYLVRDYMKQSPPESPILVHCSAGVGRTGTFIAIDRLIYQIENEN
TVDVYGIVYDLRMHRPLMVQTEDQYVFLNQCVLDIVRSQKDSKVDLIYQNTTAMTIYENLAP
VTTFGKTNGYIA

SEQ ID No. 3
MSLPVTALLLPLALLLHAARPDIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPD
GTVKLLIYHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTK
LEITKAGGGGSGGGGSGGGGSGGGGSEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYG
VSWIRQPPRKGLEWLGVIWGSETTYYNSALKSRLTIIKDNSKSQVFLKMNSLQTDDTAIYYC
AKHYYYGGSYAMDYWGQGTSVTVSSDPTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGG
AVHTRGLDFACDIFWVLVVVGGVLACYSLLVTVAFIIFWVRRVKFSRSADAPAYQQGQNQL

YNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGE
RRRGKGHDGLYQGLSTATKDTYDALHMQALPPRRAEGRGSLLTCGDVEENPGPMAVPTQ
VLGLLLLWLTDARCDIQMTQSPSSLSASVGDRVTITCRASEDIYFNLVWYQQKPGKAPKLLI
YDTNRLADGVPSRFSGSGSGTQYTLTISSLQPEDFATYYCQHYKNYPLTFGQGTKLEIKRS
GGGGSGGGGSGGGGSGGGGSRSEVQLVESGGGLVQPGGSLRLSCAASGFTLSNYGMH
WIRQAPGKGLEWVSSISLNGGSTYYRDSVKGRFTISRDNAKSTLYLQMNSLRAEDTAVYYC
AAQDAYTGGYFDYWGQGTLVTVSSMDPAEPKSPDKTHTCPPCPAPPVAGPSVFLFPPKPK
DTLMIARTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL
HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE
ALHNHYTQKSLSLSPGKKDPKALIAFLAFLIIVTSIALLVVLYKIYDLHKKRSCNLDEQQELVER
DDEKQLMNVEPIHADILLETYKRKIADEGRLFLAEFQSIPRVFSKFPIKEARKPFNQNKNRYV
DILPYDYNRVELSEINGDAGSNYINASYIDGFKEPRKYIAAQGPRDETVDDFWRMIWEQKAT
VIVMVTRCEEGNRNKCAEYWPSMEEGTRAFGDVVVKINQHKRCPDYIIQKLNIVNKKEKAT
GREVTHIQFTSWPDHGVPEDPHLLLKLRRRVNAFSNFFSGPIVVHCSAGVGRTGTYIGIDA
MLEGLEAENKVDVYGYVVKLRRQRCLMVQVEAQYILIHQALVEYNQFGETEVNLSELHPYL
HNMKKRDPPSEPSPLEAEFQRLPSYRSWRTQHIGNQEENKSKNRNSNVIPYDYNRVPLKH
ELEMSKESEHDSDESSDDDSDSEEPSKYINASFIMSYWKPEVMIAAQGPLKETIGDFWQMI
FQRKVKVIVMLTELKHGDQEICAQYWGEGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKR
KDSRTVYQYQYTNWSVEQLPAEPKELISMIQVVKQKLPQKNSSEGNKHHKSTPLLIHCRDG
SQQTGIFCALLNLLESAETEEVVDIFQVVKALRKARPGMVSTFEQYQFLYDVIASTYPAQNG
QVKKNNHQEDKIEFDNEVDKVKQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSV
NGPASPALNQGS

SEQ ID No. 4

MSLPVTALLLPLALLLHAARPDIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPD
GTVKLLIYHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTK
LEITKAGGGGSGGGGSGGGGSGGGGSEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYG
VSWIRQPPRKGLEWLGVIWGSETTYYNSALKSRLTIIKDNSKSQVFLKMNSLQTDDTAIYYC
AKHYYYGGSYAMDYWGQGTSVTVSSDPTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGG
AVHTRGLDFACDIFWVLVVVGGVLACYSLLVTVAFIIFWVRRVKFSRSADAPAYQQGQNQL
YNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGE
RRRGKGHDGLYQGLSTATKDTYDALHMQALPPRRAEGRGSLLTCGDVEENPGPMAVPTQ
VLGLLLLWLTDARCDIQMTQSPSSLSASVGDRVTITCRASEDIYFNLVWYQQKPGKAPKLLI
YDTNRLADGVPSRFSGSGSGTQYTLTISSLQPEDFATYYCQHYKNYPLTFGQGTKLEIKRS
GGGGSGGGGSGGGGSGGGGSRSEVQLVESGGGLVQPGGSLRLSCAASGFTLSNYGMH
WIRQAPGKGLEWVSSISLNGGSTYYRDSVKGRFTISRDNAKSTLYLQMNSLRAEDTAVYYC

AAQDAYTGGYFDYWGQGTLVTVSSMDPATTTKPVLRTPSPVHPTGTSQPQRPEDCRPRG
SVKGTGLDFACDIYWAPLAGICVALLLSLIITLICYHRSRKRVCKSGGGSFWEEFESLQKQEV
KNLHQRLEGQRPENKGKNRYKNILPFDHSRVILQGRDSNIPGSDYINANYIKNQLLGPDENA
KTYIASQGCLEATVNDFWQMAWQENSRVIVMTTREVEKGRNKCVPYWPEVGMQRAYGPY
SVTNCGEHDTTEYKLRTLQVSPLDNGDLIREIWHYQYLSWPDHGVPSEPGGVLSFLDQINQ
RQESLPHAGPIIVHCSAGIGRTGTIIVIDMLMENISTKGLDCDIDIQKTIQMVRAQRSGMVQTE
AQYKFIYVAIAQFIETTKKKL

SEQ ID No. 5
MSLPVTALLLPLALLLHAARPDIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPD
GTVKLLIYHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTK
LEITKAGGGGSGGGGSGGGGSGGGGSEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYG
VSWIRQPPRKGLEWLGVIWGSETTYYNSALKSRLTIIKDNSKSQVFLKMNSLQTDDTAIYYC
AKHYYYGGSYAMDYWGQGTSVTVSSDPTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGG
AVHTRGLDFACDIFWVLVVVGGVLACYSLLVTVAFIIFWVRRVKFSRSADAPAYQQGQNQL
YNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGE
RRRGKGHDGLYQGLSTATKDTYDALHMQALPPRRAEGRGSLLTCGDVEENPGPMAVPTQ
VLGLLLLWLTDARCDIQMTQSPSSLSASVGDRVTITCRASEDIYFNLVWYQQKPGKAPKLLI
YDTNRLADGVPSRFSGSGSGTQYTLTISSLQPEDFATYYCQHYKNYPLTFGQGTKLEIKRS
GGGGSGGGGSGGGGSGGGGSRSEVQLVESGGGLVQPGGSLRLSCAASGFTLSNYGMH
WIRQAPGKGLEWVSSISLNGGSTYYRDSVKGRFTISRDNAKSTLYLQMNSLRAEDTAVYYC
AAQDAYTGGYFDYWGQGTLVTVSSMDPATTTKPVLRTPSPVHPTGTSQPQRPEDCRPRG
SVKGTGLDFACDILIGVSVVFLFCLLLLVLFCLHRQNQIKQGPPRSKDEEQKPQQRPDLAVD
VLERTADKATVNGLPEKDRETDTSALAAGSSQEVTYAQLDHWALTQRTARAVSPQSTKPM
AESITYAAVARH

SEQ ID No. 6
MSLPVTALLLPLALLLHAARPDIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPD
GTVKLLIYHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTK
LEITKAGGGGSGGGGSGGGGSGGGGSEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYG
VSWIRQPPRKGLEWLGVIWGSETTYYNSALKSRLTIIKDNSKSQVFLKMNSLQTDDTAIYYC
AKHYYYGGSYAMDYWGQGTSVTVSSDPTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGG
AVHTRGLDFACDIFWVLVVVGGVLACYSLLVTVAFIIFWVRRVKFSRSADAPAYQQGQNQL
YNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGE
RRRGKGHDGLYQGLSTATKDTYDALHMQALPPRRAEGRGSLLTCGDVEENPGPMAVPTQ
VLGLLLLWLTDARCDIQMTQSPSSLSASVGDRVTITCRASEDIYFNLVWYQQKPGKAPKLLI
YDTNRLADGVPSRFSGSGSGTQYTLTISSLQPEDFATYYCQHYKNYPLTFGQGTKLEIKRS

GGGGSGGGGSGGGGSGGGGSRSEVQLVESGGGLVQPGGSLRLSCAASGFTLSNYGMH
WIRQAPGKGLEWVSSISLNGGSTYYRDSVKGRFTISRDNAKSTLYLQMNSLRAEDTAVYYC
AAQDAYTGGYFDYWGQGTLVTVSSMDPATTTKPVLRTPSPVHPTGTSQPQRPEDCRPRG
SVKGTGLDFACDILIGVSVVFLFCLLLLVLFCLHRQNQIKQGPPRSKDEEQKPQQRPDLAVD
VLERTADKATVNGLPEKDRETDTSALAAGSSQEVTYAQLDHWALTQRTARAVSPQSTKPM
AESITYAAVARHRAEGRGSLLTCGDVEENPGPWYHGHMSGGQAETLLQAKGEPWTFLVR
ESLSQPGDFVLSVLSDQPKAGPGSPLRVTHIKVMCEGGRYTVGGLETFDSLTDLVEHFKKT
GIEEASGAFVYLRQPYSGGGGSFEAYFKKQQADSNCGFAEEYEDLKLVGISQPKYAAELAE
NRGKNRYNNVLPYDISRVKLSVQTHSTDDYINANYMPGYHSKKDFIATQGPLPNTLKDFWR
MVWEKNVYAIIMLTKCVEQGRTKCEEYWPSKQAQDYGDITVAMTSEIVLPEWTIRDFTVKNI
QTSESHPLRQFHFTSWPDHGVPDTTDLLINFRYLVRDYMKQSPPESPILVHCSAGVGRTGT
FIAIDRLIYQIENENTVDVYGIVYDLRMHRPLMVQTEDQYVFLNQCVLDIVRSQKDSKVDLIY
QNTTAMTIYENLAPVTTFGKTNGYIASGS

The CAR may comprise a variant of the CAR-encoding part of the sequence shown as SEQ ID No. 1, 2, 3, 4, 5 or 6 having at least 80, 85, 90, 95, 98 or 99% sequence identity, provided that the variant sequence is a CAR having the required properties.

Methods of sequence alignment are well known in the art and are accomplished using suitable alignment programs. The % sequence identity refers to the percentage of amino acid or nucleotide residues that are identical in the two sequences when they are optimally aligned. Nucleotide and protein sequence homology or identity may be determined using standard algorithms such as a BLAST program (Basic Local Alignment Search Tool at the National Center for Biotechnology Information) using default parameters, which is publicly available at http://blast.ncbi.nlm.nih.gov. Other algorithms for determining sequence identity or homology include: LALIGN (http://www.ebi.ac.uk/Tools/psa/lalign/ and http://www.ebi.ac.uk/Tools/psa/lalign/nucleotide.html), AMAS (Analysis of Multiply Aligned Sequences, at http://www.compbio.dundee.ac.uk/Software/Amas/amas.html), FASTA (http://www.ebi.ac.uk/Tools/sss/fasta/) , Clustal Omega (http://www.ebi.ac.uk/Tools/msa/clustalo/), SIM (http://web.expasy.org/sim/), and EMBOSS Needle (http://www.ebi.ac.uk/Tools/psa/emboss_needle/nucleotide.html).

CAR LOGICAL OR GATE

In this embodiment, the antigen binding domains of the first and second CARs of the present invention bind to different antigens and both CARs comprise an activating endodomain. Both CARs have different spacer domains to prevent cross-pairing of the two different receptors. A T cell can hence be engineered to activate upon recognition of either or both antigens.

This is useful in the field of oncology as indicated by the Goldie-Coldman hypothesis: sole targeting of a single antigen may result in tumour escape by modulation of said antigen due to the high mutation rate inherent in most cancers. By simultaneously targeting two antigens, the probably of such escape is exponentially reduced.

Various tumour associated antigens are known as shown in the following Table 4. For a given disease, the first CAR and second CAR may bind to two different TAAs associated with that disease. In this way, tumour escape by modulating a single antigen is prevented, since a second antigen is also targeted. For example, when targeting a B-cell malignancy, both CD19 and CD20 can be simultaneously targeted. In this embodiment, it is important that the two CARs do not heterodimerize.

TABLE 4

Cancer type	**TAA**
Diffuse Large B-cell Lymphoma	CD19, CD20
Breast cancer	ErbB2, MUC1
AML	CD13, CD33
Neuroblastoma	GD2, NCAM
B-CLL	CD19, CD52
Colorectal cancer	Folate binding protein, CA-125

KINETIC SEGREGATION MODEL

Subsequent pairing of CARs to generate the AND gate and the AND NOT gate are based on the kinetic segregation model (KS) of T-cell activation. This is a functional model, backed by experimental data, which explains how antigen recognition by a T-cell receptor is converted into down-stream activation signals. Briefly: at the ground state, the signalling components on the T-cell membrane are in dynamic homeostasis whereby dephosphorylated ITAMs are favoured over phosphorylated ITAMs. This is due to greater activity of the transmembrane CD45/CD148 phosphatases over membrane-tethered kinases such as lck. When a T-cell engages a target cell through a T-cell receptor (or CAR) recognition of cognate antigen, tight immunological synapses form. This close juxtapositioning of the T-cell and target membranes excludes CD45/CD148 due to their large ectodomains which cannot fit into the synapse. Segregation of a high concentration of T-cell receptor associated ITAMs and kinases in the synapse, in the absence of phosphatases, leads to a state whereby phosphorylated ITAMs are favoured. ZAP70 recognizes a threshold of phosphorylated ITAMs and propagates a T-cell activation signal. This advanced understanding of T-cell

activation is exploited by the present invention. In particular, the invention is based on this understanding of how ectodomains of different length and/or bulk and/or charge and/or configuration and/or glycosylation result in differential segregation upon synapse formation.

THE CAR LOGICAL AND GATE

In this embodiment, one CAR comprises an activating endodomain and one CAR comprises an inhibitory endodomain whereby the inhibitory CAR constitutively inhibits the first activating CAR, but upon recognition of its cognate antigen releases its inhibition of the activating CAR. In this manner, a T-cell can be engineered to trigger only if a target cell expresses both cognate antigens. This behaviour is achieved by the activating CAR comprising an activating endodomain containing ITAM domains for example the endodomain of CD3 Zeta, and the inhibitory CAR comprising the endodomain from a phosphatase able to dephosphorylate an ITAM (e.g. CD45 or CD148). Crucially, the spacer domains of both CARs are significantly different in size and/or shape and/or charge etc. When only the activating CAR is ligated, the inhibitory CAR is in solution on the T-cell surface and can diffuse in and out of the synapse inhibiting the activating CAR. When both CARs are ligated, due to differences in spacer properties, the activating and inhibiting CAR are differentially segregated allowing the activating CAR to trigger T-cell activation unhindered by the inhibiting CAR.

This is of considerable utility in the field of cancer therapy. Currently, immunotherapies typically target a single antigen. Most cancers cannot be differentiated from normal tissues on the basis of a single antigen. Hence, considerable "on-target off-tumour" toxicity occurs whereby normal tissues are damaged by the therapy. For instance, whilst targeting CD20 to treat B-cell lymphomas with Rituximab, the entire normal B-cell compartment is depleted. For instance, whilst targeting CD52 to treat chronic lymphocytic leukaemia, the entire lymphoid compartment is depleted. For instance, whilst targeting CD33 to treat acute myeloid leukaemia, the entire myeloid compartment is damaged etc. By restricting activity to a pair of antigens, much more refined targeting, and hence less toxic therapy can be developed. A practical example is targeting of CLL which expresses both CD5 and CD19. Only a small proportion of normal B-cells express both antigens, so the off-target toxicity of targeting both antigens with a logical AND gate is substantially less than targeting each antigen individually.

The design of the present invention is a considerable improvement on previous implementation as described by Wilkie *et al.* ((2012). *J. Clin. Immunol.* **32,** 1059–1070) and then tested *in vivo* (Kloss *et al* (2013) *Nat. Biotechnol.* **31,** 71–75). In this implementation, the first CAR comprises of an activating endodomain, and the second a co-stimulatory

domain. This way, a T-cell only receives an activating and co-stimulatory signal when both antigens are present. However, the T-cell still will activate in the sole presence of the first antigen resulting in the potential for off-target toxicity. Further, the implementation of the present invention allows for multiple compound linked gates whereby a cell can interpret a complex pattern of antigens.

TABLE 5

Cancer Type	*Antigens*
Chronic Lymphocytic Leukaemia	CD5, CD19
Neuroblastoma	ALK, GD2
Glioma	EGFR, Vimentin
Multiple myeloma	BCMA, CD138
Renal Cell Carcinoma	Carbonic anhydrase IX, G250
T-ALL	CD2, N-Cadherin
Prostate Cancer	PSMA, hepsin (or others)

THE CAR LOGICAL AND NOT GATE

In this embodiment, one CAR comprises an activating endodomain and one CAR comprises an inhibitory endodomain such that this inhibitory CAR is only active when it recognizes its cognate antigen. Hence a T-cell engineered in this manner is activated in response to the sole presence of the first antigen but is not activated when both antigens are present. This invention is implemented by inhibitory CARs with a spacer that co-localise with the first CAR but either the phosphatase activity of the inhibitory CAR should not be so potent that it inhibits in solution, or the inhibitory endodomain in fact recruits a phosphatase solely when the inhibitory CAR recognizes its cognate target. Such endodomains are termed "ligation-on" or semi-inhibitory herein.

This invention is of use in refining targeting when a tumour can be distinguished from normal tissue by the presence of tumour associated antigen and the loss of an antigen expressed on normal tissue. The AND NOT gate is of considerable utility in the field of oncology as it allows targeting of an antigen which is expressed by a normal cell, which normal cell also expresses the antigen recognised by the CAR comprising the activating endodomain. An example of such an antigen is CD33 which is expressed by normal stem cells and acute myeloid leukaemia (AML) cells. CD34 is expressed on stem cells but not typically expressed on AML cells. A T-cell recognizing CD33 AND NOT CD34 would result in destruction of leukaemia cells but sparing of normal stem cells.

Potential antigen pairs for use with AND NOT gates are shown in Table 6.

TABLE 6

Disease	TAA	Normal cell which expresses TAA	Antigen expressed by normal cell but not cancer cell
AML	CD33	stem cells	CD34
Myeloma	BCMA	Dendritic cells	CD1c
B-CLL	CD160	Natural Killer cells	CD56
Prostate cancer	PSMA	Neural Tissue	NCAM
Bowel cancer	A33	Normal bowel epithelium	HLA class I

COMPOUND GATES

The kinetic segregation model with the above components allows compound gates to be made e.g. a T-cell which triggers in response to patterns of more than two target antigens. For example, it is possible to make a T cell which only triggers when three antigens are present (A AND B AND C). Here, a cell expresses three CARs, each recognizing antigens A, B and C. One CAR is excitatory and two are inhibitory, which each CAR having spacer domains which result in differential segregation. Only when all three are ligated, will the T-cell activate. A further example: (A OR B) AND C: here, CARs recognizing antigens A and B are activating and have spacers which co-localise, while CAR recognizing antigen C is inhibitory and has a spacer which results in different co-segregation. A further example (A AND NOT B) AND C: Here CAR against antigen A has an activating endodomain and co-localises with CAR against antigen B which has a conditionally inhibiting endodomain. CAR against antigen C has a spacer who segregates differently from A or B and is inhibitory. In fact, ever more complex boolean logic can be programmed with these simple components of the invention with any number of CARs and spacers.

SIGNAL PEPTIDE

The CARs of the T cell of the present invention may comprise a signal peptide so that when the CAR is expressed inside a cell, such as a T-cell, the nascent protein is directed to the endoplasmic reticulum and subsequently to the cell surface, where it is expressed.

The core of the signal peptide may contain a long stretch of hydrophobic amino acids that has a tendency to form a single alpha-helix. The signal peptide may begin with a short positively charged stretch of amino acids, which helps to enforce proper topology of the polypeptide during translocation. At the end of the signal peptide there is typically a stretch of amino acids that is recognized and cleaved by signal peptidase. Signal peptidase may cleave either during or after completion of translocation to generate a free signal peptide and a mature protein. The free signal peptides are then digested by specific proteases.

The signal peptide may be at the amino terminus of the molecule.

The signal peptide may comprise the SEQ ID No. 7, 8 or 9 or a variant thereof having 5, 4, 3, 2 or 1 amino acid mutations (insertions, substitutions or additions) provided that the signal peptide still functions to cause cell surface expression of the CAR.

SEQ ID No. 7: MGTSLLCWMALCLLGADHADG

The signal peptide of SEQ ID No. 7 is compact and highly efficient. It is predicted to give about 95% cleavage after the terminal glycine, giving efficient removal by signal peptidase.

SEQ ID No. 8: MSLPVTALLLPLALLLHAARP

The signal peptide of SEQ ID No. 8 is derived from IgG1.

SEQ ID No. 9: MAVPTQVLGLLLLWLTDARC

The signal peptide of SEQ ID No. 9 is derived from CD8.

The signal peptide for the first CAR may have a different sequence from the signal peptide of the second CAR (and from the 3rd CAR and 4th CAR etc).

ANTIGEN BINDING DOMAIN

The antigen binding domain is the portion of the CAR which recognizes antigen. Numerous antigen-binding domains are known in the art, including those based on the antigen binding site of an antibody, antibody mimetics, and T-cell receptors. For example, the antigen-binding domain may comprise: a single-chain variable fragment (scFv) derived from a monoclonal antibody; a natural ligand of the target antigen; a peptide with sufficient affinity

for the target; a single domain antibody; an artificial single binder such as a Darpin (designed ankyrin repeat protein); or a single-chain derived from a T-cell receptor.

The antigen binding domain may comprise a domain which is not based on the antigen binding site of an antibody. For example the antigen binding domain may comprise a domain based on a protein/peptide which is a soluble ligand for a tumour cell surface receptor (e.g. a soluble peptide such as a cytokine or a chemokine); or an extracellular domain of a membrane anchored ligand or a receptor for which the binding pair counterpart is expressed on the tumour cell.

Examples 11 to 13 relate to a CAR which binds BCMA, in which the antigen binding doaimn comprises APRIL, a ligand for BCMA.

The antigen binding domain may be based on a natural ligand of the antigen.

The antigen binding domain may comprise an affinity peptide from a combinatorial library or a *de novo* designed affinity protein/peptide.

SPACER DOMAIN

CARs comprise a spacer sequence to connect the antigen-binding domain with the transmembrane domain and spatially separate the antigen-binding domain from the endodomain. A flexible spacer allows the antigen-binding domain to orient in different directions to facilitate binding.

In the T cell of the present invention, the first and second CARs comprise different spacer molecules. For example, the spacer sequence may, for example, comprise an IgG1 Fc region, an IgG1 hinge or a human CD8 stalk or the mouse CD8 stalk. The spacer may alternatively comprise an alternative linker sequence which has similar length and/or domain spacing properties as an IgG1 Fc region, an IgG1 hinge or a CD8 stalk. A human IgG1 spacer may be altered to remove Fc binding motifs.

Examples of amino acid sequences for these spacers are given below:

SEQ ID No. 10 (hinge-CH2CH3 of human IgG1)

AEPKSPDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMIARTPEVTCVVVDVSHEDPEVKFN

WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS

KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL
DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKKD

SEQ ID No. 11 (human CD8 stalk):
TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDI

SEQ ID No. 12 (human IgG1 hinge):
AEPKSPDKTHTCPPCPKDPK

SEQ ID No. 13 (CD2 ectodomain)
KEITNALETWGALGQDINLDIPSFQMSDDIDDIKWEKTSDKKKIAQFRKEKETFKEKDTYKLF
KNGTLKIKHLKTDDQDIYKVSIYDTKGKNVLEKIFDLKIQERVSKPKISWTCINTTLTCEVMNG
TDPELNLYQDGKHLKLSQRVITHKWTTSLSAKFKCTAGNKVSKESSVEPVSCP
EKGLD

SEQ ID no. 14 (CD34 ectodomain)
SLDNNGTATPELPTQGTFSNVSTNVSYQETTTPSTLGSTSLHPVSQHGNEATTNITETTVKF
TSTSVITSVYGNTNSSVQSQTSVISTVFTTPANVSTPETTLKPSLSPGNVSDLSTTSTSLATS
PTKPYTSSSPILSDIKAEIKCSGIREVKLTQGICLEQNKTSSCAEFKKDRGEGLARVLCGEEQ
ADADAGAQVCSLLLAQSEVRPQCLLLVLANRTEISSKLQLMKKHQSDLKKLGILDFTEQDVA
SHQSYSQKT

Since CARs are typically homodimers (see Figure 1a), cross-pairing may result in a heterodimeric chimeric antigen receptor. This is undesirable for various reasons, for example: (1) the epitope may not be at the same "level" on the target cell so that a cross-paired CAR may only be able to bind to one antigen; (2) the VH and VL from the two different scFv could swap over and either fail to recognize target or worse recognize an unexpected and unpredicted antigen. For the “OR” gate and the “AND NOT” gate, the spacer of the first CAR is sufficiently different from the spacer of the second CAR in order to avoid cross-pairing. The amino acid sequence of the first spacer may share less that 50%, 40%, 30% or 20% identity at the amino acid level with the second spacer.

In other aspects of the invention (for example the AND gate) it is important that the spacer of the first CAR has a different length, and/or charge and/or shape and/or configuration and/or glycosylation, such that when both first and second CARs bind their target antigen, the difference in spacer charge or dimensions results in spatial separation of the two types of CAR to different parts of the membrane to result in activation as predicted by the kinetic

separation model. In these aspects, the different length, shape and/or configuration of the spacers is carefully chosen bearing in mind the size and binding epitope on the target antigen to allow differential segregation upon cognate target recognition. For example the IgG1 Hinge, CD8 stalk, IgG1 Fc, ectodomain of CD34, ectodomain of CD45 are expected to differentially segregate.

Examples of spacer pairs which differentially segregate and are therefore suitable for use with the AND gate are shown in the following Table:

Stimulatory CAR spacer	Inhibitory CAR spacer
Human-CD8STK	Human-IgG-Hinge-CH2CH3
Human-CD3z ectodomain	Human-IgG-Hinge-CH2CH3
Human-IgG-Hinge	Human-IgG-Hinge-CH2CH3
Human-CD28STK	Human-IgG-Hinge-CH2CH3
Human-CD8STK	Human-IgM-Hinge-CH2CH3CD4
Human-CD3z ectodomain	Human-IgM-Hinge-CH2CH3CD4
Human-IgG-Hinge	Human-IgM-Hinge-CH2CH3CD4
Human-CD28STK	Human-IgM-Hinge-CH2CH3CD4

In other aspects of the invention (for example the AND NOT gate), it is important that the spacer be sufficiently different as to prevent cross-pairing, but to be sufficiently similar to co-localise. Pairs of orthologous spacer sequences may be employed. Examples are murine and human CD8 stalks, or alternatively spacer domains which are monomeric – for instance the ectodomain of CD2.

Examples of spacer pairs which co-localise and are therefore suitable for use with the AND NOT gate are shown in the following Table:

Stimulatory CAR spacer	Inhibitory CAR spacer
Human-CD8aSTK	Mouse CD8aSTK
Human-CD28STK	Mouse CD8aSTK
Human-IgG-Hinge	Human-CD3z ectodomain
Human-CD8aSTK	Mouse CD28STK
Human-CD28STK	Mouse CD28STK
Human-IgG-Hinge-CH2CH3	Human-IgM-Hinge-CH2CH3CD4

All the spacer domains mentioned above form homodimers. However the mechanism is not limited to using homodimeric receptors and should work with monomeric receptors as long as the spacer is sufficiently rigid. An example of such a spacer is CD2 or truncated CD22.

TRANSMEMBRANE DOMAIN

The transmembrane domain is the sequence of the CAR that spans the membrane.

A transmembrane domain may be any protein structure which is thermodynamically stable in a membrane. This is typically an alpha helix comprising of several hydrophobic residues. The transmembrane domain of any transmembrane protein can be used to supply the transmembrane portion of the invention. The presence and span of a transmembrane domain of a protein can be determined by those skilled in the art using the TMHMM algorithm (http://www.cbs.dtu.dk/services/TMHMM-2.0/). Further, given that the transmembrane domain of a protein is a relatively simple structure, i.e a polypeptide sequence predicted to form a hydrophobic alpha helix of sufficient length to span the membrane, an artificially designed TM domain may also be used (US 7052906 B1 describes synthetic transmembrane components).

The transmembrane domain may be derived from CD28, which gives good receptor stability.

ACTIVATING ENDODOMAIN

The endodomain is the signal-transmission portion of the CAR. After antigen recognition, receptors cluster, native CD45 and CD148 are excluded from the synapse and a signal is transmitted to the cell. The most commonly used endodomain component is that of CD3-zeta which contains 3 ITAMs. This transmits an activation signal to the T cell after antigen is bound. CD3-zeta may not provide a fully competent activation signal and additional co-stimulatory signaling may be needed. For example, chimeric CD28 and OX40 can be used with CD3-Zeta to transmit a proliferative / survival signal, or all three can be used together.

Where the T cell of the present invention comprises a CAR with an activating endodomain, it may comprise the CD3-Zeta endodomain alone, the CD3-Zeta endodomain with that of either CD28 or OX40 or the CD28 endodomain and OX40 and CD3-Zeta endodomain.

Any endodomain which contains an ITAM motif can act as an activation endodomain in this invention. Several proteins are known to contain endodomains with one or more ITAM motifs. Examples of such proteins include the CD3 epsilon chain, the CD3 gamma chain and the CD3 delta chain to name a few. The ITAM motif can be easily recognized as a tyrosine separated from a leucine or isoleucine by any two other amino acids, giving the signature YxxL/I. Typically, but not always, two of these motifs are separated by between 6 and 8 amino acids in the tail of the molecule (YxxL/Ix(6-8)YxxL/I). Hence, one skilled in the art can

readily find existing proteins which contain one or more ITAM to transmit an activation signal. Further, given the motif is simple and a complex secondary structure is not required, one skilled in the art can design polypeptides containing artificial ITAMs to transmit an activation signal (see WO 2000063372, which relates to synthetic signalling molecules).

The transmembrane and intracellular T-cell signalling domain (endodomain) of a CAR with an activating endodomain may comprise the sequence shown as SEQ ID No. 15, 16 or 17 or a variant thereof having at least 80% sequence identity.

SEQ ID No. 15 comprising CD28 transmembrane domain and CD3 Z endodomain
FWVLVVVGGVLACYSLLVTVAFIIFWVRRVKFSRSADAPAYQQGQNQLYNELNLGRREEY
DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLY
QGLSTATKDTYDALHMQALPPR

SEQ ID No. 16 comprising CD28 transmembrane domain and CD28 and CD3 Zeta endodomains
FWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPP
RDFAAYRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRR
KNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALP
PR

SEQ ID No. 17 comprising CD28 transmembrane domain and CD28, OX40 and CD3 Zeta endodomains.
FWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPP
RDFAAYRSRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAKIRVKFSRSADAPAYQQG
QNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIG
MKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

A variant sequence may have at least 80%, 85%, 90%, 95%, 98% or 99% sequence identity to SEQ ID No. 15, 16 or 17, provided that the sequence provides an effective trans-membrane domain and an effective intracellular T cell signaling domain.

"LIGATION-OFF" INHIBITORY ENDODOMAIN

In the embodiment referred above as the AND gate, one of the CARs comprises an inhibitory endodomain such that the inhibitory CAR inhibits T-cell activation by the activating CAR in the absence of inhibitory CAR ligation, but does not significantly inhibit T-cell

activation by the activating CAR when the inhibitory CAR is ligated. This is termed a "ligation-off" inhibitory endodomain.

In this case, the spacer of the inhibitory CAR is of a different length, charge, shape and/or configuration and/or glycosylation from the spacer of the activating CAR, such that when both receptors are ligated, the difference in spacer dimensions results in isolation of the activating CARs and the inhibitory CARs in different membrane compartments of the immunological synapse, so that the activating endodomain is released from inhibition by the inhibitory endodomain.

The inhibitory endodomains for use in a ligation-off inhibitory CAR may therefore comprise any sequence which inhibits T-cell signaling by the activating CAR when it is in the same membrane compartment (i.e. in the absence of the antigen for the inhibitory CAR) but which does not significantly inhibit T cell signaling when it is isolated in a separate part of the membrane from the inhibitory CAR.

The ligation-off inhibitory endodomain may be or comprise a tyrosine phosphatase, such as a receptor-like tyrosine phosphatase. An inhibitory endodomain may be or comprise any tyrosine phosphatase that is capable of inhibiting the TCR signalling when only the stimulatory receptor is ligated. An inhibitory endodomain may be or comprise any tyrosine phosphatase with a sufficiently fast catalytic rate for phosphorylated ITAMs that is capable of inhibiting the TCR signalling when only the stimulatory receptor is ligated.

For example, the inhibitory endodomain of an AND gate may comprise the endodomain of CD148 or CD45. CD148 and CD45 have been shown to act naturally on the phosphorylated tyrosines up-stream of TCR signalling.

CD148 is a receptor-like protein tyrosine phosphatase which negatively regulates TCR signaling by interfering with the phosphorylation and function of PLCγ1 and LAT.

CD45 present on all hematopoetic cells, is a protein tyrosine phosphatase which is capable of regulating signal transduction and functional responses, again by phosphorylating PLC γ1.

An inhibitory endodomain may comprise all of part of a receptor-like tyrosine phosphatase. The phospatase may interfere with the phosphorylation and/or function of elements involved in T-cell signalling, such as PLCγ1 and/or LAT.

The transmembrane and endodomain of CD45 and CD148 is shown as SEQ ID No. 18 and No.19 respectively.

SEQ ID 18 - CD45 trans-membrane and endodomain sequence
ALIAFLAFLIIVTSIALLVVLYKIYDLHKKRSCNLDEQQELVERDDEKQLMNVEPIHADILLETYK
RKIADEGRLFLAEFQSIPRVFSKFPIKEARKPFNQNKNRYVDILPYDYNRVELSEINGDAGSN
YINASYIDGFKEPRKYIAAQGPRDETVDDFWRMIWEQKATVIVMVTRCEEGNRNKCAEYWP
SMEEGTRAFGDVVVKINQHKRCPDYIIQKLNIVNKKEKATGREVTHIQFTSWPDHGVPEDPH
LLLKLRRRVNAFSNFFSGPIVVHCSAGVGRTGTYIGIDAMLEGLEAENKVDVYGYVVKLRRQ
RCLMVQVEAQYILIHQALVEYNQFGETEVNLSELHPYLHNMKKRDPPSEPSPLEAEFQRLP
SYRSWRTQHIGNQEENKSKNRNSNVIPYDYNRVPLKHELEMSKESEHDSDESSDDDSDSE
EPSKYINASFIMSYWKPEVMIAAQGPLKETIGDFWQMIFQRKVKVIVMLTELKHGDQEICAQ
YWGEGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKRKDSRTVYQYQYTNWSVEQLPAEP
KELISMIQVVKQKLPQKNSSEGNKHHKSTPLLIHCRDGSQQTGIFCALLNLLESAETEEVVDI
FQVVKALRKARPGMVSTFEQYQFLYDVIASTYPAQNGQVKKNNHQEDKIEFDNEVDKVKQ
DANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGPASPALNQGS

SEQ ID 19 - CD148 trans-membrane and endodomain sequence
AVFGCIFGALVIVTVGGFIFWRKKRKDAKNNEVSFSQIKPKKSKLIRVENFEAYFKKQQADSN
CGFAEEYEDLKLVGISQPKYAAELAENRGKNRYNNVLPYDISRVKLSVQTHSTDDYINANYM
PGYHSKKDFIATQGPLPNTLKDFWRMVWEKNVYAIIMLTKCVEQGRTKCEEYWPSKQAQD
YGDITVAMTSEIVLPEWTIRDFTVKNIQTSESHPLRQFHFTSWPDHGVPDTTDLLINFRYLVR
DYMKQSPPESPILVHCSAGVGRTGTFIAIDRLIYQIENENTVDVYGIVYDLRMHRPLMVQTED
QYVFLNQCVLDIVRSQKDSKVDLIYQNTTAMTIYENLAPVTTFGKTNGYIA

An inhibitory CAR may comprise all or part of SEQ ID No 18 or 19 (for example, it may comprise the phosphatase function of the endodomain). It may comprise a variant of the sequence or part thereof having at least 80% sequence identity, as long as the variant retains the capacity to basally inhibit T cell signalling by the activating CAR.

Other spacers and endodomains may be tested for example using the model system exemplified herein. Target cell populations can be created by transducing a suitable cell line such as a SupT1 cell line either singly or doubly to establish cells negative for both antigens (the wild-type), positive for either and positive for both (e.g. CD19-CD33-, CD19+CD33-, CD19-CD33+ and CD19+CD33+). T cells such as the mouse T cell line BW5147 which releases IL-2 upon activation may be transduced with pairs of CARs and their ability to function in a logic gate measured through measurement of IL-2 release (for example by

ELISA). For example, it is shown in Example 4 that both CD148 and CD45 endodomains can function as inhibitory CARs in combination with an activating CAR containing a CD3 Zeta endodomain. These CARs rely upon a short/non-bulky CD8 stalk spacer on one CAR and a bulky Fc spacer on the other CAR to achieve AND gating. When both receptors are ligated, the difference in spacer dimensions results in isolation of the different receptors in different membrane compartments, releasing the CD3 Zeta receptor from inhibition by the CD148 or CD45 endodomains. In this way, activation only occurs once both receptors are activated. It can be readily seen that this modular system can be used to test alternative spacer pairs and inhibitory endodomains. If the spacers do not achieve isolation following ligation of both receptors, the inhibition would not be released and so no activation would occur. If the inhibitory endodomain under test is ineffective, activation would be expected in the presence of ligation of the activating CAR irrespective of the ligation status of the inhibitory CAR.

"LIGATION-ON" ENDODOMAIN

In the embodiment referred above as the AND NOT gate, one of the CARs comprises a "ligation-on" inhibitory endodomain such that the inhibitory CAR does not significantly inhibit T-cell activation by the activating CAR in the absence of inhibitory CAR ligation, but inhibits T-cell activation by the activating CAR when the inhibitory CAR is ligated.

The "ligation-on" inhibitory endodomain may be or comprise a tyrosine phosphatase that is incapable of inhibiting the TCR signalling when only the stimulatory receptor is ligated.

The "ligation-on" inhibitory endodomain may be or comprise a tyrosine phosphatase with a sufficiently slow catalytic rate for phosphorylated ITAMs that is incapable of inhibiting the TCR signalling when only the stimulatory receptor is ligated but it is capable of inhibiting the TCR signalling response when concentrated at the synapse. Concentration at the synapse is achieved through inhibitory receptor ligation.

If a tyrosine phosphatase has a catalytic rate which is too fast for a "ligation-on" inhibitory endodomain, then it is possible to tune-down the catalytic rates of phosphatase through modification such as point mutations and short linkers (which cause steric hindrance) to make it suitable for a "ligation-on" inhibitory endodomain.

In this first embodiment the endodomain may be or comprise a phosphatase which is considerably less active than CD45 or CD148, such that significant dephosphorylation of ITAMS only occurs when activating and inhibitory endodomains are co-localised. Many

suitable sequences are known in the art. For example, the inhibitory endodomain of a NOT AND gate may comprise all or part of a protein-tyrosine phosphatase such as PTPN6.

Protein tyrosine phosphatases (PTPs) are signaling molecules that regulate a variety of cellular processes including cell growth, differentiation, mitotic cycle, and oncogenic transformation. The N-terminal part of this PTP contains two tandem Src homolog (SH2) domains, which act as protein phospho-tyrosine binding domains, and mediate the interaction of this PTP with its substrates. This PTP is expressed primarily in hematopoietic cells, and functions as an important regulator of multiple signaling pathways in hematopoietic cells.

The inhibitor domain may comprise all of PTPN6 (SEQ ID No. 20) or just the phosphatase domain (SEQ ID No. 21).

SEQ ID 20 – sequence of PTPN6

MVRWFHRDLSGLDAETLLKGRGVHGSFLARPSRKNQGDFSLSVRVGDQVTHIRIQNSGDF
YDLYGGEKFATLTELVEYYTQQQGVLQDRDGTIIHLKYPLNCSDPTSERWYHGHMSGGQA
ETLLQAKGEPWTFLVRESLSQPGDFVLSVLSDQPKAGPGSPLRVTHIKVMCEGGRYTVGG
LETFDSLTDLVEHFKKTGIEEASGAFVYLRQPYYATRVNAADIENRVLELNKKQESEDTAKA
GFWEEFESLQKQEVKNLHQRLEGQRPENKGKNRYKNILPFDHSRVILQGRDSNIPGSDYIN
ANYIKNQLLGPDENAKTYIASQGCLEATVNDFWQMAWQENSRVIVMTTREVEKGRNKCVP
YWPEVGMQRAYGPYSVTNCGEHDTTEYKLRTLQVSPLDNGDLIREIWHYQYLSWPDHGV
PSEPGGVLSFLDQINQRQESLPHAGPIIVHCSAGIGRTGTIIVIDMLMENISTKGLDCDIDIQKT
IQMVRAQRSGMVQTEAQYKFIYVAIAQFIETTKKKLEVLQSQKGQESEYGNITYPPAMKNAH
AKASRTSSKHKEDVYENLHTKNKREEKVKKQRSADKEKSKGSLKRK

SEQ ID 21 – sequence of phosphatase domain of PTPN6

FWEEFESLQKQEVKNLHQRLEGQRPENKGKNRYKNILPFDHSRVILQGRDSNIPGSDYINA
NYIKNQLLGPDENAKTYIASQGCLEATVNDFWQMAWQENSRVIVMTTREVEKGRNKCVPY
WPEVGMQRAYGPYSVTNCGEHDTTEYKLRTLQVSPLDNGDLIREIWHYQYLSWPDHGVP
SEPGGVLSFLDQINQRQESLPHAGPIIVHCSAGIGRTGTIIVIDMLMENISTKGLDCDIDIQKTI
QMVRAQRSGMVQTEAQYKFIYVAIAQF

A second embodiment of a ligation-on inhibitory endodomain is an ITIM (Immunoreceptor Tyrosine-based Inhibition motif) containing endodomain such as that from CD22, LAIR-1, the Killer inhibitory receptor family (KIR), LILRB1, CTLA4, PD-1, BTLA etc. When phosphorylated, ITIMs recruits endogenous PTPN6 through its SH2 domain. If co-localised

with an ITAM containing endodomain, dephosphorylation occurs and the activating CAR is inhibited.

An ITIM is a conserved sequence of amino acids (S/I/V/LxYxxI/V/L) that is found in the cytoplasmic tails of many inhibitory receptors of the immune system. One skilled in the art can easily find protein domains containing an ITIM. A list of human candidate ITIM-containing proteins has been generated by proteome-wide scans (Staub, et al (2004) Cell. Signal. 16, 435–456). Further, since the consensus sequence is well known and little secondary structure appears to be required, one skilled in the art could generate an artificial ITIM.

ITIM endodomains from PDCD1, BTLA4, LILRB1, LAIR1, CTLA4, KIR2DL1, KIR2DL4, KIR2DL5, KIR3DL1 and KIR3DL3 are shown in SEQ ID 22 to 31 respectively

SEQ ID 22 PDCD1 endodomain
CSRAARGTIGARRTGQPLKEDPSAVPVFSVDYGELDFQWREKTPEPPVPCVPEQTEYATI
VFPSGMGTSSPARRGSADGPRSAQPLRPEDGHCSWPL

SEQ ID 23 BTLA4
KLQRRWKRTQSQQGLQENSSGQSFFVRNKKVRRAPLSEGPHSLGCYNPMMEDGISYTTL
RFPEMNIPRTGDAESSEMQRPPPDCDDTVTYSALHKRQVGDYENVIPDFPEDEGIHYSELI
QFGVGERPQAQENVDYVILKH

SEQ ID 24 LILRB1
LRHRRQGKHWTSTQRKADFQHPAGAVGPEPTDRGLQWRSSPAADAQEENLYAAVKHTQ
PEDGVEMDTRSPHDEDPQAVTYAEVKHSRPRREMASPPSPLSGEFLDTKDRQAEEDRQM
DTEAAASEAPQDVTYAQLHSLTLRREATEPPPSQEGPSPAVPSIYATLAIH

SEQ ID 25 LAIR1
HRQNQIKQGPPRSKDEEQKPQQRPDLAVDVLERTADKATVNGLPEKDRETDTSALAAGSS
QEVTYAQLDHWALTQRTARAVSPQSTKPMAESITYAAVARH

SEQ ID 26 CTLA4
FLLWILAAVSSGLFFYSFLLTAVSLSKMLKKRSPLTTGVYVKMPPTEPECEKQFQPYFIPIN

SEQ ID 27 KIR2DL1
GNSRHLHVLIGTSVVIIPFAILLFFLLHRWCANKKNAVVMDQEPAGNRTVNREDSDEQDP

QEVTYTQLNHCVFTQRKITRPSQRPKTPPTDIIVYTELPNAESRSKVVSCP

SEQ ID 28 KIR2DL4
GIARHLHAVIRYSVAIILFTILPFFLLHRWCSKKKENAAVMNQEPAGHRTVNREDSDEQDPQ
EVTYAQLDHCIFTQRKITGPSQRSKRPSTDTSVCIELPNAEPRALSPAHEHHSQALMGSSRE
TTALSQTQLASSNVPAAGI

SEQ ID 29 KIR2DL5
TGIRRHLHILIGTSVAIILFIILFFFLLHCCCSNKKNAAVMDQEPAGDRTVNREDSDDQDPQEV
TYAQLDHCVFTQTKITSPSQRPKTPPTDTTMYMELPNAKPRSLSPAHKHHSQALRGSSRET
TALSQNRVASSHVPAAGI

SEQ ID 30 KIR3DL1
KDPRHLHILIGTSVVIILFILLLFFLLHLWCSNKKNAAVMDQEPAGNRTANSEDSDEQDPEEV
TYAQLDHCVFTQRKITRPSQRPKTPPTDTILYTELPNAKPRSKVVSCP

SEQ ID 31 KIR3DL3
KDPGNSRHLHVLIGTSVVIIPFAILLFFLLHRWCANKKNAVVMDQEPAGNRTVNREDSDEQD
PQEVTYAQLNHCVFTQRKITRPSQRPKTPPTDTSV

A third embodiment of a ligation-on inhibitory endodomain is an ITIM containing endodomain co-expressed with a fusion protein. The fusion protein may comprise at least part of a protein-tyrosine phosphatase and at least part of a receptor-like tyrosine phosphatase. The fusion may comprise one or more SH2 domains from the protein-tyrosine phosphatase. For example, the fusion may be between a PTPN6 SH2 domain and CD45 endodomain or between a PTPN6 SH2 domain and CD148 endodomain. When phosphorylated, the ITIM domains recruit the fusion protein bring the highly potent CD45 or CD148 phosphatase to proximity to the activating endodomain blocking activation.

SEQUENCES of fusion proteins are listed 32 and 33

SEQ ID 32 PTPN6-CD45 fusion protein
WYHGHMSGGQAETLLQAKGEPWTFLVRESLSQPGDFVLSVLSDQPKAGPGSPLRVTHIKV
MCEGGRYTVGGLETFDSLTDLVEHFKKTGIEEASGAFVYLRQPYKIYDLHKKRSCNLDEQQ
ELVERDDEKQLMNVEPIHADILLETYKRKIADEGRLFLAEFQSIPRVFSKFPIKEARKPFNQN
KNRYVDILPYDYNRVELSEINGDAGSNYINASYIDGFKEPRKYIAAQGPRDETVDDFWRMIW
EQKATVIVMVTRCEEGNRNKCAEYWPSMEEGTRAFGDVVVKINQHKRCPDYIIQKLNIVNK

KEKATGREVTHIQFTSWPDHGVPEDPHLLLKLRRRVNAFSNFFSGPIVVHCSAGVGRTGTY
IGIDAMLEGLEAENKVDVYGYVVKLRRQRCLMVQVEAQYILIHQALVEYNQFGETEVNLSEL
HPYLHNMKKRDPPSEPSPLEAEFQRLPSYRSWRTQHIGNQEENKSKNRNSNVIPYDYNRV
LKHELEMSKESEHDSDESSDDDSDSEEPSKYINASFIMSYWKPEVMIAAQGPLKETIGDFMI
QRKVKVIVMLTELKHGDQEICAQYWGEGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKRK
DSRTVYQYQYTNWSVEQLPAEPKELISMIQVVKQKLPQKNSSEGNKHHKSTPLLIHCRDGS
QQTGIFCALLNLLESAETEEVVDIFQVVKALRKARPGMVSTFEQYQFLYDVIASTYPAQNGQ
VKKNNHQEDKIEFDNEVDKVKQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVN
GPASPALNQGS

SEQ ID 33 PTPN6-CD148 fusion
ETLLQAKGEPWTFLVRESLSQPGDFVLSVLSDQPKAGPGSPLRVTHIKVMCEGGRYTVGG
LETFDSLTDLVEHFKKTGIEEASGAFVYLRQPYRKKRKDAKNNEVSFSQIKPKKSKLIRVENF
EAYFKKQQADSNCGFAEEYEDLKLVGISQPKYAAELAENRGKNRYNNVLPYDISRVKLSVQ
THSTDDYINANYMPGYHSKKDFIATQGPLPNTLKDFWRMVWEKNVYAIIMLTKCVEQGRTK
CEEYWPSKQAQDYGDITVAMTSEIVLPEWTIRDFTVKNIQTSESHPLRQFHFTSWPDHGVP
DTTDLLINFRYLVRDYMKQSPPESPILVHCSAGVGRTGTFIAIDRLIYQIENENTVDVYGIVYD
LRMHRPLMVQTEDQYVFLNQCVLDIVRSQKDSKVDLIYQNTTAMTIYENLAPVTTFGKTNGY
IA

A ligation-on inhibitory CAR may comprise all or part of SEQ ID No 20 or 21. It may comprise all or part of SEQ ID 22 to 31. It may comprise all or part of SEQ ID 22 to 31 co-expressed with either SEQ ID 32 or 33. It may comprise a variant of the sequence or part thereof having at least 80% sequence identity, as long as the variant retains the capacity to inhibit T cell signaling by the activating CAR upon ligation of the inhibitory CAR.

As above, alternative spacers and endodomains may be tested for example using the model system exemplified herein. It is shown in Example 5 that the PTPN6 endodomain can function as a semi-inhibitory CAR in combination with an activating CAR containing a CD3 Zeta endodomain. These CARs rely upon a human CD8 stalk spacer on one CAR and a mouse CD8 stalk spacer on the other CAR. The orthologous sequences prevent cross pairing. However, when both receptors are ligated, the similarity between the spacers results in co-segregation of the different receptors in the same membrane compartments. This results in inhibition of the CD3 Zeta receptor by the PTPN6 endodomain. If only the activating CAR is ligated the PTPN6 endodomain is not sufficiently active to prevent T cell activation. In this way, activation only occurs if the activating CAR is ligated and the inhibitory CAR is not ligated (AND NOT gating). It can be readily seen that this modular

system can be used to test alternative spacer pairs and inhibitory domains. If the spacers do not achieve co-segregation following ligation of both receptors, the inhibition would not be effective and so activation would occur. If the semi-inhibitory endodomain under test is ineffective, activation would be expected in the presence of ligation of the activating CAR irrespective of the ligation status of the semi-inhibitory CAR.

CO-EXPRESSION SITE

The second aspect of the invention relates to a nucleic acid which encodes the first and second CARs.

The nucleic acid may produce a polypeptide which comprises the two CAR molecules joined by a cleavage site. The cleavage site may be self-cleaving, such that when the polypeptide is produced, it is immediately cleaved into the first and second CARs without the need for any external cleavage activity.

Various self-cleaving sites are known, including the Foot-and-Mouth disease virus (FMDV) 2a self-cleaving peptide, which has the sequence shown as SEQ ID No. 34:

SEQ ID No. 34
RAEGRGSLLTCGDVEENPGP.

The co-expressing sequence may be an internal ribosome entry sequence (IRES). The co-expressing sequence may be an internal promoter.

CELL

The first aspect of the invention relates to a cell which co-expresses a first CAR and a second CAR at the cell surface.

The cell may be any eukaryotic cell capable of expressing a CAR at the cell surface, such as an immunological cell.

In particular the cell may be an immune effector cell such as a T cell or a natural killer (NK) cell

T cells or T lymphocytes are a type of lymphocyte that play a central role in cell-mediated immunity. They can be distinguished from other lymphocytes, such as B cells and natural

killer cells (NK cells), by the presence of a T-cell receptor (TCR) on the cell surface. There are various types of T cell, as summarised below.

Helper T helper cells (TH cells) assist other white blood cells in immunologic processes, including maturation of B cells into plasma cells and memory B cells, and activation of cytotoxic T cells and macrophages. TH cells express CD4 on their surface. TH cells become activated when they are presented with peptide antigens by MHC class II molecules on the surface of antigen presenting cells (APCs). These cells can differentiate into one of several subtypes, including TH1, TH2, TH3, TH17, Th9, or TFH, which secrete different cytokines to facilitate different types of immune responses.

Cytotoxic T cells (TC cells, or CTLs) destroy virally infected cells and tumor cells, and are also implicated in transplant rejection. CTLs express the CD8 at their surface. These cells recognize their targets by binding to antigen associated with MHC class I, which is present on the surface of all nucleated cells. Through IL-10, adenosine and other molecules secreted by regulatory T cells, the CD8+ cells can be inactivated to an anergic state, which prevent autoimmune diseases such as experimental autoimmune encephalomyelitis.

Memory T cells are a subset of antigen-specific T cells that persist long-term after an infection has resolved. They quickly expand to large numbers of effector T cells upon re-exposure to their cognate antigen, thus providing the immune system with "memory" against past infections. Memory T cells comprise three subtypes: central memory T cells (TCM cells) and two types of effector memory T cells (TEM cells and TEMRA cells). Memory cells may be either CD4+ or CD8+. Memory T cells typically express the cell surface protein CD45RO.

Regulatory T cells (Treg cells), formerly known as suppressor T cells, are crucial for the maintenance of immunological tolerance. Their major role is to shut down T cell-mediated immunity toward the end of an immune reaction and to suppress auto-reactive T cells that escaped the process of negative selection in the thymus.

Two major classes of CD4+ Treg cells have been described — naturally occurring Treg cells and adaptive Treg cells.

Naturally occurring Treg cells (also known as CD4+CD25+FoxP3+ Treg cells) arise in the thymus and have been linked to interactions between developing T cells with both myeloid (CD11c+) and plasmacytoid (CD123+) dendritic cells that have been activated with TSLP.

Naturally occurring Treg cells can be distinguished from other T cells by the presence of an intracellular molecule called FoxP3. Mutations of the FOXP3 gene can prevent regulatory T cell development, causing the fatal autoimmune disease IPEX.

Adaptive Treg cells (also known as Tr1 cells or Th3 cells) may originate during a normal immune response.

The T cell of the invention may be any of the T cell types mentioned above, in particular a CTL.

Natural killer (NK) cells are a type of cytolytic cell which forms part of the innate immune system. NK cells provide rapid responses to innate signals from virally infected cells in an MHC independent manner

NK cells (belonging to the group of innate lymphoid cells) are defined as large granular lymphocytes (LGL) and constitute the third kind of cells differentiated from the common lymphoid progenitor generating B and T lymphocytes. NK cells are known to differentiate and mature in the bone marrow, lymph node, spleen, tonsils and thymus where they then enter into the circulation.

The CAR cells of the invention may be any of the cell types mentioned above.

CAR- expressing cells , such as CAR-expressing T or NK cells, may either be created *ex vivo* either from a patient's own peripheral blood (1st party), or in the setting of a haematopoietic stem cell transplant from donor peripheral blood (2nd party), or peripheral blood from an unconnected donor (3rd party).

The present invention also provide a cell composition comprising CAR expressing T cells and/or CAR expressing NK cells according to the present invention. The cell composition may be made by tranducing or transfecting a blood-sample ex vivo with a nucleic acid according to the present invention.

Alternatively, CAR-expressing cells may be derived from *ex vivo* differentiation of inducible progenitor cells or embryonic progenitor cells to the relevant cell type, such as T cells. Alternatively, an immortalized cell line such as a T-cell line which retains its lytic function and could act as a therapeutic may be used.

In all these embodiments, CAR cells are generated by introducing DNA or RNA coding for the CARs by one of many means including transduction with a viral vector, transfection with DNA or RNA.

A CAR T cell of the invention may be an *ex vivo* T cell from a subject. The T cell may be from a peripheral blood mononuclear cell (PBMC) sample. T cells may be activated and/or expanded prior to being transduced with CAR-encoding nucleic acid, for example by treatment with an anti-CD3 monoclonal antibody.

A CAR T cell of the invention may be made by:

(i) isolation of a T cell-containing sample from a subject or other sources listed above; and

(ii) transduction or transfection of the T cells with one or more nucleic acid sequence(s) encoding the first and second CAR.

The T cells may then by purified, for example, selected on the basis of co-expression of the first and second CAR.

NUCLEIC ACID SEQUENCES

The second aspect of the invention relates to one or more nucleic acid sequence(s) which codes for a first CAR and a second CAR as defined in the first aspect of the invention.

The nucleic acid sequence may comprise one of the following sequences, or a variant thereof

SEQ ID 35 OR gate
SEQ ID 36 AND gate using CD45
SEQ ID 37 AND gate using CD148
SEQ ID 38 AND NOT gate using PTPN6 as endodomain
SEQ ID 39 AND NOT gate using LAIR1 endodomain
SEQ ID 40 AND NOT gate using LAIR1 and PTPN6 SH2 fusion with CD148 phosphatase

SEQ ID No. 35:
>MP13974.SFG.aCD19fmc63-CD8STK-CD28tmZ-2A-aCD33glx-HCH2CH3pvaa-CD28tmZw

ATGAGCCTGCCCGTGACCGCCCTGCTGCTGCCCCTGGCCCTGCTGCTGCACGCCGCC
AGACCAGACATCCAGATGACCCAGACCACCAGCAGCCTGAGCGCCAGCCTGGGCGAC
CGGGTGACCATCAGCTGCAGAGCCAGCCAGGACATCAGCAAGTACCTGAACTGGTACC
AGCAGAAGCCCGACGGCACCGTGAAGCTGCTGATCTACCACACCAGCCGGCTGCACA
GCGGCGTGCCCAGCCGGTTCAGCGGCAGCGGCAGCGGCACCGACTACAGCCTGACC
ATCAGCAACCTGGAGCAGGAGGACATCGCCACCTACTTCTGCCAGCAGGGCAACACCC
TGCCCTACACCTTCGGAGGCGGCACCAAGCTGGAGATCACCAAGGCCGGAGGCGGAG
GCTCTGGCGGAGGCGGCTCTGGCGGAGGCGGCTCTGGCGGAGGCGGCAGCGAGGT
GAAGCTGCAGGAGTCTGGCCCAGGCCTGGTGGCCCCAAGCCAGAGCCTGAGCGTGAC
CTGCACCGTGAGCGGCGTGAGCCTGCCCGACTACGGCGTGAGCTGGATCAGGCAGCC
CCCACGGAAGGGCCTGGAGTGGCTGGGCGTGATCTGGGGCAGCGAGACCACCTACTA
CAACAGCGCCCTGAAGAGCCGGCTGACCATCATCAAGGACAACAGCAAGAGCCAGGT
GTTCCTGAAGATGAACAGCCTGCAGACCGACGACACCGCCATCTACTACTGCGCCAAG
CACTACTACTATGGCGGCAGCTACGCTATGGACTACTGGGGCCAGGGCACCAGCGTG
ACCGTGAGCTCAGATCCCACCACGACGCCAGCGCCGCGACCACCAACACCGGCGCCC
ACCATCGCGTCGCAGCCCCTGTCCCTGCGCCCAGAGGCGTGCCGGCCAGCGGCGGG
GGGCGCAGTGCACACGAGGGGGCTGGACTTCGCCTGTGATATCTTTTGGGTGCTGGT
GGTGGTTGGTGGAGTCCTGGCTTGCTATAGCTTGCTAGTAACAGTGGCCTTTATTATTT
TCTGGGTGAGGAGAGTGAAGTTCAGCAGGAGCGCAGACGCCCCCGCGTACCAGCAGG
GCCAGAACCAGCTCTATAACGAGCTCAATCTAGGACGAAGAGAGGAGTACGATGTTTT
GGACAAGAGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAGAACC
CTCAGGAAGGCCTGTACAATGAACTGCAGAAAGATAAGATGGCGGAGGCCTACAGTGA
GATTGGGATGAAAGGCGAGCGCCGGAGGGGCAAGGGGCACGATGGCCTTTACCAGG
GTCTCAGTACAGCCACCAAGGACACCTACGACGCCCTTCACATGCAGGCCCTGCCTCC
TCGCAGAGCCGAGGGCAGGGGAAGTCTTCTAACATGCGGGGACGTGGAGGAAAATCC
CGGGCCCATGGCCGTGCCCACTCAGGTCCTGGGGTTGTTGCTACTGTGGCTTACAGAT
GCCAGATGTGACATCCAGATGACACAGTCTCCATCTTCCCTGTCTGCATCTGTCGGAGA
TCGCGTCACCATCACCTGTCGAGCAAGTGAGGACATTTATTTTAATTTAGTGTGGTATCA
GCAGAAACCAGGAAAGGCCCCTAAGCTCCTGATCTATGATACAAATCGCTTGGCAGAT
GGGGTCCCATCACGGTTCAGTGGCTCTGGATCTGGCACACAGTATACTCTAACCATAA
GTAGCCTGCAACCCGAAGATTTCGCAACCTATTATTGTCAACACTATAAGAATTATCCGC
TCACGTTCGGTCAGGGGACCAAGCTGGAAATCAAAAGATCTGGTGGCGGAGGGTCAG
GAGGCGGAGGCAGCGGAGGCGGTGGCTCGGGAGGCGGAGGCTCGAGATCTGAGGTG
CAGTTGGTGGAGTCTGGGGGCGGCTTGGTGCAGCCTGGAGGGTCCCTGAGGCTCTCC
TGTGCAGCCTCAGGATTCACTCTCAGTAATTATGGCATGCACTGGATCAGGCAGGCTC
CAGGGAAGGGTCTGGAGTGGGTCTCGTCTATTAGTCTTAATGGTGGTAGCACTTACTAT
CGAGACTCCGTGAAGGGCCGATTCACTATCTCCAGGGACAATGCAAAAAGCACCCTCT

ACCTTCAAATGAATAGTCTGAGGGCCGAGGACACGGCCGTCTATTACTGTGCAGCACA
GGACGCTTATACGGGAGGTTACTTTGATTACTGGGGCCAAGGAACGCTGGTCACAGTC
TCGTCTATGGATCCCGCCGAGCCCAAATCTCCTGACAAAACTCACACATGCCCACCGT
GCCCAGCACCTCCCGTGGCCGGCCCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGA
CACCCTCATGATCGCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCA
CGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCC
AAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC
ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACA
AAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGA
ACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAG
CCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAG
CAATGGGCAACCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGG
CTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAC
GTCTTCTCATGCTCCGTGATGCATGAGGCCCTGCACAATCACTATACCCAGAAATCTCT
GAGTCTGAGCCCAGGCAAGAAGGACCCCAAGTTCTGGGTCCTGGTGGTGGTGGGAGG
CGTGCTGGCCTGTTACTCTCTCCTGGTGACCGTGGCCTTCATCATCTTTTGGGTGCGCT
CCCGGGTGAAGTTTTCTCGCTCTGCCGATGCCCCAGCCTATCAGCAGGGCCAGAATCA
GCTGTACAATGAACTGAACCTGGGCAGGCGGGAGGAGTACGACGTGCTGGATAAGCG
GAGAGGCAGAGACCCCGAGATGGGCGGCAAACCACGGCGCAAAAATCCCCAGGAGG
GACTCTATAACGAGCTGCAGAAGGACAAAATGGCCGAGGCCTATTCCGAGATCGGCAT
GAAGGGAGAGAGAAGACGCGGAAAGGGCCACGACGGCCTGTATCAGGGATTGTCCAC
CGCTACAAAAGATACATATGATGCCCTGCACATGCAGGCCCTGCCACCCAGATGA

SEQ ID No. 36
>MP14802.SFG.aCD19fmc63_clean-CD8STK-CD28tmZ-2A-aCD33glx-HCH2CH3pvaa-dCD45
ATGAGCCTGCCCGTGACCGCCCTGCTGCTGCCCCTGGCCCTGCTGCTGCACGCCGCC
AGACCAGACATCCAGATGACCCAGACCACCAGCAGCCTGAGCGCCAGCCTGGGCGAC
CGGGTGACCATCAGCTGCAGAGCCAGCCAGGACATCAGCAAGTACCTGAACTGGTACC
AGCAGAAGCCCGACGGCACCGTGAAGCTGCTGATCTACCACACCAGCCGGCTGCACA
GCGGCGTGCCCAGCCGGTTCAGCGGCAGCGGCAGCGGCACCGACTACAGCCTGACC
ATCAGCAACCTGGAGCAGGAGGACATCGCCACCTACTTCTGCCAGCAGGGCAACACCC
TGCCCTACACCTTCGGAGGCGGCACCAAGCTGGAGATCACCAAGGCCGGAGGCGGAG
GCTCTGGCGGAGGCGGCTCTGGCGGAGGCGGCTCTGGCGGAGGCGGCAGCGAGGT
GAAGCTGCAGGAGTCTGGCCCAGGCCTGGTGGCCCCAAGCCAGAGCCTGAGCGTGAC
CTGCACCGTGAGCGGCGTGAGCCTGCCCGACTACGGCGTGAGCTGGATCAGGCAGCC
CCCACGGAAGGGCCTGGAGTGGCTGGGCGTGATCTGGGGCAGCGAGACCACCTACTA

CAACAGCGCCCTGAAGAGCCGGCTGACCATCATCAAGGACAACAGCAAGAGCCAGGT
GTTCCTGAAGATGAACAGCCTGCAGACCGACGACACCGCCATCTACTACTGCGCCAAG
CACTACTACTATGGCGGCAGCTACGCTATGGACTACTGGGGCCAGGGCACCAGCGTG
ACCGTGAGCTCAGATCCCACCACGACGCCAGCGCCGCGACCACCAACACCGGCGCCC
ACCATCGCGTCGCAGCCCCTGTCCCTGCGCCCAGAGGCGTGCCGGCCAGCGGCGGG
GGGCGCAGTGCACACGAGGGGGCTGGACTTCGCCTGTGATATCTTTTGGGTGCTGGT
GGTGGTTGGTGGAGTCCTGGCTTGCTATAGCTTGCTAGTAACAGTGGCCTTTATTATTT
TCTGGGTGAGGAGAGTGAAGTTCAGCAGGAGCGCAGACGCCCCCGCGTACCAGCAGG
GCCAGAACCAGCTCTATAACGAGCTCAATCTAGGACGAAGAGAGGAGTACGATGTTTT
GGACAAGAGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAGAACC
CTCAGGAAGGCCTGTACAATGAACTGCAGAAAGATAAGATGGCGGAGGCCTACAGTGA
GATTGGGATGAAAGGCGAGCGCCGGAGGGGCAAGGGGCACGATGGCCTTTACCAGG
GTCTCAGTACAGCCACCAAGGACACCTACGACGCCCTTCACATGCAGGCCCTGCCTCC
TCGCAGAGCCGAGGGCAGGGGAAGTCTTCTAACATGCGGGGACGTGGAGGAAAATCC
CGGGCCCATGGCCGTGCCCACTCAGGTCCTGGGGTTGTTGCTACTGTGGCTTACAGAT
GCCAGATGTGACATCCAGATGACACAGTCTCCATCTTCCCTGTCTGCATCTGTCGGAGA
TCGCGTCACCATCACCTGTCGAGCAAGTGAGGACATTTATTTTAATTTAGTGTGGTATCA
GCAGAAACCAGGAAAGGCCCCTAAGCTCCTGATCTATGATACAAATCGCTTGGCAGAT
GGGGTCCCATCACGGTTCAGTGGCTCTGGATCTGGCACACAGTATACTCTAACCATAA
GTAGCCTGCAACCCGAAGATTTCGCAACCTATTATTGTCAACACTATAAGAATTATCCGC
TCACGTTCGGTCAGGGGACCAAGCTGGAAATCAAAAGATCTGGTGGCGGAGGGTCAG
GAGGCGGAGGCAGCGGAGGCGGTGGCTCGGGAGGCGGAGGCTCGAGATCTGAGGTG
CAGTTGGTGGAGTCTGGGGGCGGCTTGGTGCAGCCTGGAGGGTCCCTGAGGCTCTCC
TGTGCAGCCTCAGGATTCACTCTCAGTAATTATGGCATGCACTGGATCAGGCAGGCTC
CAGGGAAGGGTCTGGAGTGGGTCTCGTCTATTAGTCTTAATGGTGGTAGCACTTACTAT
CGAGACTCCGTGAAGGGCCGATTCACTATCTCCAGGGACAATGCAAAAAGCACCCTCT
ACCTTCAAATGAATAGTCTGAGGGCCGAGGACACGGCCGTCTATTACTGTGCAGCACA
GGACGCTTATACGGGAGGTTACTTTGATTACTGGGGCCAAGGAACGCTGGTCACAGTC
TCGTCTATGGATCCCGCCGAGCCCAAATCTCCTGACAAAACTCACACATGCCCACCGT
GCCCAGCACCTCCCGTGGCCGGCCCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGA
CACCCTCATGATCGCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCA
CGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCC
AAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC
ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACA
AAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGA
ACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAG
CCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAG

CAATGGGCAACCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGG
CTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAC
GTCTTCTCATGCTCCGTGATGCATGAGGCCCTGCACAATCACTATACCCAGAAATCTCT
GAGTCTGAGCCCAGGCAAGAAGGACCCCAAGGCACTGATAGCATTTCTGGCATTTCTG
ATTATTGTGACATCAATAGCCCTGCTTGTTGTTCTCTACAAAATCTATGATCTACATAAGA
AAAGATCCTGCAATTTAGATGAACAGCAGGAGCTTGTTGAAAGGGATGATGAAAAACAA
CTGATGAATGTGGAGCCAATCCATGCAGATATTTTGTTGGAAACTTATAAGAGGAAGAT
TGCTGATGAAGGAAGACTTTTTCTGGCTGAATTTCAGAGCATCCCGCGGGTGTTCAGCA
AGTTTCCTATAAAGGAAGCTCGAAAGCCCTTTAACCAGAATAAAAACCGTTATGTTGACA
TTCTTCCTTATGATTATAACCGTGTTGAACTCTCTGAGATAAACGGAGATGCAGGGTCAA
ACTACATAAATGCCAGCTATATTGATGGTTTCAAAGAACCCAGGAAATACATTGCTGCAC
AAGGTCCCAGGGATGAAACTGTTGATGATTTCTGGAGGATGATTTGGGAACAGAAAGC
CACAGTTATTGTCATGGTCACTCGATGTGAAGAAGGAAACAGGAACAAGTGTGCAGAAT
ACTGGCCGTCAATGGAAGAGGGCACTCGGGCTTTTGGAGATGTTGTTGTAAAGATCAA
CCAGCACAAAAGATGTCCAGATTACATCATTCAGAAATTGAACATTGTAAATAAAAAAGA
AAAAGCAACTGGAAGAGAGGTGACTCACATTCAGTTCACCAGCTGGCCAGACCACGGG
GTGCCTGAGGATCCTCACTTGCTCCTCAAACTGAGAAGGAGAGTGAATGCCTTCAGCA
ATTTCTTCAGTGGTCCCATTGTGGTGCACTGCAGTGCTGGTGTTGGGCGCACAGGAAC
CTATATCGGAATTGATGCCATGCTAGAAGGCCTGGAAGCCGAGAACAAAGTGGATGTTT
ATGGTTATGTTGTCAAGCTAAGGCGACAGAGATGCCTGATGGTTCAAGTAGAGGCCCA
GTACATCTTGATCCATCAGGCTTTGGTGGAATACAATCAGTTTGGAGAAACAGAAGTGA
ATTTGTCTGAATTACATCCATATCTACATAACATGAAGAAAAGGGATCCACCCAGTGAGC
CGTCTCCACTAGAGGCTGAATTCCAGAGACTTCCTTCATATAGGAGCTGGAGGACACA
GCACATTGGAAATCAAGAAGAAAATAAAAGTAAAAACAGGAATTCTAATGTCATCCCATA
TGACTATAACAGAGTGCCACTTAAACATGAGCTGGAAATGAGTAAAGAGAGTGAGCATG
ATTCAGATGAATCCTCTGATGATGACAGTGATTCAGAGGAACCAAGCAAATACATCAAT
GCATCTTTTATAATGAGCTACTGGAAACCTGAAGTGATGATTGCTGCTCAGGGACCACT
GAAGGAGACCATTGGTGACTTTTGGCAGATGATCTTCCAAAGAAAAGTCAAAGTTATTG
TTATGCTGACAGAACTGAAACATGGAGACCAGGAAATCTGTGCTCAGTACTGGGGAGA
AGGAAAGCAAACATATGGAGATATTGAAGTTGACCTGAAAGACACAGACAAATCTTCAA
CTTATACCCTTCGTGTCTTTGAACTGAGACATTCCAAGAGGAAAGACTCTCGAACTGTG
TACCAGTACCAATATACAAACTGGAGTGTGGAGCAGCTTCCTGCAGAACCCAAGGAATT
AATCTCTATGATTCAGGTCGTCAAACAAAAACTTCCCCAGAAGAATTCCTCTGAAGGGA
ACAAGCATCACAAGAGTACACCTCTACTCATTCACTGCAGGGATGGATCTCAGCAAACG
GGAATATTTTGTGCTTTGTTAAATCTCTTAGAAAGTGCGGAAACAGAAGAGGTAGTGGA
TATTTTTCAAGTGGTAAAAGCTCTACGCAAAGCTAGGCCAGGCATGGTTTCCACATTCG
AGCAATATCAATTCCTATATGACGTCATTGCCAGCACCTACCCTGCTCAGAATGGACAA

GTAAAGAAAAACAACCATCAAGAAGATAAAATTGAATTTGATAATGAAGTGGACAAAGTA
AAGCAGGATGCTAATTGTGTTAATCCACTTGGTGCCCCAGAAAAGCTCCCTGAAGCAAA
GGAACAGGCTGAAGGTTCTGAACCCACGAGTGGCACTGAGGGGCCAGAACATTCTGTC
AATGGTCCTGCAAGTCCAGCTTTAAATCAAGGTTCATAG

SEQ ID No. 37:
>MP14801.SFG.aCD19fmc63_clean-CD8STK-CD28tmZ-2A-aCD33glx-HCH2CH3pvaa-dCD148
ATGAGCCTGCCCGTGACCGCCCTGCTGCTGCCCCTGGCCCTGCTGCTGCACGCCGCC
AGACCAGACATCCAGATGACCCAGACCACCAGCAGCCTGAGCGCCAGCCTGGGCGAC
CGGGTGACCATCAGCTGCAGAGCCAGCCAGGACATCAGCAAGTACCTGAACTGGTACC
AGCAGAAGCCCGACGGCACCGTGAAGCTGCTGATCTACCACACCAGCCGGCTGCACA
GCGGCGTGCCCAGCCGGTTCAGCGGCAGCGGCAGCGGCACCGACTACAGCCTGACC
ATCAGCAACCTGGAGCAGGAGGACATCGCCACCTACTTCTGCCAGCAGGGCAACACCC
TGCCCTACACCTTCGGAGGCGGCACCAAGCTGGAGATCACCAAGGCCGGAGGCGGAG
GCTCTGGCGGAGGCGGCTCTGGCGGAGGCGGCTCTGGCGGAGGCGGCAGCGAGGT
GAAGCTGCAGGAGTCTGGCCCAGGCCTGGTGGCCCCAAGCCAGAGCCTGAGCGTGAC
CTGCACCGTGAGCGGCGTGAGCCTGCCCGACTACGGCGTGAGCTGGATCAGGCAGCC
CCCACGGAAGGGCCTGGAGTGGCTGGGCGTGATCTGGGGCAGCGAGACCACCTACTA
CAACAGCGCCCTGAAGAGCCGGCTGACCATCATCAAGGACAACAGCAAGAGCCAGGT
GTTCCTGAAGATGAACAGCCTGCAGACCGACGACACCGCCATCTACTACTGCGCCAAG
CACTACTACTATGGCGGCAGCTACGCTATGGACTACTGGGGCCAGGGCACCAGCGTG
ACCGTGAGCTCAGATCCCACCACGACGCCAGCGCCGCGACCACCAACACCGGCGCCC
ACCATCGCGTCGCAGCCCCTGTCCCTGCGCCCAGAGGCGTGCCGGCCAGCGGCGGG
GGGCGCAGTGCACACGAGGGGGCTGGACTTCGCCTGTGATATCTTTTGGGTGCTGGT
GGTGGTTGGTGGAGTCCTGGCTTGCTATAGCTTGCTAGTAACAGTGGCCTTTATTATTT
TCTGGGTGAGGAGAGTGAAGTTCAGCAGGAGCGCAGACGCCCCCGCGTACCAGCAGG
GCCAGAACCAGCTCTATAACGAGCTCAATCTAGGACGAAGAGAGGAGTACGATGTTTT
GGACAAGAGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAGAACC
CTCAGGAAGGCCTGTACAATGAACTGCAGAAAGATAAGATGGCGGAGGCCTACAGTGA
GATTGGGATGAAAGGCGAGCGCCGGAGGGGCAAGGGGCACGATGGCCTTTACCAGG
GTCTCAGTACAGCCACCAAGGACACCTACGACGCCCTTCACATGCAGGCCCTGCCTCC
TCGCAGAGCCGAGGGCAGGGGAAGTCTTCTAACATGCGGGGACGTGGAGGAAAATCC
CGGGCCCATGGCCGTGCCCACTCAGGTCCTGGGGTTGTTGCTACTGTGGCTTACAGAT
GCCAGATGTGACATCCAGATGACACAGTCTCCATCTTCCCTGTCTGCATCTGTCGGAGA
TCGCGTCACCATCACCTGTCGAGCAAGTGAGGACATTTATTTTAATTTAGTGTGGTATCA
GCAGAAACCAGGAAAGGCCCCTAAGCTCCTGATCTATGATACAAATCGCTTGGCAGAT

GGGGTCCCATCACGGTTCAGTGGCTCTGGATCTGGCACACAGTATACTCTAACCATAA
GTAGCCTGCAACCCGAAGATTTCGCAACCTATTATTGTCAACACTATAAGAATTATCCGC
TCACGTTCGGTCAGGGGACCAAGCTGGAAATCAAAAGATCTGGTGGCGGAGGGTCAG
GAGGCGGAGGCAGCGGAGGCGGTGGCTCGGGAGGCGGAGGCTCGAGATCTGAGGTG
CAGTTGGTGGAGTCTGGGGGCGGCTTGGTGCAGCCTGGAGGGTCCCTGAGGCTCTCC
TGTGCAGCCTCAGGATTCACTCTCAGTAATTATGGCATGCACTGGATCAGGCAGGCTC
CAGGGAAGGGTCTGGAGTGGGTCTCGTCTATTAGTCTTAATGGTGGTAGCACTTACTAT
CGAGACTCCGTGAAGGGCCGATTCACTATCTCCAGGGACAATGCAAAAAGCACCCTCT
ACCTTCAAATGAATAGTCTGAGGGCCGAGGACACGGCCGTCTATTACTGTGCAGCACA
GGACGCTTATACGGGAGGTTACTTTGATTACTGGGGCCAAGGAACGCTGGTCACAGTC
TCGTCTATGGATCCCGCCGAGCCCAAATCTCCTGACAAAACTCACACATGCCCACCGT
GCCCAGCACCTCCCGTGGCCGGCCCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGA
CACCCTCATGATCGCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCA
CGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCC
AAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC
ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACA
AAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGA
ACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAG
CCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAG
CAATGGGCAACCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGG
CTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAC
GTCTTCTCATGCTCCGTGATGCATGAGGCCCTGCACAATCACTATACCCAGAAATCTCT
GAGTCTGAGCCCAGGCAAGAAGGACCCCAAGGCGGTTTTTGGCTGTATCTTTGGTGCC
CTGGTTATTGTGACTGTGGGAGGCTTCATCTTCTGGAGAAAGAAGAGGAAAGATGCAAA
GAATAATGAAGTGTCCTTTTCTCAAATTAAACCTAAAAAATCTAAGTTAATCAGAGTGGA
GAATTTTGAGGCCTACTTCAAGAAGCAGCAAGCTGACTCCAACTGTGGGTTCGCAGAG
GAATACGAAGATCTGAAGCTTGTTGGAATTAGTCAACCTAAATATGCAGCAGAACTGGC
TGAGAATAGAGGAAAGAATCGCTATAATAATGTTCTGCCCTATGATATTTCCCGTGTCAA
ACTTTCGGTCCAGACCCATTCAACGGATGACTACATCAATGCCAACTACATGCCTGGCT
ACCACTCCAAGAAAGATTTTATTGCCACACAAGGACCTTTACCGAACACTTTGAAAGATT
TTTGGCGTATGGTTTGGGAGAAAAATGTATATGCCATCATTATGTTGACTAAATGTGTTG
AACAGGGAAGAACCAAATGTGAGGAGTATTGGCCCTCCAAGCAGGCTCAGGACTATGG
AGACATAACTGTGGCAATGACATCAGAAATTGTTCTTCCGGAATGGACCATCAGAGATT
TCACAGTGAAAAATATCCAGACAAGTGAGAGTCACCCTCTGAGACAGTTCCATTTCACC
TCCTGGCCAGACCACGGTGTTCCCGACACCACTGACCTGCTCATCAACTTCCGGTACC
TCGTTCGTGACTACATGAAGCAGAGTCCTCCCGAATCGCCGATTCTGGTGCATTGCAGT
GCTGGGGTCGGAAGGACGGGCACTTTCATTGCCATTGATCGTCTCATCTACCAGATAG

AGAATGAGAACACCGTGGATGTGTATGGGATTGTGTATGACCTTCGAATGCATAGGCCT
TTAATGGTGCAGACAGAGGACCAGTATGTTTTCCTCAATCAGTGTGTTTTGGATATTGTC
AGATCCCAGAAAGACTCAAAAGTAGATCTTATCTACCAGAACACAACTGCAATGACAAT
CTATGAAAACCTTGCGCCCGTGACCACATTTGGAAAGACCAATGGTTACATCGCCTAA

SEQ ID No. 38
>16076.SFG.aCD19fmc63-CD8STK-CD28tmZ-2A-aCD33glx-muCD8STK-tm-dPTPN6
ATGAGCCTGCCCGTGACCGCCCTGCTGCTGCCCCTGGCCCTGCTGCTGCACGCCGCC
AGACCAGACATCCAGATGACCCAGACCACCAGCAGCCTGAGCGCCAGCCTGGGCGAC
CGGGTGACCATCAGCTGCAGAGCCAGCCAGGACATCAGCAAGTACCTGAACTGGTACC
AGCAGAAGCCCGACGGCACCGTGAAGCTGCTGATCTACCACACCAGCCGGCTGCACA
GCGGCGTGCCCAGCCGGTTCAGCGGCAGCGGCAGCGGCACCGACTACAGCCTGACC
ATCAGCAACCTGGAGCAGGAGGACATCGCCACCTACTTCTGCCAGCAGGGCAACACCC
TGCCCTACACCTTCGGAGGCGGCACCAAGCTGGAGATCACCAAGGCCGGAGGCGGAG
GCTCTGGCGGAGGCGGCTCTGGCGGAGGCGGCTCTGGCGGAGGCGGCAGCGAGGT
GAAGCTGCAGGAGTCTGGCCCAGGCCTGGTGGCCCCAAGCCAGAGCCTGAGCGTGAC
CTGCACCGTGAGCGGCGTGAGCCTGCCCGACTACGGCGTGAGCTGGATCAGGCAGCC
CCCACGGAAGGGCCTGGAGTGGCTGGGCGTGATCTGGGGCAGCGAGACCACCTACTA
CAACAGCGCCCTGAAGAGCCGGCTGACCATCATCAAGGACAACAGCAAGAGCCAGGT
GTTCCTGAAGATGAACAGCCTGCAGACCGACGACACCGCCATCTACTACTGCGCCAAG
CACTACTACTATGGCGGCAGCTACGCTATGGACTACTGGGGCCAGGGCACCAGCGTG
ACCGTGAGCTCAGATCCCACCACGACGCCAGCGCCGCGACCACCAACACCGGCGCCC
ACCATCGCGTCGCAGCCCCTGTCCCTGCGCCCAGAGGCGTGCCGGCCAGCGGCGGG
GGGCGCAGTGCACACGAGGGGGCTGGACTTCGCCTGTGATATCTTTTGGGTGCTGGT
GGTGGTTGGTGGAGTCCTGGCTTGCTATAGCTTGCTAGTAACAGTGGCCTTTATTATTT
TCTGGGTGAGGAGAGTGAAGTTCAGCAGGAGCGCAGACGCCCCCGCGTACCAGCAGG
GCCAGAACCAGCTCTATAACGAGCTCAATCTAGGACGAAGAGAGGAGTACGATGTTTT
GGACAAGAGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAGAACC
CTCAGGAAGGCCTGTACAATGAACTGCAGAAAGATAAGATGGCGGAGGCCTACAGTGA
GATTGGGATGAAAGGCGAGCGCCGGAGGGGCAAGGGGCACGATGGCCTTTACCAGG
GTCTCAGTACAGCCACCAAGGACACCTACGACGCCCTTCACATGCAGGCCCTGCCTCC
TCGCAGAGCCGAGGGCAGGGGAAGTCTTCTAACATGCGGGGACGTGGAGGAAAATCC
CGGGCCCATGGCCGTGCCCACTCAGGTCCTGGGGTTGTTGCTACTGTGGCTTACAGAT
GCCAGATGTGACATCCAGATGACACAGTCTCCATCTTCCCTGTCTGCATCTGTCGGAGA
TCGCGTCACCATCACCTGTCGAGCAAGTGAGGACATTTATTTTAATTTAGTGTGGTATCA
GCAGAAACCAGGAAAGGCCCCTAAGCTCCTGATCTATGATACAAATCGCTTGGCAGAT
GGGGTCCCATCACGGTTCAGTGGCTCTGGATCTGGCACACAGTATACTCTAACCATAA

GTAGCCTGCAACCCGAAGATTTCGCAACCTATTATTGTCAACACTATAAGAATTATCCGC
TCACGTTCGGTCAGGGGACCAAGCTGGAAATCAAAAGATCTGGTGGCGGAGGGTCAG
GAGGCGGAGGCAGCGGAGGCGGTGGCTCGGGAGGCGGAGGCTCGAGATCTGAGGTG
CAGTTGGTGGAGTCTGGGGGCGGCTTGGTGCAGCCTGGAGGGTCCCTGAGGCTCTCC
TGTGCAGCCTCAGGATTCACTCTCAGTAATTATGGCATGCACTGGATCAGGCAGGCTC
CAGGGAAGGGTCTGGAGTGGGTCTCGTCTATTAGTCTTAATGGTGGTAGCACTTACTAT
CGAGACTCCGTGAAGGGCCGATTCACTATCTCCAGGGACAATGCAAAAAGCACCCTCT
ACCTTCAAATGAATAGTCTGAGGGCCGAGGACACGGCCGTCTATTACTGTGCAGCACA
GGACGCTTATACGGGAGGTTACTTTGATTACTGGGGCCAAGGAACGCTGGTCACAGTC
TCGTCTATGGATCCCGCCACCACAACCAAGCCCGTGCTGCGGACCCCAAGCCCTGTGC
ACCCTACCGGCACCAGCCAGCCTCAGAGACCCGAGGACTGCCGGCCTCGGGGCAGC
GTGAAGGGCACCGGCCTGGACTTCGCCTGCGACATCTACTGGGCACCTCTGGCCGGA
ATATGCGTGGCACTGCTGCTGAGCCTCATCATCACCCTGATCTGTTATCACCGAAGCCG
CAAGCGGGTGTGTAAAAGTGGAGGCGGAAGCTTCTGGGAGGAGTTTGAGAGTTTGCA
GAAGCAGGAGGTGAAGAACTTGCACCAGCGTCTGGAAGGGCAGCGGCCAGAGAACAA
GGGCAAGAACCGCTACAAGAACATTCTCCCCTTTGACCACAGCCGAGTGATCCTGCAG
GGACGGGACAGTAACATCCCCGGGTCCGACTACATCAATGCCAACTACATCAAGAACC
AGCTGCTAGGCCCTGATGAGAACGCTAAGACCTACATCGCCAGCCAGGGCTGTCTGGA
GGCCACGGTCAATGACTTCTGGCAGATGGCGTGGCAGGAGAACAGCCGTGTCATCGT
CATGACCACCCGAGAGGTGGAGAAAGGCCGGAACAAATGCGTCCCATACTGGCCCGA
GGTGGGCATGCAGCGTGCTTATGGGCCCTACTCTGTGACCAACTGCGGGGAGCATGA
CACAACCGAATACAAACTCCGTACCTTACAGGTCTCCCCGCTGGACAATGGAGACCTG
ATTCGGGAGATCTGGCATTACCAGTACCTGAGCTGGCCCGACCACGGGGTCCCCAGT
GAGCCTGGGGGTGTCCTCAGCTTCCTGGACCAGATCAACCAGCGGCAGGAAAGTCTG
CCTCACGCAGGGCCCATCATCGTGCACTGCAGCGCCGGCATCGGCCGCACAGGCACC
ATCATTGTCATCGACATGCTCATGGAGAACATCTCCACCAAGGGCCTGGACTGTGACAT
TGACATCCAGAAGACCATCCAGATGGTGCGGGCGCAGCGCTCGGGCATGGTGCAGAC
GGAGGCGCAGTACAAGTTCATCTACGTGGCCATCGCCCAGTTCATTGAAACCACTAAG
AAGAAGCTGTGA

SEQ ID No. 39

>MP16091.SFG.aCD19fmc63-CD8STK-CD28tmZ-2A-aCD33glx-muCD8STK-LAIR1tm-endo

ATGAGCCTGCCCGTGACCGCCCTGCTGCTGCCCCTGGCCCTGCTGCTGCACGCCGCC
AGACCAGACATCCAGATGACCCAGACCACCAGCAGCCTGAGCGCCAGCCTGGGCGAC
CGGGTGACCATCAGCTGCAGAGCCAGCCAGGACATCAGCAAGTACCTGAACTGGTACC
AGCAGAAGCCCGACGGCACCGTGAAGCTGCTGATCTACCACACCAGCCGGCTGCACA
GCGGCGTGCCCAGCCGGTTCAGCGGCAGCGGCAGCGGCACCGACTACAGCCTGACC

ATCAGCAACCTGGAGCAGGAGGACATCGCCACCTACTTCTGCCAGCAGGGCAACACCC
TGCCCTACACCTTCGGAGGCGGCACCAAGCTGGAGATCACCAAGGCCGGAGGCGGAG
GCTCTGGCGGAGGCGGCTCTGGCGGAGGCGGCTCTGGCGGAGGCGGCAGCGAGGT
GAAGCTGCAGGAGTCTGGCCCAGGCCTGGTGGCCCCAAGCCAGAGCCTGAGCGTGAC
CTGCACCGTGAGCGGCGTGAGCCTGCCCGACTACGGCGTGAGCTGGATCAGGCAGCC
CCCACGGAAGGGCCTGGAGTGGCTGGGCGTGATCTGGGGCAGCGAGACCACCTACTA
CAACAGCGCCCTGAAGAGCCGGCTGACCATCATCAAGGACAACAGCAAGAGCCAGGT
GTTCCTGAAGATGAACAGCCTGCAGACCGACGACACCGCCATCTACTACTGCGCCAAG
CACTACTACTATGGCGGCAGCTACGCTATGGACTACTGGGGCCAGGGCACCAGCGTG
ACCGTGAGCTCAGATCCCACCACGACGCCAGCGCCGCGACCACCAACACCGGCGCCC
ACCATCGCGTCGCAGCCCCTGTCCCTGCGCCCAGAGGCGTGCCGGCCAGCGGCGGG
GGGCGCAGTGCACACGAGGGGGCTGGACTTCGCCTGTGATATCTTTTGGGTGCTGGT
GGTGGTTGGTGGAGTCCTGGCTTGCTATAGCTTGCTAGTAACAGTGGCCTTTATTATTT
TCTGGGTGAGGAGAGTGAAGTTCAGCAGGAGCGCAGACGCCCCCGCGTACCAGCAGG
GCCAGAACCAGCTCTATAACGAGCTCAATCTAGGACGAAGAGAGGAGTACGATGTTTT
GGACAAGAGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAGAACC
CTCAGGAAGGCCTGTACAATGAACTGCAGAAAGATAAGATGGCGGAGGCCTACAGTGA
GATTGGGATGAAAGGCGAGCGCCGGAGGGGCAAGGGGCACGATGGCCTTTACCAGG
GTCTCAGTACAGCCACCAAGGACACCTACGACGCCCTTCACATGCAGGCCCTGCCTCC
TCGCAGAGCCGAGGGCAGGGGAAGTCTTCTAACATGCGGGGACGTGGAGGAAAATCC
CGGGCCCATGGCCGTGCCCACTCAGGTCCTGGGGTTGTTGCTACTGTGGCTTACAGAT
GCCAGATGTGACATCCAGATGACACAGTCTCCATCTTCCCTGTCTGCATCTGTCGGAGA
TCGCGTCACCATCACCTGTCGAGCAAGTGAGGACATTTATTTTAATTTAGTGTGGTATCA
GCAGAAACCAGGAAAGGCCCCTAAGCTCCTGATCTATGATACAAATCGCTTGGCAGAT
GGGGTCCCATCACGGTTCAGTGGCTCTGGATCTGGCACACAGTATACTCTAACCATAA
GTAGCCTGCAACCCGAAGATTTCGCAACCTATTATTGTCAACACTATAAGAATTATCCGC
TCACGTTCGGTCAGGGGACCAAGCTGGAAATCAAAAGATCTGGTGGCGGAGGGTCAG
GAGGCGGAGGCAGCGGAGGCGGTGGCTCGGGAGGCGGAGGCTCGAGATCTGAGGTG
CAGTTGGTGGAGTCTGGGGGCGGCTTGGTGCAGCCTGGAGGGTCCCTGAGGCTCTCC
TGTGCAGCCTCAGGATTCACTCTCAGTAATTATGGCATGCACTGGATCAGGCAGGCTC
CAGGGAAGGGTCTGGAGTGGGTCTCGTCTATTAGTCTTAATGGTGGTAGCACTTACTAT
CGAGACTCCGTGAAGGGCCGATTCACTATCTCCAGGGACAATGCAAAAAGCACCCTCT
ACCTTCAAATGAATAGTCTGAGGGCCGAGGACACGGCCGTCTATTACTGTGCAGCACA
GGACGCTTATACGGGAGGTTACTTTGATTACTGGGGCCAAGGAACGCTGGTCACAGTC
TCGTCTATGGATCCCGCCACCACAACCAAGCCCGTGCTGCGGACCCCAAGCCCTGTGC
ACCCTACCGGCACCAGCCAGCCTCAGAGACCCGAGGACTGCCGGCCTCGGGGCAGC
GTGAAGGGCACCGGCCTGGACTTCGCCTGCGACATTCTCATCGGGGTCTCAGTGGTCT

TCCTCTTCTGTCTCCTCCTCCTGGTCCTCTTCTGCCTCCATCGCCAGAATCAGATAAAG
CAGGGGCCCCCCAGAAGCAAGGACGAGGAGCAGAAGCCACAGCAGAGGCCTGACCT
GGCTGTTGATGTTCTAGAGAGGACAGCAGACAAGGCCACAGTCAATGGACTTCCTGAG
AAGGACCGGGAGACCGACACCAGCGCCCTGGCTGCAGGGAGTTCCCAGGAGGTGAC
GTATGCTCAGCTGGACCACTGGGCCCTCACACAGAGGACAGCCCGGGCTGTGTCCCC
ACAGTCCACAAAGCCCATGGCCGAGTCCATCACGTATGCAGCCGTTGCCAGACACTGA

SEQ ID no. 40
>MP16092.SFG.aCD19fmc63-CD8STK-CD28tmZ-2A-aCD33glx-muCD8STK-LAIR1tm-endo-2A-PTPN6_SH2-dCD148

ATGAGCCTGCCCGTGACCGCCCTGCTGCTGCCCCTGGCCCTGCTGCTGCACGCCGCC
AGACCAGACATCCAGATGACCCAGACCACCAGCAGCCTGAGCGCCAGCCTGGGCGAC
CGGGTGACCATCAGCTGCAGAGCCAGCCAGGACATCAGCAAGTACCTGAACTGGTACC
AGCAGAAGCCCGACGGCACCGTGAAGCTGCTGATCTACCACACCAGCCGGCTGCACA
GCGGCGTGCCCAGCCGGTTCAGCGGCAGCGGCAGCGGCACCGACTACAGCCTGACC
ATCAGCAACCTGGAGCAGGAGGACATCGCCACCTACTTCTGCCAGCAGGGCAACACCC
TGCCCTACACCTTCGGAGGCGGCACCAAGCTGGAGATCACCAAGGCCGGAGGCGGAG
GCTCTGGCGGAGGCGGCTCTGGCGGAGGCGGCTCTGGCGGAGGCGGCAGCGAGGT
GAAGCTGCAGGAGTCTGGCCCAGGCCTGGTGGCCCCAAGCCAGAGCCTGAGCGTGAC
CTGCACCGTGAGCGGCGTGAGCCTGCCCGACTACGGCGTGAGCTGGATCAGGCAGCC
CCCACGGAAGGGCCTGGAGTGGCTGGGCGTGATCTGGGGCAGCGAGACCACCTACTA
CAACAGCGCCCTGAAGAGCCGGCTGACCATCATCAAGGACAACAGCAAGAGCCAGGT
GTTCCTGAAGATGAACAGCCTGCAGACCGACGACACCGCCATCTACTACTGCGCCAAG
CACTACTACTATGGCGGCAGCTACGCTATGGACTACTGGGGCCAGGGCACCAGCGTG
ACCGTGAGCTCAGATCCCACCACGACGCCAGCGCCGCGACCACCAACACCGGCGCCC
ACCATCGCGTCGCAGCCCCTGTCCCTGCGCCCAGAGGCGTGCCGGCCAGCGGCGGG
GGGCGCAGTGCACACGAGGGGGCTGGACTTCGCCTGTGATATCTTTTGGGTGCTGGT
GGTGGTTGGTGGAGTCCTGGCTTGCTATAGCTTGCTAGTAACAGTGGCCTTTATTATTT
TCTGGGTGAGGAGAGTGAAGTTCAGCAGGAGCGCAGACGCCCCCGCGTACCAGCAGG
GCCAGAACCAGCTCTATAACGAGCTCAATCTAGGACGAAGAGAGGAGTACGATGTTTT
GGACAAGAGACGTGGCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAGAACC
CTCAGGAAGGCCTGTACAATGAACTGCAGAAAGATAAGATGGCGGAGGCCTACAGTGA
GATTGGGATGAAAGGCGAGCGCCGGAGGGGCAAGGGGCACGATGGCCTTTACCAGG
GTCTCAGTACAGCCACCAAGGACACCTACGACGCCCTTCACATGCAGGCCCTGCCTCC
TCGCAGAGCCGAGGGCAGGGGAAGTCTTCTAACATGCGGGGACGTGGAGGAAAATCC
CGGGCCCATGGCCGTGCCCACTCAGGTCCTGGGGTTGTTGCTACTGTGGCTTACAGAT
GCCAGATGTGACATCCAGATGACACAGTCTCCATCTTCCCTGTCTGCATCTGTCGGAGA

TCGCGTCACCATCACCTGTCGAGCAAGTGAGGACATTTATTTTAATTTAGTGTGGTATCA
GCAGAAACCAGGAAAGGCCCCTAAGCTCCTGATCTATGATACAAATCGCTTGGCAGAT
GGGGTCCCATCACGGTTCAGTGGCTCTGGATCTGGCACACAGTATACTCTAACCATAA
GTAGCCTGCAACCCGAAGATTTCGCAACCTATTATTGTCAACACTATAAGAATTATCCGC
TCACGTTCGGTCAGGGGACCAAGCTGGAAATCAAAAGATCTGGTGGCGGAGGGTCAG
GAGGCGGAGGCAGCGGAGGCGGTGGCTCGGGAGGCGGAGGCTCGAGATCTGAGGTG
CAGTTGGTGGAGTCTGGGGGCGGCTTGGTGCAGCCTGGAGGGTCCCTGAGGCTCTCC
TGTGCAGCCTCAGGATTCACTCTCAGTAATTATGGCATGCACTGGATCAGGCAGGCTC
CAGGGAAGGGTCTGGAGTGGGTCTCGTCTATTAGTCTTAATGGTGGTAGCACTTACTAT
CGAGACTCCGTGAAGGGCCGATTCACTATCTCCAGGGACAATGCAAAAAGCACCCTCT
ACCTTCAAATGAATAGTCTGAGGGCCGAGGACACGGCCGTCTATTACTGTGCAGCACA
GGACGCTTATACGGGAGGTTACTTTGATTACTGGGGCCAAGGAACGCTGGTCACAGTC
TCGTCTATGGATCCCGCCACCACAACCAAGCCCGTGCTGCGGACCCCAAGCCCTGTGC
ACCCTACCGGCACCAGCCAGCCTCAGAGACCCGAGGACTGCCGGCCTCGGGGCAGC
GTGAAGGGCACCGGCCTGGACTTCGCCTGCGACATTCTCATCGGGGTCTCAGTGGTCT
TCCTCTTCTGTCTCCTCCTCCTGGTCCTCTTCTGCCTCCATCGCCAGAATCAGATAAAG
CAGGGGCCCCCCAGAAGCAAGGACGAGGAGCAGAAGCCACAGCAGAGGCCTGACCT
GGCTGTTGATGTTCTAGAGAGGACAGCAGACAAGGCCACAGTCAATGGACTTCCTGAG
AAGGACCGGGAGACCGACACCAGCGCCCTGGCTGCAGGGAGTTCCCAGGAGGTGAC
GTATGCTCAGCTGGACCACTGGGCCCTCACACAGAGGACAGCCCGGGCTGTGTCCCC
ACAGTCCACAAAGCCCATGGCCGAGTCCATCACGTATGCAGCCGTTGCCAGACACAGG
GCAGAAGGAAGAGGTAGCCTGCTGACTTGCGGGGACGTGGAAGAGAACCCAGGGCCA
TGGTATCATGGCCACATGTCTGGCGGGCAGGCAGAGACGCTGCTGCAGGCCAAGGGC
GAGCCCTGGACGTTTCTTGTGCGTGAGAGCCTCAGCCAGCCTGGAGACTTCGTGCTTT
CTGTGCTCAGTGACCAGCCCAAGGCTGGCCCAGGCTCCCCGCTCAGGGTCACCCACA
TCAAGGTCATGTGCGAGGGTGGACGCTACACAGTGGGTGGTTTGGAGACCTTCGACAG
CCTCACGGACCTGGTGGAGCATTTCAAGAAGACGGGGATTGAGGAGGCCTCAGGCGC
CTTTGTCTACCTGCGGCAGCCGTACAGCGGTGGCGGTGGCAGCTTTGAGGCCTACTTC
AAGAAGCAGCAAGCTGACTCCAACTGTGGGTTCGCAGAGGAATACGAAGATCTGAAGC
TTGTTGGAATTAGTCAACCTAAATATGCAGCAGAACTGGCTGAGAATAGAGGAAAGAAT
CGCTATAATAATGTTCTGCCCTATGATATTTCCCGTGTCAAACTTTCGGTCCAGACCCAT
TCAACGGATGACTACATCAATGCCAACTACATGCCTGGCTACCACTCCAAGAAAGATTT
TATTGCCACACAAGGACCTTTACCGAACACTTTGAAAGATTTTTGGCGTATGGTTTGGG
AGAAAAATGTATATGCCATCATTATGTTGACTAAATGTGTTGAACAGGGAAGAACCAAAT
GTGAGGAGTATTGGCCCTCCAAGCAGGCTCAGGACTATGGAGACATAACTGTGGCAAT
GACATCAGAAATTGTTCTTCCGGAATGGACCATCAGAGATTTCACAGTGAAAAATATCC
AGACAAGTGAGAGTCACCCTCTGAGACAGTTCCATTTCACCTCCTGGCCAGACCACGG

TGTTCCCGACACCACTGACCTGCTCATCAACTTCCGGTACCTCGTTCGTGACTACATGA
AGCAGAGTCCTCCCGAATCGCCGATTCTGGTGCATTGCAGTGCTGGGGTCGGAAGGA
CGGGCACTTTCATTGCCATTGATCGTCTCATCTACCAGATAGAGAATGAGAACACCGTG
GATGTGTATGGGATTGTGTATGACCTTCGAATGCATAGGCCTTTAATGGTGCAGACAGA
GGACCAGTATGTTTTCCTCAATCAGTGTGTTTTGGATATTGTCAGATCCCAGAAAGACTC
AAAAGTAGATCTTATCTACCAGAACACAACTGCAATGACAATCTATGAAAACCTTGCGCC
CGTGACCACATTTGGAAAGACCAATGGTTACATCGCCAGCGGTAGCTAA

The nucleic acid sequence may encode the same amino acid sequence as that encoded by SEQ ID No. 35, 36, 37, 38, 39 or 40, but may have a different nucleic acid sequence, due to the degeneracy of the genetic code. The nucleic acid sequence may have at least 80, 85, 90, 95, 98 or 99% identity to the sequence shown as SEQ ID No. 35, 36, 37, 38, 39 or 40, provided that it encodes a first CAR and a second CAR as defined in the first aspect of the invention.

VECTOR

The present invention also provides a vector, or kit of vectors which comprises one or more CAR-encoding nucleic acid sequence(s). Such a vector may be used to introduce the nucleic acid sequence(s) into a host cell so that it expresses the first and second CARs.

The vector may, for example, be a plasmid or a viral vector, such as a retroviral vector or a lentiviral vector, or a transposon based vector or synthetic mRNA.

The vector may be capable of transfecting or transducing a T cell.

PHARMACEUTICAL COMPOSITION

The present invention also relates to a pharmaceutical composition containing a plurality of CAR-expressing cells, such as T cells or NK cells according to the first aspect of the invention. The pharmaceutical composition may additionally comprise a pharmaceutically acceptable carrier, diluent or excipient. The pharmaceutical composition may optionally comprise one or more further pharmaceutically active polypeptides and/or compounds. Such a formulation may, for example, be in a form suitable for intravenous infusion.

METHOD OF TREATMENT

The T cells of the present invention may be capable of killing target cells, such as cancer cells. The target cell may be recognisable by a defined pattern of antigen expression, for example the expression of antigen A AND antigen B; the expression of antigen A OR antigen B; or the expression of antigen A AND NOT antigen B or complex iterations of these gates.

T cells of the present invention may be used for the treatment of an infection, such as a viral infection.

T cells of the invention may also be used for the control of pathogenic immune responses, for example in autoimmune diseases, allergies and graft-vs-host rejection.

T cells of the invention may be used for the treatment of a cancerous disease, such as bladder cancer, breast cancer, colon cancer, endometrial cancer, kidney cancer (renal cell), leukemia, lung cancer, melanoma, non-Hodgkin lymphoma, pancreatic cancer, prostate cancer and thyroid cancer.

It is particularly suited for treatment of solid tumours where the availability of good selective single targets is limited.

T cells of the invention may be used to treat: cancers of the oral cavity and pharynx which includes cancer of the tongue, mouth and pharynx; cancers of the digestive system which includes oesophageal, gastric and colorectal cancers; cancers of the liver and biliary tree which includes hepatocellular carcinomas and cholangiocarcinomas; cancers of the respiratory system which includes bronchogenic cancers and cancers of the larynx; cancers of bone and joints which includes osteosarcoma; cancers of the skin which includes melanoma; breast cancer; cancers of the genital tract which include uterine, ovarian and cervical cancer in women, prostate and testicular cancer in men; cancers of the renal tract which include renal cell carcinoma and transitional cell carcinomas of the utterers or bladder; brain cancers including gliomas, glioblastoma multiforme and medullobastomas; cancers of the endocrine system including thyroid cancer, adrenal carcinoma and cancers associated with multiple endocrine neoplasm syndromes; lymphomas including Hodgkin's lymphoma and non-Hodgkin lymphoma; Multiple Myeloma and plasmacytomas; leukaemias both acute and chronic, myeloid or lymphoid; and cancers of other and unspecified sites including neuroblastoma.

Treatment with the T cells of the invention may help prevent the escape or release of tumour cells which often occurs with standard approaches.

The invention will now be further described by way of Examples, which are meant to serve to assist one of ordinary skill in the art in carrying out the invention and are not intended in any way to limit the scope of the invention.

EXAMPLES

Example 1 - Creation of target cell populations

For the purposes of proving the principle of the invention, receptors based on anti-CD19 and anti-CD33 were arbitrarily chosen. Using retroviral vectors, CD19 and CD33 were cloned. These proteins were truncated so that they do not signal and could be stably expressed for prolonged periods. Next, these vectors were used to transduce the SupT1 cell line either singly or doubly to establish cells negative for both antigen (the wild-type), positive for either and positive for both. The expression data are shown in Figure 3.

Example 2 - Design and function of the OR gate

To construct the OR gate, a pair of receptors recognizing CD19 and CD33 were co-expressed. Different spacers were used to prevent cross-pairing. Both receptors had a trans-membrane domain derived from CD28 to improve surface stability and an endodomain derived from that of CD3 Zeta to provide a simple activating signal. In this way, a pair of independent 1st generation CARs were co-expressed. The retroviral vector cassette used to co-express the sequences utilizes a foot-and-mouth 2A self-cleaving peptide to allow co-expression 1:1 of both receptors. The cassette design is shown in Figure 4, and the protein structures in Figure 5. The nucleotide sequence of homologous regions was codon-wobbled to prevent recombination during retroviral vector reverse transcription.

Example 3 - Testing the OR gate

Expression of both CARs was tested on the T-cell surface by staining with cognate antigen fused to Fc. By using different species of Fc domains (mouse for CD19 and rabbit for CD33), co-expression of both CARs was determined on the cell surface by staining with

different secondary antibodies conjugated with different fluorophores. This is shown in Figure 6.

Functional testing was then carried out using the mouse T-cell line BW5147. This cell line releases IL2 upon activation allowing a simple quantitative readout. These T-cells were co-cultured with increasing amounts of the artificial target cells described above. T-cells responded to target cells expressing either antigen, as shown by IL2 release measured by ELISA. Both CARs were shown to be expressed on the cell surfaces and the T-cells were shown to respond to either or both antigens. These data are show in Figure 7.

Example 4 - Design and function of the AND gate

The AND gate combines a simple activating receptor with a receptor which basally inhibits activity, but whose inhibition is turned off once the receptor is ligated. This was achieved by combining a standard 1st generation CAR with a short / non-bulky CD8 stalk spacer and a CD3 Zeta endodomain with a second receptor with a bulky Fc spacer whose endodomain contained either CD148 or CD45 endodomains. When both receptors are ligated, the difference in spacer dimensions results in isolation of the different receptors in different membrane compartments, releasing the CD3 Zeta receptor from inhibition by the CD148 or CD45 endodomains. In this way, activation only occurs once both receptors are activated. CD148 and CD45 were chosen for this as they function in this manner natively: for instance, the very bulky CD45 ectodomain excludes the entire receptor from the immunological synapse. The expression cassette is depicted in Figure 8 and the subsequent proteins in Figure 9.

Surface staining for the different specificity showed that both receptor pairs could be effectively expressed on the cell surface shown in Figure 10. Function in BW5147 shows that the T-cell is only activated in the presence of both antigens (Figure 11).

Example 5: Demonstration of Generalizability of the AND gate

To ensure that the observations were not a manifestation of some specific characteristic of CD19 / CD33 and their binders which had been used, the two targeting scFvs were swapped such that now, the activation (ITAM) signal was transmitted upon recognition of CD33, rather than CD19; and the inhibitory (CD148) signal was transmitted upon recognition of CD19, rather than of CD33. Since CD45 and CD148 endodomains are considered to be functionally similar, experimentation was restricted to AND gates with CD148 endodomain. This should

still result in a functional AND gate. T-cells expressing the new logic gate where challenged with targets bearing either CD19 or CD33 alone, or both. The T-cells responded to targets expressing both CD19 and CD33, but not to targets expressing only one or none of these antigens. This shows that the AND gate is still functional in this format (Figure 18B).

On the same lines, it was sought to establish how generalizable our AND gate is: the AND gate should be generalizable across different targets. While there may be lesser or greater fidelity of the gate given relative antigen density, cognate scFv binding kinetics and precise distance of the scFv binding epitope, one would expect to see some AND gate manifestations with a wide set of targets and binders. To test this, three additional AND gates were generated. Once again, experimentation was restricted to the CD148 version of the AND gate. The second scFv from the original CD148 AND gate was replaced with the anti-GD2 scFv huK666 (SEQ ID 41 and SEQ ID 42), or with the anti-CD5 scFv (SEQ ID 43 and SEQ ID 44), or the anti-EGFRvIII scFv MR1.1 (SEQ ID 45 AND SEQ ID 46) to generate the following CAR AND gates: CD19 AND GD2; CD19 AND CD5; CD19 AND EGFRvIII. The following artificial antigen expressing cell lines were also generated: by transducing SupT1, and our SupT1.CD19 with GM3 and GD2 synthases SupT1.GD2 and SupT1.CD19.GD2 were generated. By transducing SupT1 and SupT1.CD19 with a retroviral vector coding for EGFRvIII SupT1.EGFRvIII and SupT1.CD19.EGFRvIII were generated. Since CD5 is expressed on SupT1 cells, a different cell line was used to generate the target cells: 293T cells were generated which express CD19 alone, CD5 alone and both CD5 and CD19 together. Expression was confirmed by flow-cytometry (Figure 19). T-cells expressing the three new CAR AND gates were challenged with SupT1.CD19 and respective cognate double positive and single positive target cells. All three AND gates demonstrated reduced activation by the double positive cell lines in comparison with the single positive targets (Figure 20). This demonstrates generalizability of the AND gate design to arbitrary targets and cognate binders.

Example 6: Experimental proof of Kinetic segregation model of CAR AND gate

The aim was to prove the model that differential segregation caused by different spacers is the central mechanism behind the ability to generate these logic CAR gates. The model is that if only the activating CAR is ligated, the potent inhibiting 'ligation off' type CAR is in solution in the membrane and can inhibit the activating CAR. Once both CARs are ligated, if both CAR spacers are sufficiently different, they will segregate within the synapse and not co-localize. Hence, a key requirement is that the spacers are sufficiently different. If the model is correct, if both spacers are sufficiently similar so they co-localize when both

receptors are ligated, the gate will fail to function. To test this, the "bulky" Fc spacer in the original CAR we replaced with a murine CD8 spacer. It was predicted that this has the similar length, bulk and charge as human CD8 but so should not cross-pair with it. Hence, the new gate had a first CAR which recognizes CD19, a human CD8 stalk spacer and an activatory endodomain; while the second CAR recognizes CD33, has a mouse CD8 stalk spacer and a CD148 endodomain (Figure 18C). T-cells were transduced to express this new CAR gate. These T-cells were then challenged with SupT1 cells expressing CD19 alone, CD33 alone or CD19 and CD33 together. T-cells did not respond to SupT1 cells expressing either antigen alone as per the original AND gate. However, CAR T-cells failed to respond to SupT1 cells expressing both antigens, thereby confirming the model (Figure 18C). A functional AND gate requires both CARs to have spacers sufficiently different so that they do not co-localize within an immunological synapse (Figure 23A and B).

Example 7 - Design and function of an AND NOT gate

Phosphatases such as CD45 and CD148 are so potent that even a small amount entering an immunological synapse can inhibit ITAM activation. This is the basis of inhibition of the logical AND gate. Other classes of phosphatases are not as potent e.g. PTPN6 and related phosphatases. It was predicted that a small amount of PTPN6 entering a synapse by diffusion would not inhibit activation. In addition, it was predicted that if an inhibitory CAR had a sufficiently similar spacer to an activating CAR, it could co-localize within a synapse if both CARs were ligated. In this case, large amounts of the inhibitory endodomain would be sufficient to stop the ITAMS from activating when both antigens were present. In this way, an AND NOT gate could be created.

For the NOT AND gate, the second signal needs to "veto" activation. This is done by bringing an inhibitory signal into the immunological synapse, for example by bringing in the phosphatase of an enzyme such as PTPN6. We hence generated an initial AND NOT gate as follows: two CARs co-expressed whereby the first recognizes CD19, has a human CD8 stalk spacer and an activating endodomain; co-expressed with an anti-CD33 CAR with a mouse CD8 stalk spacer and an endodomain comprising of the catalytic domain of PTPN6 (SEQ ID 38, Figure 13 A with B). A suitable cassette is shown in Figure 12 and preliminary functional data are shown in Figure 14.

In addition, an alternative strategy was developed for generating an AND NOT gate. Immune Tyrosinase Inhibitory Motifs (ITIMs) are activated in a similar manner to ITAMS, in that they become phosphorylated by lck upon clustering and exclusion of phosphatases.

Instead of triggering activation by binding ZAP70, phosphorylated ITIMs recruit phosphatases like PTPN6 through their cognate SH2 domains. An ITIM can function as an inhibitory endodomain, as long as the spacers on the activating and inhibiting CARs can co-localize. To generate this construct, an AND NOT gate was generated as follows: two CARs co-expressed - the first recognizes CD19, has a human CD8 stalk spacer and an activating endodomain; co-expressed with an anti-CD33 CAR with a mouse CD8 stalk spacer and an ITIM containing endodomain derived from that of LAIR1 (SEQ ID 39, Figure 13 A with C).

A further, more complex AND NOT gate was also developed, whereby an ITIM is enhanced by the presence of an additional chimeric protein: an intracellular fusion of the SH2 domain of PTPN6 and the endodomain of CD148. In this design three proteins are expressed - the first recognizes CD19, has a human CD8 stalk spacer and an activating endodomain; co-expressed with an anti-CD33 CAR with a mouse CD8 stalk spacer and an ITIM containing endodomain derived from that of LAIR1. A further 2A peptide, allows co-expression of the PTPN6-CD148 fusion (SEQ ID 40, Figure 13 A and D). It was predicted that these AND NOT gates would have a different range of inhibition: PTPN6-CD148 > PTPN6 > > ITIM.

T-cells were transduced with these gates and challenged with targets expressing either CD19 or CD33 alone, or both CD19 and CD33 together. All three gates responded to targets expressing only CD19, but not targets expressing both CD19 and CD33 together (Figure 21), confirming that all three of the AND NOT gates were functional.

Example 8: Experimental proof of Kinetic segregation model of PTPN6 based AND NOT gate.

The model of the AND NOT gate centres around the fact that the nature of the spacers used in both CARs is pivotal for the correct function of the gate. In the functional AND NOT gate with PTPN6, both CAR spacers are sufficiently similar that when both CARs are ligated, both co-localize within the synapse so the high concentration even the weak PTPN6 is sufficient to inhibit activation. If the spacers were different, segregation in the synapse will isolate the PTPN6 from the ITAM allowing activation disrupting the AND NOT gate. To test this, a control was generated replacing the murine CD8 stalk spacer with that of Fc. In this case, the test gate consisted of two CARs, the first recognizes CD19, has a human CD8 stalk spacer and an ITAM endodomain; while the second CAR recognizes CD33, has an Fc spacer and an endodomain comprising of the phosphatase from PTPN6. This gate activates in response to CD19, but also activates in response to CD19 and CD33 together (Figure 22B, where function of this gate is compared with that of the original AND NOT, and the

control AND gate variant described in Example 6). This experimental data proves the model that for a functional AND NOT gate with PTPN6, co-localizing spacers are needed.

Example 9: Experimental proof of kinetic segregation model of ITIM based AND NOT gate.

Similar to the PTPN6 based AND NOT gate, the ITIM based gate also requires co-localization in an immunological synapse to function as an AND NOT gate. To prove this hypothesis, a control ITIM based gate was generated as follows: two CARs co-expressed - the first recognizes CD19, has a human CD8 stalk spacer and an activating endodomain; co-expressed with an anti-CD33 CAR with an Fc spacer and an ITIM containing endodomain derived from that of LAIR1. The activity of this gate was compared with that of the original ITIM based AND NOT gate. In this case, the modified gate activated in response to targets expressing CD19, but also activated in response to cells expressing both CD19 and CD33. These data indicate that ITIM based AND NOT gates follow the kinetic segregation based model and a correct spacer must be selected to create a functional gate (Figure 23B).

Example 10: Summary of model of CAR logic gates generated by kinetic segregation

Based on current understanding of the kinetic-segregation model and the experimental data described herein, a summary of the model for a two-CAR gate is presented in Figure 24. The Figure shows a cell expressing two CARs, each recognizing a different antigen. When either or both CARs recognize a target antigen on a cell, a synapse forms and native CD45 and CD148 are excluded from the synapse due to the bulk of their ectodomain. This sets the stage for T-cell activation. In the case that the target cell bears only one cognate antigen, the cognate CAR is ligated and the cognate CAR segregates into the synapse. The unligated CAR remains in solution on the T-cell membrane and can diffuse in and out of the synapse so that an area of high local concentration of ligated CAR with low concentration of unligated CAR forms. In this case, if the ligated CAR has an ITAM and the non-ligated CAR has 'ligation off" type inhibitory endodomain such as that of CD148, the amount of non-ligated CAR is sufficient to inhibit activation and the gate is off. In contrast, in this case, if the ligated CAR has an ITAM and the non-ligated CAR has a 'ligation on' type inhibitory endodomain such as PTPN6, the amount of non-ligated CAR is insufficient to inhibit and the gate is on. When challenged by a target cell bearing both cognate antigens, both cognate CARs are ligated and form part of an immunological synapse. Importantly, if the CAR spacers are sufficiently similar, the CARs co-localize in the synapse but if the CAR spacers are sufficiently different the CARs segregate within the synapse. In this latter case, areas of membrane form whereby high concentrations of one CAR are present but the other CAR is

absent. In this case since segregation is complete, even if the inhibitory endodomain is a 'ligation off' type, the gate is on. In the former case, areas of membrane form with high concentrations of both CARs mixed together. In this case, since both endodomains are concentrated, even if the inhibitory endodomain is 'ligation on' type, the gate is off. By selecting the correct combination of spacer and endodomain logic can be programmed into a CAR T-cell.

Based on our work above, we have established a series of design rules to allow generation of logic-gated CARs (illustrated in figure 31). To generate an "antigen A OR antigen B" gated CAR T-cell, anti-A and anti-B CARs must be generated such that (1) each CAR has a spacer which simply allows antigen access and synapse formation such that the CAR functions, and (2) Each CAR has an activating endodomain; To generate an "antigen A AND NOT B" gated CAR T-cell, anti-A and anti-B CARs must be generated such that (1) both CARs have spacers which do not cross-pair, but which will allow the CARs to co-segregate upon recognition of both cognate antigens on the target cell, (2) and one CAR has an activating endodomain, while the other CAR has an endodomain which comprises or recruits a weak phosphatase (e.g. PTPN6); (3) To generate an "antigen A AND antigen B" gated CAR T-cell, anti-A and anti-B CARs must be generated such that (1) one CAR has a spacer sufficiently different from the other CAR such that both CARs will not co-segregate upon recognition of both cognate antigens on the target cell, (2) one CAR has an activating endodomain, while the other car has an endodomain which comprises of a potent phosphatase (e.g. that of CD45 or CD148). The correct spacers to achieve the desired effect can be selected from a set of spacers with known size/shape etc as well as taking into consideration size/shape etc of the target antigen (for instance see figure 30) and the location of the cognate epitope on the target antigen.

SEQ ID No 41: SFG.aCD19-CD8STK-CD28tmZ-2A-aGD2-HCH2CH3pvaa-dCD148

MSLPVTALLLPLALLLHAARPDIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDGTVKLL
IYHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTKLEITKAGGGGSG
GGGSGGGGSGGGGSEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSWIRQPPRKGLEWLGVIWGS
ETTYYNSALKSRLTIIKDNSKSQVFLKMNSLQTDDTAIYYCAKHYYYGGSYAMDYWGQGTSVTVSSDP
TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIFWVLVVVGGVLACYSLLVTVAF
IIFWVRRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL
QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPRRAEGRGSLLTCGDVEENP
GPMETDTLLLWVLLLWVPGSTGQVQLQESGPGLVKPSQTLSITCTVSGFSLASYNIHWVRQPPGKGLE
WLGVIWAGGSTNYNSALMSRLTISKDNSKNQVFLKMSSLTAADTAVYYCAKRSDDYSWFAYWGQGTLV
TVSSGGGGSGGGGSGGGGSENQMTQSPSSLSASVGDRVTMTCRASSSVSSSYLHWYQQKSGKAPKVWI
YSTSNLASGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCQQYSGYPITFGQGTKVEIKRSDPAEPKS
PDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMIARTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD

ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
CSVMHEALHNHYTQKSLSLSPGKKDPKAVFGCIFGALVIVTVGGFIFWRKKRKDAKNNEVSFSQIKPK
KSKLIRVENFEAYFKKQQADSNCGFAEEYEDLKLVGISQPKYAAELAENRGKNRYNNVLPYDISRVKL
SVQTHSTDDYINANYMPGYHSKKDFIATQGPLPNTLKDFWRMVWEKNVYAIIMLTKCVEQGRTKCEEY
WPSKQAQDYGDITVAMTSEIVLPEWTIRDFTVKNIQTSESHPLRQFHFTSWPDHGVPDTTDLLINFRY
LVRDYMKQSPPESPILVHCSAGVGRTGTFIAIDRLIYQIENENTVDVYGIVYDLRMHRPLMVQTEDQY
VFLNQCVLDIVRSQKDSKVDLIYQNTTAMTIYENLAPVTTFGKTNGYIA

SEQ ID No. 42: SFG.aCD19-CD8STK-CD28tmZ-2A-aGD2-HCH2CH3pvaa-dCD148

ATGAGCCTGCCCGTGACCGCCCTGCTGCTGCCCCTGGCCCTGCTGCTGCACGCCGCCAGACCAGACAT
CCAGATGACCCAGACCACCAGCAGCCTGAGCGCCAGCCTGGGCGACCGGGTGACCATCAGCTGCAGAG
CCAGCCAGGACATCAGCAAGTACCTGAACTGGTACCAGCAGAAGCCCGACGGCACCGTGAAGCTGCTG
ATCTACCACACCAGCCGGCTGCACAGCGGCGTGCCCAGCCGGTTCAGCGGCAGCGGCAGCGGCACCGA
CTACAGCCTGACCATCAGCAACCTGGAGCAGGAGGACATCGCCACCTACTTCTGCCAGCAGGGCAACA
CCCTGCCCTACACCTTCGGAGGCGGCACCAAGCTGGAGATCACCAAGGCCGGAGGCGGAGGCTCTGGC
GGAGGCGGCTCTGGCGGAGGCGGCTCTGGCGGAGGCGGCAGCGAGGTGAAGCTGCAGGAGTCTGGCCC
AGGCCTGGTGGCCCCAAGCCAGAGCCTGAGCGTGACCTGCACCGTGAGCGGCGTGAGCCTGCCCGACT
ACGGCGTGAGCTGGATCAGGCAGCCCCCACGGAAGGGCCTGGAGTGGCTGGGCGTGATCTGGGGCAGC
GAGACCACCTACTACAACAGCGCCCTGAAGAGCCGGCTGACCATCATCAAGGACAACAGCAAGAGCCA
GGTGTTCCTGAAGATGAACAGCCTGCAGACCGACGACACCGCCATCTACTACTGCGCCAAGCACTACT
ACTATGGCGGCAGCTACGCTATGGACTACTGGGGCCAGGGCACCAGCGTGACCGTGAGCTCAGATCCC
ACCACGACGCCAGCGCCGCGACCACCAACACCGGCGCCCACCATCGCGTCGCAGCCCCTGTCCCTGCG
CCCAGAGGCGTGCCGGCCAGCGGCGGGGGGCGCAGTGCACACGAGGGGGCTGGACTTCGCCTGTGATA
TCTTTTGGGTGCTGGTGGTGGTTGGTGGAGTCCTGGCTTGCTATAGCTTGCTAGTAACAGTGGCCTTT
ATTATTTTCTGGGTGAGGAGAGTGAAGTTCAGCAGGAGCGCAGACGCCCCCGCGTACCAGCAGGGCCA
GAACCAGCTCTATAACGAGCTCAATCTAGGACGAAGAGAGGAGTACGATGTTTTGGACAAGAGACGTG
GCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAGAACCCTCAGGAAGGCCTGTACAATGAACTG
CAGAAAGATAAGATGGCGGAGGCCTACAGTGAGATTGGGATGAAAGGCGAGCGCCGGAGGGGCAAGGG
GCACGATGGCCTTTACCAGGGTCTCAGTACAGCCACCAAGGACACCTACGACGCCCTTCACATGCAGG
CCCTGCCTCCTCGCAGAGCCGAGGGCAGGGGAAGTCTTCTAACATGCGGGGACGTGGAGGAAAATCCC
GGGCCCATGGAGACCGACACCCTGCTGCTGTGGGTGCTGCTGCTGTGGGTGCCAGGCAGCACCGGCCA
GGTGCAGCTGCAGGAGTCTGGCCCAGGCCTGGTGAAGCCCAGCCAGACCCTGAGCATCACCTGCACCG
TGAGCGGCTTCAGCCTGGCCAGCTACAACATCCACTGGGTGCGGCAGCCCCCAGGCAAGGGCCTGGAG
TGGCTGGGCGTGATCTGGGCTGGCGGCAGCACCAACTACAACAGCGCCCTGATGAGCCGGCTGACCAT
CAGCAAGGACAACAGCAAGAACCAGGTGTTCCTGAAGATGAGCAGCCTGACAGCCGCCGACACCGCCG
TGTACTACTGCGCCAAGCGGAGCGACGACTACAGCTGGTTCGCCTACTGGGGCCAGGGCACCCTGGTG
ACCGTGAGCTCTGGCGGAGGCGGCTCTGGCGGAGGCGGCTCTGGCGGAGGCGGCAGCGAGAACCAGAT
GACCCAGAGCCCCAGCAGCTTGAGCGCCAGCGTGGGCGACCGGGTGACCATGACCTGCAGAGCCAGCA
GCAGCGTGAGCAGCAGCTACCTGCACTGGTACCAGCAGAAGAGCGGCAAGGCCCCAAAGGTGTGGATC
TACAGCACCAGCAACCTGGCCAGCGGCGTGCCCAGCCGGTTCAGCGGCAGCGGCAGCGGCACCGACTA
CACCCTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCTACTACTGCCAGCAGTACAGCGGCT
ACCCCATCACCTTCGGCCAGGGCACCAAGGTGGAGATCAAGCGGTCGGATCCCGCCGAGCCCAAATCT
CCTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTCCCGTGGCCGGCCCGTCAGTCTTCCTCTT
CCCCCCAAAACCCAAGGACACCCTCATGATCGCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACG
TGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAG
ACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCA
GGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGA
AAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAT

GAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT
GGAGTGGGAGAGCAATGGGCAACCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG
GCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA
TGCTCCGTGATGCATGAGGCCCTGCACAATCACTATACCCAGAAATCTCTGAGTCTGAGCCCAGGCAA
GAAGGACCCCAAGGCGGTTTTTGGCTGTATCTTTGGTGCCCTGGTTATTGTGACTGTGGGAGGCTTCA
TCTTCTGGAGAAAGAAGAGGAAAGATGCAAAGAATAATGAAGTGTCCTTTTCTCAAATTAAACCTAAA
AAATCTAAGTTAATCAGAGTGGAGAATTTTGAGGCCTACTTCAAGAAGCAGCAAGCTGACTCCAACTG
TGGGTTCGCAGAGGAATACGAAGATCTGAAGCTTGTTGGAATTAGTCAACCTAAATATGCAGCAGAAC
TGGCTGAGAATAGAGGAAAGAATCGCTATAATAATGTTCTGCCCTATGATATTTCCCGTGTCAAACTT
TCGGTCCAGACCCATTCAACGGATGACTACATCAATGCCAACTACATGCCTGGCTACCACTCCAAGAA
AGATTTTATTGCCACACAAGGACCTTTACCGAACACTTTGAAAGATTTTTGGCGTATGGTTTGGGAGA
AAAATGTATATGCCATCATTATGTTGACTAAATGTGTTGAACAGGGAAGAACCAAATGTGAGGAGTAT
TGGCCCTCCAAGCAGGCTCAGGACTATGGAGACATAACTGTGGCAATGACATCAGAAATTGTTCTTCC
GGAATGGACCATCAGAGATTTCACAGTGAAAAATATCCAGACAAGTGAGAGTCACCCTCTGAGACAGT
TCCATTTCACCTCCTGGCCAGACCACGGTGTTCCCGACACCACTGACCTGCTCATCAACTTCCGGTAC
CTCGTTCGTGACTACATGAAGCAGAGTCCTCCCGAATCGCCGATTCTGGTGCATTGCAGTGCTGGGGT
CGGAAGGACGGGCACTTTCATTGCCATTGATCGTCTCATCTACCAGATAGAGAATGAGAACACCGTGG
ATGTGTATGGGATTGTGTATGACCTTCGAATGCATAGGCCTTTAATGGTGCAGACAGAGGACCAGTAT
GTTTTCCTCAATCAGTGTGTTTTGGATATTGTCAGATCCCAGAAAGACTCAAAAGTAGATCTTATCTA
CCAGAACACAACTGCAATGACAATCTATGAAAACCTTGCGCCCGTGACCACATTTGGAAAGACCAATG
GTTACATCGCCTAA

SEQ ID No. 43: SFG.aCD19-CD8STK-CD28tmZ-2A-aCD5-HCH2CH3pvaa-dCD148

MSLPVTALLLPLALLLHAARPDIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDGTVKLL
IYHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTKLEITKAGGGGSG
GGGSGGGGSGGGGSEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSWIRQPPRKGLEWLGVIWGS
ETTYYNSALKSRLTIIKDNSKSQVFLKMNSLQTDDTAIYYCAKHYYYGGSYAMDYWGQGTSVTVSSDP
TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIFWVLVVVGGVLACYSLLVTVAF
IIFWVRRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL
QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPRRAEGRGSLLTCGDVEENP
GPMETDTLLLWVLLLWVPGSTGQVTLKESGPGILKPSQTLSLTCSFSGFSLSTSGMGVGWIRQPSGKG
LEWLAHIWWDDDVYYNPSLKNQLTISKDASRDQVFLKITNLDTADTATYYCVRRRATGTGFDYWGQGT
TLTVSSGGGGSGGGGSGGGGSNIVMTQSHKFMSTSVGDRVSIACKASQDVGTAVAWYQQKPGQSPKLL
IYWTSTRHTGVPDRFTGSGSGTDFTLTITNVQSEDLADYFCHQYNSYNTFGSGTRLELKRSDPAEPKS
PDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMIARTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
CSVMHEALHNHYTQKSLSLSPGKKDPKAVFGCIFGALVIVTVGGFIFWRKKRKDAKNNEVSFSQIKPK
KSKLIRVENFEAYFKKQQADSNCGFAEEYEDLKLVGISQPKYAAELAENRGKNRYNNVLPYDISRVKL
SVQTHSTDDYINANYMPGYHSKKDFIATQGPLPNTLKDFWRMVWEKNVYAIIMLTKCVEQGRTKCEEY
WPSKQAQDYGDITVAMTSEIVLPEWTIRDFTVKNIQTSESHPLRQFHFTSWPDHGVPDTTDLLINFRY
LVRDYMKQSPPESPILVHCSAGVGRTGTFIAIDRLIYQIENENTVDVYGIVYDLRMHRPLMVQTEDQY
VFLNQCVLDIVRSQKDSKVDLIYQNTTAMTIYENLAPVTTFGKTNGYIA

SEQ ID No. 44: SFG.aCD19-CD8STK-CD28tmZ-2A-aCD5-HCH2CH3pvaa-dCD148

ATGAGCCTGCCCGTGACCGCCCTGCTGCTGCCCCTGGCCCTGCTGCTGCACGCCGCCAGACCAGACAT
CCAGATGACCCAGACCACCAGCAGCCTGAGCGCCAGCCTGGGCGACCGGGTGACCATCAGCTGCAGAG

CCAGCCAGGACATCAGCAAGTACCTGAACTGGTACCAGCAGAAGCCCGACGGCACCGTGAAGCTGCTG
ATCTACCACACCAGCCGGCTGCACAGCGGCGTGCCCAGCCGGTTCAGCGGCAGCGGCAGCGGCACCGA
CTACAGCCTGACCATCAGCAACCTGGAGCAGGAGGACATCGCCACCTACTTCTGCCAGCAGGGCAACA
CCCTGCCCTACACCTTCGGAGGCGGCACCAAGCTGGAGATCACCAAGGCCGGAGGCGGAGGCTCTGGC
GGAGGCGGCTCTGGCGGAGGCGGCTCTGGCGGAGGCGGCAGCGAGGTGAAGCTGCAGGAGTCTGGCCC
AGGCCTGGTGGCCCCAAGCCAGAGCCTGAGCGTGACCTGCACCGTGAGCGGCGTGAGCCTGCCCGACT
ACGGCGTGAGCTGGATCAGGCAGCCCCCACGGAAGGGCCTGGAGTGGCTGGGCGTGATCTGGGGCAGC
GAGACCACCTACTACAACAGCGCCCTGAAGAGCCGGCTGACCATCATCAAGGACAACAGCAAGAGCCA
GGTGTTCCTGAAGATGAACAGCCTGCAGACCGACGACACCGCCATCTACTACTGCGCCAAGCACTACT
ACTATGGCGGCAGCTACGCTATGGACTACTGGGGCCAGGGCACCAGCGTGACCGTGAGCTCAGATCCC
ACCACGACGCCAGCGCCGCGACCACCAACACCGGCGCCCACCATCGCGTCGCAGCCCCTGTCCCTGCG
CCCAGAGGCGTGCCGGCCAGCGGCGGGGGGCGCAGTGCACACGAGGGGGCTGGACTTCGCCTGTGATA
TCTTTTGGGTGCTGGTGGTGGTTGGTGGAGTCCTGGCTTGCTATAGCTTGCTAGTAACAGTGGCCTTT
ATTATTTTCTGGGTGAGGAGAGTGAAGTTCAGCAGGAGCGCAGACGCCCCCGCGTACCAGCAGGGCCA
GAACCAGCTCTATAACGAGCTCAATCTAGGACGAAGAGAGGAGTACGATGTTTTGGACAAGAGACGTG
GCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAGAACCCTCAGGAAGGCCTGTACAATGAACTG
CAGAAAGATAAGATGGCGGAGGCCTACAGTGAGATTGGGATGAAAGGCGAGCGCCGGAGGGGCAAGGG
GCACGATGGCCTTTACCAGGGTCTCAGTACAGCCACCAAGGACACCTACGACGCCCTTCACATGCAGG
CCCTGCCTCCTCGCAGAGCCGAGGGCAGGGGAAGTCTTCTAACATGCGGGGACGTGGAGGAAAATCCC
GGGCCCATGGAGACCGACACCCTGCTGCTGTGGGTGCTGCTGCTGTGGGTGCCCGGCAGCACCGGCCA
GGTGACCCTGAAGGAGAGCGGTCCCGGCATCCTGAAGCCCAGCCAGACCCTGAGCCTGACCTGCAGCT
TCAGCGGCTTCAGCCTGAGCACCAGCGGCATGGGCGTGGGCTGGATTCGGCAGCCCAGCGGCAAGGGC
CTGGAGTGGCTGGCCCACATCTGGTGGGACGACGACGTGTACTACAACCCCAGCCTGAAGAACCAGCT
GACCATCAGCAAGGACGCCAGCCGGGACCAGGTGTTCCTGAAGATCACCAACCTGGACACCGCCGACA
CCGCCACCTACTACTGCGTGCGGCGCCGGGCCACCGGCACCGGCTTCGACTACTGGGGCCAGGGCACC
ACCCTGACCGTGAGCAGCGGTGGCGGTGGCAGCGGCGGCGGCGGAAGCGGAGGTGGTGGCAGCAACAT
CGTGATGACCCAGAGCCACAAGTTCATGAGCACCAGCGTGGGCGACCGGGTGAGCATCGCCTGCAAGG
CCAGCCAGGACGTGGGCACCGCCGTGGCCTGGTACCAGCAGAAGCCTGGCCAGAGCCCCAAGCTGCTG
ATCTACTGGACCAGCACCCGGCACACCGGCGTGCCCGACCGGTTCACCGGCAGCGGCAGCGGCACCGA
CTTCACCCTGACCATCACCAACGTGCAGAGCGAGGACCTGGCCGACTACTTCTGCCACCAGTACAACA
GCTACAACACCTTCGGCAGCGGCACCCGGCTGGAGCTGAAGCGGTCGGATCCCGCCGAGCCCAAATCT
CCTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTCCCGTGGCCGGCCCGTCAGTCTTCCTCTT
CCCCCCAAAACCCAAGGACACCCTCATGATCGCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACG
TGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAG
ACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCA
GGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGA
AAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAT
GAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT
GGAGTGGGAGAGCAATGGGCAACCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG
GCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA
TGCTCCGTGATGCATGAGGCCCTGCACAATCACTATACCCAGAAATCTCTGAGTCTGAGCCCAGGCAA
GAAGGACCCCAAGGCGGTTTTTGGCTGTATCTTTGGTGCCCTGGTTATTGTGACTGTGGGAGGCTTCA
TCTTCTGGAGAAAGAAGAGGAAAGATGCAAAGAATAATGAAGTGTCCTTTTCTCAAATTAAACCTAAA
AAATCTAAGTTAATCAGAGTGGAGAATTTTGAGGCCTACTTCAAGAAGCAGCAAGCTGACTCCAACTG
TGGGTTCGCAGAGGAATACGAAGATCTGAAGCTTGTTGGAATTAGTCAACCTAAATATGCAGCAGAAC
TGGCTGAGAATAGAGGAAAGAATCGCTATAATAATGTTCTGCCCTATGATATTTCCCGTGTCAAACTT
TCGGTCCAGACCCATTCAACGGATGACTACATCAATGCCAACTACATGCCTGGCTACCACTCCAAGAA
AGATTTTATTGCCACACAAGGACCTTTACCGAACACTTTGAAAGATTTTTGGCGTATGGTTTGGGAGA

AAAATGTATATGCCATCATTATGTTGACTAAATGTGTTGAACAGGGAAGAACCAAATGTGAGGAGTAT
TGGCCCTCCAAGCAGGCTCAGGACTATGGAGACATAACTGTGGCAATGACATCAGAAATTGTTCTTCC
GGAATGGACCATCAGAGATTTCACAGTGAAAAATATCCAGACAAGTGAGAGTCACCCTCTGAGACAGT
TCCATTTCACCTCCTGGCCAGACCACGGTGTTCCCGACACCACTGACCTGCTCATCAACTTCCGGTAC
CTCGTTCGTGACTACATGAAGCAGAGTCCTCCCGAATCGCCGATTCTGGTGCATTGCAGTGCTGGGGT
CGGAAGGACGGGCACTTTCATTGCCATTGATCGTCTCATCTACCAGATAGAGAATGAGAACACCGTGG
ATGTGTATGGGATTGTGTATGACCTTCGAATGCATAGGCCTTTAATGGTGCAGACAGAGGACCAGTAT
GTTTTCCTCAATCAGTGTGTTTTGGATATTGTCAGATCCCAGAAAGACTCAAAAGTAGATCTTATCTA
CCAGAACACAACTGCAATGACAATCTATGAAAACCTTGCGCCCGTGACCACATTTGGAAAGACCAATG
GTTACATCGCCTAA

SEQ ID No. 45: SFG.aCD19-CD8STK-CD28tmZ-2A-aEGFRvIII-HCH2CH3pvaa-dCD148

MSLPVTALLLPLALLLHAARPDIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDGTVKLL
IYHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTKLEITKAGGGGSG
GGGSGGGGSGGGGSEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSWIRQPPRKGLEWLGVIWGS
ETTYYNSALKSRLTIIKDNSKSQVFLKMNSLQTDDTAIYYCAKHYYYGGSYAMDYWGQGTSVTVSSDP
TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIFWVLVVVGGVLACYSLLVTVAF
IIFWVRRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL
QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPRRAEGRGSLLTCGDVEENP
GPMETDTLLLWVLLLWVPGSTGQVKLQQSGGGLVKPGASLKLSCVTSGFTFRKFGMSWVRQTSDKRLE
WVASISTGGYNTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCTRGYSSTSYAMDYWGQGT
TVTVSSGGGGSGGGGSGGGGSDIELTQSPASLSVATGEKVTIRCMTSTDIDDDMNWYQQKPGEPPKFL
ISEGNTLRPGVPSRFSSSGTGTDFVFTIENTLSEDVGDYYCLQSFNVPLTFGDGTKLEIKRSDPAEPK
SPDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMIARTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA
KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF
SCSVMHEALHNHYTQKSLSLSPGKKDPKAVFGCIFGALVIVTVGGFIFWRKKRKDAKNNEVSFSQIKP
KKSKLIRVENFEAYFKKQQADSNCGFAEEYEDLKLVGISQPKYAAELAENRGKNRYNNVLPYDISRVK
LSVQTHSTDDYINANYMPGYHSKKDFIATQGPLPNTLKDFWRMVWEKNVYAIIMLTKCVEQGRTKCEE
YWPSKQAQDYGDITVAMTSEIVLPEWTIRDFTVKNIQTSESHPLRQFHFTSWPDHGVPDTTDLLINFR
YLVRDYMKQSPPESPILVHCSAGVGRTGTFIAIDRLIYQIENENTVDVYGIVYDLRMHRPLMVQTEDQ
YVFLNQCVLDIVRSQKDSKVDLIYQNTTAMTIYENLAPVTTFGKTNGYIA

SEQ ID No. 46: SFG.aCD19-CD8STK-CD28tmZ-2A-aEGFRvIII-HCH2CH3pvaa-dCD148

ATGAGCCTGCCCGTGACCGCCCTGCTGCTGCCCCTGGCCCTGCTGCTGCACGCCGCCAGACCAGACAT
CCAGATGACCCAGACCACCAGCAGCCTGAGCGCCAGCCTGGGCGACCGGGTGACCATCAGCTGCAGAG
CCAGCCAGGACATCAGCAAGTACCTGAACTGGTACCAGCAGAAGCCCGACGGCACCGTGAAGCTGCTG
ATCTACCACACCAGCCGGCTGCACAGCGGCGTGCCCAGCCGGTTCAGCGGCAGCGGCAGCGGCACCGA
CTACAGCCTGACCATCAGCAACCTGGAGCAGGAGGACATCGCCACCTACTTCTGCCAGCAGGGCAACA
CCCTGCCCTACACCTTCGGAGGCGGCACCAAGCTGGAGATCACCAAGGCCGGAGGCGGAGGCTCTGGC
GGAGGCGGCTCTGGCGGAGGCGGCTCTGGCGGAGGCGGCAGCGAGGTGAAGCTGCAGGAGTCTGGCCC
AGGCCTGGTGGCCCCAAGCCAGAGCCTGAGCGTGACCTGCACCGTGAGCGGCGTGAGCCTGCCCGACT
ACGGCGTGAGCTGGATCAGGCAGCCCCCACGGAAGGGCCTGGAGTGGCTGGGCGTGATCTGGGGCAGC
GAGACCACCTACTACAACAGCGCCCTGAAGAGCCGGCTGACCATCATCAAGGACAACAGCAAGAGCCA
GGTGTTCCTGAAGATGAACAGCCTGCAGACCGACGACACCGCCATCTACTACTGCGCCAAGCACTACT
ACTATGGCGGCAGCTACGCTATGGACTACTGGGGCCAGGGCACCAGCGTGACCGTGAGCTCAGATCCC

ACCACGACGCCAGCGCCGCGACCACCAACACCGGCGCCCACCATCGCGTCGCAGCCCCTGTCCCTGCG
CCCAGAGGCGTGCCGGCCAGCGGCGGGGGGCGCAGTGCACACGAGGGGGCTGGACTTCGCCTGTGATA
TCTTTTGGGTGCTGGTGGTGGTTGGTGGAGTCCTGGCTTGCTATAGCTTGCTAGTAACAGTGGCCTTT
ATTATTTTCTGGGTGAGGAGAGTGAAGTTCAGCAGGAGCGCAGACGCCCCCGCGTACCAGCAGGGCCA
GAACCAGCTCTATAACGAGCTCAATCTAGGACGAAGAGAGGAGTACGATGTTTTGGACAAGAGACGTG
GCCGGGACCCTGAGATGGGGGGAAAGCCGAGAAGGAAGAACCCTCAGGAAGGCCTGTACAATGAACTG
CAGAAAGATAAGATGGCGGAGGCCTACAGTGAGATTGGGATGAAAGGCGAGCGCCGGAGGGGCAAGGG
GCACGATGGCCTTTACCAGGGTCTCAGTACAGCCACCAAGGACACCTACGACGCCCTTCACATGCAGG
CCCTGCCTCCTCGCAGAGCCGAGGGCAGGGGAAGTCTTCTAACATGCGGGGACGTGGAGGAAAATCCC
GGGCCCATGGAGACCGACACCCTGCTGCTGTGGGTGCTGCTGCTGTGGGTGCCCGGCAGCACCGGCCA
GGTGAAGCTGCAGCAGAGCGGCGGAGGCCTGGTGAAGCCCGGCGCCAGCCTGAAGCTGAGCTGCGTGA
CCAGCGGCTTCACCTTCCGGAAGTTCGGCATGAGCTGGGTGCGGCAGACCAGCGACAAGCGGCTGGAG
TGGGTGGCCAGCATCAGCACCGGCGGCTACAACACCTACTACAGCGACAACGTGAAGGGCCGGTTCAC
CATCAGCCGGGAGAACGCCAAGAACACCCTGTACCTGCAGATGAGCAGCCTGAAGAGCGAGGACACCG
CCCTGTACTACTGCACCCGGGGCTACAGCAGCACCAGCTACGCTATGGACTACTGGGGCCAGGGCACC
ACCGTGACAGTGAGCAGCGGCGGAGGAGGCAGTGGTGGGGGTGGATCTGGCGGAGGTGGCAGCGACAT
CGAGCTGACCCAGAGCCCCGCCAGCCTGAGCGTGGCCACCGGCGAGAAGGTGACCATCCGGTGCATGA
CCAGCACCGACATCGACGACGACATGAACTGGTACCAGCAGAAGCCCGGCGAGCCCCCAAAGTTCCTG
ATCAGCGAGGGCAACACCCTGCGGCCCGGCGTGCCCAGCCGGTTCAGCAGCAGCGGCACCGGCACCGA
CTTCGTGTTCACCATCGAGAACACCCTGAGCGAGGACGTGGGCGACTACTACTGCCTGCAGAGCTTCA
ACGTGCCCCTGACCTTCGGCGACGGCACCAAGCTGGAGATCAAGCGGTCGGATCCCGCCGAGCCCAAA
TCTCCTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTCCCGTGGCCGGCCCGTCAGTCTTCCT
CTTCCCCCCAAAACCCAAGGACACCCTCATGATCGCCCGGACCCCTGAGGTCACATGCGTGGTGGTGG
ACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCC
AAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCA
CCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCG
AGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG
GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGC
CGTGGAGTGGGAGAGCAATGGGCAACCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCG
ACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC
TCATGCTCCGTGATGCATGAGGCCCTGCACAATCACTATACCCAGAAATCTCTGAGTCTGAGCCCAGG
CAAGAAGGACCCCAAGGCGGTTTTTGGCTGTATCTTTGGTGCCCTGGTTATTGTGACTGTGGGAGGCT
TCATCTTCTGGAGAAAGAAGAGGAAAGATGCAAAGAATAATGAAGTGTCCTTTTCTCAAATTAAACCT
AAAAAATCTAAGTTAATCAGAGTGGAGAATTTTGAGGCCTACTTCAAGAAGCAGCAAGCTGACTCCAA
CTGTGGGTTCGCAGAGGAATACGAAGATCTGAAGCTTGTTGGAATTAGTCAACCTAAATATGCAGCAG
AACTGGCTGAGAATAGAGGAAAGAATCGCTATAATAATGTTCTGCCCTATGATATTTCCCGTGTCAAA
CTTTCGGTCCAGACCCATTCAACGGATGACTACATCAATGCCAACTACATGCCTGGCTACCACTCCAA
GAAAGATTTTATTGCCACACAAGGACCTTTACCGAACACTTTGAAAGATTTTTGGCGTATGGTTTGGG
AGAAAAATGTATATGCCATCATTATGTTGACTAAATGTGTTGAACAGGGAAGAACCAAATGTGAGGAG
TATTGGCCCTCCAAGCAGGCTCAGGACTATGGAGACATAACTGTGGCAATGACATCAGAAATTGTTCT
TCCGGAATGGACCATCAGAGATTTCACAGTGAAAAATATCCAGACAAGTGAGAGTCACCCTCTGAGAC
AGTTCCATTTCACCTCCTGGCCAGACCACGGTGTTCCCGACACCACTGACCTGCTCATCAACTTCCGG
TACCTCGTTCGTGACTACATGAAGCAGAGTCCTCCCGAATCGCCGATTCTGGTGCATTGCAGTGCTGG
GGTCGGAAGGACGGGCACTTTCATTGCCATTGATCGTCTCATCTACCAGATAGAGAATGAGAACACCG
TGGATGTGTATGGGATTGTGTATGACCTTCGAATGCATAGGCCTTTAATGGTGCAGACAGAGGACCAG
TATGTTTTCCTCAATCAGTGTGTTTTGGATATTGTCAGATCCCAGAAAGACTCAAAAGTAGATCTTAT
CTACCAGAACACAACTGCAATGACAATCTATGAAAACCTTGCGCCCGTGACCACATTTGGAAAGACCA
ATGGTTACATCGCCTAA

Example 11: Design and construction of APRIL based CARs.

APRIL in its natural form is a secreted type II protein. The use of APRIL as a BCMA binding domain for a CAR requires conversion of this type II secreted protein to a type I membrane bound protein and for this protein to be stable and to retain binding to BCMA in this form. To generate candidate molecules, the extreme amino-terminus of APRIL was deleted to remove binding to proteoglycans. Next, a signal peptide was added to direct the nascent protein to the endoplasmic reticulum and hence the cell surface. Also, because the nature of spacer used can alter the function of a CAR, three different spacer domains were tested: an APRIL based CAR was generated comprising (i) a human IgG1 spacer altered to remove Fc binding motifs; (ii) a CD8 stalk; and (iii) the IgG1 hinge alone (cartoon in Figure 25 and amino acid sequences in Figure 26). These CARs were expressed in a bicistronic retroviral vector (Figure 27A) so that a marker protein – truncated CD34 could be co-expressed as a convenient marker gene.

Example 12: Expression and function of APRIL based CARs.

The aim of this study was to test whether the APRIL based CARs which had been constructed were expressed on the cell surface and whether APRIL had folded to form the native protein. T-cells were transduced with these different CAR constructs and stained using a commercially available anti-APRIL mAb, along with staining for the marker gene and analysed by flow-cytometry. The results of this experiment are shown in Figure 27B where APRIL binding is plotting against marker gene fluorescence. These data show that in this format, the APRIL based CARs are expressed on the cell surface and APRIL folds sufficiently to be recognized by an anti-APRIL mAb.

Next, it was determined whether APRIL in this format could recognize BCMA and TACI. Recombinant BCMA and TACI were generated as fusions with mouse IgG2a-Fc. These recombinant proteins were incubated with the transduced T-cells. After this, the cells were washed and stained with an anti-mouse fluorophore conjugated antibody and an antibody to detect the marker gene conjugated to a different fluorophore. The cells were analysed by flow cytometry and the results are presented in Figure 27C. The different CARs were able to bind both BCMA and TACI. Surprisingly, the CARs were better able to bind BCMA than TACI. Also, surprisingly CARs with a CD8 stalk or IgG1 hinge spacer were better able to bind BCMA and TACI than CAR with an Fc spacer.

Example 13: APRIL based chimeric antigen receptors are active against BCMA expressing cells

T-cells from normal donors were transduced with the different APRIL CARs and tested against SupT1 cells either wild-type, or engineered to express BCMA and TACI. Several different assays were used to determine function. A classical chromium release assay was performed. Here, the target cells (the SupT1 cells) were labelled with 51Cr and mixed with effectors (the transduced T-cells) at different ratio. Lysis of target cells was determined by counting 51Cr in the co-culture supernatant (Figure 28A shows the cumulative data).

In addition, supernatant from T-cells cultured 1:1 with SupT1 cells was assayed by ELISA for Interferon-gamma (Figure 28B shows cumulative data). Measurement of T-cell expansion after one week of co-culture with SupT1 cells was also performed (Figure 28C). T-cells were counted by flow-cytometry calibrated with counting beads. These experimental data show that APRIL based CARs can kill BCMA expressing targets. Further, these data show that CARs based on the CD8 stalk or IgG1 hinge performed better than the Fc-pvaa based CAR.

Example 14: Functional analysis of the AND gate in primary cells

PBMCs were isolated from blood and stimulated using PHA and IL-2. Two days later the cells were transduced on retronectin coated plates with retro virus containing the CD19:CD33 AND gate construct. On day 5 the expression level of the two CARs translated by the AND gate construct was evaluated via flow cytometry and the cells were depleted of CD56+ cells (predominantly NK cells). On day 6 the PBMCs were placed in a co-culture with target cells at a 1:2 effector to target cell ratio. On day 8 the supernatant was collected and analysed for IFN-gamma secretion via ELISA (Figure 29).

These data demonstrate that the AND gate functions in primary cells.

All publications mentioned in the above specification are herein incorporated by reference. Various modifications and variations of the described methods and system of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the 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 molecular biology, cell biology or related fields are intended to be within the scope of the following claims.

EDITORAL NOTE

2014351557

Please note that there is no page

78. The claim pages start at 79 to

82

2014351557 25 Mar 2019

CLAIMS

1. A T cell which co-expresses a first chimeric antigen receptor (CAR) and second CAR at the cell surface, each CAR comprising:

(i) an antigen-binding domain;

(ii) a spacer

(iii) a trans-membrane domain; and

(iv) an endodomain

wherein the antigen binding domains of the first and second CARs bind to different antigens, wherein the spacer of the first CAR is different to the spacer of the second CAR and wherein one of the first or second CARs is an activating CAR comprising an activating endodomain and the other CAR is an inhibitory CAR comprising a ligation-off inhibitory endodomain.

2. A T cell according to claim 1, wherein the spacer of the first CAR has a different length and/or charge and/or size and/or configuration and/or glycosylation of the spacer of the second CAR, such that when the first CAR and the second CAR bind their respective target antigens, the first CAR and second CAR become spatially separated on the T cell membrane.

3. A T cell according to claim 2, wherein either the first spacer or the second spacer comprises a CD8 stalk and the other spacer comprises the hinge, CH2 and CH3 domain of IgG1.

4. A T cell according to claim 2 or 3, wherein the inhibitory endodomain comprises all or part of the endodomain from CD148 or CD45.

5 A T cell according to claim 4, wherein the antigen-binding domain of the first CAR binds CD5 and the antigen-binding domain of the second CAR binds CD19.

6. A T cell which comprises more than two CARs as defined in the preceding claims such that it is specifically stimulated by a cell, such as a T cell, bearing a distinct pattern of more than two antigens.

7. A nucleic acid sequence encoding both the first and second chimeric antigen receptors (CARs) as defined in any of claims 1 to 6.

8. A nucleic acid sequence according to claim 7, which has the following structure:

2014351557 25 Mar 2019

AgB1-spacer1-TM1-endo1-coexpr-AbB2-spacer2-TM2-endo2

in which
AgB1 is a nucleic acid sequence encoding the antigen-binding domain of the first CAR;
spacer 1 is a nucleic acid sequence encoding the spacer of the first CAR;
TM1 is a nucleic acid sequence encoding the transmembrane domain of the first CAR;
endo 1 is a nucleic acid sequence encoding the endodomain of the first CAR;
coexpr is a nucleic acid sequence enabling co-expression of both CARs
AgB2 is a nucleic acid sequence encoding the antigen-binding domain of the second CAR;
spacer 2 is a nucleic acid sequence encoding the spacer of the second CAR;
TM2 is a nucleic acid sequence encoding the transmembrane domain of the second CAR;
endo 2 is a nucleic acid sequence encoding the endodomain of the second CAR;
which nucleic acid sequence, when expressed in a T cell, encodes a polypeptide which is cleaved at the cleavage site such that the first and second CARs are co-expressed at the T cell surface.

9. A nucleic acid sequence according to claim 8, wherein coexpr encodes a sequence comprising a self-cleaving peptide.

10. A nucleic acid sequence according to claim 9 wherein alternative codons are used in regions of sequence encoding the same or similar amino acid sequences, in order to avoid homologous recombination.

11. A kit which comprises

(i) a first nucleic acid sequence encoding the first chimeric antigen receptor (CAR) as defined in any of claims 1 to 6, which nucleic acid sequence has the following structure:

AgB1-spacer1-TM1-endo1
in which
AgB1 is a nucleic acid sequence encoding the antigen-binding domain of the first CAR;
spacer 1 is a nucleic acid sequence encoding the spacer of the first CAR;
TM1 is a nucleic acid sequence encoding the transmembrane domain of the first CAR;
endo 1 is a nucleic acid sequence encoding the endodomain of the first CAR; and

(ii) a second nucleic acid sequence encoding the second chimeric antigen receptor (CAR) as defined in any of claims 1 to 7, which nucleic acid sequence has the following structure:

AgB2-spacer2-TM2-endo2
AgB2 is a nucleic acid sequence encoding the antigen-binding domain of the second CAR;
spacer 2 is a nucleic acid sequence encoding the spacer of the second CAR;
TM2 is a a nucleic acid sequence encoding the transmembrane domain of the second CAR;
endo 2 is a nucleic acid sequence encoding the endodomain of the second CAR.

12. A kit comprising: a first vector which comprises the first nucleic acid sequence as defined in claim 11; and a second vector which comprises the second nucleic acid sequence as defined in claim 11.

13. A kit according to claim 12, wherein the vectors are integrating viral vectors or transposons.

14. A vector comprising a nucleic acid sequence according to any of claims 7to 10.

15. A retroviral vector or a lentiviral vector or a transposon according to claim 14.

16. A method for making a T cell according to any of claim 1 to 6, which comprises the step of introducing: a nucleic acid sequence according to any of claims 7 to 10; a first nucleic acid sequence and a second nucleic acid sequence as defined in claim 11; and/or a first vector and a second vector as defined in claim 12 or a vector according to claim 14 or 15, into a T cell.

17. A method according to claim 16, wherein the T cell is from a sample isolated from a subject.

18 A pharmaceutical composition comprising a plurality of T cells according to any of claims 1 to 6.

19. A method for treating and/or preventing a disease, which comprises the step of administering a pharmaceutical composition according to claim 18 to a subject.

20. A method according to claim 19, which comprises the following steps:

(i) isolation of a T cell-containing sample from a subject;

(ii) transduction or transfection of the T cells with: a nucleic acid sequence according to any of claims 7 to 10; a first nucleic acid sequence and a second nucleic acid sequence as

defined in claim 11; a first vector and a second vector as defined in claim 12 or 13 or a vector according to claim 14 or 15; and

(iii) administering the T cells from (ii) to the subject.

21. A method according to claim 19 or 20, wherein the disease is a cancer.

22. A pharmaceutical composition according to claim 18 for use in treating and/or preventing a disease.

23. The use of a T cell according to any of claims 1 to 6 in the manufacture of a medicament for treating and/or preventing a disease.

24. A natural killer (NK) cell which co-expresses a first chimeric antigen receptor (CAR) and second CAR at the cell surface, each CAR comprising:

(i) an antigen-binding domain;

(ii) a spacer

(iii) a trans-membrane domain; and

(iv) an endodomain

wherein the antigen binding domains of the first and second CARs bind to different antigens, wherein the spacer of the first CAR is different to the spacer of the second CAR and wherein one of the first or second CARs is an activating CAR comprising an activating endodomain and the other CAR is an inhibitory CAR comprising a ligation-off inhibitory endodomain.

25. A cell composition comprising CAR expressing T cells according to claim 1 and/or CAR expressing NK cells according to claim 25 made by tranducing a blood-sample ex vivo with a nucleic acid encoding the first and second CARs

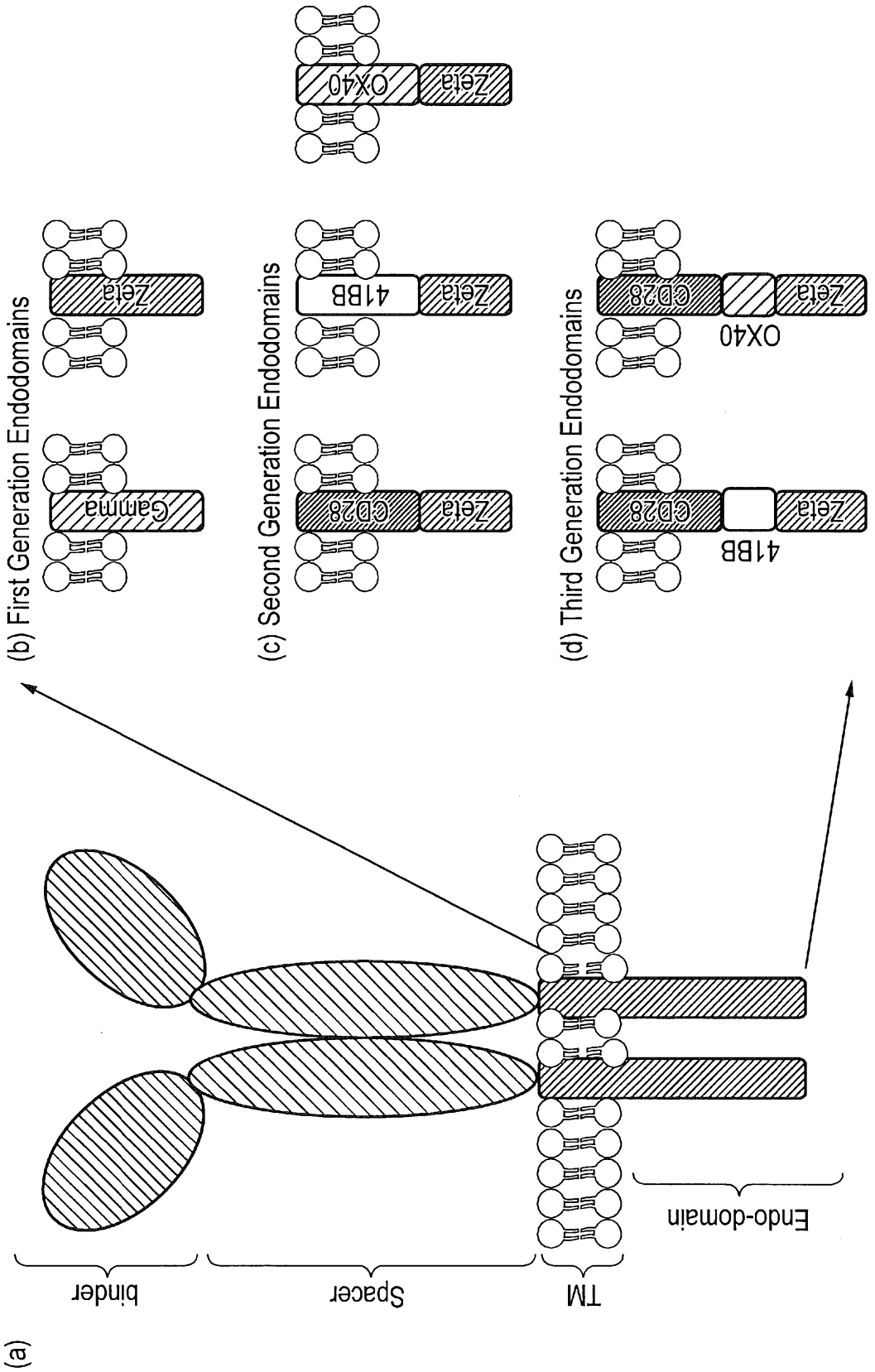

(a)
binder
Spacer
TM
Endo-domain
(b) First Generation Endodomains
Zeta
Gamma
(c) Second Generation Endodomains
Zeta
41BB
Zeta
CD28
Zeta
OX40
(d) Third Generation Endodomains
Zeta
CD28
OX40
Zeta
CD28
41BB

FIG. 1

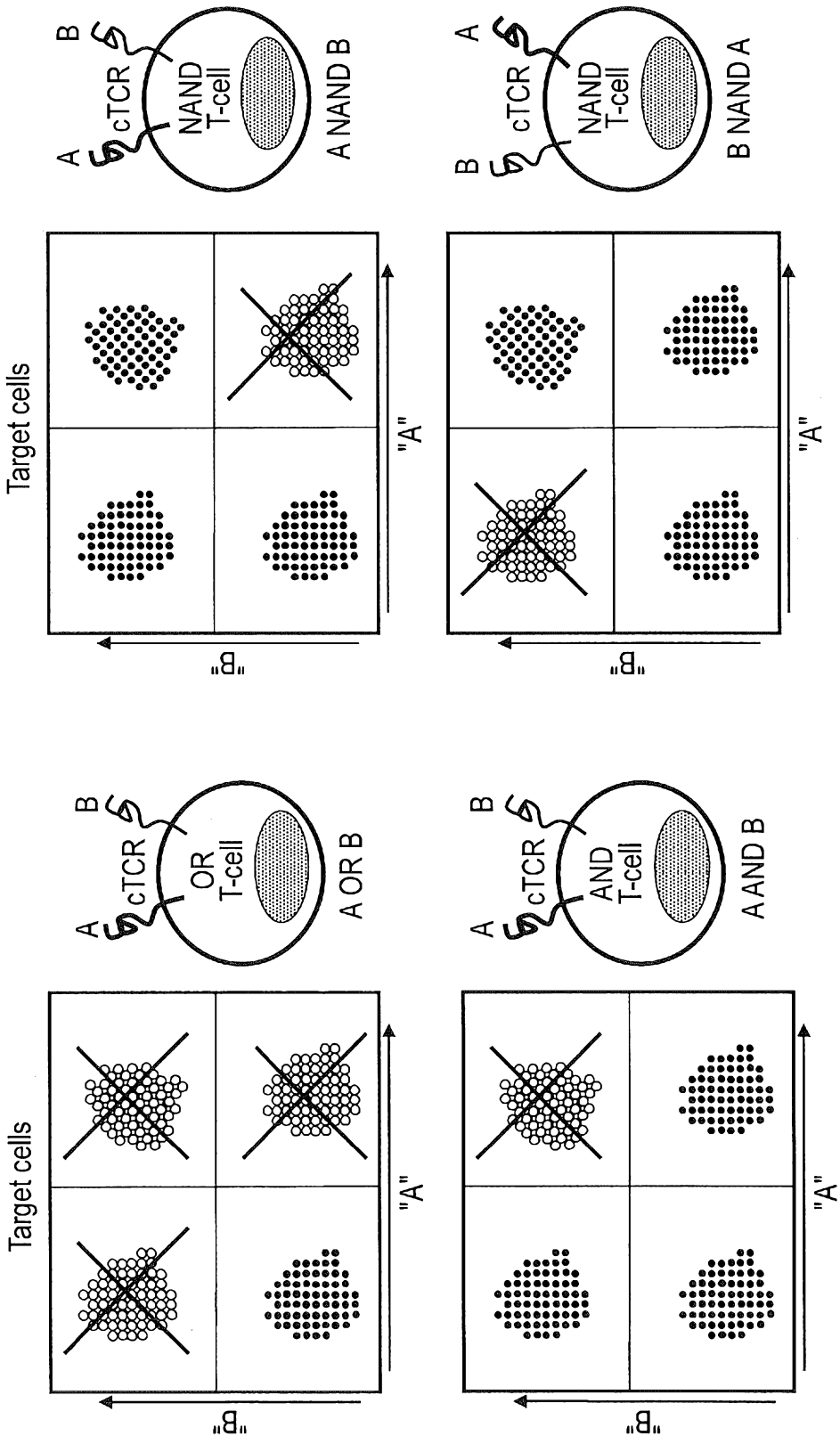

A
B
cTCR
NAND
T-cell
A NAND B
B NAND A
AND
T-cell
A AND B
OR
T-cell
A OR B
Target cells
"A"
"B"

FIG. 2

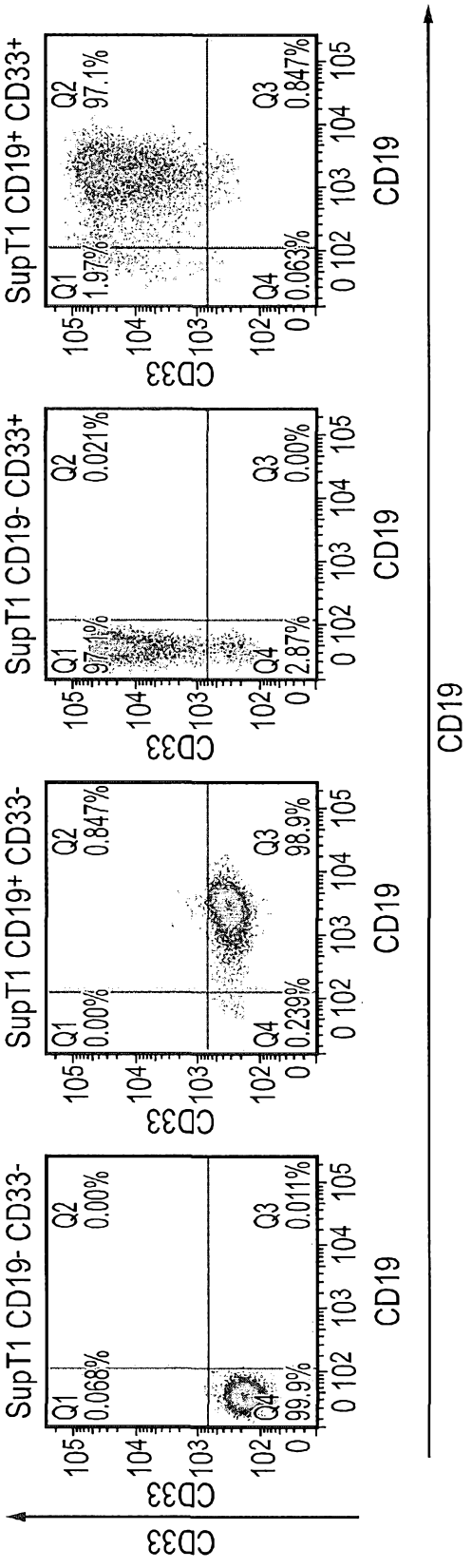

SupT1 CD19- CD33-
Q1 0.068%
Q2 0.00%
Q4 99.9%
Q3 0.011%
SupT1 CD19+ CD33-
Q1 0.00%
Q2 0.847%
Q4 0.239%
Q3 98.9%
SupT1 CD19- CD33+
Q1 97.1%
Q2 0.021%
Q4 2.87%
Q3 0.00%
SupT1 CD19+ CD33+
Q1 1.97%
Q2 97.1%
Q4 0.063%
Q3 0.847%
CD33
CD19
0 102 103 104 105

FIG. 3

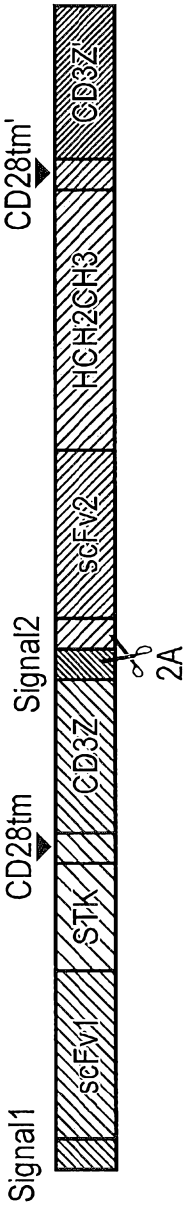

Signal1
scFv1
STK
CD28tm
CD3Z
Signal2
2A
scFv2
HCH2CH3
CD28tm'
CD3Z

FIG. 4

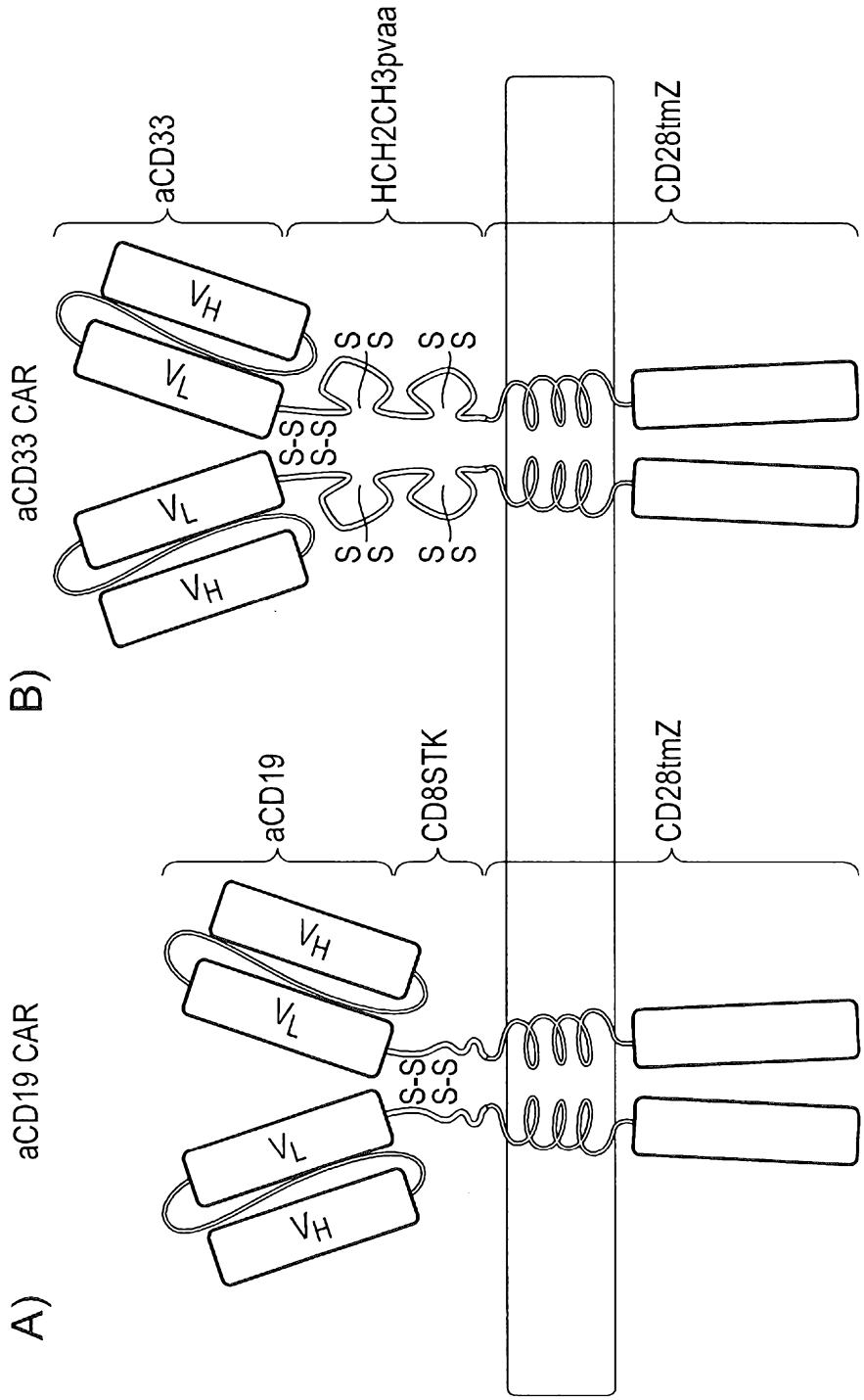

A)
aCD19 CAR
aCD19
CD8STK
CD28tmZ
VH
VL
S-S
B)
aCD33 CAR
aCD33
HCH2CH3pvaa
CD28tmZ
S

FIG. 5

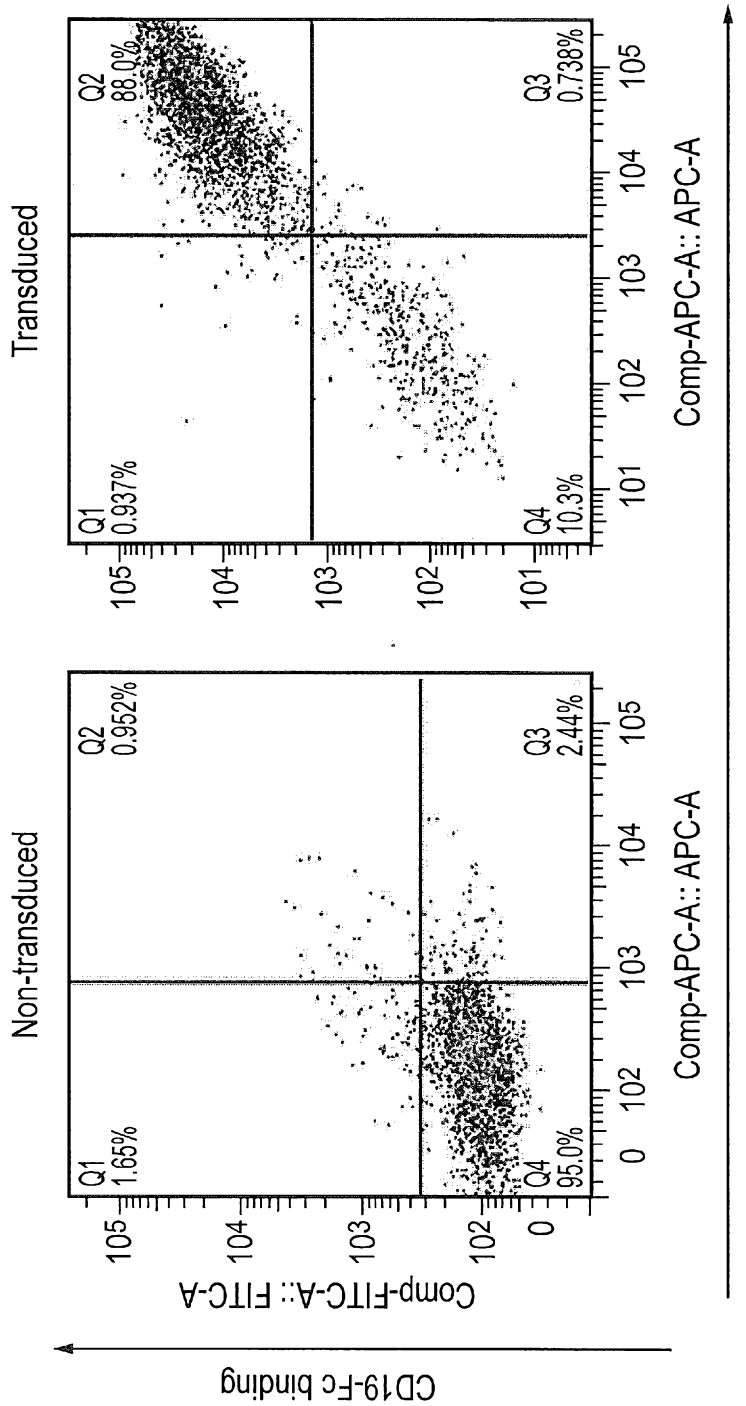

Non-transduced
Transduced
Q1
1.65%
Q2
0.952%
Q3
2.44%
Q4
95.0%
Q1
0.937%
Q2
88.0%
Q3
0.738%
Q4
10.3%
Comp-FITC-A:: FITC-A
Comp-APC-A:: APC-A
CD19-Fc binding
CD33-Fc binding

FIG. 6

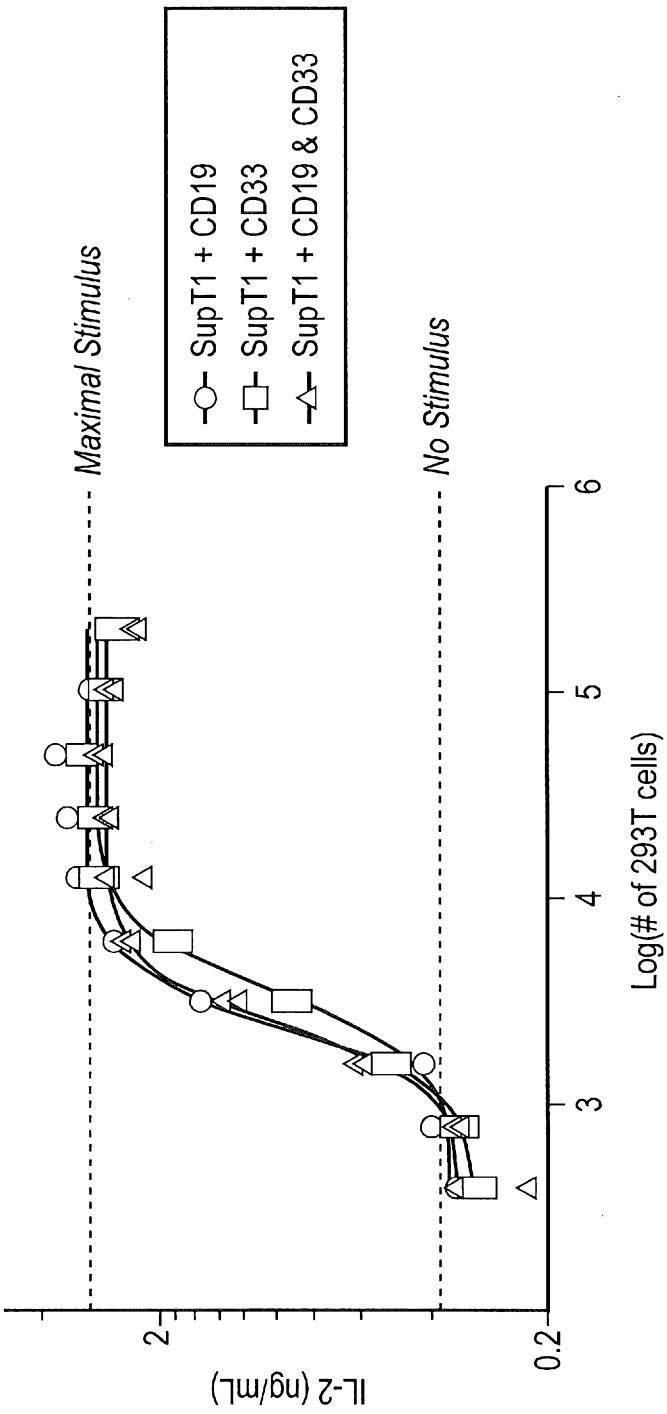

SupT1 + CD19
SupT1 + CD33
SupT1 + CD19 & CD33
Maximal Stimulus
No Stimulus
IL-2 (ng/mL)
2
0.2
3
4
5
6
Log(# of 293T cells)

FIG. 7

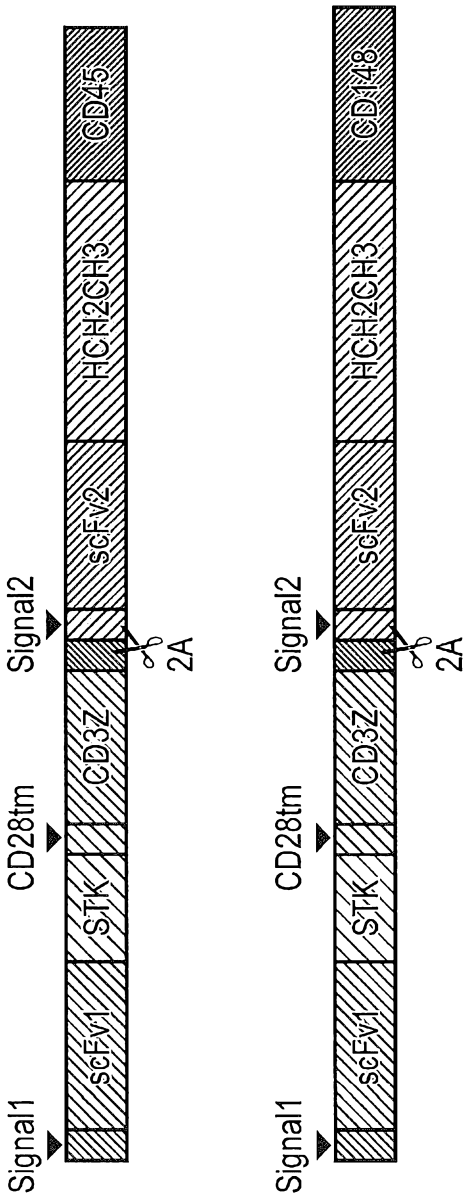

Signal1
scFv1
STK
CD28tm
CD3Z
2A
Signal2
scFv2
HCH2CH3
CD45
Signal1
scFv1
STK
CD28tm
CD3Z
2A
Signal2
scFv2
HCH2CH3
CD148

FIG. 8

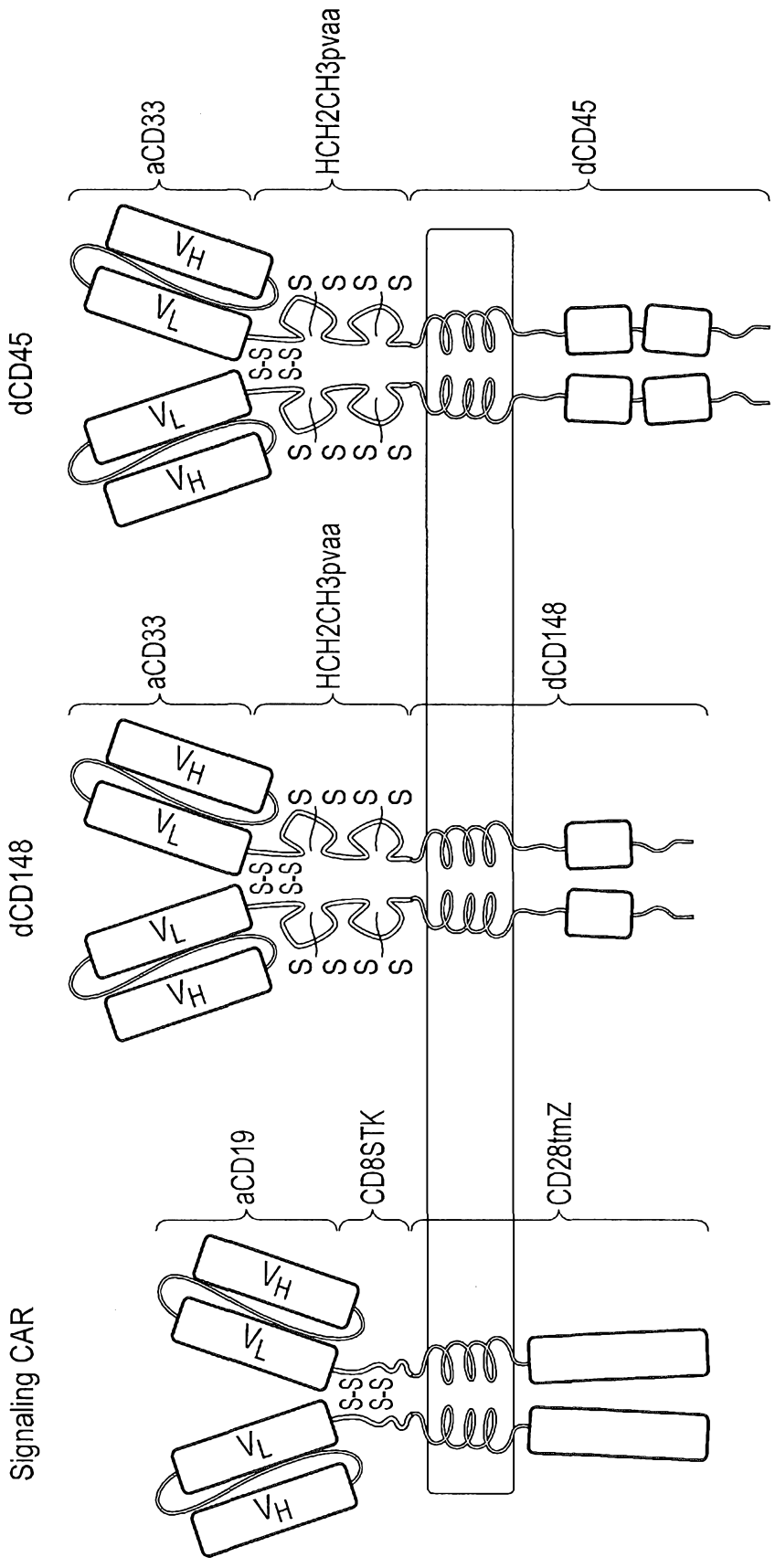

Signaling CAR
aCD19
CD8STK
CD28tmZ
dCD148
aCD33
HCH2CH3pvaa
dCD148
dCD45
aCD33
HCH2CH3pvaa
dCD45
VH
VL
S-S
S

FIG. 9

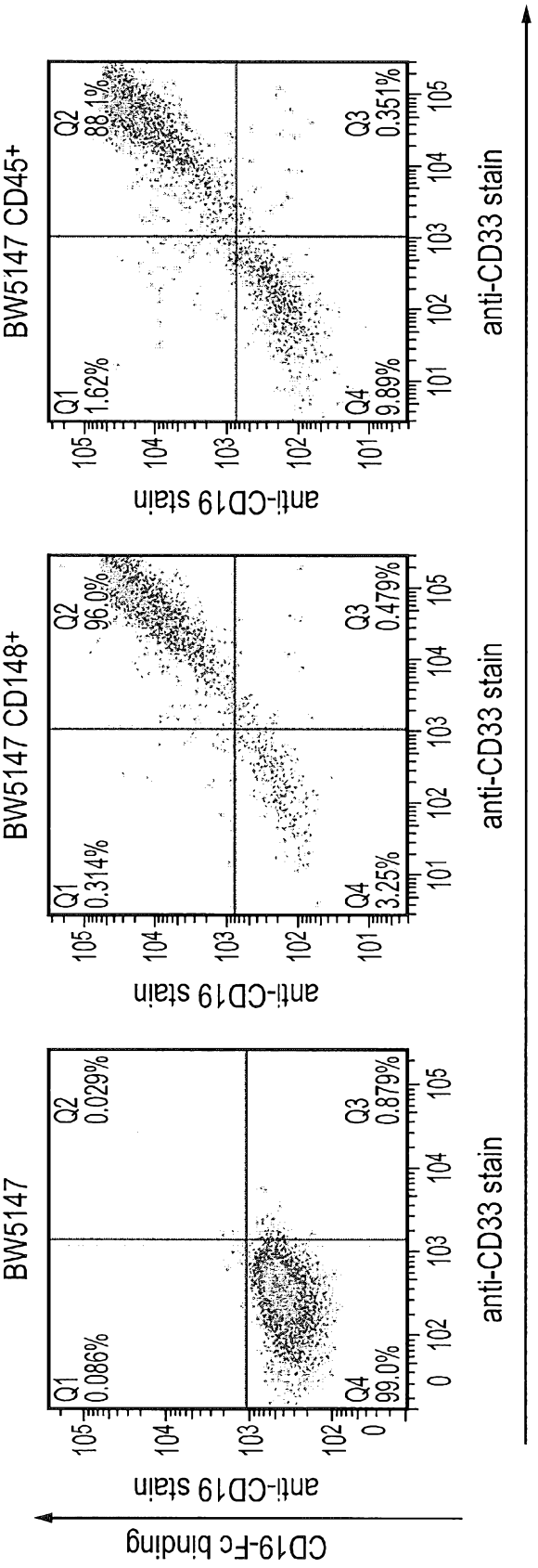

BW5147
BW5147 CD148+
BW5147 CD45+
Q1
0.086%
Q2
0.029%
Q3
0.879%
Q4
99.0%
Q1
0.314%
Q2
96.0%
Q3
0.479%
Q4
3.25%
Q1
1.62%
Q2
88.1%
Q3
0.351%
Q4
9.89%
anti-CD19 stain
anti-CD33 stain
CD19-Fc binding
CD33-Fc binding

FIG. 10

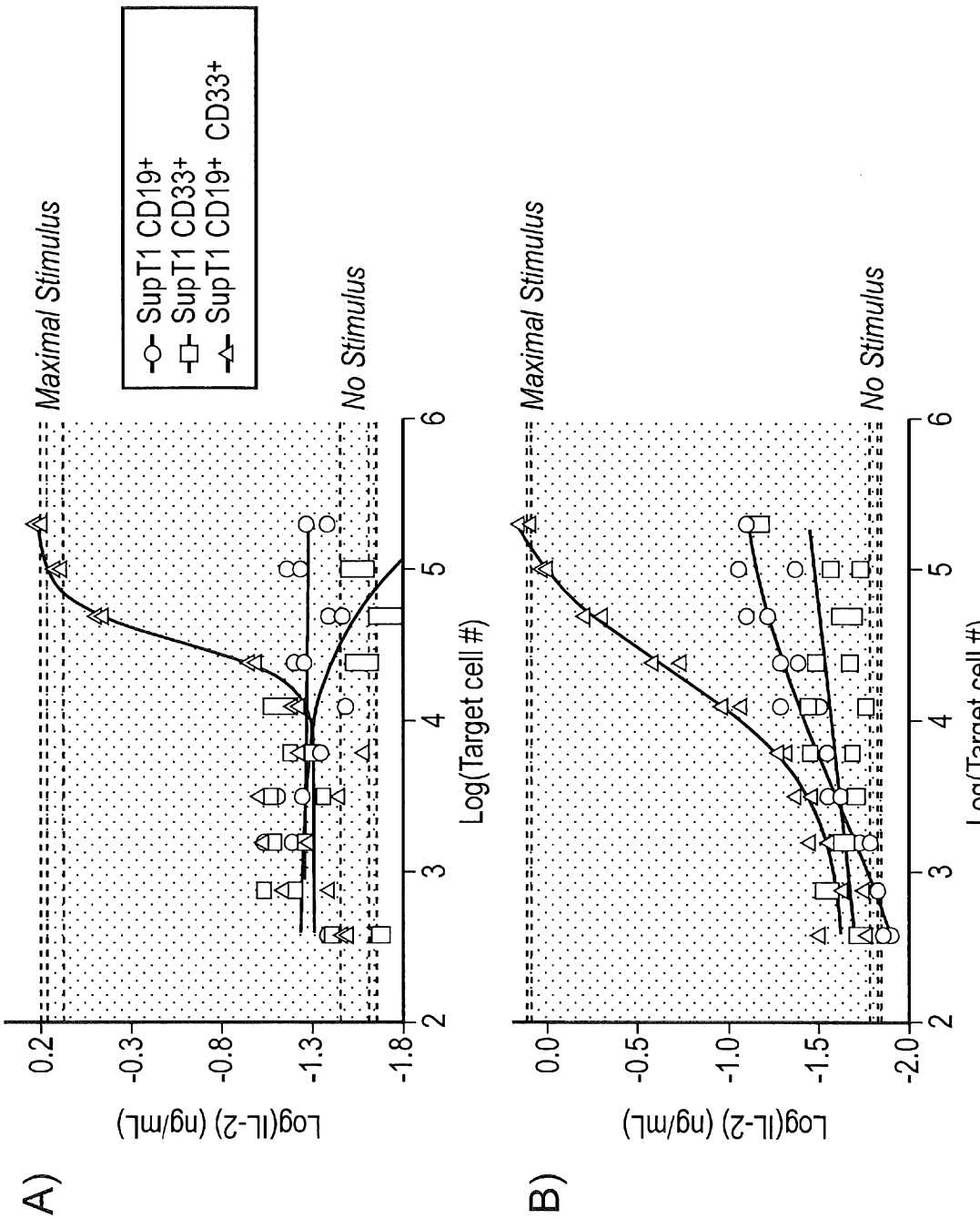

A)
B)
Maximal Stimulus
No Stimulus
SupT1 CD19+
SupT1 CD33+
SupT1 CD19+ CD33+
Log(IL-2) (ng/mL)
Log(Target cell #)
0.2
-0.3
-0.8
-1.3
-1.8
0.0
-0.5
-1.0
-1.5
-2.0
2
3
4
5
6

FIG. 11

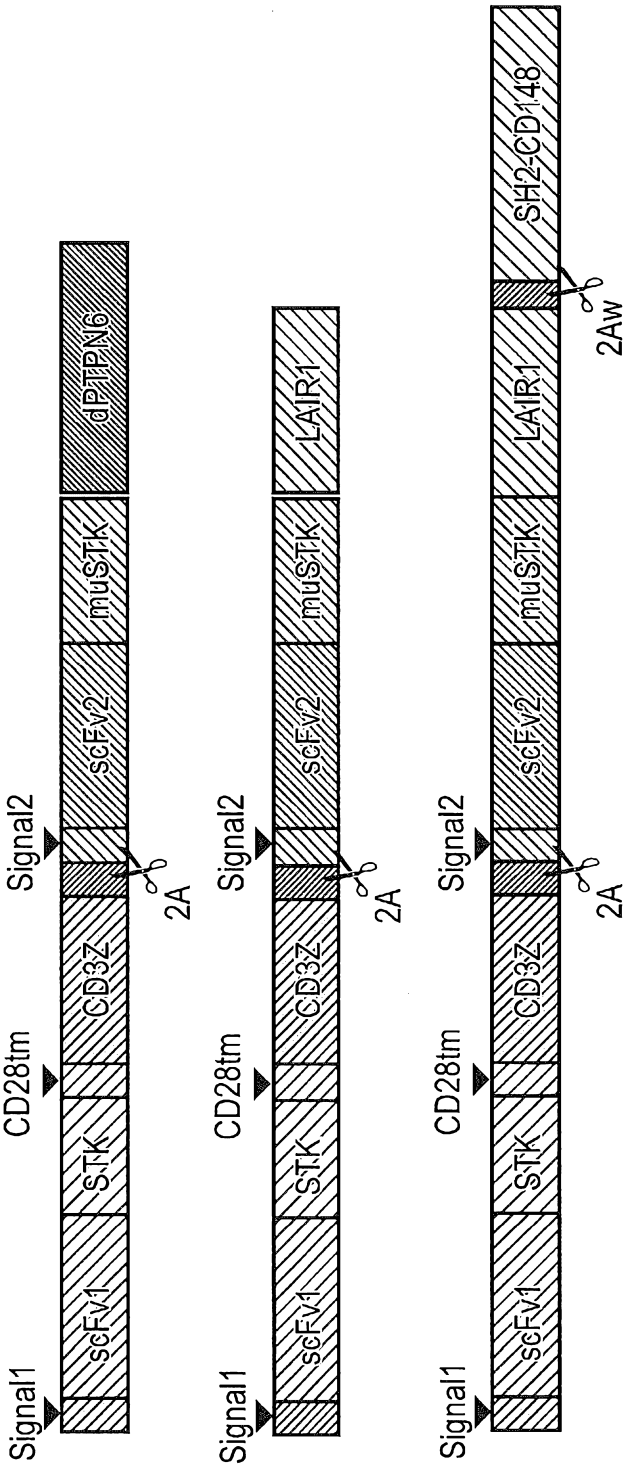

Signal1
scFv1
STK
CD28tm
CD3Z
2A
Signal2
scFv2
muSTK
dPTPN6
Signal1
scFv1
STK
CD28tm
CD3Z
2A
Signal2
scFv2
muSTK
LAIR1
Signal1
scFv1
STK
CD28tm
CD3Z
2A
Signal2
scFv2
muSTK
LAIR1
2Aw
SH2-CD148

FIG. 12

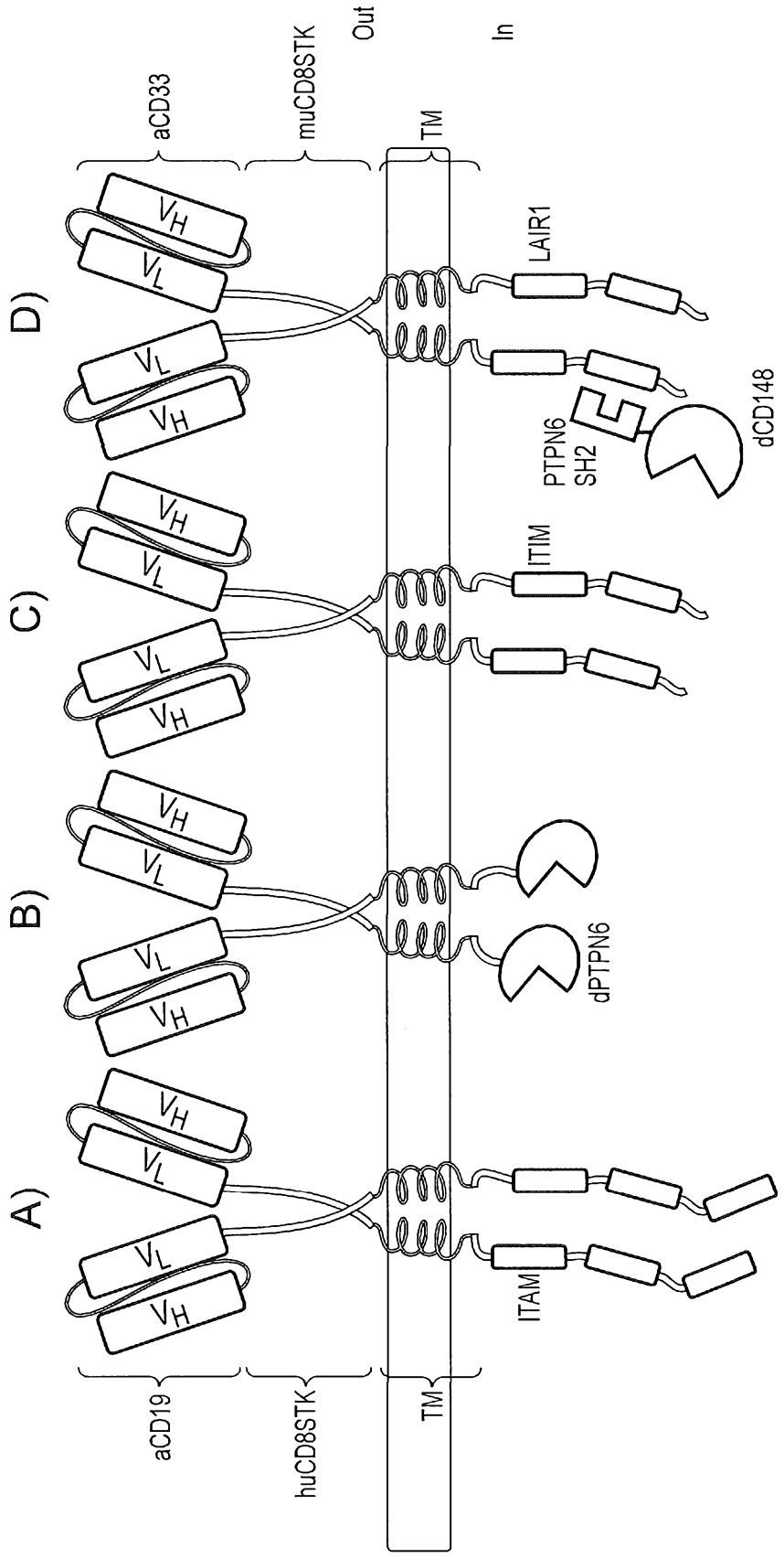

A)
B)
C)
D)
aCD19
huCD8STK
TM
aCD33
muCD8STK
TM
Out
In
ITAM
dPTPN6
ITIM
LAIR1
PTPN6
SH2
dCD148

FIG. 13

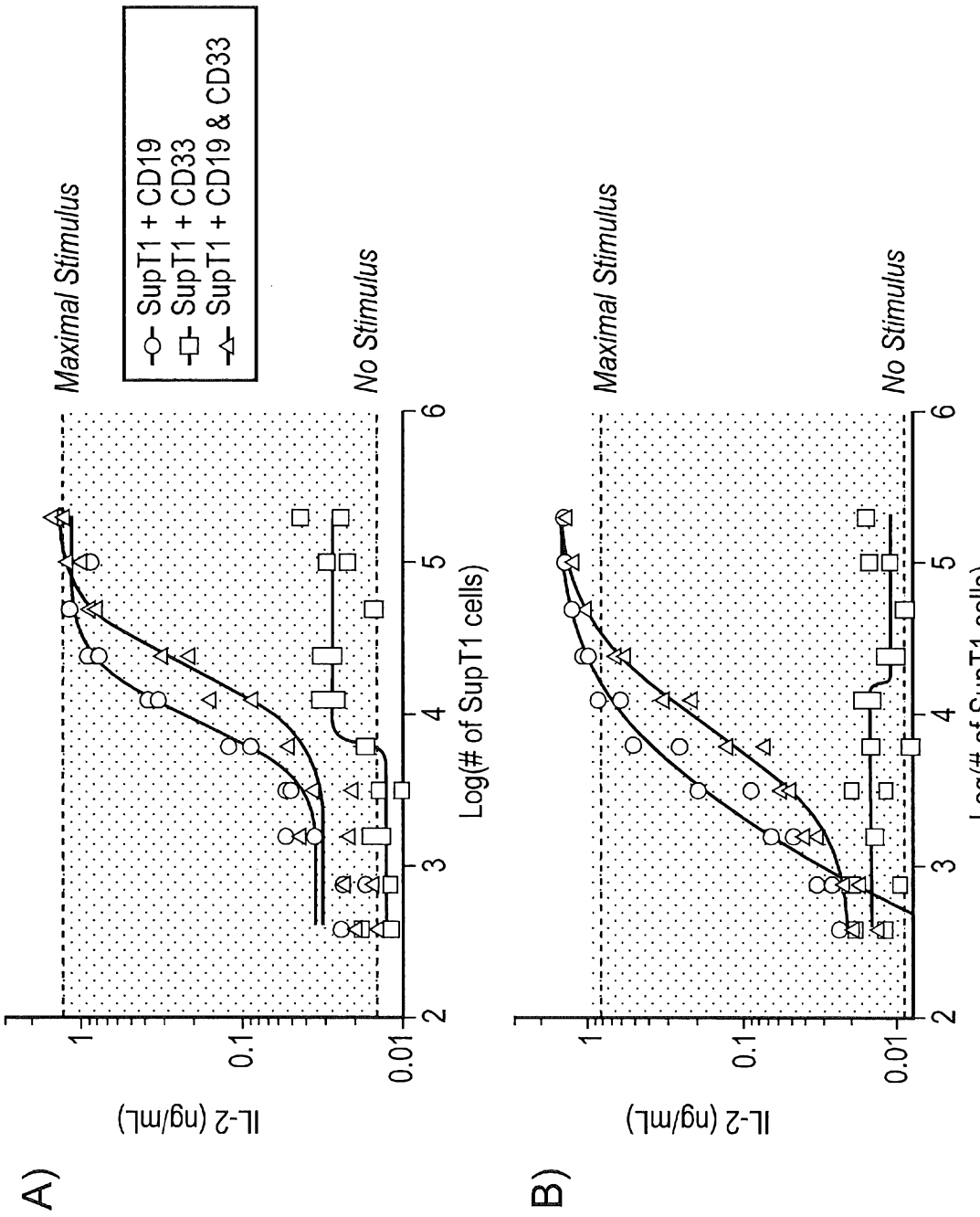

A)
B)
IL-2 (ng/mL)
Log(# of SupT1 cells)
Maximal Stimulus
No Stimulus
SupT1 + CD19
SupT1 + CD33
SupT1 + CD19 & CD33
0.01
0.1
1
2
3
4
5
6

FIG. 14

>MP13974.SFG.aCD19fmc63_clean-CD8STK-CD28tmZ-2A-aCD33glx-HCH2CH3pvaa-CD28tmZw

MSLPVTALLLPLALLLHAARPDIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDGTVKLLIYHTSRLHSGVPSRF
SGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTKLEITKAGGGGSGGGGSGGGGSGGGGSEVKLQESGPGLVAPSQ
SLSVTCTVSGVSLPDYGVSWIRQPPRKGLEWLGVIWGSETTYYNSALKSRLTIIKDNSKSQVFLKMNSLQTDDTAIYYCAKHY
YYGGSYAMDYWGQGTSVTVS**SDP**TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIFWVLVVVGGVLACY
SLLVTVAFIIFWVRRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAE
AYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR**RAEGRGSLLTCGDVEENPGP**MAVPTQVLGLLLLWLTDARC
DIQMTQSPSSLSASVGDRVTITCRASEDIYFNLVWYQQKPGKAPKLLIYDTNRLADGVPSRFSGSGSGTQYTLTISSLQPEDF
ATYYCQHYKNYPLTFGQGTKLEIKRSGGGGSGGGGSGGGGSGGGGSRSEVQLVESGGGLVQPGGSLRLSCAASGFTLSNYGMH
WIRQAPGKGLEWVSSISLNGGSTYYRDSVKGRFTISRDNAKSTLYLQMNSLRAEDTAVYYCAAQDAYTGGYFDYWGQGTLVTV
SS**MDP**AEPKSPDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMIARTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSD
IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKKDPKFWVLVVVG
GVLACYSLLVTVAFIIFWVRSRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL
QKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

Region	*Description*
Signal1	Signal peptide 1
scFv1	scFv 1 – anti-CD19
SDP	Linker and chain break
STK	CD8alpha stalk
CD28tmZ	CD28 transmembrane domain and CD3 Zeta endodomain
FMD-2A	Foot-and-mouth disease 2A peptide
Signal2	Signal peptide 2
scFv2	scFv 2 – anti-CD33
MDP	Linker and chain break
HCH2CH3	Hinge, CH2 and CH3 of human IgG1
CD28tmZ'	CD28 transmembrane domain and CD3 Zeta endodomain

FIG. 15

>MP14801.SFG.aCD19fmc63_clean-CD8STK-CD28tmZ-2A-aCD33glx-HCH2CH3pvaa-dCD148

MSLPVTALLLPLALLLHAARPDIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDGTVKLLIYHTSRLHSGVPSRF
SGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTKLEITKAGGGGSGGGGSGGGGSGGGGSEVKLQESGPGLVAPSQ
SLSVTCTVSGVSLPDYGVSWIRQPPRKGLEWLGVIWGSETTYYNSALKSRLTIIKDNSKSQVFLKMNSLQTDDTAIYYCAKHY
YYGGSYAMDYWGQGTSVTVSSDPTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIFWVLVVVGGVLACY
SLLVTVAFIIFWVRRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAE
AYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPRRAEGRGSLLTCGDVEENPGPMAVPTQVLGLLLLWLTDARC
DIQMTQSPSSLSASVGDRVTITCRASEDIYFNLVWYQQKPGKAPKLLIYDTNRLADGVPSRFSGSGSGTQYTLTISSLQPEDF
ATYYCQHYKNYPLTFGQGTKLEIKRSGGGGSGGGGSGGGGSGGGGSRSEVQLVESGGGLVQPGGSLRLSCAASGFTLSNYGMH
WIRQAPGKGLEWVSSISLSNGGSTYYRDSVKGRFTLSRDNAKSTLYLQMNSLRAEDTAVYYCAAQDAYTGGYEDYWGQGTLVTV
SSMDPAEPKSPDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMIARTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSD
IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKKDPKAVFGCIFG
ALVIVTVGGFIFWRKKRKDAKNNEVSFSQIKPKKSKLIRVENFEAYFKKQQADSNCGFAEEYEDLKLVGISQPKYAAELAENR
GKNRYNNVLPYDISRVKLSVQTHSTDDYINANYMPGYHSKKDFIATQGPLPNTLKDFWRMVWEKNVYAIIMLTKCVEQGRTKC
EEYWPSKQAQDYGDITVAMTSEIVLPEWTIRDFTVKNIQTSESHPLRQFHFTSWPDHGVPDTTDLLINFRYLVRDYMKQSPPE
SPILVHCSAGVGRTGTFIAIDRLIYQIENENTVDVYGIVYDLRMHRPLMVQTEDQYVFLNQCVLDIVRSQKDSKVDLIYQNTT
AMTIYENLAPVTTFGKTNGYIA

MP14802. SFG.aCD19fmc63_clean-CD8STK-CD28tmZ-2A-aCD33glx-HCH2CH3pvaa-dCD45

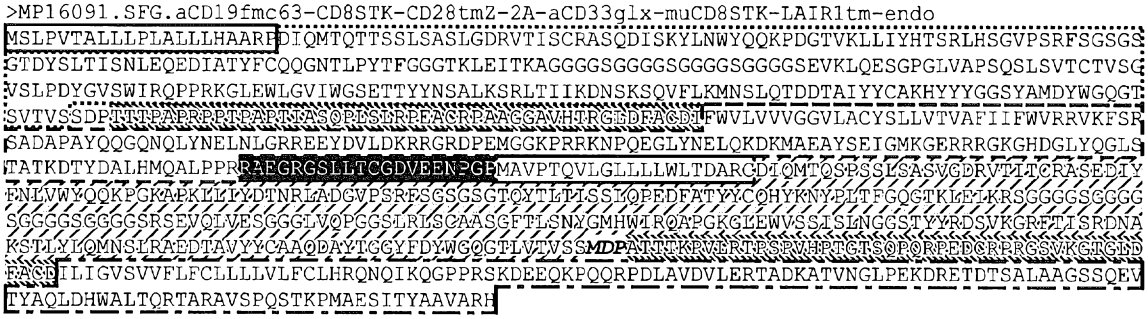
MSLPVTALLLPLALLLHAARPDIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDGTVKLLIYHTSRLHSGVPSRF
SGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTKLEITKAGGGGSGGGGSGGGGSGGGGSEVKLQESGPGLVAPSQ
SLSVTCTVSGVSLPDYGVSWIRQPPRKGLEWLGVIWGSETTYYNSALKSRLTIIKDNSKSQVFLKMNSLQTDDTAIYYCAKHY
YYGGSYAMDYWGQGTSVTVSSDPTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIFWVLVVVGGVLACY
SLLVTVAFIIFWVRRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAE
AYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPRRAEGRGSLLTCGDVEENPGPMAVPTQVLGLLLLWLTDARC
DIQMTQSPSSLSASVGDRVTITCRASEDIYFNLVWYQQKPGKAPKLLIYDTNRLADGVPSRFSGSGSGTQYTLTISSLQPEDF
ATYYCQHYKNYPLTFGQGTKLEIKRSGGGGSGGGGSGGGGSGGGGSRSEVQLVESGGGLVQPGGSLRLSCAASGFTLSNYGMH
WIRQAPGKGLEWVSSISLSNGGSTYYRDSVKGRFTISRDNAKSTLYLQMNSLRAEDTAVYYCAAQDAYTGGYFDYWGQGTLVTV
SSMDPAEPKSPDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMIARTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSD
IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKKDPKALIAFLAF
LIIVTSIALLVVLYKIYDLHKKRSCNLDEQQELVERDDEKQLMNVEPIHADILLETYKRKIADEGRLFLAEFQSIPRVFSKFP
IKEARKPFNQNKNRYVDILPYDYNRVELSEINGDAGSNYINASYIDGFKEPRKYIAAQGPRDETVDDFWRMIWEQKATVIVMV
TRCEEGNRNKCAEYWPSMEEGTRAFGDVVVKINQHKRCPDYIIQKLNIVNKKEKATGREVTHIQFTSWPDHGVPEDPHLLLKL
RRRVNAFSNFFSGPIVVHCSAGVGRTGTYIGIDAMLEGLEAENKVDVYGYVVKLRRQRCLMVQVEAQYILIHQALVEYNQFGE
TEVNLSELHPYLHNMKKRDPPSEPSPLEAEFQRLPSYRSWRTQHIGNQEENKSKNRNSNVIPYDYNRVPLKHELEMSKESEHD
SDESSDDDSDSEEPSKYINASFIMSYWKPEVMIAAQGPLKETIGDFWQMIFQRKVKVIVMLTELKHGDQEICAQYWGEGKQTY
GDIEVDLKDTDKSSTYTLRVFELRHSKRKDSRTVYQYQYTNWSVEQLPAEPKELISMIQVVKQKLPQKNSSEGNKHHKSTPLL
IHCRDGSQQTGIFCALLNLLESAETEEVVDIFQVVKALRKARPGMVSTFEQYQFLYDVIASTYPAQNGQVKKNNHQEDKIEFD
NEVDKVKQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGPASPALNQGS

Region	*Description*
Signal1	Signal peptide 1
scFv1	scFv 1 – anti-CD19
SDP	Linker and chain break
STK	CD8alpha stalk
CD28tmZ	CD28 transmembrane domain and CD3 Zeta endodomain
FMD-2A	Foot-and-mouth disease 2A peptide
Signal2	Signal peptide 2
scFv2	scFv 2 – anti-CD33
MDP	Linker and chain break
HCH2CH3	Hinge, CH2 and CH3 of human IgG1
dCD148 / dCD45	Trans-membrane and endo-domains of CD148 and CD45

FIG. 16

>16076.SFG.aCD19fmc63-CD8STK-CD28tmZ-2A-aCD33glx-muCD8STK-tm-dPTPN6

>MP16091.SFG.aCD19fmc63-CD8STK-CD28tmZ-2A-aCD33glx-muCD8STK-LAIR1tm-endo



>MP16092.SFG.aCD19fmc63-CD8STK-CD28tmZ-2A-aCD33glx-muCD8STK-LAIR1tm-endo-2A-PTPN6_SH2-dCD148

Region	*Description*
Signal1	Signal peptide 1
scFv1	scFv 1 – anti-CD19
SDP	Linker and chain break
STK	Human CD8alpha stalk
CD28tmZ	CD28 transmembrane domain and CD3 Zeta endodomain
FMD-2A	Foot-and-mouth disease 2A peptide
Signal2	Signal peptide 2
scFv2	scFv 2 – anti-CD33
MDP	Linker and chain break
STK	Mouse CD8alpha stalk
dLAIR1	Hinge, CH2 and CH3 of human IgG1
dPTPN6	Phosphatase domain of PTPN6
FMD-2A	Foot-and-mouth disease 2A peptide codon wobbled
PTPN6-SH2	SH2 domain of PTPN6
SGGGGS	Serine glycine linker and chain break
dCD148	Phosphatase domain of CD148

FIG. 17

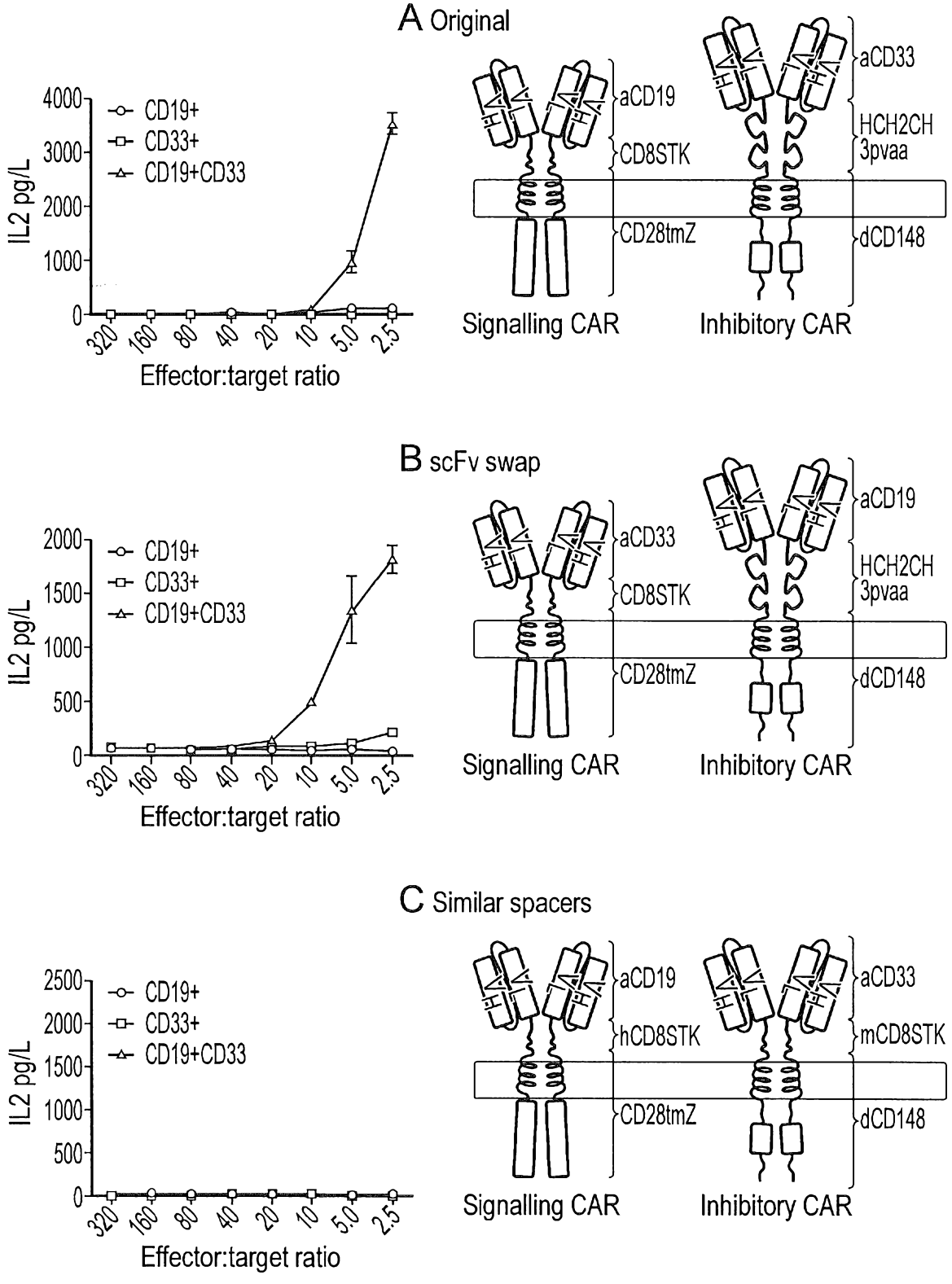

A Original
IL2 pg/L
4000
3000
2000
1000
0
CD19+
CD33+
CD19+CD33
320
160
80
40
20
10
5.0
2.5
Effector:target ratio
aCD19
CD8STK
CD28tmZ
aCD33
HCH2CH
3pvaa
dCD148
Signalling CAR
Inhibitory CAR
B scFv swap
IL2 pg/L
2000
1500
1000
500
0
CD19+
CD33+
CD19+CD33
320
160
80
40
20
10
5.0
2.5
Effector:target ratio
aCD33
CD8STK
CD28tmZ
aCD19
HCH2CH
3pvaa
dCD148
Signalling CAR
Inhibitory CAR
C Similar spacers
IL2 pg/L
2500
2000
1500
1000
500
0
CD19+
CD33+
CD19+CD33
320
160
80
40
20
10
5.0
2.5
Effector:target ratio
aCD19
hCD8STK
CD28tmZ
aCD33
mCD8STK
dCD148
Signalling CAR
Inhibitory CAR

FIG. 18

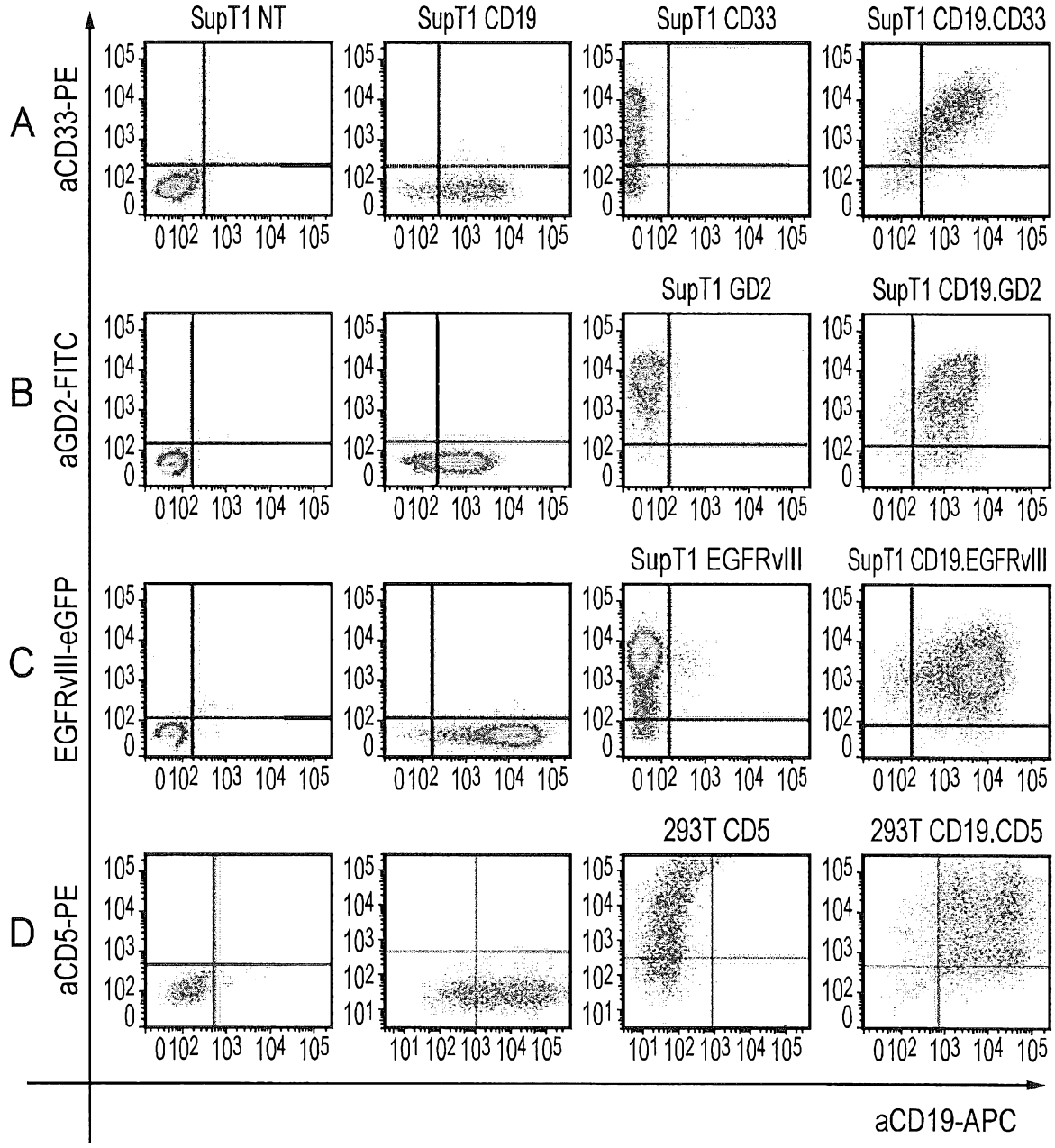

SupT1 NT
SupT1 CD19
SupT1 CD33
SupT1 CD19.CD33
A
aCD33-PE
SupT1 GD2
SupT1 CD19.GD2
B
aGD2-FITC
SupT1 EGFRvIII
SupT1 CD19.EGFRvIII
C
EGFRvIII-eGFP
293T CD5
293T CD19.CD5
D
aCD5-PE
aCD19-APC

FIG. 19

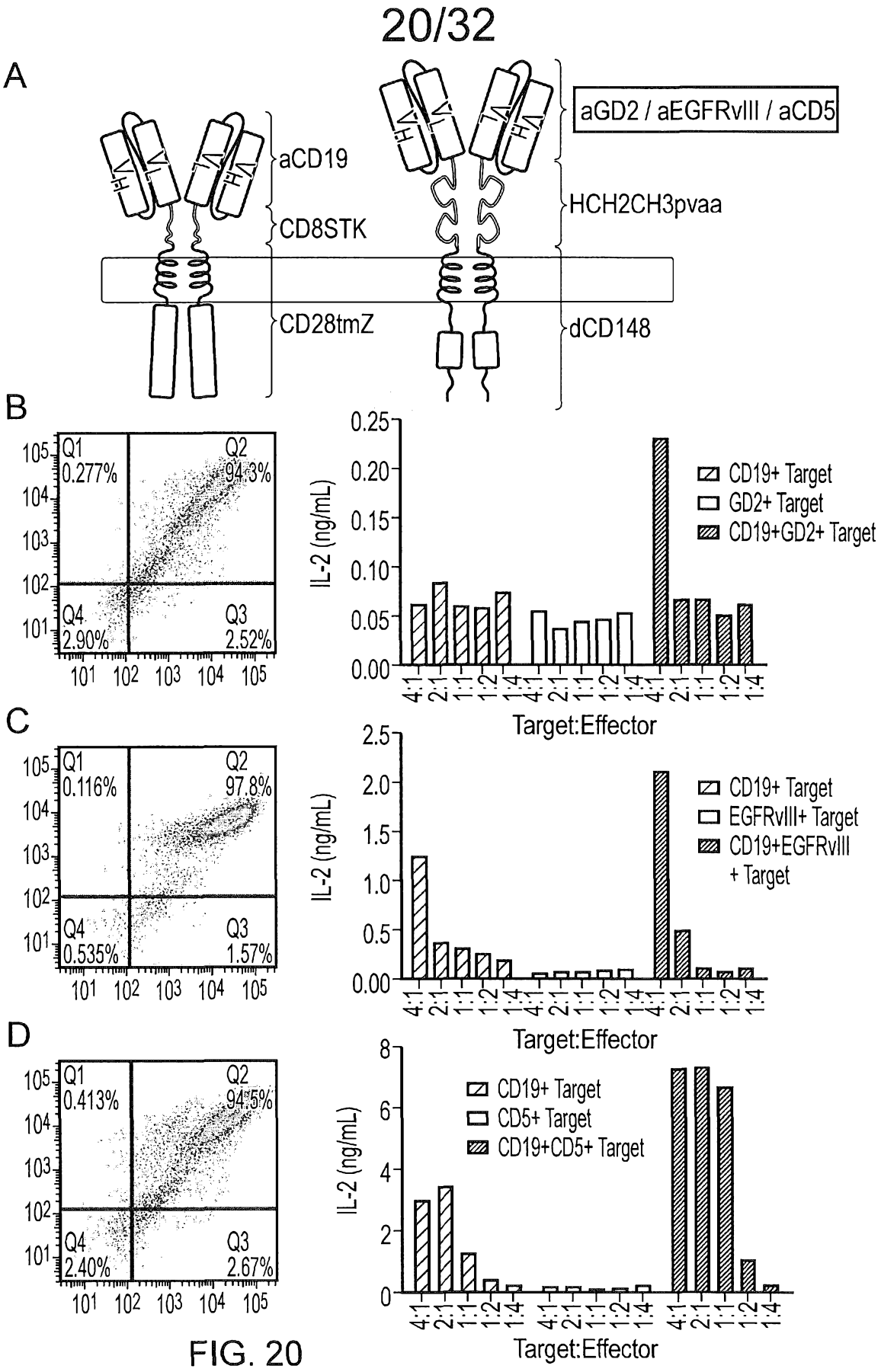

A
aGD2 / aEGFRvIII / aCD5
aCD19
CD8STK
HCH2CH3pvaa
CD28tmZ
dCD148
B
Q1 0.277%
Q2 94.3%
Q4 2.90%
Q3 2.52%
IL-2 (ng/mL)
CD19+ Target
GD2+ Target
CD19+GD2+ Target
Target:Effector
C
Q1 0.116%
Q2 97.8%
Q4 0.535%
Q3 1.57%
IL-2 (ng/mL)
CD19+ Target
EGFRvIII+ Target
CD19+EGFRvIII + Target
Target:Effector
D
Q1 0.413%
Q2 94.5%
Q4 2.40%
Q3 2.67%
IL-2 (ng/mL)
CD19+ Target
CD5+ Target
CD19+CD5+ Target
Target:Effector

FIG. 20

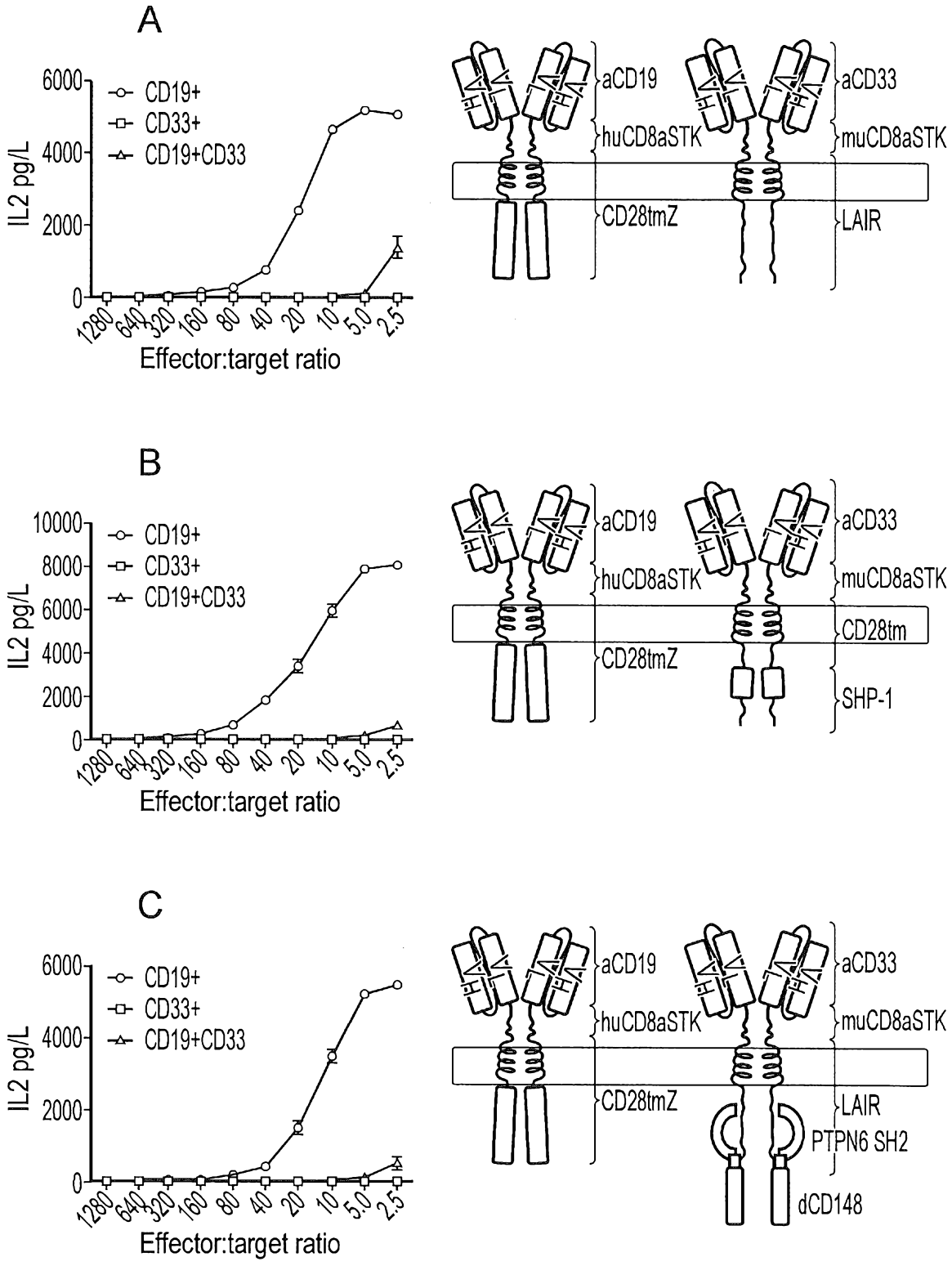

A
6000
4000
2000
0
IL2 pg/L
CD19+
CD33+
CD19+CD33
1280
640
320
160
80
40
20
10
5.0
2.5
Effector:target ratio
aCD19
huCD8aSTK
CD28tmZ
aCD33
muCD8aSTK
LAIR
B
10000
8000
6000
4000
2000
0
IL2 pg/L
CD19+
CD33+
CD19+CD33
Effector:target ratio
aCD19
huCD8aSTK
CD28tmZ
aCD33
muCD8aSTK
CD28tm
SHP-1
C
6000
4000
2000
0
IL2 pg/L
CD19+
CD33+
CD19+CD33
Effector:target ratio
aCD19
huCD8aSTK
CD28tmZ
aCD33
muCD8aSTK
LAIR
PTPN6 SH2
dCD148

FIG. 21

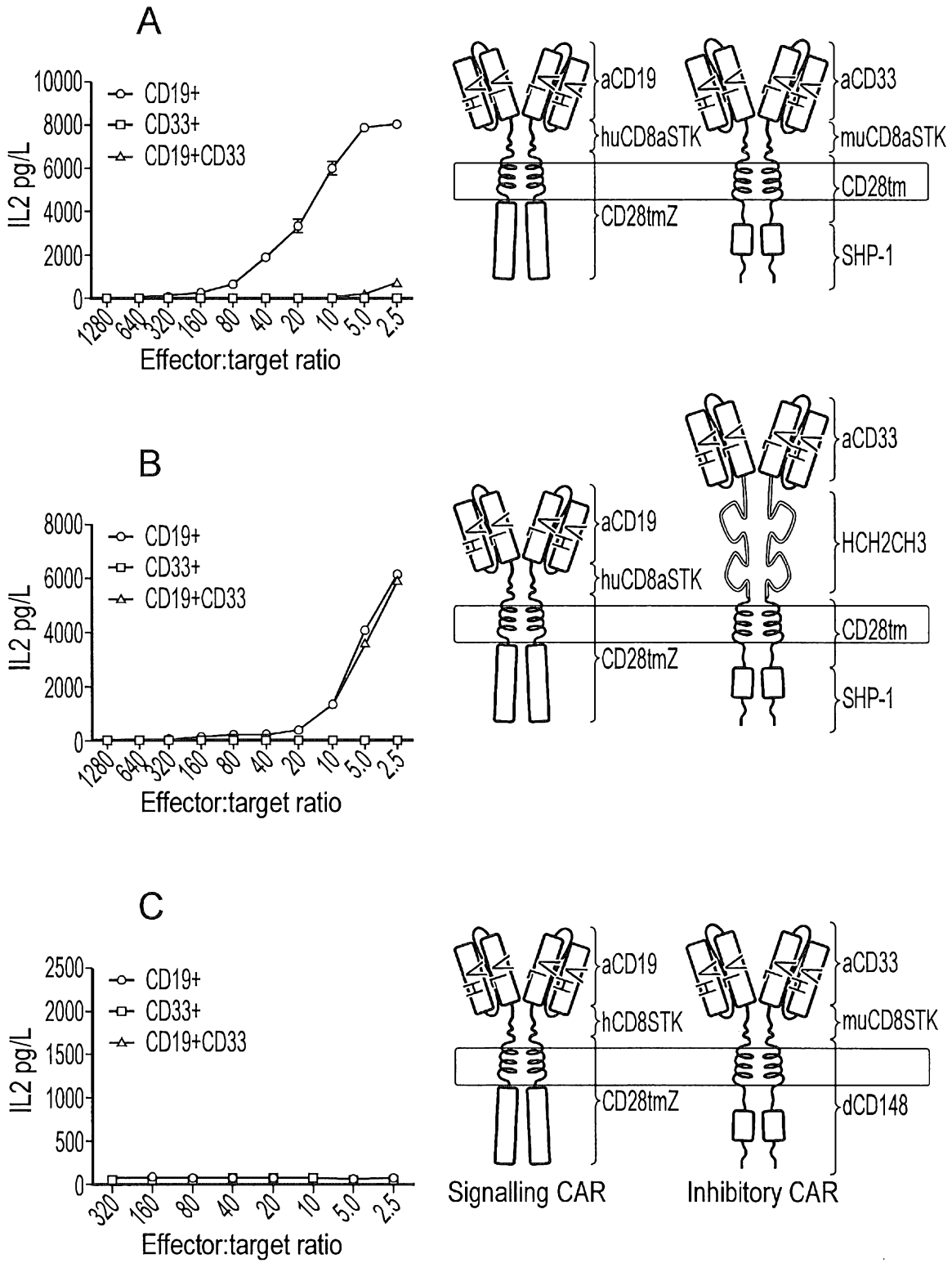

A
IL2 pg/L
10000
8000
6000
4000
2000
0
CD19+
CD33+
CD19+CD33
1280
640
320
160
80
40
20
10
5.0
2.5
Effector:target ratio
aCD19
huCD8aSTK
CD28tmZ
aCD33
muCD8aSTK
CD28tm
SHP-1
B
IL2 pg/L
8000
6000
4000
2000
0
CD19+
CD33+
CD19+CD33
Effector:target ratio
aCD19
huCD8aSTK
CD28tmZ
aCD33
HCH2CH3
CD28tm
SHP-1
C
IL2 pg/L
2500
2000
1500
1000
500
0
CD19+
CD33+
CD19+CD33
320
160
80
40
20
10
5.0
2.5
Effector:target ratio
aCD19
hCD8STK
CD28tmZ
aCD33
muCD8STK
dCD148
Signalling CAR
Inhibitory CAR

FIG. 22

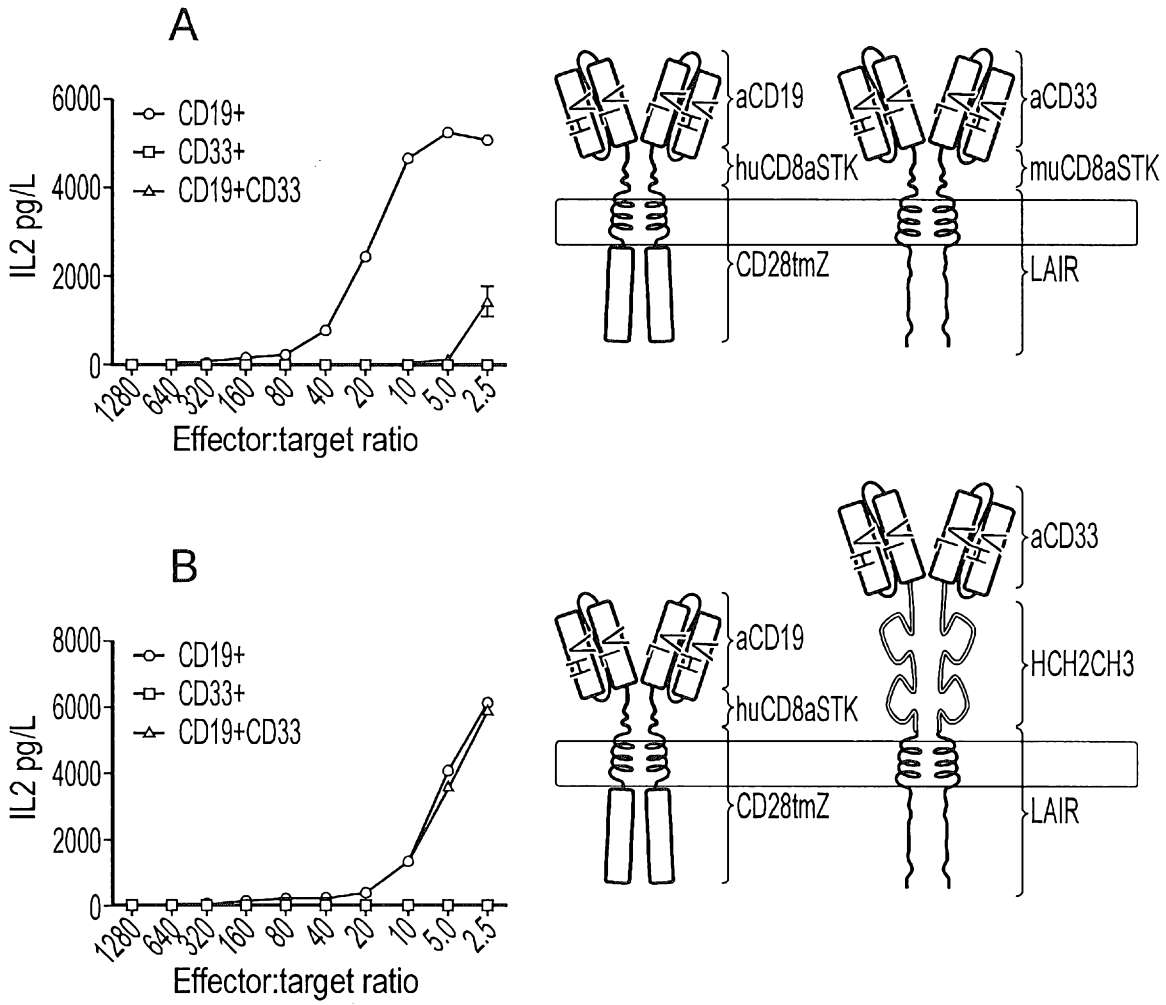

A
6000
4000
2000
0
IL2 pg/L
CD19+
CD33+
CD19+CD33
1280
640
320
160
80
40
20
10
5.0
2.5
Effector:target ratio
aCD19
huCD8aSTK
CD28tmZ
aCD33
muCD8aSTK
LAIR
B
8000
6000
4000
2000
0
IL2 pg/L
CD19+
CD33+
CD19+CD33
1280
640
320
160
80
40
20
10
5.0
2.5
Effector:target ratio
aCD33
aCD19
huCD8aSTK
CD28tmZ
HCH2CH3
LAIR

FIG. 23

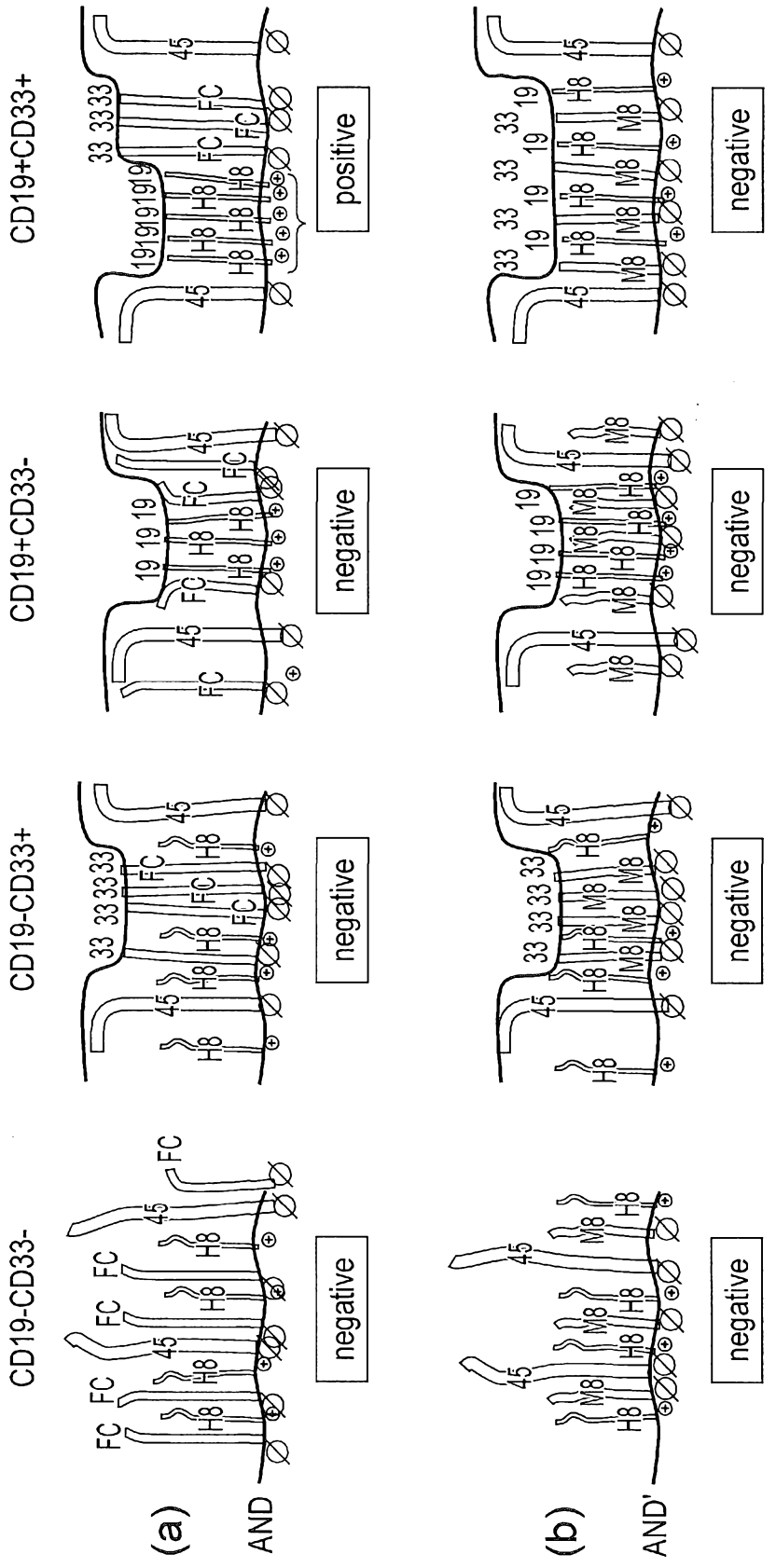

CD19-CD33-
CD19-CD33+
CD19+CD33-
CD19+CD33+
(a)
AND
(b)
AND'
negative
negative
negative
positive
negative
negative
negative
negative

FIG. 24

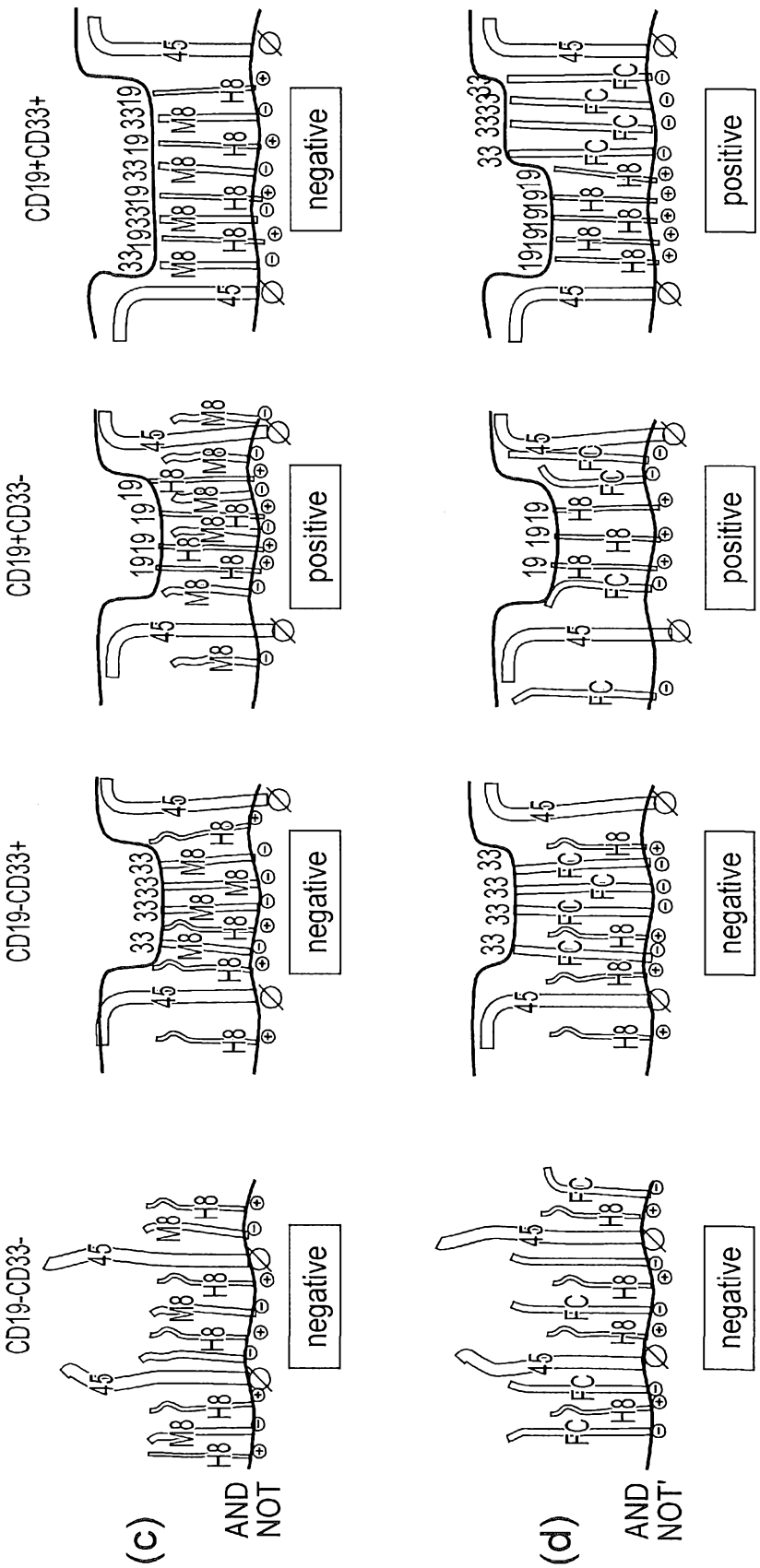


FIG. 24 (Continued)

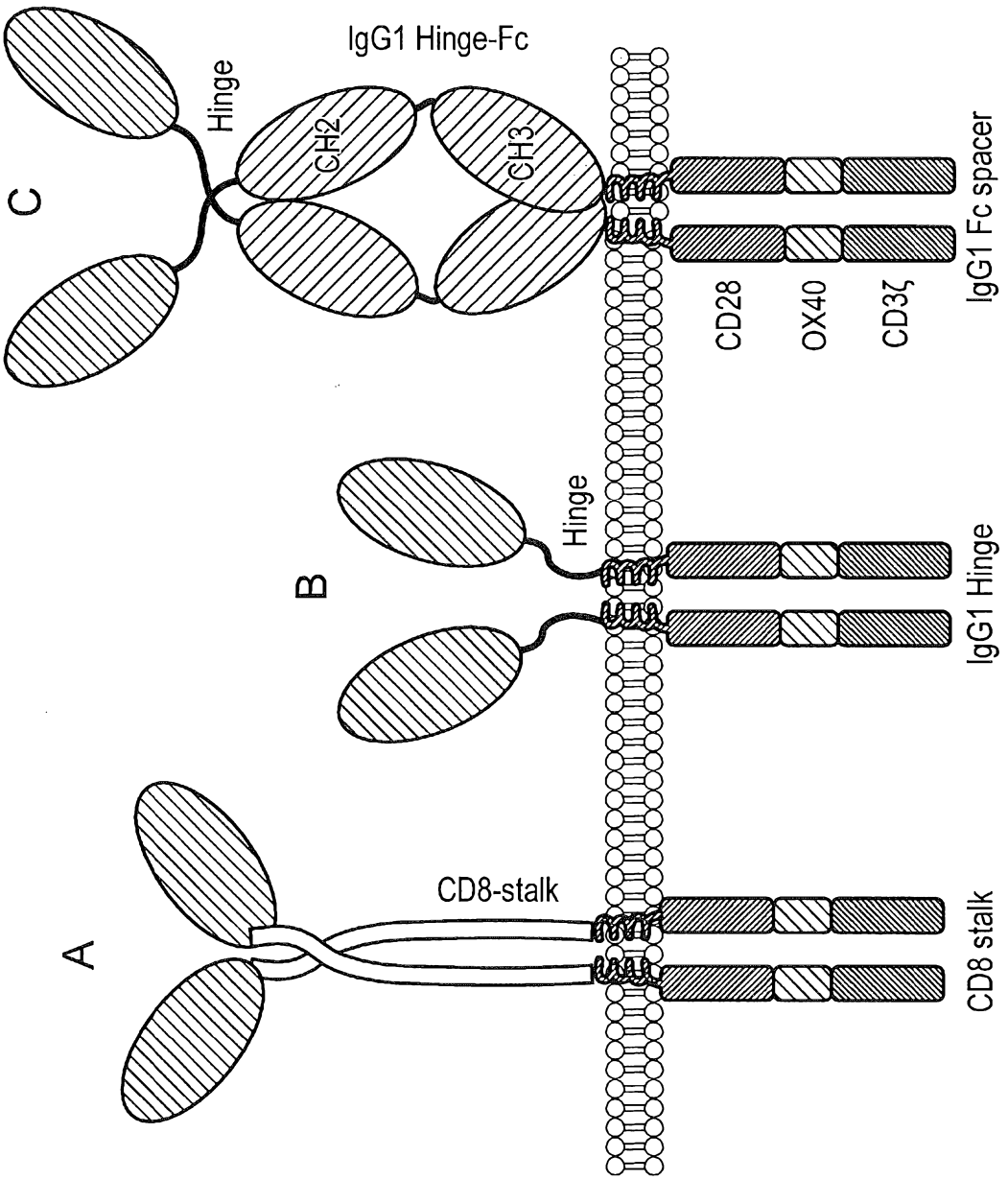
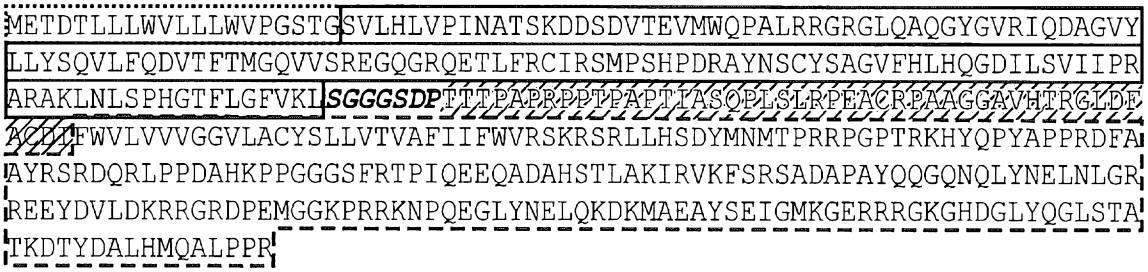
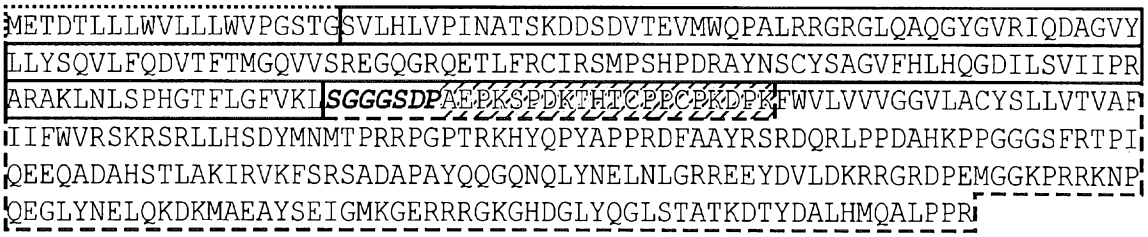

IgG1 Hinge-Fc
Hinge
CH2
CH3
C
CD28
OX40
CD3ζ
IgG1 Fc spacer
Hinge
B
IgG1 Hinge
CD8-stalk
A
CD8 stalk

FIG. 25

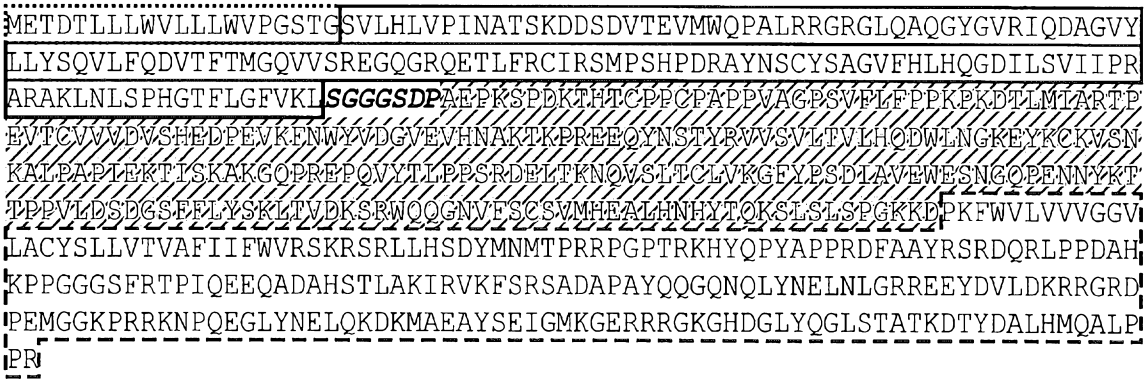
A



B



C



Signal Peptide	Efficient signal peptide
dAPRIL	Truncated APRIL
Spacer	Either hinge-CH2CH3 of human IgG1, human CD8 stalk and human IgG1 hinge
TM and endodomain	Compound endodomain comprising of the CD28TM domain, CD28 endodomain and OX40 and CD3-Zeta endodomains

FIG. 26

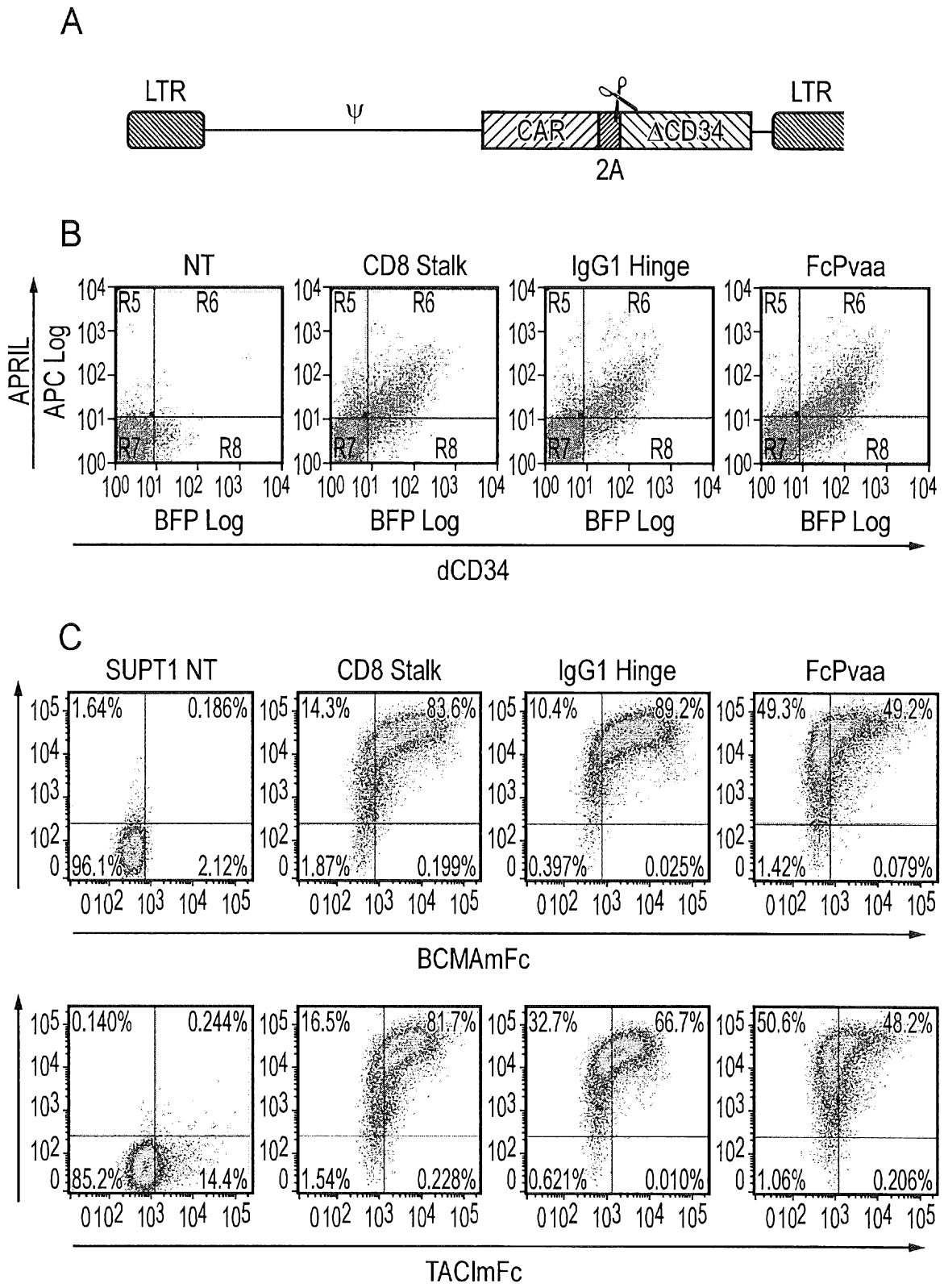

A
LTR
ψ
CAR
ΔCD34
LTR
2A
B
NT
CD8 Stalk
IgG1 Hinge
FcPvaa
APRIL
APC Log
R5
R6
R7
R8
BFP Log
dCD34
C
SUPT1 NT
CD8 Stalk
IgG1 Hinge
FcPvaa
1.64%
0.186%
96.1%
2.12%
14.3%
83.6%
1.87%
0.199%
10.4%
89.2%
0.397%
0.025%
49.3%
49.2%
1.42%
0.079%
BCMAmFc
0.140%
0.244%
85.2%
14.4%
16.5%
81.7%
1.54%
0.228%
32.7%
66.7%
0.621%
0.010%
50.6%
48.2%
1.06%
0.206%
TACImFc

FIG. 27

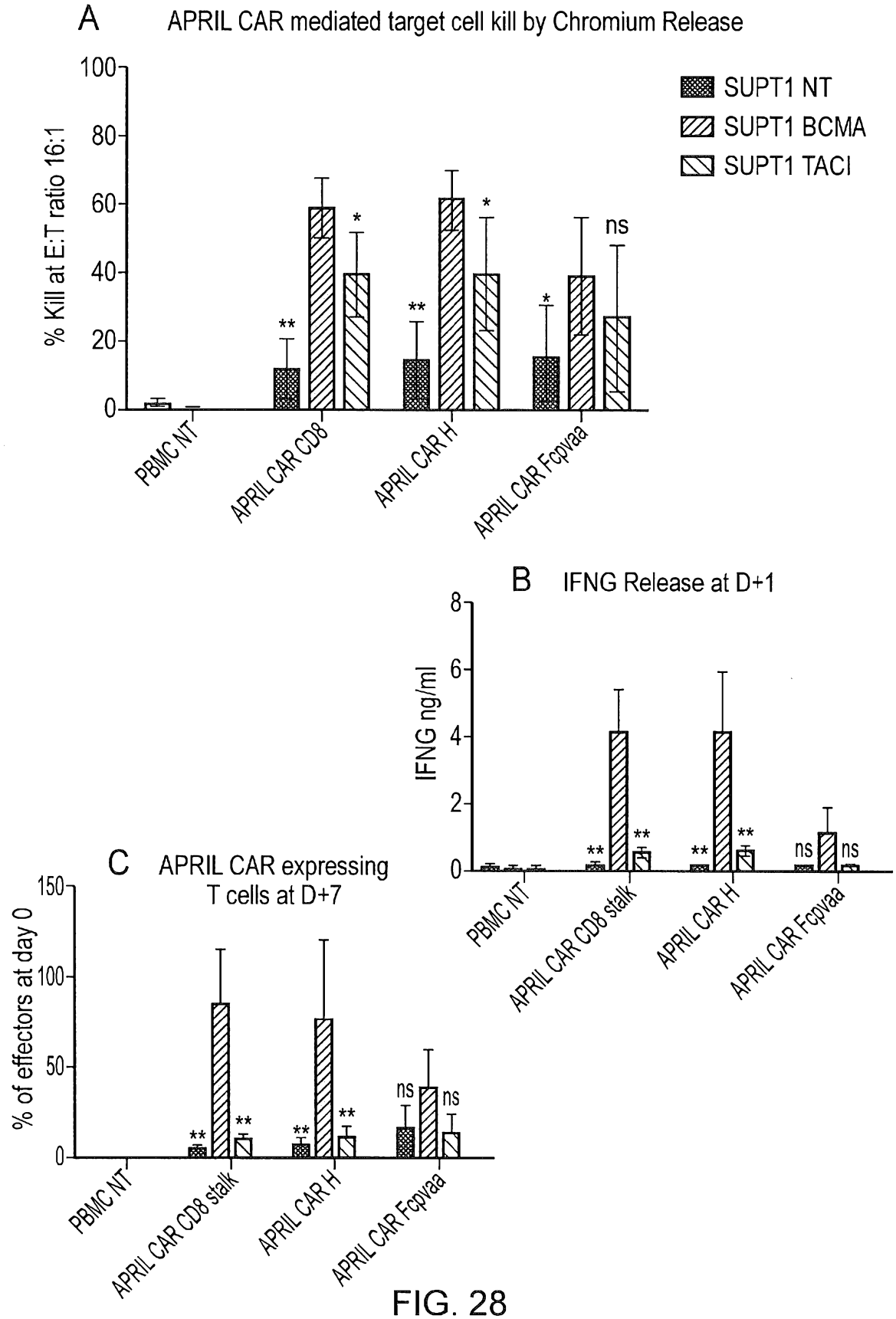

A
APRIL CAR mediated target cell kill by Chromium Release
% Kill at E:T ratio 16:1
100
80
60
40
20
0
SUPT1 NT
SUPT1 BCMA
SUPT1 TACI
**
*
**
*
*
ns
PBMC NT
APRIL CAR CD8
APRIL CAR H
APRIL CAR Fcpvaa
B
IFNG Release at D+1
IFNG ng/ml
8
6
4
2
0
**
**
**
**
ns
ns
PBMC NT
APRIL CAR CD8 stalk
APRIL CAR H
APRIL CAR Fcpvaa
C
APRIL CAR expressing
T cells at D+7
% of effectors at day 0
150
100
50
0
**
**
**
**
ns
ns
PBMC NT
APRIL CAR CD8 stalk
APRIL CAR H
APRIL CAR Fcpvaa

FIG. 28

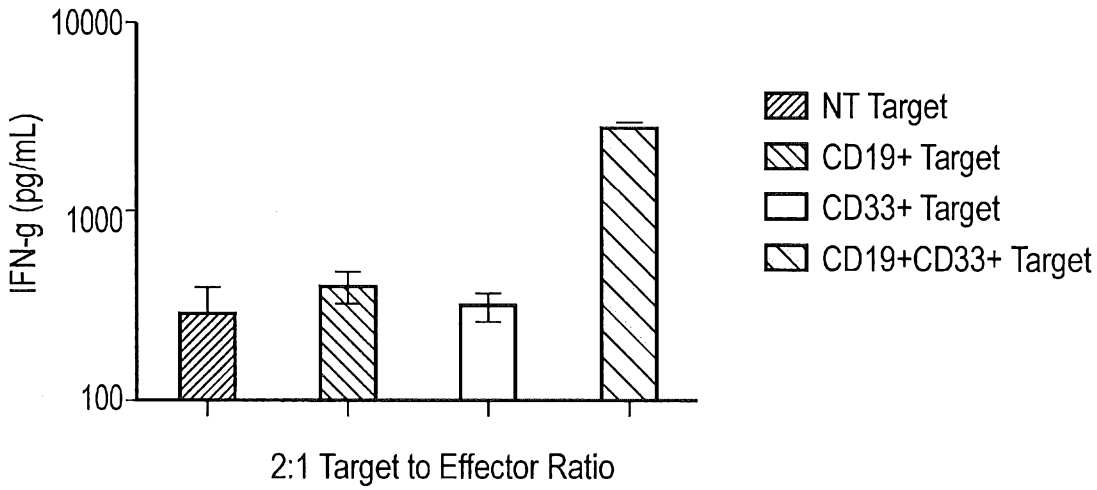

10000
1000
100
IFN-g (pg/mL)
2:1 Target to Effector Ratio
NT Target
CD19+ Target
CD33+ Target
CD19+CD33+ Target

FIG. 29

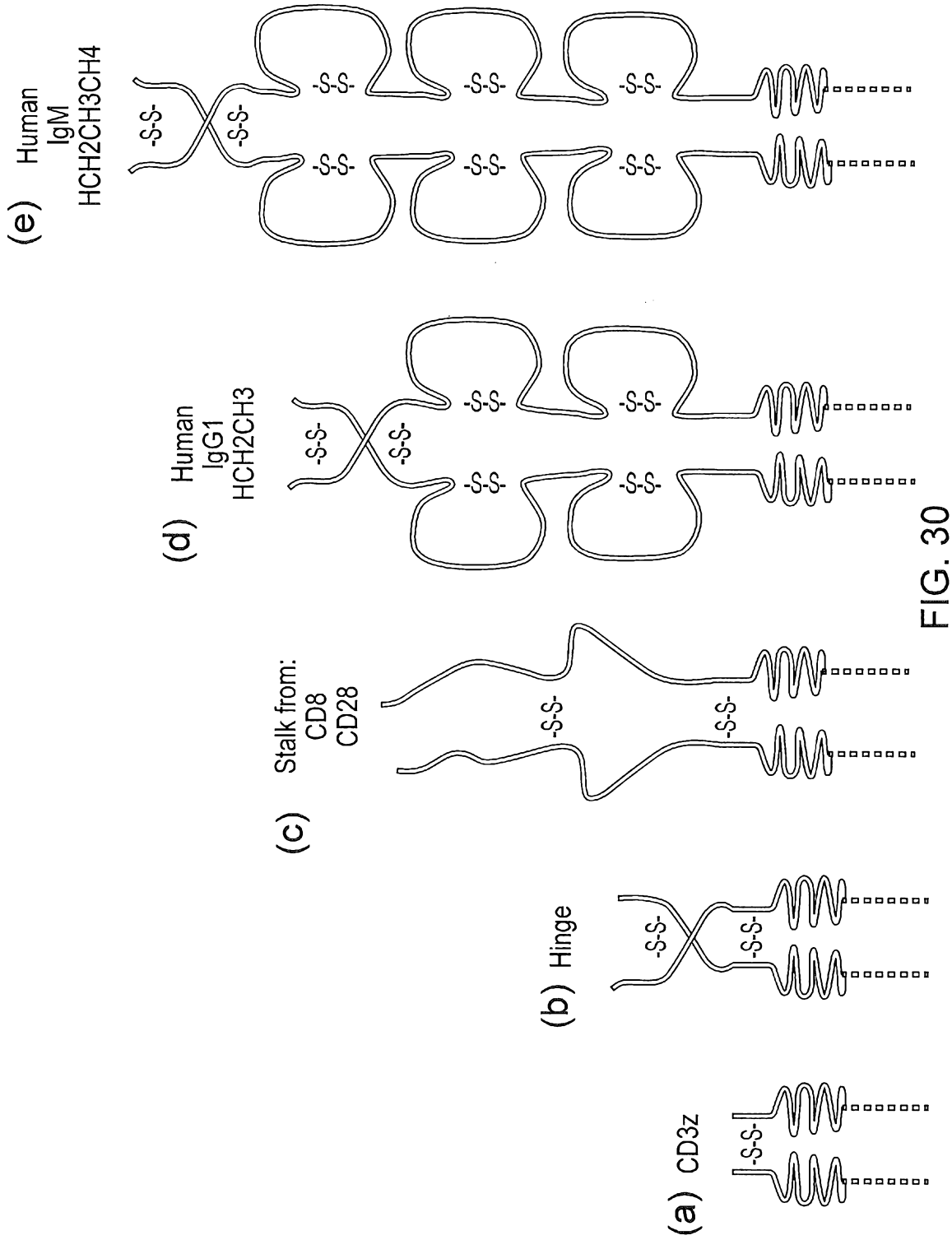

(e) Human IgM HCH2CH3CH4
-S-S-
(d) Human IgG1 HCH2CH3
(c) Stalk from: CD8 CD28
(b) Hinge
(a) CD3z

FIG. 30

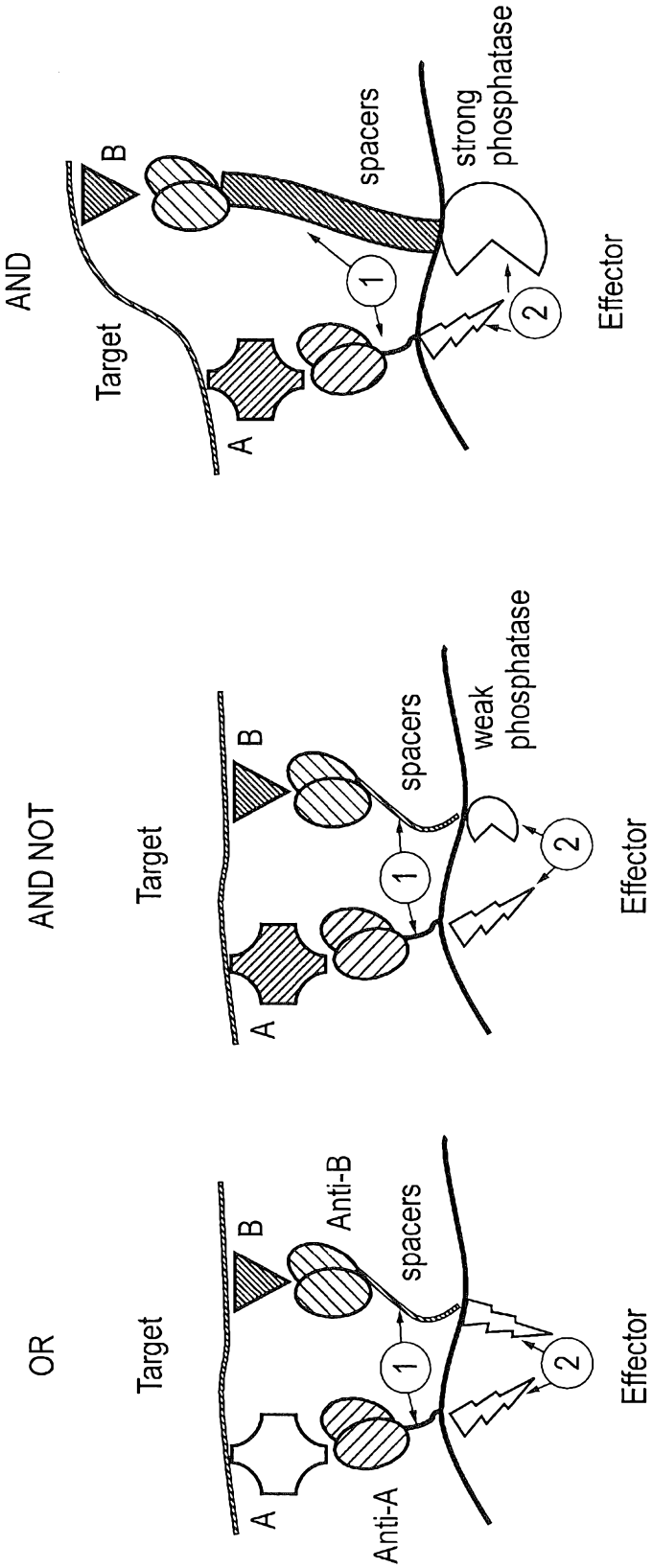

AND
Target
A
B
spacers
strong phosphatase
1
2
Effector
AND NOT
Target
A
B
spacers
weak phosphatase
1
2
Effector
OR
Target
A
Anti-A
B
Anti-B
spacers
1
2
Effector

FIG. 31

SEQUENCE LISTING

<110> UCL Business PLC

<120> T Cell

<130> P103294PCT1

<150> GB 1410934.2
<151> 2014-06-19

<160> 53

<170> PatentIn version 3.5

<210> 1
<211> 1129
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric antigen receptor (CAR)

<400> 1

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

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

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

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

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65                  70                  75                  80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
                85                  90                  95

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
            100                 105                 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
        115                 120                 125

Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser Gly Pro Gly
145                 150                 155                 160
```

```
Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys Thr Val Ser Gly
                165                 170                 175

Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg
            180                 185                 190

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr
        195                 200                 205

Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile Lys Asp Asn Ser
    210                 215                 220

Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr
225                 230                 235                 240

Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala
                245                 250                 255

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp Pro
            260                 265                 270

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
        275                 280                 285

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
    290                 295                 300

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Phe Trp
305                 310                 315                 320

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
                325                 330                 335

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Arg Val Lys Phe Ser Arg
            340                 345                 350

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
        355                 360                 365

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
    370                 375                 380

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
385                 390                 395                 400

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
```

405 410 415

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
420 425 430

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
435 440 445

Ala Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Glu Gly Arg Gly
450 455 460

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala
465 470 475 480

Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr Asp Ala
485 490 495

Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
500 505 510

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp Ile Tyr
515 520 525

Phe Asn Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
530 535 540

Leu Ile Tyr Asp Thr Asn Arg Leu Ala Asp Gly Val Pro Ser Arg Phe
545 550 555 560

Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser Ser Leu
565 570 575

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Lys Asn Tyr
580 585 590

Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ser Gly
595 600 605

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
610 615 620

Gly Gly Ser Arg Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
625 630 635 640

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
645 650 655

```
Thr Leu Ser Asn Tyr Gly Met His Trp Ile Arg Gln Ala Pro Gly Lys
            660                 665                 670

Gly Leu Glu Trp Val Ser Ser Ile Ser Leu Asn Gly Gly Ser Thr Tyr
        675                 680                 685

Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
    690                 695                 700

Lys Ser Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
705                 710                 715                 720

Ala Val Tyr Tyr Cys Ala Ala Gln Asp Ala Tyr Thr Gly Gly Tyr Phe
                725                 730                 735

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Met Asp Pro
            740                 745                 750

Ala Glu Pro Lys Ser Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro
        755                 760                 765

Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
    770                 775                 780

Lys Asp Thr Leu Met Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val
785                 790                 795                 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
                805                 810                 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
            820                 825                 830

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
        835                 840                 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
    850                 855                 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
865                 870                 875                 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
                885                 890                 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
            900                 905                 910
```

```
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
        915                 920                 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
    930                 935                 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
945                 950                 955                 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
                965                 970                 975

Ser Leu Ser Leu Ser Pro Gly Lys Lys Asp Pro Lys Phe Trp Val Leu
            980                 985                 990

Val Val Val Gly Gly Val Leu Ala  Cys Tyr Ser Leu Leu  Val Thr Val
        995                 1000                1005

Ala Phe  Ile Ile Phe Trp Val  Arg Ser Arg Val Lys  Phe Ser Arg
    1010                1015                1020

Ser Ala  Asp Ala Pro Ala Tyr  Gln Gln Gly Gln Asn  Gln Leu Tyr
    1025                1030                1035

Asn Glu  Leu Asn Leu Gly Arg  Arg Glu Glu Tyr Asp  Val Leu Asp
    1040                1045                1050

Lys Arg  Arg Gly Arg Asp Pro  Glu Met Gly Gly Lys  Pro Arg Arg
    1055                1060                1065

Lys Asn  Pro Gln Glu Gly Leu  Tyr Asn Glu Leu Gln  Lys Asp Lys
    1070                1075                1080

Met Ala  Glu Ala Tyr Ser Glu  Ile Gly Met Lys Gly  Glu Arg Arg
    1085                1090                1095

Arg Gly  Lys Gly His Asp Gly  Leu Tyr Gln Gly Leu  Ser Thr Ala
    1100                1105                1110

Thr Lys  Asp Thr Tyr Asp Ala  Leu His Met Gln Ala  Leu Pro Pro
    1115                1120                1125

Arg
```

<210> 2
<211> 1350

<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric antigen receptor (CAR)

<400> 2

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

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

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

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

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65                  70                  75                  80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
                85                  90                  95

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
            100                 105                 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
        115                 120                 125

Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser Gly Pro Gly
145                 150                 155                 160

Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys Thr Val Ser Gly
                165                 170                 175

Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg
            180                 185                 190

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr
        195                 200                 205

Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile Lys Asp Asn Ser
    210                 215                 220
```

```
Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr
225                 230                 235                 240

Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala
                245                 250                 255

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp Pro
            260                 265                 270

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
        275                 280                 285

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
    290                 295                 300

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Phe Trp
305                 310                 315                 320

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
                325                 330                 335

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Arg Val Lys Phe Ser Arg
            340                 345                 350

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
        355                 360                 365

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
    370                 375                 380

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
385                 390                 395                 400

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
                405                 410                 415

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
            420                 425                 430

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
        435                 440                 445

Ala Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Glu Gly Arg Gly
    450                 455                 460

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala
465                 470                 475                 480
```

```
Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr Asp Ala
                485                 490                 495

Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
            500                 505                 510

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp Ile Tyr
        515                 520                 525

Phe Asn Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
    530                 535                 540

Leu Ile Tyr Asp Thr Asn Arg Leu Ala Asp Gly Val Pro Ser Arg Phe
545                 550                 555                 560

Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser Ser Leu
                565                 570                 575

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Lys Asn Tyr
            580                 585                 590

Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ser Gly
        595                 600                 605

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    610                 615                 620

Gly Gly Ser Arg Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
625                 630                 635                 640

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
                645                 650                 655

Thr Leu Ser Asn Tyr Gly Met His Trp Ile Arg Gln Ala Pro Gly Lys
            660                 665                 670

Gly Leu Glu Trp Val Ser Ser Ile Ser Leu Asn Gly Gly Ser Thr Tyr
        675                 680                 685

Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
    690                 695                 700

Lys Ser Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
705                 710                 715                 720

Ala Val Tyr Tyr Cys Ala Ala Gln Asp Ala Tyr Thr Gly Gly Tyr Phe
```

725 730 735

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Met Asp Pro
740 745 750

Ala Glu Pro Lys Ser Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro
755 760 765

Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
770 775 780

Lys Asp Thr Leu Met Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val
785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
820 825 830

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
965 970 975

```
Ser Leu Ser Leu Ser Pro Gly Lys Lys Asp Pro Lys Ala Val Phe Gly
            980                 985                 990

Cys Ile Phe Gly Ala Leu Val Ile  Val Thr Val Gly Gly  Phe Ile Phe
        995                 1000                1005

Trp Arg  Lys Lys Arg Lys Asp  Ala Lys Asn Asn Glu  Val Ser Phe
    1010                1015                1020

Ser Gln  Ile Lys Pro Lys Lys  Ser Lys Leu Ile Arg  Val Glu Asn
    1025                1030                1035

Phe Glu  Ala Tyr Phe Lys Lys  Gln Gln Ala Asp Ser  Asn Cys Gly
    1040                1045                1050

Phe Ala  Glu Glu Tyr Glu Asp  Leu Lys Leu Val Gly  Ile Ser Gln
    1055                1060                1065

Pro Lys  Tyr Ala Ala Glu Leu  Ala Glu Asn Arg Gly  Lys Asn Arg
    1070                1075                1080

Tyr Asn  Asn Val Leu Pro Tyr  Asp Ile Ser Arg Val  Lys Leu Ser
    1085                1090                1095

Val Gln  Thr His Ser Thr Asp  Asp Tyr Ile Asn Ala  Asn Tyr Met
    1100                1105                1110

Pro Gly  Tyr His Ser Lys Lys  Asp Phe Ile Ala Thr  Gln Gly Pro
    1115                1120                1125

Leu Pro  Asn Thr Leu Lys Asp  Phe Trp Arg Met Val  Trp Glu Lys
    1130                1135                1140

Asn Val  Tyr Ala Ile Ile Met  Leu Thr Lys Cys Val  Glu Gln Gly
    1145                1150                1155

Arg Thr  Lys Cys Glu Glu Tyr  Trp Pro Ser Lys Gln  Ala Gln Asp
    1160                1165                1170

Tyr Gly  Asp Ile Thr Val Ala  Met Thr Ser Glu Ile  Val Leu Pro
    1175                1180                1185

Glu Trp  Thr Ile Arg Asp Phe  Thr Val Lys Asn Ile  Gln Thr Ser
    1190                1195                1200

Glu Ser  His Pro Leu Arg Gln  Phe His Phe Thr Ser  Trp Pro Asp
    1205                1210                1215
```

```
His Gly  Val Pro Asp Thr Thr  Asp Leu Leu Ile Asn  Phe Arg Tyr
    1220                 1225                 1230


Leu Val  Arg Asp Tyr Met Lys  Gln Ser Pro Pro Glu  Ser Pro Ile
    1235                 1240                 1245


Leu Val  His Cys Ser Ala Gly  Val Gly Arg Thr Gly  Thr Phe Ile
    1250                 1255                 1260


Ala Ile  Asp Arg Leu Ile Tyr  Gln Ile Glu Asn Glu  Asn Thr Val
    1265                 1270                 1275


Asp Val  Tyr Gly Ile Val Tyr  Asp Leu Arg Met His  Arg Pro Leu
    1280                 1285                 1290


Met Val  Gln Thr Glu Asp Gln  Tyr Val Phe Leu Asn  Gln Cys Val
    1295                 1300                 1305


Leu Asp  Ile Val Arg Ser Gln  Lys Asp Ser Lys Val  Asp Leu Ile
    1310                 1315                 1320


Tyr Gln  Asn Thr Thr Ala Met  Thr Ile Tyr Glu Asn  Leu Ala Pro
    1325                 1330                 1335


Val Thr  Thr Phe Gly Lys Thr  Asn Gly Tyr Ile Ala
    1340                 1345                 1350


<210>  3
<211>  1717
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Chimeric antigen receptor (CAR)

<400>  3

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


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


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


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

```
Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65                  70                  75                  80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
                85                  90                  95

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
            100                 105                 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
        115                 120                 125

Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser Gly Pro Gly
145                 150                 155                 160

Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys Thr Val Ser Gly
                165                 170                 175

Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg
            180                 185                 190

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr
        195                 200                 205

Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile Lys Asp Asn Ser
    210                 215                 220

Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr
225                 230                 235                 240

Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala
                245                 250                 255

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp Pro
            260                 265                 270

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
        275                 280                 285

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
    290                 295                 300

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Phe Trp
305                 310                 315                 320
```

```
Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
                325                 330                 335

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Arg Val Lys Phe Ser Arg
            340                 345                 350

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
        355                 360                 365

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
    370                 375                 380

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
385                 390                 395                 400

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
                405                 410                 415

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
            420                 425                 430

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
        435                 440                 445

Ala Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Glu Gly Arg Gly
    450                 455                 460

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala
465                 470                 475                 480

Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr Asp Ala
                485                 490                 495

Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
            500                 505                 510

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp Ile Tyr
        515                 520                 525

Phe Asn Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
    530                 535                 540

Leu Ile Tyr Asp Thr Asn Arg Leu Ala Asp Gly Val Pro Ser Arg Phe
545                 550                 555                 560

Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser Ser Leu
                565                 570                 575
```

```
Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Lys Asn Tyr
            580                 585                 590

Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ser Gly
        595                 600                 605

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    610                 615                 620

Gly Gly Ser Arg Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
625                 630                 635                 640

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
                645                 650                 655

Thr Leu Ser Asn Tyr Gly Met His Trp Ile Arg Gln Ala Pro Gly Lys
            660                 665                 670

Gly Leu Glu Trp Val Ser Ser Ile Ser Leu Asn Gly Gly Ser Thr Tyr
        675                 680                 685

Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
    690                 695                 700

Lys Ser Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
705                 710                 715                 720

Ala Val Tyr Tyr Cys Ala Ala Gln Asp Ala Tyr Thr Gly Gly Tyr Phe
                725                 730                 735

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Met Asp Pro
            740                 745                 750

Ala Glu Pro Lys Ser Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro
        755                 760                 765

Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
    770                 775                 780

Lys Asp Thr Leu Met Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val
785                 790                 795                 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
                805                 810                 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
```

```
            820                 825                 830

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
        835                 840                 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
    850                 855                 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
865                 870                 875                 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
                885                 890                 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
            900                 905                 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
        915                 920                 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
    930                 935                 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
945                 950                 955                 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
                965                 970                 975

Ser Leu Ser Leu Ser Pro Gly Lys Lys Asp Pro Lys Ala Leu Ile Ala
            980                 985                 990

Phe Leu Ala Phe Leu Ile Ile Val  Thr Ser Ile Ala Leu  Leu Val Val
        995                 1000                1005

Leu Tyr  Lys Ile Tyr Asp Leu  His Lys Lys Arg Ser  Cys Asn Leu
    1010                1015                1020

Asp Glu  Gln Gln Glu Leu Val  Glu Arg Asp Asp Glu  Lys Gln Leu
    1025                1030                1035

Met Asn  Val Glu Pro Ile His  Ala Asp Ile Leu Leu  Glu Thr Tyr
    1040                1045                1050

Lys Arg  Lys Ile Ala Asp Glu  Gly Arg Leu Phe Leu  Ala Glu Phe
    1055                1060                1065
```

```
Gln Ser  Ile Pro Arg Val Phe  Ser Lys Phe Pro Ile  Lys Glu Ala
    1070                1075                1080

Arg Lys  Pro Phe Asn Gln Asn  Lys Asn Arg Tyr Val  Asp Ile Leu
    1085                1090                1095

Pro Tyr  Asp Tyr Asn Arg Val  Glu Leu Ser Glu Ile  Asn Gly Asp
    1100                1105                1110

Ala Gly  Ser Asn Tyr Ile Asn  Ala Ser Tyr Ile Asp  Gly Phe Lys
    1115                1120                1125

Glu Pro  Arg Lys Tyr Ile Ala  Ala Gln Gly Pro Arg  Asp Glu Thr
    1130                1135                1140

Val Asp  Asp Phe Trp Arg Met  Ile Trp Glu Gln Lys  Ala Thr Val
    1145                1150                1155

Ile Val  Met Val Thr Arg Cys  Glu Glu Gly Asn Arg  Asn Lys Cys
    1160                1165                1170

Ala Glu  Tyr Trp Pro Ser Met  Glu Glu Gly Thr Arg  Ala Phe Gly
    1175                1180                1185

Asp Val  Val Val Lys Ile Asn  Gln His Lys Arg Cys  Pro Asp Tyr
    1190                1195                1200

Ile Ile  Gln Lys Leu Asn Ile  Val Asn Lys Lys Glu  Lys Ala Thr
    1205                1210                1215

Gly Arg  Glu Val Thr His Ile  Gln Phe Thr Ser Trp  Pro Asp His
    1220                1225                1230

Gly Val  Pro Glu Asp Pro His  Leu Leu Leu Lys Leu  Arg Arg Arg
    1235                1240                1245

Val Asn  Ala Phe Ser Asn Phe  Phe Ser Gly Pro Ile  Val Val His
    1250                1255                1260

Cys Ser  Ala Gly Val Gly Arg  Thr Gly Thr Tyr Ile  Gly Ile Asp
    1265                1270                1275

Ala Met  Leu Glu Gly Leu Glu  Ala Glu Asn Lys Val  Asp Val Tyr
    1280                1285                1290

Gly Tyr  Val Val Lys Leu Arg  Arg Gln Arg Cys Leu  Met Val Gln
    1295                1300                1305
```

```
Val Glu  Ala Gln Tyr Ile Leu  Ile His Gln Ala Leu  Val Glu Tyr
    1310                1315                1320

Asn Gln  Phe Gly Glu Thr Glu  Val Asn Leu Ser Glu  Leu His Pro
    1325                1330                1335

Tyr Leu  His Asn Met Lys Lys  Arg Asp Pro Pro Ser  Glu Pro Ser
    1340                1345                1350

Pro Leu  Glu Ala Glu Phe Gln  Arg Leu Pro Ser Tyr  Arg Ser Trp
    1355                1360                1365

Arg Thr  Gln His Ile Gly Asn  Gln Glu Glu Asn Lys  Ser Lys Asn
    1370                1375                1380

Arg Asn  Ser Asn Val Ile Pro  Tyr Asp Tyr Asn Arg  Val Pro Leu
    1385                1390                1395

Lys His  Glu Leu Glu Met Ser  Lys Glu Ser Glu His  Asp Ser Asp
    1400                1405                1410

Glu Ser  Ser Asp Asp Asp Ser  Asp Ser Glu Glu Pro  Ser Lys Tyr
    1415                1420                1425

Ile Asn  Ala Ser Phe Ile Met  Ser Tyr Trp Lys Pro  Glu Val Met
    1430                1435                1440

Ile Ala  Ala Gln Gly Pro Leu  Lys Glu Thr Ile Gly  Asp Phe Trp
    1445                1450                1455

Gln Met  Ile Phe Gln Arg Lys  Val Lys Val Ile Val  Met Leu Thr
    1460                1465                1470

Glu Leu  Lys His Gly Asp Gln  Glu Ile Cys Ala Gln  Tyr Trp Gly
    1475                1480                1485

Glu Gly  Lys Gln Thr Tyr Gly  Asp Ile Glu Val Asp  Leu Lys Asp
    1490                1495                1500

Thr Asp  Lys Ser Ser Thr Tyr  Thr Leu Arg Val Phe  Glu Leu Arg
    1505                1510                1515

His Ser  Lys Arg Lys Asp Ser  Arg Thr Val Tyr Gln  Tyr Gln Tyr
    1520                1525                1530

Thr Asn  Trp Ser Val Glu Gln  Leu Pro Ala Glu Pro  Lys Glu Leu
    1535                1540                1545
```

```
Ile Ser  Met Ile Gln Val Val  Lys Gln Lys Leu Pro  Gln Lys Asn
    1550                 1555                 1560

Ser Ser  Glu Gly Asn Lys His  His Lys Ser Thr Pro  Leu Leu Ile
    1565                 1570                 1575

His Cys  Arg Asp Gly Ser Gln  Gln Thr Gly Ile Phe  Cys Ala Leu
    1580                 1585                 1590

Leu Asn  Leu Leu Glu Ser Ala  Glu Thr Glu Glu Val  Val Asp Ile
    1595                 1600                 1605

Phe Gln  Val Val Lys Ala Leu  Arg Lys Ala Arg Pro  Gly Met Val
    1610                 1615                 1620

Ser Thr  Phe Glu Gln Tyr Gln  Phe Leu Tyr Asp Val  Ile Ala Ser
    1625                 1630                 1635

Thr Tyr  Pro Ala Gln Asn Gly  Gln Val Lys Lys Asn  Asn His Gln
    1640                 1645                 1650

Glu Asp  Lys Ile Glu Phe Asp  Asn Glu Val Asp Lys  Val Lys Gln
    1655                 1660                 1665

Asp Ala  Asn Cys Val Asn Pro  Leu Gly Ala Pro Glu  Lys Leu Pro
    1670                 1675                 1680

Glu Ala  Lys Glu Gln Ala Glu  Gly Ser Glu Pro Thr  Ser Gly Thr
    1685                 1690                 1695

Glu Gly  Pro Glu His Ser Val  Asn Gly Pro Ala Ser  Pro Ala Leu
    1700                 1705                 1710

Asn Gln  Gly Ser
    1715


<210>  4
<211>  1114
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Chimeric antigen receptor (CAR)

<400>  4

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

```
His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu
            20                  25                  30

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

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

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65                  70                  75                  80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
                85                  90                  95

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
            100                 105                 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
        115                 120                 125

Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser Gly Pro Gly
145                 150                 155                 160

Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys Thr Val Ser Gly
                165                 170                 175

Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg
            180                 185                 190

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr
        195                 200                 205

Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile Lys Asp Asn Ser
    210                 215                 220

Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr
225                 230                 235                 240

Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala
                245                 250                 255

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp Pro
            260                 265                 270
```

```
Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
        275                 280                 285

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
    290                 295                 300

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Phe Trp
305                 310                 315                 320

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
                325                 330                 335

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Arg Val Lys Phe Ser Arg
            340                 345                 350

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
        355                 360                 365

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
    370                 375                 380

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
385                 390                 395                 400

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
                405                 410                 415

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
            420                 425                 430

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
        435                 440                 445

Ala Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Glu Gly Arg Gly
    450                 455                 460

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala
465                 470                 475                 480

Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr Asp Ala
                485                 490                 495

Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
            500                 505                 510

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp Ile Tyr
```

```
        515                 520                 525

Phe Asn Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
    530                 535                 540

Leu Ile Tyr Asp Thr Asn Arg Leu Ala Asp Gly Val Pro Ser Arg Phe
545                 550                 555                 560

Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser Ser Leu
                565                 570                 575

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Lys Asn Tyr
            580                 585                 590

Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ser Gly
        595                 600                 605

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    610                 615                 620

Gly Gly Ser Arg Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
625                 630                 635                 640

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
                645                 650                 655

Thr Leu Ser Asn Tyr Gly Met His Trp Ile Arg Gln Ala Pro Gly Lys
            660                 665                 670

Gly Leu Glu Trp Val Ser Ser Ile Ser Leu Asn Gly Gly Ser Thr Tyr
        675                 680                 685

Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
    690                 695                 700

Lys Ser Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
705                 710                 715                 720

Ala Val Tyr Tyr Cys Ala Ala Gln Asp Ala Tyr Thr Gly Gly Tyr Phe
                725                 730                 735

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Met Asp Pro
            740                 745                 750

Ala Thr Thr Thr Lys Pro Val Leu Arg Thr Pro Ser Pro Val His Pro
        755                 760                 765
```

```
Thr Gly Thr Ser Gln Pro Gln Arg Pro Glu Asp Cys Arg Pro Arg Gly
    770                 775                 780

Ser Val Lys Gly Thr Gly Leu Asp Phe Ala Cys Asp Ile Tyr Trp Ala
785                 790                 795                 800

Pro Leu Ala Gly Ile Cys Val Ala Leu Leu Leu Ser Leu Ile Ile Thr
                805                 810                 815

Leu Ile Cys Tyr His Arg Ser Arg Lys Arg Val Cys Lys Ser Gly Gly
            820                 825                 830

Gly Ser Phe Trp Glu Glu Phe Glu Ser Leu Gln Lys Gln Glu Val Lys
        835                 840                 845

Asn Leu His Gln Arg Leu Glu Gly Gln Arg Pro Glu Asn Lys Gly Lys
    850                 855                 860

Asn Arg Tyr Lys Asn Ile Leu Pro Phe Asp His Ser Arg Val Ile Leu
865                 870                 875                 880

Gln Gly Arg Asp Ser Asn Ile Pro Gly Ser Asp Tyr Ile Asn Ala Asn
                885                 890                 895

Tyr Ile Lys Asn Gln Leu Leu Gly Pro Asp Glu Asn Ala Lys Thr Tyr
            900                 905                 910

Ile Ala Ser Gln Gly Cys Leu Glu Ala Thr Val Asn Asp Phe Trp Gln
        915                 920                 925

Met Ala Trp Gln Glu Asn Ser Arg Val Ile Val Met Thr Thr Arg Glu
    930                 935                 940

Val Glu Lys Gly Arg Asn Lys Cys Val Pro Tyr Trp Pro Glu Val Gly
945                 950                 955                 960

Met Gln Arg Ala Tyr Gly Pro Tyr Ser Val Thr Asn Cys Gly Glu His
                965                 970                 975

Asp Thr Thr Glu Tyr Lys Leu Arg Thr Leu Gln Val Ser Pro Leu Asp
            980                 985                 990

Asn Gly Asp Leu Ile Arg Glu Ile  Trp His Tyr Gln Tyr  Leu Ser Trp
        995                 1000                1005

Pro Asp  His Gly Val Pro Ser  Glu Pro Gly Gly Val  Leu Ser Phe
    1010                1015                1020
```

```
Leu Asp  Gln Ile Asn Gln Arg  Gln Glu Ser Leu Pro  His Ala Gly
    1025                1030                1035

Pro Ile  Ile Val His Cys Ser  Ala Gly Ile Gly Arg  Thr Gly Thr
    1040                1045                1050

Ile Ile  Val Ile Asp Met Leu  Met Glu Asn Ile Ser  Thr Lys Gly
    1055                1060                1065

Leu Asp  Cys Asp Ile Asp Ile  Gln Lys Thr Ile Gln  Met Val Arg
    1070                1075                1080

Ala Gln  Arg Ser Gly Met Val  Gln Thr Glu Ala Gln  Tyr Lys Phe
    1085                1090                1095

Ile Tyr  Val Ala Ile Ala Gln  Phe Ile Glu Thr Thr  Lys Lys Lys
    1100                1105                1110

Leu
```

<210> 5
<211> 918
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric antigen receptor (CAR)

<400> 5

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

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

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

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

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65                  70                  75                  80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
                85                  90                  95
```

```
Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
            100                 105                 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
        115                 120                 125

Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser Gly Pro Gly
145                 150                 155                 160

Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys Thr Val Ser Gly
                165                 170                 175

Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg
            180                 185                 190

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr
        195                 200                 205

Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile Lys Asp Asn Ser
    210                 215                 220

Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr
225                 230                 235                 240

Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala
                245                 250                 255

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp Pro
            260                 265                 270

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
        275                 280                 285

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
    290                 295                 300

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Phe Trp
305                 310                 315                 320

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
                325                 330                 335

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Arg Val Lys Phe Ser Arg
            340                 345                 350
```

```
Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
        355                 360                 365

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
    370                 375                 380

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
385                 390                 395                 400

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
                405                 410                 415

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
            420                 425                 430

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
        435                 440                 445

Ala Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Glu Gly Arg Gly
    450                 455                 460

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala
465                 470                 475                 480

Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr Asp Ala
                485                 490                 495

Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
            500                 505                 510

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp Ile Tyr
        515                 520                 525

Phe Asn Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
    530                 535                 540

Leu Ile Tyr Asp Thr Asn Arg Leu Ala Asp Gly Val Pro Ser Arg Phe
545                 550                 555                 560

Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser Ser Leu
                565                 570                 575

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Lys Asn Tyr
            580                 585                 590

Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ser Gly
        595                 600                 605
```

```
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    610                 615                 620

Gly Gly Ser Arg Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
625                 630                 635                 640

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
                645                 650                 655

Thr Leu Ser Asn Tyr Gly Met His Trp Ile Arg Gln Ala Pro Gly Lys
            660                 665                 670

Gly Leu Glu Trp Val Ser Ser Ile Ser Leu Asn Gly Gly Ser Thr Tyr
        675                 680                 685

Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
    690                 695                 700

Lys Ser Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
705                 710                 715                 720

Ala Val Tyr Tyr Cys Ala Ala Gln Asp Ala Tyr Thr Gly Gly Tyr Phe
                725                 730                 735

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Met Asp Pro
            740                 745                 750

Ala Thr Thr Thr Lys Pro Val Leu Arg Thr Pro Ser Pro Val His Pro
        755                 760                 765

Thr Gly Thr Ser Gln Pro Gln Arg Pro Glu Asp Cys Arg Pro Arg Gly
    770                 775                 780

Ser Val Lys Gly Thr Gly Leu Asp Phe Ala Cys Asp Ile Leu Ile Gly
785                 790                 795                 800

Val Ser Val Val Phe Leu Phe Cys Leu Leu Leu Leu Val Leu Phe Cys
                805                 810                 815

Leu His Arg Gln Asn Gln Ile Lys Gln Gly Pro Pro Arg Ser Lys Asp
            820                 825                 830

Glu Glu Gln Lys Pro Gln Gln Arg Pro Asp Leu Ala Val Asp Val Leu
        835                 840                 845

Glu Arg Thr Ala Asp Lys Ala Thr Val Asn Gly Leu Pro Glu Lys Asp
```

850 855 860

Arg Glu Thr Asp Thr Ser Ala Leu Ala Ala Gly Ser Ser Gln Glu Val
865 870 875 880

Thr Tyr Ala Gln Leu Asp His Trp Ala Leu Thr Gln Arg Thr Ala Arg
885 890 895

Ala Val Ser Pro Gln Ser Thr Lys Pro Met Ala Glu Ser Ile Thr Tyr
900 905 910

Ala Ala Val Ala Arg His
915

<210> 6
<211> 1363
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric antigen receptor (CAR)

<400> 6

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

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

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

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

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
85 90 95

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
115 120 125

Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

```
Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser Gly Pro Gly
145                 150                 155                 160

Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys Thr Val Ser Gly
                165                 170                 175

Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg
            180                 185                 190

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr
        195                 200                 205

Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile Lys Asp Asn Ser
    210                 215                 220

Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr
225                 230                 235                 240

Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala
                245                 250                 255

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp Pro
            260                 265                 270

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
        275                 280                 285

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
    290                 295                 300

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Phe Trp
305                 310                 315                 320

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
                325                 330                 335

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Arg Val Lys Phe Ser Arg
            340                 345                 350

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
        355                 360                 365

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
    370                 375                 380

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
```

```
385                 390                 395                 400

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
                405                 410                 415

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
            420                 425                 430

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
        435                 440                 445

Ala Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Glu Gly Arg Gly
    450                 455                 460

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala
465                 470                 475                 480

Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr Asp Ala
                485                 490                 495

Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
            500                 505                 510

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp Ile Tyr
        515                 520                 525

Phe Asn Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
    530                 535                 540

Leu Ile Tyr Asp Thr Asn Arg Leu Ala Asp Gly Val Pro Ser Arg Phe
545                 550                 555                 560

Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser Ser Leu
                565                 570                 575

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Lys Asn Tyr
            580                 585                 590

Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ser Gly
        595                 600                 605

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    610                 615                 620

Gly Gly Ser Arg Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
625                 630                 635                 640
```

```
Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
                645                 650                 655

Thr Leu Ser Asn Tyr Gly Met His Trp Ile Arg Gln Ala Pro Gly Lys
            660                 665                 670

Gly Leu Glu Trp Val Ser Ser Ile Ser Leu Asn Gly Gly Ser Thr Tyr
        675                 680                 685

Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
    690                 695                 700

Lys Ser Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
705                 710                 715                 720

Ala Val Tyr Tyr Cys Ala Ala Gln Asp Ala Tyr Thr Gly Gly Tyr Phe
                725                 730                 735

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Met Asp Pro
            740                 745                 750

Ala Thr Thr Thr Lys Pro Val Leu Arg Thr Pro Ser Pro Val His Pro
        755                 760                 765

Thr Gly Thr Ser Gln Pro Gln Arg Pro Glu Asp Cys Arg Pro Arg Gly
    770                 775                 780

Ser Val Lys Gly Thr Gly Leu Asp Phe Ala Cys Asp Ile Leu Ile Gly
785                 790                 795                 800

Val Ser Val Val Phe Leu Phe Cys Leu Leu Leu Leu Val Leu Phe Cys
                805                 810                 815

Leu His Arg Gln Asn Gln Ile Lys Gln Gly Pro Pro Arg Ser Lys Asp
            820                 825                 830

Glu Glu Gln Lys Pro Gln Gln Arg Pro Asp Leu Ala Val Asp Val Leu
        835                 840                 845

Glu Arg Thr Ala Asp Lys Ala Thr Val Asn Gly Leu Pro Glu Lys Asp
    850                 855                 860

Arg Glu Thr Asp Thr Ser Ala Leu Ala Ala Gly Ser Ser Gln Glu Val
865                 870                 875                 880

Thr Tyr Ala Gln Leu Asp His Trp Ala Leu Thr Gln Arg Thr Ala Arg
                885                 890                 895
```

```
Ala Val Ser Pro Gln Ser Thr Lys Pro Met Ala Glu Ser Ile Thr Tyr
            900                 905                 910

Ala Ala Val Ala Arg His Arg Ala Glu Gly Arg Gly Ser Leu Leu Thr
        915                 920                 925

Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Trp Tyr His Gly His Met
    930                 935                 940

Ser Gly Gly Gln Ala Glu Thr Leu Leu Gln Ala Lys Gly Glu Pro Trp
945                 950                 955                 960

Thr Phe Leu Val Arg Glu Ser Leu Ser Gln Pro Gly Asp Phe Val Leu
                965                 970                 975

Ser Val Leu Ser Asp Gln Pro Lys Ala Gly Pro Gly Ser Pro Leu Arg
            980                 985                 990

Val Thr His Ile Lys Val Met Cys  Glu Gly Gly Arg Tyr  Thr Val Gly
        995                 1000                1005

Gly Leu  Glu Thr Phe Asp Ser  Leu Thr Asp Leu Val  Glu His Phe
    1010                1015                1020

Lys Lys  Thr Gly Ile Glu Glu  Ala Ser Gly Ala Phe  Val Tyr Leu
    1025                1030                1035

Arg Gln  Pro Tyr Ser Gly Gly  Gly Gly Ser Phe Glu  Ala Tyr Phe
    1040                1045                1050

Lys Lys  Gln Gln Ala Asp Ser  Asn Cys Gly Phe Ala  Glu Glu Tyr
    1055                1060                1065

Glu Asp  Leu Lys Leu Val Gly  Ile Ser Gln Pro Lys  Tyr Ala Ala
    1070                1075                1080

Glu Leu  Ala Glu Asn Arg Gly  Lys Asn Arg Tyr Asn  Asn Val Leu
    1085                1090                1095

Pro Tyr  Asp Ile Ser Arg Val  Lys Leu Ser Val Gln  Thr His Ser
    1100                1105                1110

Thr Asp  Asp Tyr Ile Asn Ala  Asn Tyr Met Pro Gly  Tyr His Ser
    1115                1120                1125

Lys Lys  Asp Phe Ile Ala Thr  Gln Gly Pro Leu Pro  Asn Thr Leu
    1130                1135                1140
```

```
Lys Asp  Phe Trp Arg Met Val  Trp Glu Lys Asn Val  Tyr Ala Ile
    1145                1150                1155

Ile Met  Leu Thr Lys Cys Val  Glu Gln Gly Arg Thr  Lys Cys Glu
    1160                1165                1170

Glu Tyr  Trp Pro Ser Lys Gln  Ala Gln Asp Tyr Gly  Asp Ile Thr
    1175                1180                1185

Val Ala  Met Thr Ser Glu Ile  Val Leu Pro Glu Trp  Thr Ile Arg
    1190                1195                1200

Asp Phe  Thr Val Lys Asn Ile  Gln Thr Ser Glu Ser  His Pro Leu
    1205                1210                1215

Arg Gln  Phe His Phe Thr Ser  Trp Pro Asp His Gly  Val Pro Asp
    1220                1225                1230

Thr Thr  Asp Leu Leu Ile Asn  Phe Arg Tyr Leu Val  Arg Asp Tyr
    1235                1240                1245

Met Lys  Gln Ser Pro Pro Glu  Ser Pro Ile Leu Val  His Cys Ser
    1250                1255                1260

Ala Gly  Val Gly Arg Thr Gly  Thr Phe Ile Ala Ile  Asp Arg Leu
    1265                1270                1275

Ile Tyr  Gln Ile Glu Asn Glu  Asn Thr Val Asp Val  Tyr Gly Ile
    1280                1285                1290

Val Tyr  Asp Leu Arg Met His  Arg Pro Leu Met Val  Gln Thr Glu
    1295                1300                1305

Asp Gln  Tyr Val Phe Leu Asn  Gln Cys Val Leu Asp  Ile Val Arg
    1310                1315                1320

Ser Gln  Lys Asp Ser Lys Val  Asp Leu Ile Tyr Gln  Asn Thr Thr
    1325                1330                1335

Ala Met  Thr Ile Tyr Glu Asn  Leu Ala Pro Val Thr  Thr Phe Gly
    1340                1345                1350

Lys Thr  Asn Gly Tyr Ile Ala  Ser Gly Ser
    1355                1360
```

<210> 7

<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Signal peptide

<400> 7

Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
1 5 10 15

Asp His Ala Asp Gly
20

<210> 8
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Signal peptide

<400> 8

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

His Ala Ala Arg Pro
20

<210> 9
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Signal peptide

<400> 9

Met Ala Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr
1 5 10 15

Asp Ala Arg Cys
20

<210> 10
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer (hinge-CH2CH3 of human IgG1)

<400> 10

```
Ala Glu Pro Lys Ser Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1               5                   10                  15

Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30

Lys Asp Thr Leu Met Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Lys Lys Asp
225                 230


<210>  11
<211>  46
<212>  PRT
```

<213> Artificial Sequence

<220>
<223> Spacer (human CD8 stalk)

<400> 11

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1 5 10 15

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
20 25 30

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

<210> 12
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer (human IgG1 hinge)

<400> 12

Ala Glu Pro Lys Ser Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

Lys Asp Pro Lys
20

<210> 13
<211> 185
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer (CD2 ectodomain)

<400> 13

Lys Glu Ile Thr Asn Ala Leu Glu Thr Trp Gly Ala Leu Gly Gln Asp
1 5 10 15

Ile Asn Leu Asp Ile Pro Ser Phe Gln Met Ser Asp Asp Ile Asp Asp
20 25 30

Ile Lys Trp Glu Lys Thr Ser Asp Lys Lys Lys Ile Ala Gln Phe Arg
35 40 45

Lys Glu Lys Glu Thr Phe Lys Glu Lys Asp Thr Tyr Lys Leu Phe Lys
50 55 60

Asn Gly Thr Leu Lys Ile Lys His Leu Lys Thr Asp Asp Gln Asp Ile
65 70 75 80

Tyr Lys Val Ser Ile Tyr Asp Thr Lys Gly Lys Asn Val Leu Glu Lys
85 90 95

Ile Phe Asp Leu Lys Ile Gln Glu Arg Val Ser Lys Pro Lys Ile Ser
100 105 110

Trp Thr Cys Ile Asn Thr Thr Leu Thr Cys Glu Val Met Asn Gly Thr
115 120 125

Asp Pro Glu Leu Asn Leu Tyr Gln Asp Gly Lys His Leu Lys Leu Ser
130 135 140

Gln Arg Val Ile Thr His Lys Trp Thr Thr Ser Leu Ser Ala Lys Phe
145 150 155 160

Lys Cys Thr Ala Gly Asn Lys Val Ser Lys Glu Ser Ser Val Glu Pro
165 170 175

Val Ser Cys Pro Glu Lys Gly Leu Asp
180 185

<210> 14
<211> 259
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer (CD34 ectodomain)

<400> 14

Ser Leu Asp Asn Asn Gly Thr Ala Thr Pro Glu Leu Pro Thr Gln Gly
1 5 10 15

Thr Phe Ser Asn Val Ser Thr Asn Val Ser Tyr Gln Glu Thr Thr Thr
20 25 30

Pro Ser Thr Leu Gly Ser Thr Ser Leu His Pro Val Ser Gln His Gly
35 40 45

Asn Glu Ala Thr Thr Asn Ile Thr Glu Thr Thr Val Lys Phe Thr Ser
50 55 60

Thr Ser Val Ile Thr Ser Val Tyr Gly Asn Thr Asn Ser Ser Val Gln
65 70 75 80

Ser Gln Thr Ser Val Ile Ser Thr Val Phe Thr Thr Pro Ala Asn Val

85 90 95

Ser Thr Pro Glu Thr Thr Leu Lys Pro Ser Leu Ser Pro Gly Asn Val
100 105 110

Ser Asp Leu Ser Thr Thr Ser Thr Ser Leu Ala Thr Ser Pro Thr Lys
115 120 125

Pro Tyr Thr Ser Ser Ser Pro Ile Leu Ser Asp Ile Lys Ala Glu Ile
130 135 140

Lys Cys Ser Gly Ile Arg Glu Val Lys Leu Thr Gln Gly Ile Cys Leu
145 150 155 160

Glu Gln Asn Lys Thr Ser Ser Cys Ala Glu Phe Lys Lys Asp Arg Gly
165 170 175

Glu Gly Leu Ala Arg Val Leu Cys Gly Glu Glu Gln Ala Asp Ala Asp
180 185 190

Ala Gly Ala Gln Val Cys Ser Leu Leu Leu Ala Gln Ser Glu Val Arg
195 200 205

Pro Gln Cys Leu Leu Leu Val Leu Ala Asn Arg Thr Glu Ile Ser Ser
210 215 220

Lys Leu Gln Leu Met Lys Lys His Gln Ser Asp Leu Lys Lys Leu Gly
225 230 235 240

Ile Leu Asp Phe Thr Glu Gln Asp Val Ala Ser His Gln Ser Tyr Ser
245 250 255

Gln Lys Thr

<210> 15
<211> 140
<212> PRT
<213> Artificial Sequence

<220>
<223> CD28 transmembrane domain and CD3 Z endodomains

<400> 15

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
1 5 10 15

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Arg Val Lys Phe
20 25 30

```
Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
        35                  40                  45

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
    50                  55                  60

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
65                  70                  75                  80

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
                85                  90                  95

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
            100                 105                 110

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
        115                 120                 125

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
    130                 135                 140
```

<210> 16
<211> 180
<212> PRT
<213> Artificial Sequence

<220>
<223> CD28 transmembrane domain and CD28 and CD3 Zeta endodomains

<400> 16

```
Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
1               5                   10                  15

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
            20                  25                  30

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
        35                  40                  45

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
    50                  55                  60

Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
65                  70                  75                  80

Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
                85                  90                  95
```

```
Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
            100                 105                 110

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
        115                 120                 125

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
    130                 135                 140

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
145                 150                 155                 160

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
                165                 170                 175

Leu Pro Pro Arg
            180


<210>  17
<211>  216
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD28 transmembrane domain and CD28, OX40 and CD3 Zeta endodomains

<400>  17

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
1               5                   10                  15

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
            20                  25                  30

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
        35                  40                  45

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
    50                  55                  60

Ala Tyr Arg Ser Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro
65                  70                  75                  80

Pro Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp
                85                  90                  95

Ala His Ser Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala
            100                 105                 110
```

```
Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
        115                 120                 125

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
    130                 135                 140

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
145                 150                 155                 160

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
                165                 170                 175

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
            180                 185                 190

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
        195                 200                 205

His Met Gln Ala Leu Pro Pro Arg
    210                 215


<210>  18
<211>  729
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD45 transmembrane and endodomain

<400>  18

Ala Leu Ile Ala Phe Leu Ala Phe Leu Ile Ile Val Thr Ser Ile Ala
1               5                   10                  15

Leu Leu Val Val Leu Tyr Lys Ile Tyr Asp Leu His Lys Lys Arg Ser
            20                  25                  30

Cys Asn Leu Asp Glu Gln Gln Glu Leu Val Glu Arg Asp Asp Glu Lys
        35                  40                  45

Gln Leu Met Asn Val Glu Pro Ile His Ala Asp Ile Leu Leu Glu Thr
    50                  55                  60

Tyr Lys Arg Lys Ile Ala Asp Glu Gly Arg Leu Phe Leu Ala Glu Phe
65                  70                  75                  80

Gln Ser Ile Pro Arg Val Phe Ser Lys Phe Pro Ile Lys Glu Ala Arg
                85                  90                  95

Lys Pro Phe Asn Gln Asn Lys Asn Arg Tyr Val Asp Ile Leu Pro Tyr
```

```
            100                 105                 110

Asp Tyr Asn Arg Val Glu Leu Ser Glu Ile Asn Gly Asp Ala Gly Ser
        115                 120                 125

Asn Tyr Ile Asn Ala Ser Tyr Ile Asp Gly Phe Lys Glu Pro Arg Lys
    130                 135                 140

Tyr Ile Ala Ala Gln Gly Pro Arg Asp Glu Thr Val Asp Asp Phe Trp
145                 150                 155                 160

Arg Met Ile Trp Glu Gln Lys Ala Thr Val Ile Val Met Val Thr Arg
                165                 170                 175

Cys Glu Glu Gly Asn Arg Asn Lys Cys Ala Glu Tyr Trp Pro Ser Met
            180                 185                 190

Glu Glu Gly Thr Arg Ala Phe Gly Asp Val Val Val Lys Ile Asn Gln
        195                 200                 205

His Lys Arg Cys Pro Asp Tyr Ile Ile Gln Lys Leu Asn Ile Val Asn
    210                 215                 220

Lys Lys Glu Lys Ala Thr Gly Arg Glu Val Thr His Ile Gln Phe Thr
225                 230                 235                 240

Ser Trp Pro Asp His Gly Val Pro Glu Asp Pro His Leu Leu Leu Lys
                245                 250                 255

Leu Arg Arg Arg Val Asn Ala Phe Ser Asn Phe Phe Ser Gly Pro Ile
            260                 265                 270

Val Val His Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Tyr Ile Gly
        275                 280                 285

Ile Asp Ala Met Leu Glu Gly Leu Glu Ala Glu Asn Lys Val Asp Val
    290                 295                 300

Tyr Gly Tyr Val Val Lys Leu Arg Arg Gln Arg Cys Leu Met Val Gln
305                 310                 315                 320

Val Glu Ala Gln Tyr Ile Leu Ile His Gln Ala Leu Val Glu Tyr Asn
                325                 330                 335

Gln Phe Gly Glu Thr Glu Val Asn Leu Ser Glu Leu His Pro Tyr Leu
            340                 345                 350
```

```
His Asn Met Lys Lys Arg Asp Pro Pro Ser Glu Pro Ser Pro Leu Glu
        355                 360                 365

Ala Glu Phe Gln Arg Leu Pro Ser Tyr Arg Ser Trp Arg Thr Gln His
    370                 375                 380

Ile Gly Asn Gln Glu Glu Asn Lys Ser Lys Asn Arg Asn Ser Asn Val
385                 390                 395                 400

Ile Pro Tyr Asp Tyr Asn Arg Val Pro Leu Lys His Glu Leu Glu Met
                405                 410                 415

Ser Lys Glu Ser Glu His Asp Ser Asp Glu Ser Ser Asp Asp Asp Ser
            420                 425                 430

Asp Ser Glu Glu Pro Ser Lys Tyr Ile Asn Ala Ser Phe Ile Met Ser
        435                 440                 445

Tyr Trp Lys Pro Glu Val Met Ile Ala Ala Gln Gly Pro Leu Lys Glu
    450                 455                 460

Thr Ile Gly Asp Phe Trp Gln Met Ile Phe Gln Arg Lys Val Lys Val
465                 470                 475                 480

Ile Val Met Leu Thr Glu Leu Lys His Gly Asp Gln Glu Ile Cys Ala
                485                 490                 495

Gln Tyr Trp Gly Glu Gly Lys Gln Thr Tyr Gly Asp Ile Glu Val Asp
            500                 505                 510

Leu Lys Asp Thr Asp Lys Ser Ser Thr Tyr Thr Leu Arg Val Phe Glu
        515                 520                 525

Leu Arg His Ser Lys Arg Lys Asp Ser Arg Thr Val Tyr Gln Tyr Gln
    530                 535                 540

Tyr Thr Asn Trp Ser Val Glu Gln Leu Pro Ala Glu Pro Lys Glu Leu
545                 550                 555                 560

Ile Ser Met Ile Gln Val Val Lys Gln Lys Leu Pro Gln Lys Asn Ser
                565                 570                 575

Ser Glu Gly Asn Lys His His Lys Ser Thr Pro Leu Leu Ile His Cys
            580                 585                 590

Arg Asp Gly Ser Gln Gln Thr Gly Ile Phe Cys Ala Leu Leu Asn Leu
        595                 600                 605
```

```
Leu Glu Ser Ala Glu Thr Glu Glu Val Val Asp Ile Phe Gln Val Val
    610                 615                 620

Lys Ala Leu Arg Lys Ala Arg Pro Gly Met Val Ser Thr Phe Glu Gln
625                 630                 635                 640

Tyr Gln Phe Leu Tyr Asp Val Ile Ala Ser Thr Tyr Pro Ala Gln Asn
                645                 650                 655

Gly Gln Val Lys Lys Asn Asn His Gln Glu Asp Lys Ile Glu Phe Asp
            660                 665                 670

Asn Glu Val Asp Lys Val Lys Gln Asp Ala Asn Cys Val Asn Pro Leu
        675                 680                 685

Gly Ala Pro Glu Lys Leu Pro Glu Ala Lys Glu Gln Ala Glu Gly Ser
    690                 695                 700

Glu Pro Thr Ser Gly Thr Glu Gly Pro Glu His Ser Val Asn Gly Pro
705                 710                 715                 720

Ala Ser Pro Ala Leu Asn Gln Gly Ser
                725
```

<210> 19
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<223> CD148 transmembrane and endodomain

<400> 19

```
Ala Val Phe Gly Cys Ile Phe Gly Ala Leu Val Ile Val Thr Val Gly
1               5                   10                  15

Gly Phe Ile Phe Trp Arg Lys Lys Arg Lys Asp Ala Lys Asn Asn Glu
            20                  25                  30

Val Ser Phe Ser Gln Ile Lys Pro Lys Lys Ser Lys Leu Ile Arg Val
        35                  40                  45

Glu Asn Phe Glu Ala Tyr Phe Lys Lys Gln Gln Ala Asp Ser Asn Cys
    50                  55                  60

Gly Phe Ala Glu Glu Tyr Glu Asp Leu Lys Leu Val Gly Ile Ser Gln
65                  70                  75                  80
```

```
Pro Lys Tyr Ala Ala Glu Leu Ala Glu Asn Arg Gly Lys Asn Arg Tyr
                85                  90                  95

Asn Asn Val Leu Pro Tyr Asp Ile Ser Arg Val Lys Leu Ser Val Gln
            100                 105                 110

Thr His Ser Thr Asp Asp Tyr Ile Asn Ala Asn Tyr Met Pro Gly Tyr
        115                 120                 125

His Ser Lys Lys Asp Phe Ile Ala Thr Gln Gly Pro Leu Pro Asn Thr
    130                 135                 140

Leu Lys Asp Phe Trp Arg Met Val Trp Glu Lys Asn Val Tyr Ala Ile
145                 150                 155                 160

Ile Met Leu Thr Lys Cys Val Glu Gln Gly Arg Thr Lys Cys Glu Glu
                165                 170                 175

Tyr Trp Pro Ser Lys Gln Ala Gln Asp Tyr Gly Asp Ile Thr Val Ala
            180                 185                 190

Met Thr Ser Glu Ile Val Leu Pro Glu Trp Thr Ile Arg Asp Phe Thr
        195                 200                 205

Val Lys Asn Ile Gln Thr Ser Glu Ser His Pro Leu Arg Gln Phe His
    210                 215                 220

Phe Thr Ser Trp Pro Asp His Gly Val Pro Asp Thr Thr Asp Leu Leu
225                 230                 235                 240

Ile Asn Phe Arg Tyr Leu Val Arg Asp Tyr Met Lys Gln Ser Pro Pro
                245                 250                 255

Glu Ser Pro Ile Leu Val His Cys Ser Ala Gly Val Gly Arg Thr Gly
            260                 265                 270

Thr Phe Ile Ala Ile Asp Arg Leu Ile Tyr Gln Ile Glu Asn Glu Asn
        275                 280                 285

Thr Val Asp Val Tyr Gly Ile Val Tyr Asp Leu Arg Met His Arg Pro
    290                 295                 300

Leu Met Val Gln Thr Glu Asp Gln Tyr Val Phe Leu Asn Gln Cys Val
305                 310                 315                 320

Leu Asp Ile Val Arg Ser Gln Lys Asp Ser Lys Val Asp Leu Ile Tyr
                325                 330                 335
```

```
Gln Asn Thr Thr Ala Met Thr Ile Tyr Glu Asn Leu Ala Pro Val Thr
            340                 345                 350

Thr Phe Gly Lys Thr Asn Gly Tyr Ile Ala
        355                 360
```

<210> 20
<211> 595
<212> PRT
<213> Artificial Sequence

<220>
<223> sequence of PTPN6

<400> 20

```
Met Val Arg Trp Phe His Arg Asp Leu Ser Gly Leu Asp Ala Glu Thr
1               5                   10                  15

Leu Leu Lys Gly Arg Gly Val His Gly Ser Phe Leu Ala Arg Pro Ser
            20                  25                  30

Arg Lys Asn Gln Gly Asp Phe Ser Leu Ser Val Arg Val Gly Asp Gln
        35                  40                  45

Val Thr His Ile Arg Ile Gln Asn Ser Gly Asp Phe Tyr Asp Leu Tyr
    50                  55                  60

Gly Gly Glu Lys Phe Ala Thr Leu Thr Glu Leu Val Glu Tyr Tyr Thr
65                  70                  75                  80

Gln Gln Gln Gly Val Leu Gln Asp Arg Asp Gly Thr Ile Ile His Leu
                85                  90                  95

Lys Tyr Pro Leu Asn Cys Ser Asp Pro Thr Ser Glu Arg Trp Tyr His
            100                 105                 110

Gly His Met Ser Gly Gly Gln Ala Glu Thr Leu Leu Gln Ala Lys Gly
        115                 120                 125

Glu Pro Trp Thr Phe Leu Val Arg Glu Ser Leu Ser Gln Pro Gly Asp
    130                 135                 140

Phe Val Leu Ser Val Leu Ser Asp Gln Pro Lys Ala Gly Pro Gly Ser
145                 150                 155                 160

Pro Leu Arg Val Thr His Ile Lys Val Met Cys Glu Gly Gly Arg Tyr
                165                 170                 175
```

```
Thr Val Gly Gly Leu Glu Thr Phe Asp Ser Leu Thr Asp Leu Val Glu
            180                 185                 190

His Phe Lys Lys Thr Gly Ile Glu Glu Ala Ser Gly Ala Phe Val Tyr
        195                 200                 205

Leu Arg Gln Pro Tyr Tyr Ala Thr Arg Val Asn Ala Ala Asp Ile Glu
    210                 215                 220

Asn Arg Val Leu Glu Leu Asn Lys Lys Gln Glu Ser Glu Asp Thr Ala
225                 230                 235                 240

Lys Ala Gly Phe Trp Glu Glu Phe Glu Ser Leu Gln Lys Gln Glu Val
                245                 250                 255

Lys Asn Leu His Gln Arg Leu Glu Gly Gln Arg Pro Glu Asn Lys Gly
            260                 265                 270

Lys Asn Arg Tyr Lys Asn Ile Leu Pro Phe Asp His Ser Arg Val Ile
        275                 280                 285

Leu Gln Gly Arg Asp Ser Asn Ile Pro Gly Ser Asp Tyr Ile Asn Ala
    290                 295                 300

Asn Tyr Ile Lys Asn Gln Leu Leu Gly Pro Asp Glu Asn Ala Lys Thr
305                 310                 315                 320

Tyr Ile Ala Ser Gln Gly Cys Leu Glu Ala Thr Val Asn Asp Phe Trp
                325                 330                 335

Gln Met Ala Trp Gln Glu Asn Ser Arg Val Ile Val Met Thr Thr Arg
            340                 345                 350

Glu Val Glu Lys Gly Arg Asn Lys Cys Val Pro Tyr Trp Pro Glu Val
        355                 360                 365

Gly Met Gln Arg Ala Tyr Gly Pro Tyr Ser Val Thr Asn Cys Gly Glu
    370                 375                 380

His Asp Thr Thr Glu Tyr Lys Leu Arg Thr Leu Gln Val Ser Pro Leu
385                 390                 395                 400

Asp Asn Gly Asp Leu Ile Arg Glu Ile Trp His Tyr Gln Tyr Leu Ser
                405                 410                 415

Trp Pro Asp His Gly Val Pro Ser Glu Pro Gly Gly Val Leu Ser Phe
            420                 425                 430
```

```
Leu Asp Gln Ile Asn Gln Arg Gln Glu Ser Leu Pro His Ala Gly Pro
        435                 440                 445

Ile Ile Val His Cys Ser Ala Gly Ile Gly Arg Thr Gly Thr Ile Ile
    450                 455                 460

Val Ile Asp Met Leu Met Glu Asn Ile Ser Thr Lys Gly Leu Asp Cys
465                 470                 475                 480

Asp Ile Asp Ile Gln Lys Thr Ile Gln Met Val Arg Ala Gln Arg Ser
                485                 490                 495

Gly Met Val Gln Thr Glu Ala Gln Tyr Lys Phe Ile Tyr Val Ala Ile
            500                 505                 510

Ala Gln Phe Ile Glu Thr Thr Lys Lys Lys Leu Glu Val Leu Gln Ser
        515                 520                 525

Gln Lys Gly Gln Glu Ser Glu Tyr Gly Asn Ile Thr Tyr Pro Pro Ala
    530                 535                 540

Met Lys Asn Ala His Ala Lys Ala Ser Arg Thr Ser Ser Lys His Lys
545                 550                 555                 560

Glu Asp Val Tyr Glu Asn Leu His Thr Lys Asn Lys Arg Glu Glu Lys
                565                 570                 575

Val Lys Lys Gln Arg Ser Ala Asp Lys Glu Lys Ser Lys Gly Ser Leu
            580                 585                 590

Lys Arg Lys
        595


<210>  21
<211>  272
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  sequence of phosphatase domain of PTPN6

<400>  21

Phe Trp Glu Glu Phe Glu Ser Leu Gln Lys Gln Glu Val Lys Asn Leu
1               5                   10                  15

His Gln Arg Leu Glu Gly Gln Arg Pro Glu Asn Lys Gly Lys Asn Arg
            20                  25                  30
```

```
Tyr Lys Asn Ile Leu Pro Phe Asp His Ser Arg Val Ile Leu Gln Gly
        35                  40                  45

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

Lys Asn Gln Leu Leu Gly Pro Asp Glu Asn Ala Lys Thr Tyr Ile Ala
65                  70                  75                  80

Ser Gln Gly Cys Leu Glu Ala Thr Val Asn Asp Phe Trp Gln Met Ala
                85                  90                  95

Trp Gln Glu Asn Ser Arg Val Ile Val Met Thr Thr Arg Glu Val Glu
            100                 105                 110

Lys Gly Arg Asn Lys Cys Val Pro Tyr Trp Pro Glu Val Gly Met Gln
        115                 120                 125

Arg Ala Tyr Gly Pro Tyr Ser Val Thr Asn Cys Gly Glu His Asp Thr
    130                 135                 140

Thr Glu Tyr Lys Leu Arg Thr Leu Gln Val Ser Pro Leu Asp Asn Gly
145                 150                 155                 160

Asp Leu Ile Arg Glu Ile Trp His Tyr Gln Tyr Leu Ser Trp Pro Asp
                165                 170                 175

His Gly Val Pro Ser Glu Pro Gly Gly Val Leu Ser Phe Leu Asp Gln
            180                 185                 190

Ile Asn Gln Arg Gln Glu Ser Leu Pro His Ala Gly Pro Ile Ile Val
        195                 200                 205

His Cys Ser Ala Gly Ile Gly Arg Thr Gly Thr Ile Ile Val Ile Asp
    210                 215                 220

Met Leu Met Glu Asn Ile Ser Thr Lys Gly Leu Asp Cys Asp Ile Asp
225                 230                 235                 240

Ile Gln Lys Thr Ile Gln Met Val Arg Ala Gln Arg Ser Gly Met Val
                245                 250                 255

Gln Thr Glu Ala Gln Tyr Lys Phe Ile Tyr Val Ala Ile Ala Gln Phe
            260                 265                 270


<210>  22
<211>  97
<212>  PRT
```

<213> Artificial Sequence

<220>
<223> PDCD1 endodomain

<400> 22

Cys Ser Arg Ala Ala Arg Gly Thr Ile Gly Ala Arg Arg Thr Gly Gln
1 5 10 15

Pro Leu Lys Glu Asp Pro Ser Ala Val Pro Val Phe Ser Val Asp Tyr
20 25 30

Gly Glu Leu Asp Phe Gln Trp Arg Glu Lys Thr Pro Glu Pro Pro Val
35 40 45

Pro Cys Val Pro Glu Gln Thr Glu Tyr Ala Thr Ile Val Phe Pro Ser
50 55 60

Gly Met Gly Thr Ser Ser Pro Ala Arg Arg Gly Ser Ala Asp Gly Pro
65 70 75 80

Arg Ser Ala Gln Pro Leu Arg Pro Glu Asp Gly His Cys Ser Trp Pro
85 90 95

Leu

<210> 23
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> BTLA4 endodomain

<400> 23

Lys Leu Gln Arg Arg Trp Lys Arg Thr Gln Ser Gln Gln Gly Leu Gln
1 5 10 15

Glu Asn Ser Ser Gly Gln Ser Phe Phe Val Arg Asn Lys Lys Val Arg
20 25 30

Arg Ala Pro Leu Ser Glu Gly Pro His Ser Leu Gly Cys Tyr Asn Pro
35 40 45

Met Met Glu Asp Gly Ile Ser Tyr Thr Thr Leu Arg Phe Pro Glu Met
50 55 60

Asn Ile Pro Arg Thr Gly Asp Ala Glu Ser Ser Glu Met Gln Arg Pro
65 70 75 80

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

Gln Val Gly Asp Tyr Glu Asn Val Ile Pro Asp Phe Pro Glu Asp Glu
100 105 110

Gly Ile His Tyr Ser Glu Leu Ile Gln Phe Gly Val Gly Glu Arg Pro
115 120 125

Gln Ala Gln Glu Asn Val Asp Tyr Val Ile Leu Lys His
130 135 140

<210> 24
<211> 168
<212> PRT
<213> Artificial Sequence

<220>
<223> LILRB1 endodomain

<400> 24

Leu Arg His Arg Arg Gln Gly Lys His Trp Thr Ser Thr Gln Arg Lys
1 5 10 15

Ala Asp Phe Gln His Pro Ala Gly Ala Val Gly Pro Glu Pro Thr Asp
20 25 30

Arg Gly Leu Gln Trp Arg Ser Ser Pro Ala Ala Asp Ala Gln Glu Glu
35 40 45

Asn Leu Tyr Ala Ala Val Lys His Thr Gln Pro Glu Asp Gly Val Glu
50 55 60

Met Asp Thr Arg Ser Pro His Asp Glu Asp Pro Gln Ala Val Thr Tyr
65 70 75 80

Ala Glu Val Lys His Ser Arg Pro Arg Arg Glu Met Ala Ser Pro Pro
85 90 95

Ser Pro Leu Ser Gly Glu Phe Leu Asp Thr Lys Asp Arg Gln Ala Glu
100 105 110

Glu Asp Arg Gln Met Asp Thr Glu Ala Ala Ala Ser Glu Ala Pro Gln
115 120 125

Asp Val Thr Tyr Ala Gln Leu His Ser Leu Thr Leu Arg Arg Glu Ala
130 135 140

Thr Glu Pro Pro Pro Ser Gln Glu Gly Pro Ser Pro Ala Val Pro Ser
145 150 155 160

Ile Tyr Ala Thr Leu Ala Ile His
165

<210> 25
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> LAIR1 endodomain

<400> 25

His Arg Gln Asn Gln Ile Lys Gln Gly Pro Pro Arg Ser Lys Asp Glu
1 5 10 15

Glu Gln Lys Pro Gln Gln Arg Pro Asp Leu Ala Val Asp Val Leu Glu
20 25 30

Arg Thr Ala Asp Lys Ala Thr Val Asn Gly Leu Pro Glu Lys Asp Arg
35 40 45

Glu Thr Asp Thr Ser Ala Leu Ala Ala Gly Ser Ser Gln Glu Val Thr
50 55 60

Tyr Ala Gln Leu Asp His Trp Ala Leu Thr Gln Arg Thr Ala Arg Ala
65 70 75 80

Val Ser Pro Gln Ser Thr Lys Pro Met Ala Glu Ser Ile Thr Tyr Ala
85 90 95

Ala Val Ala Arg His
100

<210> 26
<211> 62
<212> PRT
<213> Artificial Sequence

<220>
<223> CTLA4 endodomain

<400> 26

Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe Tyr
1 5 10 15

Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys Arg
20 25 30

Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu Pro
35 40 45

Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
50 55 60

<210> 27
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> KIR2DL1 endodomain

<400> 27

Gly Asn Ser Arg His Leu His Val Leu Ile Gly Thr Ser Val Val Ile
1 5 10 15

Ile Pro Phe Ala Ile Leu Leu Phe Phe Leu Leu His Arg Trp Cys Ala
20 25 30

Asn Lys Lys Asn Ala Val Val Met Asp Gln Glu Pro Ala Gly Asn Arg
35 40 45

Thr Val Asn Arg Glu Asp Ser Asp Glu Gln Asp Pro Gln Glu Val Thr
50 55 60

Tyr Thr Gln Leu Asn His Cys Val Phe Thr Gln Arg Lys Ile Thr Arg
65 70 75 80

Pro Ser Gln Arg Pro Lys Thr Pro Pro Thr Asp Ile Ile Val Tyr Thr
85 90 95

Glu Leu Pro Asn Ala Glu Ser Arg Ser Lys Val Val Ser Cys Pro
100 105 110

<210> 28
<211> 143
<212> PRT
<213> Artificial Sequence

<220>
<223> KIR2DL4 endodomain

<400> 28

Gly Ile Ala Arg His Leu His Ala Val Ile Arg Tyr Ser Val Ala Ile
1 5 10 15

Ile Leu Phe Thr Ile Leu Pro Phe Phe Leu Leu His Arg Trp Cys Ser

20 25 30

Lys Lys Lys Glu Asn Ala Ala Val Met Asn Gln Glu Pro Ala Gly His
35 40 45

Arg Thr Val Asn Arg Glu Asp Ser Asp Glu Gln Asp Pro Gln Glu Val
50 55 60

Thr Tyr Ala Gln Leu Asp His Cys Ile Phe Thr Gln Arg Lys Ile Thr
65 70 75 80

Gly Pro Ser Gln Arg Ser Lys Arg Pro Ser Thr Asp Thr Ser Val Cys
85 90 95

Ile Glu Leu Pro Asn Ala Glu Pro Arg Ala Leu Ser Pro Ala His Glu
100 105 110

His His Ser Gln Ala Leu Met Gly Ser Ser Arg Glu Thr Thr Ala Leu
115 120 125

Ser Gln Thr Gln Leu Ala Ser Ser Asn Val Pro Ala Ala Gly Ile
130 135 140

<210> 29
<211> 143
<212> PRT
<213> Artificial Sequence

<220>
<223> KIR2DL5 endodomain

<400> 29

Thr Gly Ile Arg Arg His Leu His Ile Leu Ile Gly Thr Ser Val Ala
1 5 10 15

Ile Ile Leu Phe Ile Ile Leu Phe Phe Phe Leu Leu His Cys Cys Cys
20 25 30

Ser Asn Lys Lys Asn Ala Ala Val Met Asp Gln Glu Pro Ala Gly Asp
35 40 45

Arg Thr Val Asn Arg Glu Asp Ser Asp Asp Gln Asp Pro Gln Glu Val
50 55 60

Thr Tyr Ala Gln Leu Asp His Cys Val Phe Thr Gln Thr Lys Ile Thr
65 70 75 80

Ser Pro Ser Gln Arg Pro Lys Thr Pro Pro Thr Asp Thr Thr Met Tyr
85 90 95

Met Glu Leu Pro Asn Ala Lys Pro Arg Ser Leu Ser Pro Ala His Lys
100 105 110

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

Ser Gln Asn Arg Val Ala Ser Ser His Val Pro Ala Ala Gly Ile
130 135 140

<210> 30
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> KIR3DL1 endodomain

<400> 30

Lys Asp Pro Arg His Leu His Ile Leu Ile Gly Thr Ser Val Val Ile
1 5 10 15

Ile Leu Phe Ile Leu Leu Leu Phe Phe Leu Leu His Leu Trp Cys Ser
20 25 30

Asn Lys Lys Asn Ala Ala Val Met Asp Gln Glu Pro Ala Gly Asn Arg
35 40 45

Thr Ala Asn Ser Glu Asp Ser Asp Glu Gln Asp Pro Glu Glu Val Thr
50 55 60

Tyr Ala Gln Leu Asp His Cys Val Phe Thr Gln Arg Lys Ile Thr Arg
65 70 75 80

Pro Ser Gln Arg Pro Lys Thr Pro Pro Thr Asp Thr Ile Leu Tyr Thr
85 90 95

Glu Leu Pro Asn Ala Lys Pro Arg Ser Lys Val Val Ser Cys Pro
100 105 110

<210> 31
<211> 97
<212> PRT
<213> Artificial Sequence

<220>
<223> KIR3DL3 endodomain

<400> 31

Lys Asp Pro Gly Asn Ser Arg His Leu His Val Leu Ile Gly Thr Ser

1 5 10 15

Val Val Ile Ile Pro Phe Ala Ile Leu Leu Phe Phe Leu Leu His Arg
20 25 30

Trp Cys Ala Asn Lys Lys Asn Ala Val Val Met Asp Gln Glu Pro Ala
35 40 45

Gly Asn Arg Thr Val Asn Arg Glu Asp Ser Asp Glu Gln Asp Pro Gln
50 55 60

Glu Val Thr Tyr Ala Gln Leu Asn His Cys Val Phe Thr Gln Arg Lys
65 70 75 80

Ile Thr Arg Pro Ser Gln Arg Pro Lys Thr Pro Pro Thr Asp Thr Ser
85 90 95

Val

<210> 32
<211> 807
<212> PRT
<213> Artificial Sequence

<220>
<223> PTPN6-CD45 fusion protein

<400> 32

Trp Tyr His Gly His Met Ser Gly Gly Gln Ala Glu Thr Leu Leu Gln
1 5 10 15

Ala Lys Gly Glu Pro Trp Thr Phe Leu Val Arg Glu Ser Leu Ser Gln
20 25 30

Pro Gly Asp Phe Val Leu Ser Val Leu Ser Asp Gln Pro Lys Ala Gly
35 40 45

Pro Gly Ser Pro Leu Arg Val Thr His Ile Lys Val Met Cys Glu Gly
50 55 60

Gly Arg Tyr Thr Val Gly Gly Leu Glu Thr Phe Asp Ser Leu Thr Asp
65 70 75 80

Leu Val Glu His Phe Lys Lys Thr Gly Ile Glu Glu Ala Ser Gly Ala
85 90 95

Phe Val Tyr Leu Arg Gln Pro Tyr Lys Ile Tyr Asp Leu His Lys Lys
100 105 110

```
Arg Ser Cys Asn Leu Asp Glu Gln Gln Glu Leu Val Glu Arg Asp Asp
        115                 120                 125

Glu Lys Gln Leu Met Asn Val Glu Pro Ile His Ala Asp Ile Leu Leu
    130                 135                 140

Glu Thr Tyr Lys Arg Lys Ile Ala Asp Glu Gly Arg Leu Phe Leu Ala
145                 150                 155                 160

Glu Phe Gln Ser Ile Pro Arg Val Phe Ser Lys Phe Pro Ile Lys Glu
                165                 170                 175

Ala Arg Lys Pro Phe Asn Gln Asn Lys Asn Arg Tyr Val Asp Ile Leu
            180                 185                 190

Pro Tyr Asp Tyr Asn Arg Val Glu Leu Ser Glu Ile Asn Gly Asp Ala
        195                 200                 205

Gly Ser Asn Tyr Ile Asn Ala Ser Tyr Ile Asp Gly Phe Lys Glu Pro
    210                 215                 220

Arg Lys Tyr Ile Ala Ala Gln Gly Pro Arg Asp Glu Thr Val Asp Asp
225                 230                 235                 240

Phe Trp Arg Met Ile Trp Glu Gln Lys Ala Thr Val Ile Val Met Val
                245                 250                 255

Thr Arg Cys Glu Glu Gly Asn Arg Asn Lys Cys Ala Glu Tyr Trp Pro
            260                 265                 270

Ser Met Glu Glu Gly Thr Arg Ala Phe Gly Asp Val Val Val Lys Ile
        275                 280                 285

Asn Gln His Lys Arg Cys Pro Asp Tyr Ile Ile Gln Lys Leu Asn Ile
    290                 295                 300

Val Asn Lys Lys Glu Lys Ala Thr Gly Arg Glu Val Thr His Ile Gln
305                 310                 315                 320

Phe Thr Ser Trp Pro Asp His Gly Val Pro Glu Asp Pro His Leu Leu
                325                 330                 335

Leu Lys Leu Arg Arg Arg Val Asn Ala Phe Ser Asn Phe Phe Ser Gly
            340                 345                 350

Pro Ile Val Val His Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Tyr
```

```
        355                 360                 365

Ile Gly Ile Asp Ala Met Leu Glu Gly Leu Glu Ala Glu Asn Lys Val
    370                 375                 380

Asp Val Tyr Gly Tyr Val Val Lys Leu Arg Arg Gln Arg Cys Leu Met
385                 390                 395                 400

Val Gln Val Glu Ala Gln Tyr Ile Leu Ile His Gln Ala Leu Val Glu
                405                 410                 415

Tyr Asn Gln Phe Gly Glu Thr Glu Val Asn Leu Ser Glu Leu His Pro
            420                 425                 430

Tyr Leu His Asn Met Lys Lys Arg Asp Pro Pro Ser Glu Pro Ser Pro
        435                 440                 445

Leu Glu Ala Glu Phe Gln Arg Leu Pro Ser Tyr Arg Ser Trp Arg Thr
    450                 455                 460

Gln His Ile Gly Asn Gln Glu Glu Asn Lys Ser Lys Asn Arg Asn Ser
465                 470                 475                 480

Asn Val Ile Pro Tyr Asp Tyr Asn Arg Val Leu Lys His Glu Leu Glu
                485                 490                 495

Met Ser Lys Glu Ser Glu His Asp Ser Asp Glu Ser Ser Asp Asp Asp
            500                 505                 510

Ser Asp Ser Glu Glu Pro Ser Lys Tyr Ile Asn Ala Ser Phe Ile Met
        515                 520                 525

Ser Tyr Trp Lys Pro Glu Val Met Ile Ala Ala Gln Gly Pro Leu Lys
    530                 535                 540

Glu Thr Ile Gly Asp Phe Met Ile Gln Arg Lys Val Lys Val Ile Val
545                 550                 555                 560

Met Leu Thr Glu Leu Lys His Gly Asp Gln Glu Ile Cys Ala Gln Tyr
                565                 570                 575

Trp Gly Glu Gly Lys Gln Thr Tyr Gly Asp Ile Glu Val Asp Leu Lys
            580                 585                 590

Asp Thr Asp Lys Ser Ser Thr Tyr Thr Leu Arg Val Phe Glu Leu Arg
        595                 600                 605
```

```
His Ser Lys Arg Lys Asp Ser Arg Thr Val Tyr Gln Tyr Gln Tyr Thr
    610                 615                 620

Asn Trp Ser Val Glu Gln Leu Pro Ala Glu Pro Lys Glu Leu Ile Ser
625                 630                 635                 640

Met Ile Gln Val Val Lys Gln Lys Leu Pro Gln Lys Asn Ser Ser Glu
                645                 650                 655

Gly Asn Lys His His Lys Ser Thr Pro Leu Leu Ile His Cys Arg Asp
            660                 665                 670

Gly Ser Gln Gln Thr Gly Ile Phe Cys Ala Leu Leu Asn Leu Leu Glu
        675                 680                 685

Ser Ala Glu Thr Glu Glu Val Val Asp Ile Phe Gln Val Val Lys Ala
    690                 695                 700

Leu Arg Lys Ala Arg Pro Gly Met Val Ser Thr Phe Glu Gln Tyr Gln
705                 710                 715                 720

Phe Leu Tyr Asp Val Ile Ala Ser Thr Tyr Pro Ala Gln Asn Gly Gln
                725                 730                 735

Val Lys Lys Asn Asn His Gln Glu Asp Lys Ile Glu Phe Asp Asn Glu
            740                 745                 750

Val Asp Lys Val Lys Gln Asp Ala Asn Cys Val Asn Pro Leu Gly Ala
        755                 760                 765

Pro Glu Lys Leu Pro Glu Ala Lys Glu Gln Ala Glu Gly Ser Glu Pro
    770                 775                 780

Thr Ser Gly Thr Glu Gly Pro Glu His Ser Val Asn Gly Pro Ala Ser
785                 790                 795                 800

Pro Ala Leu Asn Gln Gly Ser
                805


<210>  33
<211>  434
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  PTPN6-CD148 fusion protein

<400>  33

Glu Thr Leu Leu Gln Ala Lys Gly Glu Pro Trp Thr Phe Leu Val Arg
```

```
1               5                   10                  15

Glu Ser Leu Ser Gln Pro Gly Asp Phe Val Leu Ser Val Leu Ser Asp
            20                  25                  30

Gln Pro Lys Ala Gly Pro Gly Ser Pro Leu Arg Val Thr His Ile Lys
        35                  40                  45

Val Met Cys Glu Gly Gly Arg Tyr Thr Val Gly Gly Leu Glu Thr Phe
    50                  55                  60

Asp Ser Leu Thr Asp Leu Val Glu His Phe Lys Lys Thr Gly Ile Glu
65                  70                  75                  80

Glu Ala Ser Gly Ala Phe Val Tyr Leu Arg Gln Pro Tyr Arg Lys Lys
                85                  90                  95

Arg Lys Asp Ala Lys Asn Asn Glu Val Ser Phe Ser Gln Ile Lys Pro
            100                 105                 110

Lys Lys Ser Lys Leu Ile Arg Val Glu Asn Phe Glu Ala Tyr Phe Lys
        115                 120                 125

Lys Gln Gln Ala Asp Ser Asn Cys Gly Phe Ala Glu Glu Tyr Glu Asp
    130                 135                 140

Leu Lys Leu Val Gly Ile Ser Gln Pro Lys Tyr Ala Ala Glu Leu Ala
145                 150                 155                 160

Glu Asn Arg Gly Lys Asn Arg Tyr Asn Asn Val Leu Pro Tyr Asp Ile
                165                 170                 175

Ser Arg Val Lys Leu Ser Val Gln Thr His Ser Thr Asp Asp Tyr Ile
            180                 185                 190

Asn Ala Asn Tyr Met Pro Gly Tyr His Ser Lys Lys Asp Phe Ile Ala
        195                 200                 205

Thr Gln Gly Pro Leu Pro Asn Thr Leu Lys Asp Phe Trp Arg Met Val
    210                 215                 220

Trp Glu Lys Asn Val Tyr Ala Ile Ile Met Leu Thr Lys Cys Val Glu
225                 230                 235                 240

Gln Gly Arg Thr Lys Cys Glu Glu Tyr Trp Pro Ser Lys Gln Ala Gln
                245                 250                 255
```

```
Asp Tyr Gly Asp Ile Thr Val Ala Met Thr Ser Glu Ile Val Leu Pro
            260                 265                 270

Glu Trp Thr Ile Arg Asp Phe Thr Val Lys Asn Ile Gln Thr Ser Glu
        275                 280                 285

Ser His Pro Leu Arg Gln Phe His Phe Thr Ser Trp Pro Asp His Gly
    290                 295                 300

Val Pro Asp Thr Thr Asp Leu Leu Ile Asn Phe Arg Tyr Leu Val Arg
305                 310                 315                 320

Asp Tyr Met Lys Gln Ser Pro Pro Glu Ser Pro Ile Leu Val His Cys
                325                 330                 335

Ser Ala Gly Val Gly Arg Thr Gly Thr Phe Ile Ala Ile Asp Arg Leu
            340                 345                 350

Ile Tyr Gln Ile Glu Asn Glu Asn Thr Val Asp Val Tyr Gly Ile Val
        355                 360                 365

Tyr Asp Leu Arg Met His Arg Pro Leu Met Val Gln Thr Glu Asp Gln
    370                 375                 380

Tyr Val Phe Leu Asn Gln Cys Val Leu Asp Ile Val Arg Ser Gln Lys
385                 390                 395                 400

Asp Ser Lys Val Asp Leu Ile Tyr Gln Asn Thr Thr Ala Met Thr Ile
                405                 410                 415

Tyr Glu Asn Leu Ala Pro Val Thr Thr Phe Gly Lys Thr Asn Gly Tyr
            420                 425                 430

Ile Ala
```

<210> 34
<211> 20
<212> PRT
<213> Foot-and-mouth disease virus

<400> 34

```
Arg Ala Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu
1               5                   10                  15

Asn Pro Gly Pro
            20
```

<210> 35
<211> 3390
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequences coding for CARs (MP13974.SFG.aCD19fmc63-CD8STK-CD28tmZ-2A-aCD33glx-HCH2CH3pvaa-CD28tmZw)

<400> 35
atgagcctgc ccgtgaccgc cctgctgctg cccctggccc tgctgctgca cgccgccaga 60

ccagacatcc agatgaccca gaccaccagc agcctgagcg ccagcctggg cgaccgggtg 120

accatcagct gcagagccag ccaggacatc agcaagtacc tgaactggta ccagcagaag 180

cccgacggca ccgtgaagct gctgatctac cacaccagcc ggctgcacag cggcgtgccc 240

agccggttca gcggcagcgg cagcggcacc gactacagcc tgaccatcag caacctggag 300

caggaggaca tcgccaccta cttctgccag cagggcaaca ccctgcccta caccttcgga 360

ggcggcacca agctggagat caccaaggcc ggaggcggag gctctggcgg aggcggctct 420

ggcggaggcg gctctggcgg aggcggcagc gaggtgaagc tgcaggagtc tggcccaggc 480

ctggtggccc caagccagag cctgagcgtg acctgcaccg tgagcggcgt gagcctgccc 540

gactacggcg tgagctggat caggcagccc ccacggaagg gcctggagtg gctgggcgtg 600

atctggggca gcgagaccac ctactacaac agcgccctga agagccggct gaccatcatc 660

aaggacaaca gcaagagcca ggtgttcctg aagatgaaca gcctgcagac cgacgacacc 720

gccatctact actgcgccaa gcactactac tatggcggca gctacgctat ggactactgg 780

ggccagggca ccagcgtgac cgtgagctca gatcccacca cgacgccagc gccgcgacca 840

ccaacaccgg cgcccaccat cgcgtcgcag cccctgtccc tgcgcccaga ggcgtgccgg 900

ccagcggcgg ggggcgcagt gcacacgagg gggctggact tcgcctgtga tatcttttgg 960

gtgctggtgg tggttggtgg agtcctggct tgctatagct tgctagtaac agtggccttt 1020

attattttct gggtgaggag agtgaagttc agcaggagcg cagacgcccc cgcgtaccag 1080

cagggccaga accagctcta taacgagctc aatctaggac gaagagagga gtacgatgtt 1140

ttggacaaga gacgtggccg ggaccctgag atgggggaa agccgagaag gaagaaccct 1200

caggaaggcc tgtacaatga actgcagaaa gataagatgg cggaggccta cagtgagatt 1260

gggatgaaag gcgagcgccg gaggggcaag gggcacgatg gcctttacca gggtctcagt 1320

acagccacca aggacaccta cgacgccctt cacatgcagg ccctgcctcc tcgcagagcc 1380

gagggcaggg gaagtcttct aacatgcggg gacgtggagg aaaatcccgg gcccatggcc 1440

gtgcccactc aggtcctggg gttgttgcta ctgtggctta cagatgccag atgtgacatc 1500

cagatgacac agtctccatc ttccctgtct gcatctgtcg gagatcgcgt caccatcacc 1560

```
tgtcgagcaa gtgaggacat ttatttaat ttagtgtggt atcagcagaa accaggaaag     1620
gcccctaagc tcctgatcta tgatacaaat cgcttggcag atggggtccc atcacggttc     1680
agtggctctg gatctggcac acagtatact ctaaccataa gtagcctgca acccgaagat     1740
ttcgcaacct attattgtca acactataag aattatccgc tcacgttcgg tcaggggacc     1800
aagctggaaa tcaaaagatc tggtggcgga gggtcaggag gcggaggcag cggaggcggt     1860
ggctcgggag gcggaggctc gagatctgag gtgcagttgg tggagtctgg gggcggcttg     1920
gtgcagcctg gagggtccct gaggctctcc tgtgcagcct caggattcac tctcagtaat     1980
tatggcatgc actggatcag gcaggctcca gggaagggtc tggagtgggt ctcgtctatt     2040
agtcttaatg gtggtagcac ttactatcga gactccgtga agggccgatt cactatctcc     2100
agggacaatg caaaaagcac cctctacctt caaatgaata gtctgagggc cgaggacacg     2160
gccgtctatt actgtgcagc acaggacgct tatacgggag gttactttga ttactggggc     2220
caaggaacgc tggtcacagt ctcgtctatg gatcccgccg agcccaaatc tcctgacaaa     2280
actcacacat gcccaccgtg cccagcacct cccgtggccg gcccgtcagt cttcctcttc     2340
cccccaaaac ccaaggacac cctcatgatc gcccggaccc ctgaggtcac atgcgtggtg     2400
gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag     2460
gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc     2520
agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc     2580
tccaacaaag ccctcccagc ccccatcgag aaaaccatct ccaaagccaa agggcagccc     2640
cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccaggtc     2700
agcctgacct gcctggtcaa aggcttctat cccagcgaca tcgccgtgga gtgggagagc     2760
aatgggcaac cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc     2820
ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc     2880
tcatgctccg tgatgcatga ggccctgcac aatcactata cccagaaatc tctgagtctg     2940
agcccaggca agaaggaccc caagttctgg gtcctggtgg tggtgggagg cgtgctggcc     3000
tgttactctc tcctggtgac cgtggccttc atcatctttt gggtgcgctc ccgggtgaag     3060
ttttctcgct ctgccgatgc cccagcctat cagcagggcc agaatcagct gtacaatgaa     3120
ctgaacctgg gcaggcggga ggagtacgac gtgctggata agcggagagg cagagacccc     3180
gagatgggcg gcaaaccacg gcgcaaaaat ccccaggagg gactctataa cgagctgcag     3240
aaggacaaaa tggccgaggc ctattccgag atcggcatga agggagagag aagacgcgga     3300
aagggccacg acggcctgta tcagggattg tccaccgcta caaaagatac atatgatgcc     3360
ctgcacatgc aggccctgcc acccagatga                                      3390
```

<210> 36
<211> 5154
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequences coding for CARs (MP14802.SFG.aCD19fmc63_clean-CD8STK-CD28tmZ-2A-aCD33glx-HCH2CH3pvaa-dCD45)

<400> 36
atgagcctgc ccgtgaccgc cctgctgctg cccctggccc tgctgctgca cgccgccaga 60

ccagacatcc agatgaccca gaccaccagc agcctgagcg ccagcctggg cgaccgggtg 120

accatcagct gcagagccag ccaggacatc agcaagtacc tgaactggta ccagcagaag 180

cccgacggca ccgtgaagct gctgatctac cacaccagcc ggctgcacag cggcgtgccc 240

agccggttca gcggcagcgg cagcggcacc gactacagcc tgaccatcag caacctggag 300

caggaggaca tcgccaccta cttctgccag cagggcaaca ccctgcccta caccttcgga 360

ggcggcacca agctggagat caccaaggcc ggaggcggag gctctggcgg aggcggctct 420

ggcggaggcg gctctggcgg aggcggcagc gaggtgaagc tgcaggagtc tggcccaggc 480

ctggtggccc caagccagag cctgagcgtg acctgcaccg tgagcggcgt gagcctgccc 540

gactacggcg tgagctggat caggcagccc ccacggaagg gcctggagtg gctgggcgtg 600

atctggggca gcgagaccac ctactacaac agcgccctga agagccggct gaccatcatc 660

aaggacaaca gcaagagcca ggtgttcctg aagatgaaca gcctgcagac cgacgacacc 720

gccatctact actgcgccaa gcactactac tatggcggca gctacgctat ggactactgg 780

ggccagggca ccagcgtgac cgtgagctca gatcccacca cgacgccagc gccgcgacca 840

ccaacaccgg cgcccaccat cgcgtcgcag cccctgtccc tgcgcccaga ggcgtgccgg 900

ccagcggcgg ggggcgcagt gcacacgagg gggctggact tcgcctgtga tatcttttgg 960

gtgctggtgg tggttggtgg agtcctggct tgctatagct tgctagtaac agtggccttt 1020

attattttct gggtgaggag agtgaagttc agcaggagcg cagacgcccc cgcgtaccag 1080

cagggccaga accagctcta taacgagctc aatctaggac gaagagagga gtacgatgtt 1140

ttggacaaga gacgtggccg ggaccctgag atgggggggaa agccgagaag gaagaaccct 1200

caggaaggcc tgtacaatga actgcagaaa gataagatgg cggaggccta cagtgagatt 1260

gggatgaaag gcgagcgccg gaggggcaag gggcacgatg gcctttacca gggtctcagt 1320

acagccacca aggacaccta cgacgccctt cacatgcagg ccctgcctcc tcgcagagcc 1380

gagggcaggg gaagtcttct aacatgcggg gacgtggagg aaaatcccgg gcccatggcc 1440

gtgcccactc aggtcctggg gttgttgcta ctgtggctta cagatgccag atgtgacatc 1500

cagatgacac agtctccatc ttccctgtct gcatctgtcg gagatcgcgt caccatcacc 1560

tgtcgagcaa gtgaggacat ttatttaat ttagtgtggt atcagcagaa accaggaaag 1620

gcccctaagc tcctgatcta tgatacaaat cgcttggcag atggggtccc atcacggttc 1680

agtggctctg gatctggcac acagtatact ctaaccataa gtagcctgca acccgaagat 1740

ttcgcaacct attattgtca acactataag aattatccgc tcacgttcgg tcaggggacc 1800

aagctggaaa tcaaaagatc tggtggcgga gggtcaggag gcggaggcag cggaggcggt 1860

ggctcgggag gcggaggctc gagatctgag gtgcagttgg tggagtctgg gggcggcttg 1920

gtgcagcctg gagggtccct gaggctctcc tgtgcagcct caggattcac tctcagtaat 1980

tatggcatgc actggatcag gcaggctcca gggaagggtc tggagtgggt ctcgtctatt 2040

agtcttaatg gtggtagcac ttactatcga gactccgtga agggccgatt cactatctcc 2100

agggacaatg caaaaagcac cctctacctt caaatgaata gtctgagggc cgaggacacg 2160

gccgtctatt actgtgcagc acaggacgct tatacgggag gttactttga ttactggggc 2220

caaggaacgc tggtcacagt ctcgtctatg gatcccgccg agcccaaatc tcctgacaaa 2280

actcacacat gcccaccgtg cccagcacct cccgtggccg gcccgtcagt cttcctcttc 2340

cccccaaaac ccaaggacac cctcatgatc gcccggaccc ctgaggtcac atgcgtggtg 2400

gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag 2460

gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc 2520

agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc 2580

tccaacaaag ccctcccagc ccccatcgag aaaaccatct ccaaagccaa agggcagccc 2640

cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccaggtc 2700

agcctgacct gcctggtcaa aggcttctat cccagcgaca tcgccgtgga gtgggagagc 2760

aatgggcaac cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 2820

ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 2880

tcatgctccg tgatgcatga ggccctgcac aatcactata cccagaaatc tctgagtctg 2940

agcccaggca agaaggaccc caaggcactg atagcatttc tggcatttct gattattgtg 3000

acatcaatag ccctgcttgt tgttctctac aaaatctatg atctacataa gaaaagatcc 3060

tgcaatttag atgaacagca ggagcttgtt gaaagggatg atgaaaaaca actgatgaat 3120

gtggagccaa tccatgcaga tattttgttg gaaacttata agaggaagat tgctgatgaa 3180

ggaagacttt ttctggctga atttcagagc atcccgcggg tgttcagcaa gtttcctata 3240

aaggaagctc gaaagccctt taaccagaat aaaaaccgtt atgttgacat tcttccttat 3300

gattataacc gtgttgaact ctctgagata aacggagatg cagggtcaaa ctacataaat 3360

gccagctata ttgatggttt caaagaaccc aggaaataca ttgctgcaca aggtcccagg 3420

gatgaaactg ttgatgattt ctggaggatg atttgggaac agaaagccac agttattgtc 3480

atggtcactc gatgtgaaga aggaaacagg aacaagtgtg cagaatactg gccgtcaatg 3540

gaagagggca ctcgggcttt tggagatgtt gttgtaaaga tcaaccagca caaaagatgt 3600

ccagattaca tcattcagaa attgaacatt gtaaataaaa aagaaaaagc aactggaaga 3660

gaggtgactc acattcagtt caccagctgg ccagaccacg gggtgcctga ggatcctcac 3720

ttgctcctca aactgagaag gagagtgaat gccttcagca atttcttcag tggtcccatt 3780

gtggtgcact gcagtgctgg tgttgggcgc acaggaacct atatcggaat tgatgccatg 3840

ctagaaggcc tggaagccga gaacaaagtg gatgtttatg gttatgttgt caagctaagg 3900

cgacagagat gcctgatggt tcaagtagag gcccagtaca tcttgatcca tcaggctttg 3960

gtggaataca atcagtttgg agaaacagaa gtgaatttgt ctgaattaca tccatatcta 4020

cataacatga agaaaaggga tccacccagt gagccgtctc cactagaggc tgaattccag 4080

agacttcctt catataggag ctggaggaca cagcacattg gaaatcaaga agaaaataaa 4140

agtaaaaaca ggaattctaa tgtcatccca tatgactata acagagtgcc acttaaacat 4200

gagctggaaa tgagtaaaga gagtgagcat gattcagatg aatcctctga tgatgacagt 4260

gattcagagg aaccaagcaa atacatcaat gcatctttta taatgagcta ctggaaacct 4320

gaagtgatga ttgctgctca gggaccactg aaggagacca ttggtgactt ttggcagatg 4380

atcttccaaa gaaaagtcaa agttattgtt atgctgacag aactgaaaca tggagaccag 4440

gaaatctgtg ctcagtactg gggagaagga aagcaaacat atggagatat tgaagttgac 4500

ctgaaagaca cagacaaatc ttcaacttat acccttcgtg tctttgaact gagacattcc 4560

aagaggaaag actctcgaac tgtgtaccag taccaatata caaactggag tgtggagcag 4620

cttcctgcag aacccaagga attaatctct atgattcagg tcgtcaaaca aaaacttccc 4680

cagaagaatt cctctgaagg gaacaagcat cacaagagta cacctctact cattcactgc 4740

agggatggat ctcagcaaac gggaatattt tgtgctttgt taaatctctt agaaagtgcg 4800

gaaacagaag aggtagtgga tatttttcaa gtggtaaaag ctctacgcaa agctaggcca 4860

ggcatggttt ccacattcga gcaatatcaa ttcctatatg acgtcattgc cagcacctac 4920

cctgctcaga atggacaagt aaagaaaaac aaccatcaag aagataaaat tgaatttgat 4980

aatgaagtgg acaaagtaaa gcaggatgct aattgtgtta atccacttgg tgccccagaa 5040

aagctccctg aagcaaagga acaggctgaa ggttctgaac ccacgagtgg cactgagggg 5100

ccagaacatt ctgtcaatgg tcctgcaagt ccagctttaa atcaaggttc atag 5154

<210> 37
<211> 4053
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequences coding for CARs (MP14801.SFG.aCD19fmc63_clean-CD8STK-CD28tmZ-2A-aCD33glx-HCH2CH3pvaa-dCD148)

<400> 37

atgagcctgc ccgtgaccgc cctgctgctg cccctggccc tgctgctgca cgccgccaga 60

ccagacatcc agatgaccca gaccaccagc agcctgagcg ccagcctggg cgaccgggtg 120

accatcagct gcagagccag ccaggacatc agcaagtacc tgaactggta ccagcagaag 180

cccgacggca ccgtgaagct gctgatctac cacaccagcc ggctgcacag cggcgtgccc 240

agccggttca gcggcagcgg cagcggcacc gactacagcc tgaccatcag caacctggag 300

caggaggaca tcgccaccta cttctgccag cagggcaaca ccctgcccta caccttcgga 360

ggcggcacca agctggagat caccaaggcc ggaggcggag gctctggcgg aggcggctct 420

ggcggaggcg gctctggcgg aggcggcagc gaggtgaagc tgcaggagtc tggcccaggc 480

ctggtggccc caagccagag cctgagcgtg acctgcaccg tgagcggcgt gagcctgccc 540

gactacggcg tgagctggat caggcagccc ccacggaagg gcctggagtg gctgggcgtg 600

atctggggca gcgagaccac ctactacaac agcgccctga agagccggct gaccatcatc 660

aaggacaaca gcaagagcca ggtgttcctg aagatgaaca gcctgcagac cgacgacacc 720

gccatctact actgcgccaa gcactactac tatggcggca gctacgctat ggactactgg 780

ggccagggca ccagcgtgac cgtgagctca gatcccacca cgacgccagc gccgcgacca 840

ccaacaccgg cgcccaccat cgcgtcgcag cccctgtccc tgcgcccaga ggcgtgccgg 900

ccagcggcgg ggggcgcagt gcacacgagg gggctggact tcgcctgtga tatcttttgg 960

gtgctggtgg tggttggtgg agtcctggct tgctatagct tgctagtaac agtggccttt 1020

attattttct gggtgaggag agtgaagttc agcaggagcg cagacgcccc cgcgtaccag 1080

cagggccaga accagctcta taacgagctc aatctaggac gaagagagga gtacgatgtt 1140

ttggacaaga gacgtggccg ggaccctgag atgggggaa agccgagaag gaagaaccct 1200

caggaaggcc tgtacaatga actgcagaaa gataagatgg cggaggccta cagtgagatt 1260

gggatgaaag gcgagcgccg gaggggcaag gggcacgatg gcctttacca gggtctcagt 1320

acagccacca aggacaccta cgacgcctt cacatgcagg ccctgcctcc tcgcagagcc 1380

gagggcaggg gaagtcttct aacatgcggg gacgtggagg aaaatcccgg gcccatggcc 1440

gtgcccactc aggtcctggg gttgttgcta ctgtggctta cagatgccag atgtgacatc 1500

cagatgacac agtctccatc ttccctgtct gcatctgtcg gagatcgcgt caccatcacc 1560

tgtcgagcaa gtgaggacat ttattttaat ttagtgtggt atcagcagaa accaggaaag 1620

gcccctaagc tcctgatcta tgatacaaat cgcttggcag atggggtccc atcacggttc 1680

agtggctctg gatctggcac acagtatact ctaaccataa gtagcctgca acccgaagat 1740

ttcgcaacct attattgtca acactataag aattatccgc tcacgttcgg tcaggggacc 1800

aagctggaaa tcaaaagatc tggtggcgga gggtcaggag gcggaggcag cggaggcggt 1860

ggctcgggag gcggaggctc gagatctgag gtgcagttgg tggagtctgg gggcggcttg 1920

gtgcagcctg gagggtccct gaggctctcc tgtgcagcct caggattcac tctcagtaat 1980

tatggcatgc actggatcag gcaggctcca gggaagggtc tggagtgggt ctcgtctatt 2040

agtcttaatg gtggtagcac ttactatcga gactccgtga agggccgatt cactatctcc 2100

agggacaatg caaaaagcac cctctacctt caaatgaata gtctgagggc cgaggacacg 2160

gccgtctatt actgtgcagc acaggacgct tatacgggag gttactttga ttactggggc 2220

caaggaacgc tggtcacagt ctcgtctatg gatcccgccg agcccaaatc tcctgacaaa 2280

actcacacat gcccaccgtg cccagcacct cccgtggccg gcccgtcagt cttcctcttc 2340

cccccaaaac ccaaggacac cctcatgatc gcccggaccc ctgaggtcac atgcgtggtg 2400

gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag 2460

gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc 2520

agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc 2580

tccaacaaag ccctcccagc ccccatcgag aaaaccatct ccaaagccaa agggcagccc 2640

cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccaggtc 2700

agcctgacct gcctggtcaa aggcttctat cccagcgaca tcgccgtgga gtgggagagc 2760

aatgggcaac cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 2820

ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 2880

tcatgctccg tgatgcatga ggccctgcac aatcactata cccagaaatc tctgagtctg 2940

agcccaggca agaaggaccc caaggcggtt tttggctgta tctttggtgc cctggttatt 3000

gtgactgtgg gaggcttcat cttctggaga aagaagagga aagatgcaaa gaataatgaa 3060

gtgtccttt ctcaaattaa acctaaaaaa tctaagttaa tcagagtgga gaattttgag 3120

gcctacttca agaagcagca agctgactcc aactgtgggt tcgcagagga atacgaagat 3180

ctgaagcttg ttggaattag tcaacctaaa tatgcagcag aactggctga gaatagagga 3240

aagaatcgct ataataatgt tctgccctat gatatttccc gtgtcaaact ttcggtccag 3300

acccattcaa cggatgacta catcaatgcc aactacatgc ctggctacca ctccaagaaa 3360

gattttattg ccacacaagg acctttaccg aacactttga aagatttttg gcgtatggtt 3420

tgggagaaaa atgtatatgc catcattatg ttgactaaat gtgttgaaca gggaagaacc 3480

aaatgtgagg agtattggcc ctccaagcag gctcaggact atggagacat aactgtggca 3540

atgacatcag aaattgttct tccggaatgg accatcagag atttcacagt gaaaaatatc 3600

cagacaagtg agagtcaccc tctgagacag ttccatttca cctcctggcc agaccacggt 3660

gttcccgaca ccactgacct gctcatcaac ttccggtacc tcgttcgtga ctacatgaag 3720

cagagtcctc ccgaatcgcc gattctggtg cattgcagtg ctggggtcgg aaggacgggc 3780

actttcattg ccattgatcg tctcatctac cagatagaga atgagaacac cgtggatgtg 3840

tatgggattg tgtatgacct tcgaatgcat aggcctttaa tggtgcagac agaggaccag 3900

tatgttttcc tcaatcagtg tgttttggat attgtcagat cccagaaaga ctcaaaagta 3960

gatcttatct accagaacac aactgcaatg acaatctatg aaaaccttgc gcccgtgacc 4020

acatttggaa agaccaatgg ttacatcgcc taa 4053

<210> 38
<211> 3345
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequences coding for CARs (16076.SFG.aCD19fmc63-CD8STK-CD28tmZ-2A-aCD33glx-muCD8STK-tm-dPTPN6)

<400> 38
atgagcctgc ccgtgaccgc cctgctgctg cccctggccc tgctgctgca cgccgccaga 60

ccagacatcc agatgaccca gaccaccagc agcctgagcg ccagcctggg cgaccgggtg 120

accatcagct gcagagccag ccaggacatc agcaagtacc tgaactggta ccagcagaag 180

cccgacggca ccgtgaagct gctgatctac cacaccagcc ggctgcacag cggcgtgccc 240

agccggttca gcggcagcgg cagcggcacc gactacagcc tgaccatcag caacctggag 300

caggaggaca tcgccaccta cttctgccag cagggcaaca ccctgcccta caccttcgga 360

ggcggcacca agctggagat caccaaggcc ggaggcggag gctctggcgg aggcggctct 420

ggcggaggcg gctctggcgg aggcggcagc gaggtgaagc tgcaggagtc tggcccaggc 480

ctggtggccc caagccagag cctgagcgtg acctgcaccg tgagcggcgt gagcctgccc 540

gactacggcg tgagctggat caggcagccc ccacggaagg gcctggagtg gctgggcgtg 600

atctggggca gcgagaccac ctactacaac agcgccctga agagccggct gaccatcatc 660

aaggacaaca gcaagagcca ggtgttcctg aagatgaaca gcctgcagac cgacgacacc 720

gccatctact actgcgccaa gcactactac tatggcggca gctacgctat ggactactgg 780

ggccagggca ccagcgtgac cgtgagctca gatcccacca cgacgccagc gccgcgacca 840

ccaacaccgg cgcccaccat cgcgtcgcag cccctgtccc tgcgcccaga ggcgtgccgg 900

ccagcggcgg ggggcgcagt gcacacgagg gggctggact tcgcctgtga tatcttttgg 960

gtgctggtgg tggttggtgg agtcctggct tgctatagct tgctagtaac agtggccttt 1020

attattttct gggtgaggag agtgaagttc agcaggagcg cagacgcccc cgcgtaccag 1080

cagggccaga accagctcta taacgagctc aatctaggac gaagagagga gtacgatgtt 1140

ttggacaaga gacgtggccg ggaccctgag atgggggaa agccgagaag gaagaaccct 1200

caggaaggcc tgtacaatga actgcagaaa gataagatgg cggaggccta cagtgagatt 1260

gggatgaaag gcgagcgccg gaggggcaag gggcacgatg gcctttacca gggtctcagt 1320

acagccacca aggacaccta cgacgccctt cacatgcagg ccctgcctcc tcgcagagcc 1380

gagggcaggg gaagtcttct aacatgcggg gacgtggagg aaaatcccgg gcccatggcc 1440

gtgcccactc aggtcctggg gttgttgcta ctgtggctta cagatgccag atgtgacatc 1500

cagatgacac agtctccatc ttccctgtct gcatctgtcg gagatcgcgt caccatcacc 1560

tgtcgagcaa gtgaggacat ttattttaat ttagtgtggt atcagcagaa accaggaaag 1620

gcccctaagc tcctgatcta tgatacaaat cgcttggcag atggggtccc atcacggttc 1680

agtggctctg gatctggcac acagtatact ctaaccataa gtagcctgca acccgaagat 1740

ttcgcaacct attattgtca acactataag aattatccgc tcacgttcgg tcaggggacc 1800

aagctggaaa tcaaaagatc tggtggcgga gggtcaggag gcggaggcag cggaggcggt 1860

ggctcgggag gcggaggctc gagatctgag gtgcagttgg tggagtctgg gggcggcttg 1920

gtgcagcctg gagggtccct gaggctctcc tgtgcagcct caggattcac tctcagtaat 1980

tatggcatgc actggatcag gcaggctcca gggaagggtc tggagtgggt ctcgtctatt 2040

agtcttaatg gtggtagcac ttactatcga gactccgtga agggccgatt cactatctcc 2100

agggacaatg caaaaagcac cctctacctt caaatgaata gtctgagggc cgaggacacg 2160

gccgtctatt actgtgcagc acaggacgct tatacgggag gttactttga ttactggggc 2220

caaggaacgc tggtcacagt ctcgtctatg gatcccgcca ccacaaccaa gcccgtgctg 2280

cggaccccaa gccctgtgca ccctaccggc accagccagc ctcagagacc cgaggactgc 2340

cggcctcggg gcagcgtgaa gggcaccggc ctggacttcg cctgcgacat ctactgggca 2400

cctctggccg gaatatgcgt ggcactgctg ctgagcctca tcatcaccct gatctgttat 2460

caccgaagcc gcaagcgggt gtgtaaaagt ggaggcggaa gcttctggga ggagtttgag 2520

agtttgcaga agcaggaggt gaagaacttg caccagcgtc tggaagggca gcggccagag 2580

aacaagggca agaaccgcta caagaacatt ctccccttg accacagccg agtgatcctg 2640

cagggacggg acagtaacat ccccgggtcc gactacatca atgccaacta catcaagaac 2700

cagctgctag gccctgatga gaacgctaag acctacatcg ccagccaggg ctgtctggag 2760

gccacggtca atgacttctg gcagatggcg tggcaggaga acagccgtgt catcgtcatg 2820

accacccgag aggtggagaa aggccggaac aaatgcgtcc catactggcc cgaggtgggc 2880

atgcagcgtg cttatgggcc ctactctgtg accaactgcg gggagcatga cacaaccgaa 2940

tacaaactcc gtaccttaca ggtctccccg ctggacaatg gagacctgat tcgggagatc 3000

tggcattacc agtacctgag ctggcccgac cacggggtcc ccagtgagcc tgggggtgtc 3060

ctcagcttcc tggaccagat caaccagcgg caggaaagtc tgcctcacgc agggcccatc 3120

atcgtgcact gcagcgccgg catcggccgc acaggcacca tcattgtcat cgacatgctc 3180

atggagaaca tctccaccaa gggcctggac tgtgacattg acatccagaa gaccatccag 3240

atggtgcggg cgcagcgctc gggcatggtg cagacggagg cgcagtacaa gttcatctac 3300

gtggccatcg cccagttcat tgaaaccact aagaagaagc tgtga 3345

<210> 39
<211> 2757
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequences coding for CARs (MP16091.SFG.aCD19fmc63-CD8STK-CD28tmZ-2A-aCD33glx-muCD8STK-LAIR1 tm-endo)

<400> 39
atgagcctgc ccgtgaccgc cctgctgctg cccctggccc tgctgctgca cgccgccaga 60

ccagacatcc agatgaccca gaccaccagc agcctgagcg ccagcctggg cgaccgggtg 120

accatcagct gcagagccag ccaggacatc agcaagtacc tgaactggta ccagcagaag 180

cccgacggca ccgtgaagct gctgatctac cacaccagcc ggctgcacag cggcgtgccc 240

agccggttca gcggcagcgg cagcggcacc gactacagcc tgaccatcag caacctggag 300

caggaggaca tcgccaccta cttctgccag cagggcaaca ccctgcccta caccttcgga 360

ggcggcacca agctggagat caccaaggcc ggaggcggag gctctggcgg aggcggctct 420

ggcggaggcg gctctggcgg aggcggcagc gaggtgaagc tgcaggagtc tggcccaggc 480

ctggtggccc caagccagag cctgagcgtg acctgcaccg tgagcggcgt gagcctgccc 540

gactacggcg tgagctggat caggcagccc ccacggaagg gcctggagtg gctgggcgtg 600

atctggggca gcgagaccac ctactacaac agcgccctga agagccggct gaccatcatc 660

aaggacaaca gcaagagcca ggtgttcctg aagatgaaca gcctgcagac cgacgacacc 720

gccatctact actgcgccaa gcactactac tatggcggca gctacgctat ggactactgg 780

ggccagggca ccagcgtgac cgtgagctca gatcccacca cgacgccagc gccgcgacca 840

ccaacaccgg cgcccaccat cgcgtcgcag cccctgtccc tgcgcccaga ggcgtgccgg 900

ccagcggcgg ggggcgcagt gcacacgagg gggctggact tcgcctgtga tatcttttgg 960

gtgctggtgg tggttggtgg agtcctggct tgctatagct tgctagtaac agtggccttt 1020

attattttct gggtgaggag agtgaagttc agcaggagcg cagacgcccc cgcgtaccag 1080

cagggccaga accagctcta taacgagctc aatctaggac gaagagagga gtacgatgtt 1140

ttggacaaga gacgtggccg ggaccctgag atgggggaa agccgagaag gaagaaccct 1200

caggaaggcc tgtacaatga actgcagaaa gataagatgg cggaggccta cagtgagatt 1260

gggatgaaag gcgagcgccg gaggggcaag gggcacgatg gcctttacca gggtctcagt 1320

acagccacca aggacaccta cgacgccctt cacatgcagg ccctgcctcc tcgcagagcc 1380

gagggcaggg gaagtcttct aacatgcggg gacgtggagg aaaatcccgg gcccatggcc 1440

gtgcccactc aggtcctggg gttgttgcta ctgtggctta cagatgccag atgtgacatc 1500

cagatgacac agtctccatc ttccctgtct gcatctgtcg gagatcgcgt caccatcacc 1560

tgtcgagcaa gtgaggacat ttattttaat ttagtgtggt atcagcagaa accaggaaag 1620

gcccctaagc tcctgatcta tgatacaaat cgcttggcag atggggtccc atcacggttc 1680

agtggctctg gatctggcac acagtatact ctaaccataa gtagcctgca acccgaagat 1740

ttcgcaacct attattgtca acactataag aattatccgc tcacgttcgg tcaggggacc 1800

aagctggaaa tcaaaagatc tggtggcgga gggtcaggag gcggaggcag cggaggcggt 1860

ggctcgggag gcggaggctc gagatctgag gtgcagttgg tggagtctgg gggcggcttg 1920

gtgcagcctg gagggtccct gaggctctcc tgtgcagcct caggattcac tctcagtaat 1980

tatggcatgc actggatcag gcaggctcca gggaagggtc tggagtgggt ctcgtctatt 2040

agtcttaatg gtggtagcac ttactatcga gactccgtga agggccgatt cactatctcc 2100

agggacaatg caaaaagcac cctctacctt caaatgaata gtctgagggc cgaggacacg 2160

gccgtctatt actgtgcagc acaggacgct tatacgggag gttactttga ttactggggc 2220

caaggaacgc tggtcacagt ctcgtctatg gatcccgcca ccacaaccaa gcccgtgctg 2280

cggaccccaa gccctgtgca ccctaccggc accagccagc ctcagagacc cgaggactgc 2340

cggcctcggg gcagcgtgaa gggcaccggc ctggacttcg cctgcgacat tctcatcggg 2400

gtctcagtgg tcttcctctt ctgtctcctc ctcctggtcc tcttctgcct ccatcgccag 2460

aatcagataa agcaggggcc ccccagaagc aaggacgagg agcagaagcc acagcagagg 2520

cctgacctgg ctgttgatgt tctagagagg acagcagaca aggccacagt caatggactt 2580

cctgagaagg accgggagac cgacaccagc gccctggctg cagggagttc ccaggaggtg 2640

acgtatgctc agctggacca ctgggccctc acacagagga cagcccgggc tgtgtcccca 2700

cagtccacaa agcccatggc cgagtccatc acgtatgcag ccgttgccag acactga 2757

<210> 40
<211> 4092
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequences coding for CARs

<400> 40
atgagcctgc ccgtgaccgc cctgctgctg cccctggccc tgctgctgca cgccgccaga 60

ccagacatcc agatgaccca gaccaccagc agcctgagcg ccagcctggg cgaccgggtg 120

accatcagct gcagagccag ccaggacatc agcaagtacc tgaactggta ccagcagaag 180

cccgacggca ccgtgaagct gctgatctac cacaccagcc ggctgcacag cggcgtgccc 240

agccggttca gcggcagcgg cagcggcacc gactacagcc tgaccatcag caacctggag 300

caggaggaca tcgccaccta cttctgccag cagggcaaca ccctgcccta caccttcgga 360

ggcggcacca agctggagat caccaaggcc ggaggcggag gctctggcgg aggcggctct 420

ggcggaggcg gctctggcgg aggcggcagc gaggtgaagc tgcaggagtc tggcccaggc 480

ctggtggccc caagccagag cctgagcgtg acctgcaccg tgagcggcgt gagcctgccc 540

gactacggcg tgagctggat caggcagccc ccacggaagg gcctggagtg gctgggcgtg 600

atctggggca gcgagaccac ctactacaac agcgccctga agagccggct gaccatcatc 660

aaggacaaca gcaagagcca ggtgttcctg aagatgaaca gcctgcagac cgacgacacc 720

gccatctact actgcgccaa gcactactac tatggcggca gctacgctat ggactactgg 780

ggccagggca ccagcgtgac cgtgagctca gatcccacca cgacgccagc gccgcgacca 840

ccaacaccgg cgcccaccat cgcgtcgcag cccctgtccc tgcgcccaga ggcgtgccgg 900

ccagcggcgg ggggcgcagt gcacacgagg gggctggact tcgcctgtga tatcttttgg 960

gtgctggtgg tggttggtgg agtcctggct tgctatagct tgctagtaac agtggccttt 1020

attattttct gggtgaggag agtgaagttc agcaggagcg cagacgcccc cgcgtaccag 1080

cagggccaga accagctcta taacgagctc aatctaggac gaagagagga gtacgatgtt 1140

ttggacaaga gacgtggccg ggaccctgag atgggggggaa agccgagaag gaagaaccct 1200

caggaaggcc tgtacaatga actgcagaaa gataagatgg cggaggccta cagtgagatt 1260

gggatgaaag gcgagcgccg gaggggcaag gggcacgatg gcctttacca gggtctcagt 1320

acagccacca aggacaccta cgacgccctt cacatgcagg ccctgcctcc tcgcagagcc 1380

gagggcaggg gaagtcttct aacatgcggg gacgtggagg aaaatcccgg gcccatggcc 1440

gtgcccactc aggtcctggg gttgttgcta ctgtggctta cagatgccag atgtgacatc 1500

cagatgacac agtctccatc ttccctgtct gcatctgtcg gagatcgcgt caccatcacc 1560

tgtcgagcaa gtgaggacat ttattttaat ttagtgtggt atcagcagaa accaggaaag 1620

gcccctaagc tcctgatcta tgatacaaat cgcttggcag atggggtccc atcacggttc 1680

agtggctctg gatctggcac acagtatact ctaaccataa gtagcctgca acccgaagat 1740

ttcgcaacct attattgtca acactataag aattatccgc tcacgttcgg tcaggggacc 1800

aagctggaaa tcaaaagatc tggtggcgga gggtcaggag gcggaggcag cggaggcggt 1860

ggctcgggag gcggaggctc gagatctgag gtgcagttgg tggagtctgg gggcggcttg 1920

gtgcagcctg gagggtccct gaggctctcc tgtgcagcct caggattcac tctcagtaat 1980

tatggcatgc actggatcag gcaggctcca gggaagggtc tggagtgggt ctcgtctatt 2040

agtcttaatg gtggtagcac ttactatcga gactccgtga agggccgatt cactatctcc 2100

agggacaatg caaaaagcac cctctacctt caaatgaata gtctgagggc cgaggacacg 2160

gccgtctatt actgtgcagc acaggacgct tatacgggag gttactttga ttactggggc 2220

caaggaacgc tggtcacagt ctcgtctatg gatcccgcca ccacaaccaa gcccgtgctg 2280

cggaccccaa gccctgtgca ccctaccggc accagccagc ctcagagacc cgaggactgc 2340

cggcctcggg gcagcgtgaa gggcaccggc ctggacttcg cctgcgacat tctcatcggg 2400

gtctcagtgg tcttcctctt ctgtctcctc ctcctggtcc tcttctgcct ccatcgccag 2460

aatcagataa agcaggggcc ccccagaagc aaggacgagg agcagaagcc acagcagagg 2520

cctgacctgg ctgttgatgt tctagagagg acagcagaca aggccacagt caatggactt 2580

cctgagaagg accgggagac cgacaccagc gccctggctg cagggagttc ccaggaggtg 2640

acgtatgctc agctggacca ctgggccctc acacagagga cagcccgggc tgtgtcccca 2700

cagtccacaa agcccatggc cgagtccatc acgtatgcag ccgttgccag acacagggca 2760

gaaggaagag gtagcctgct gacttgcggg gacgtggaag agaacccagg gccatggtat 2820

catggccaca tgtctggcgg gcaggcagag acgctgctgc aggccaaggg cgagccctgg 2880

acgtttcttg tgcgtgagag cctcagccag cctggagact tcgtgctttc tgtgctcagt 2940

gaccagccca aggctggccc aggctccccg ctcagggtca cccacatcaa ggtcatgtgc 3000

gagggtggac gctacacagt gggtggtttg gagaccttcg acagcctcac ggacctggtg 3060

gagcatttca agaagacggg gattgaggag gcctcaggcg cctttgtcta cctgcggcag 3120

ccgtacagcg gtggcggtgg cagctttgag gcctacttca agaagcagca agctgactcc 3180

aactgtgggt tcgcagagga atacgaagat ctgaagcttg ttggaattag tcaacctaaa 3240

tatgcagcag aactggctga gaatagagga aagaatcgct ataataatgt tctgccctat 3300

gatatttccc gtgtcaaact ttcggtccag acccattcaa cggatgacta catcaatgcc 3360

aactacatgc ctggctacca ctccaagaaa gattttattg ccacacaagg acctttaccg 3420

aacactttga aagatttttg gcgtatggtt tgggagaaaa atgtatatgc catcattatg 3480

ttgactaaat gtgttgaaca gggaagaacc aaatgtgagg agtattggcc ctccaagcag 3540

gctcaggact atggagacat aactgtggca atgacatcag aaattgttct tccggaatgg 3600

accatcagag atttcacagt gaaaaatatc cagacaagtg agagtcaccc tctgagacag 3660

ttccatttca cctcctggcc agaccacggt gttcccgaca ccactgacct gctcatcaac 3720

ttccggtacc tcgttcgtga ctacatgaag cagagtcctc ccgaatcgcc gattctggtg 3780

cattgcagtg ctggggtcgg aaggacgggc actttcattg ccattgatcg tctcatctac 3840

cagatagaga atgagaacac cgtggatgtg tatgggattg tgtatgacct tcgaatgcat 3900

aggcctttaa tggtgcagac agaggaccag tatgttttcc tcaatcagtg tgttttggat 3960

attgtcagat cccagaaaga ctcaaaagta gatcttatct accagaacac aactgcaatg 4020

acaatctatg aaaaccttgc gcccgtgacc acatttggaa agaccaatgg ttacatcgcc 4080

agcggtagct aa 4092

<210> 41
<211> 1341
<212> PRT
<213> Artificial Sequence

<220>
<223> Single-chain variable fragment (scFv)
SFG.aCD19-CD8STK-CD28tmZ-2A-aGD2-HCH2CH3pvaa-dCD148

<400> 41

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

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

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

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

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
85 90 95

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
115 120 125

Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

```
Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser Gly Pro Gly
145                 150                 155                 160

Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys Thr Val Ser Gly
                165                 170                 175

Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg
            180                 185                 190

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr
        195                 200                 205

Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile Lys Asp Asn Ser
    210                 215                 220

Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr
225                 230                 235                 240

Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala
                245                 250                 255

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp Pro
            260                 265                 270

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
        275                 280                 285

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
    290                 295                 300

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Phe Trp
305                 310                 315                 320

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
                325                 330                 335

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Arg Val Lys Phe Ser Arg
            340                 345                 350

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
        355                 360                 365

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
    370                 375                 380

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
385                 390                 395                 400
```

```
Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
                405                 410                 415

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
            420                 425                 430

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
        435                 440                 445

Ala Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Glu Gly Arg Gly
    450                 455                 460

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Glu
465                 470                 475                 480

Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro Gly Ser
                485                 490                 495

Thr Gly Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro
            500                 505                 510

Ser Gln Thr Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Ala
        515                 520                 525

Ser Tyr Asn Ile His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu
    530                 535                 540

Trp Leu Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala
545                 550                 555                 560

Leu Met Ser Arg Leu Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln Val
                565                 570                 575

Phe Leu Lys Met Ser Ser Leu Thr Ala Ala Asp Thr Ala Val Tyr Tyr
            580                 585                 590

Cys Ala Lys Arg Ser Asp Asp Tyr Ser Trp Phe Ala Tyr Trp Gly Gln
        595                 600                 605

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
    610                 615                 620

Gly Ser Gly Gly Gly Gly Ser Glu Asn Gln Met Thr Gln Ser Pro Ser
625                 630                 635                 640

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Arg Ala
```

645 650 655

Ser Ser Ser Val Ser Ser Ser Tyr Leu His Trp Tyr Gln Gln Lys Ser
660 665 670

Gly Lys Ala Pro Lys Val Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser
675 680 685

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr
690 695 700

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
705 710 715 720

Gln Gln Tyr Ser Gly Tyr Pro Ile Thr Phe Gly Gln Gly Thr Lys Val
725 730 735

Glu Ile Lys Arg Ser Asp Pro Ala Glu Pro Lys Ser Pro Asp Lys Thr
740 745 750

His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
755 760 765

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ala Arg Thr
770 775 780

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
785 790 795 800

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
805 810 815

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
820 825 830

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
835 840 845

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
850 855 860

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
865 870 875 880

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
885 890 895

```
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
            900                 905                 910

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
        915                 920                 925

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
    930                 935                 940

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
945                 950                 955                 960

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Lys
                965                 970                 975

Asp Pro Lys Ala Val Phe Gly Cys Ile Phe Gly Ala Leu Val Ile Val
            980                 985                 990

Thr Val Gly Gly Phe Ile Phe Trp  Arg Lys Lys Arg Lys  Asp Ala Lys
        995                 1000                1005

Asn Asn  Glu Val Ser Phe Ser  Gln Ile Lys Pro Lys  Lys Ser Lys
    1010                1015                1020

Leu Ile  Arg Val Glu Asn Phe  Glu Ala Tyr Phe Lys  Lys Gln Gln
    1025                1030                1035

Ala Asp  Ser Asn Cys Gly Phe  Ala Glu Glu Tyr Glu  Asp Leu Lys
    1040                1045                1050

Leu Val  Gly Ile Ser Gln Pro  Lys Tyr Ala Ala Glu  Leu Ala Glu
    1055                1060                1065

Asn Arg  Gly Lys Asn Arg Tyr  Asn Asn Val Leu Pro  Tyr Asp Ile
    1070                1075                1080

Ser Arg  Val Lys Leu Ser Val  Gln Thr His Ser Thr  Asp Asp Tyr
    1085                1090                1095

Ile Asn  Ala Asn Tyr Met Pro  Gly Tyr His Ser Lys  Lys Asp Phe
    1100                1105                1110

Ile Ala  Thr Gln Gly Pro Leu  Pro Asn Thr Leu Lys  Asp Phe Trp
    1115                1120                1125

Arg Met  Val Trp Glu Lys Asn  Val Tyr Ala Ile Ile  Met Leu Thr
    1130                1135                1140
```

```
Lys Cys  Val Glu Gln Gly Arg  Thr Lys Cys Glu Glu  Tyr Trp Pro
    1145                1150                1155

Ser Lys  Gln Ala Gln Asp Tyr  Gly Asp Ile Thr Val  Ala Met Thr
    1160                1165                1170

Ser Glu  Ile Val Leu Pro Glu  Trp Thr Ile Arg Asp  Phe Thr Val
    1175                1180                1185

Lys Asn  Ile Gln Thr Ser Glu  Ser His Pro Leu Arg  Gln Phe His
    1190                1195                1200

Phe Thr  Ser Trp Pro Asp His  Gly Val Pro Asp Thr  Thr Asp Leu
    1205                1210                1215

Leu Ile  Asn Phe Arg Tyr Leu  Val Arg Asp Tyr Met  Lys Gln Ser
    1220                1225                1230

Pro Pro  Glu Ser Pro Ile Leu  Val His Cys Ser Ala  Gly Val Gly
    1235                1240                1245

Arg Thr  Gly Thr Phe Ile Ala  Ile Asp Arg Leu Ile  Tyr Gln Ile
    1250                1255                1260

Glu Asn  Glu Asn Thr Val Asp  Val Tyr Gly Ile Val  Tyr Asp Leu
    1265                1270                1275

Arg Met  His Arg Pro Leu Met  Val Gln Thr Glu Asp  Gln Tyr Val
    1280                1285                1290

Phe Leu  Asn Gln Cys Val Leu  Asp Ile Val Arg Ser  Gln Lys Asp
    1295                1300                1305

Ser Lys  Val Asp Leu Ile Tyr  Gln Asn Thr Thr Ala  Met Thr Ile
    1310                1315                1320

Tyr Glu  Asn Leu Ala Pro Val  Thr Thr Phe Gly Lys  Thr Asn Gly
    1325                1330                1335

Tyr Ile  Ala
    1340


<210>  42
<211>  4026
<212>  DNA
<213>  Artificial Sequence

<220>
```

<223> Single-chain variable fragment (scFv)
SFG.aCD19-CD8STK-CD28tmZ-2A-aGD2-HCH2CH3pvaa-dCD148

<400> 42
atgagcctgc ccgtgaccgc cctgctgctg cccctggccc tgctgctgca cgccgccaga 60

ccagacatcc agatgaccca gaccaccagc agcctgagcg ccagcctggg cgaccgggtg 120

accatcagct gcagagccag ccaggacatc agcaagtacc tgaactggta ccagcagaag 180

cccgacggca ccgtgaagct gctgatctac cacaccagcc ggctgcacag cggcgtgccc 240

agccggttca gcggcagcgg cagcggcacc gactacagcc tgaccatcag caacctggag 300

caggaggaca tcgccaccta cttctgccag cagggcaaca ccctgcccta caccttcgga 360

ggcggcacca agctggagat caccaaggcc ggaggcggag gctctggcgg aggcggctct 420

ggcggaggcg gctctggcgg aggcggcagc gaggtgaagc tgcaggagtc tggcccaggc 480

ctggtggccc caagccagag cctgagcgtg acctgcaccg tgagcggcgt gagcctgccc 540

gactacggcg tgagctggat caggcagccc ccacggaagg gcctggagtg gctgggcgtg 600

atctggggca gcgagaccac ctactacaac agcgccctga agagccggct gaccatcatc 660

aaggacaaca gcaagagcca ggtgttcctg aagatgaaca gcctgcagac cgacgacacc 720

gccatctact actgcgccaa gcactactac tatggcggca gctacgctat ggactactgg 780

ggccagggca ccagcgtgac cgtgagctca gatcccacca cgacgccagc gccgcgacca 840

ccaacaccgg cgcccaccat cgcgtcgcag cccctgtccc tgcgcccaga ggcgtgccgg 900

ccagcggcgg ggggcgcagt gcacacgagg gggctggact tcgcctgtga tatcttttgg 960

gtgctggtgg tggttggtgg agtcctggct tgctatagct tgctagtaac agtggccttt 1020

attattttct gggtgaggag agtgaagttc agcaggagcg cagacgcccc cgcgtaccag 1080

cagggccaga accagctcta taacgagctc aatctaggac gaagagagga gtacgatgtt 1140

ttggacaaga gacgtggccg ggaccctgag atgggggggaa agccgagaag gaagaaccct 1200

caggaaggcc tgtacaatga actgcagaaa gataagatgg cggaggccta cagtgagatt 1260

gggatgaaag gcgagcgccg gaggggcaag gggcacgatg gcctttacca gggtctcagt 1320

acagccacca aggacaccta cgacgccctt cacatgcagg ccctgcctcc tcgcagagcc 1380

gagggcaggg gaagtcttct aacatgcggg gacgtggagg aaaatcccgg gcccatggag 1440

accgacaccc tgctgctgtg ggtgctgctg ctgtgggtgc caggcagcac cggccaggtg 1500

cagctgcagg agtctggccc aggcctggtg aagcccagcc agaccctgag catcacctgc 1560

accgtgagcg gcttcagcct ggccagctac aacatccact gggtgcggca gcccccaggc 1620

aagggcctgg agtggctggg cgtgatctgg gctggcggca gcaccaacta caacagcgcc 1680

ctgatgagcc ggctgaccat cagcaaggac aacagcaaga accaggtgtt cctgaagatg 1740

agcagcctga cagccgccga caccgccgtg tactactgcg ccaagcggag cgacgactac 1800

agctggttcg cctactgggg ccagggcacc ctggtgaccg tgagctctgg cggaggcggc 1860

tctggcggag gcggctctgg cggaggcggc agcgagaacc agatgaccca gagccccagc 1920

agcttgagcg ccagcgtggg cgaccgggtg accatgacct gcagagccag cagcagcgtg 1980

agcagcagct acctgcactg gtaccagcag aagagcggca aggccccaaa ggtgtggatc 2040

tacagcacca gcaacctggc cagcggcgtg cccagccggt tcagcggcag cggcagcggc 2100

accgactaca ccctgaccat cagcagcctg cagcccgagg acttcgccac ctactactgc 2160

cagcagtaca gcggctaccc catcaccttc ggccagggca ccaaggtgga gatcaagcgg 2220

tcggatcccg ccgagcccaa atctcctgac aaaactcaca catgcccacc gtgcccagca 2280

cctcccgtgg ccggcccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 2340

atcgcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 2400

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 2460

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 2520

tggctgaatg gcaaggagta caagtgcaag gtctccaaca aagccctccc agcccccatc 2580

gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 2640

ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 2700

tatcccagcg acatcgccgt ggagtgggag agcaatgggc aaccggagaa caactacaag 2760

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 2820

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggccctg 2880

cacaatcact atacccagaa atctctgagt ctgagcccag gcaagaagga ccccaaggcg 2940

gtttttggct gtatctttgg tgccctggtt attgtgactg tgggaggctt catcttctgg 3000

agaaagaaga ggaaagatgc aaagaataat gaagtgtcct tttctcaaat taaacctaaa 3060

aaatctaagt taatcagagt ggagaatttt gaggcctact tcaagaagca gcaagctgac 3120

tccaactgtg ggttcgcaga ggaatacgaa gatctgaagc ttgttggaat tagtcaacct 3180

aaatatgcag cagaactggc tgagaataga ggaaagaatc gctataataa tgttctgccc 3240

tatgatattt cccgtgtcaa actttcggtc cagacccatt caacggatga ctacatcaat 3300

gccaactaca tgcctggcta ccactccaag aaagatttta ttgccacaca aggaccttta 3360

ccgaacactt tgaaagattt ttggcgtatg gtttgggaga aaaatgtata tgccatcatt 3420

atgttgacta aatgtgttga acagggaaga accaaatgtg aggagtattg gccctccaag 3480

caggctcagg actatggaga cataactgtg gcaatgacat cagaaattgt tcttccggaa 3540

tggaccatca gagatttcac agtgaaaaat atccagacaa gtgagagtca ccctctgaga 3600

cagttccatt tcacctcctg gccagaccac ggtgttcccg acaccactga cctgctcatc 3660

aacttccggt acctcgttcg tgactacatg aagcagagtc ctcccgaatc gccgattctg 3720

gtgcattgca gtgctggggt cggaaggacg ggcactttca ttgccattga tcgtctcatc 3780

taccagatag agaatgagaa caccgtggat gtgtatggga ttgtgtatga ccttcgaatg 3840

cataggcctt taatggtgca gacagaggac cagtatgttt tcctcaatca gtgtgttttg 3900

gatattgtca gatcccagaa agactcaaaa gtagatctta tctaccagaa cacaactgca 3960

atgacaatct atgaaaacct tgcgcccgtg accacatttg gaaagaccaa tggttacatc 4020

gcctaa 4026

<210> 43
<211> 1341
<212> PRT
<213> Artificial Sequence

<220>
<223> Single-chain variable fragment (scFv)
SFG.aCD19-CD8STK-CD28tmZ-2A-aCD5-HCH2CH3pvaa-dCD148

<400> 43

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

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

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

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

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
85 90 95

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
115 120 125

Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser Gly Pro Gly

```
145                 150                 155                 160

Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys Thr Val Ser Gly
                165                 170                 175

Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg
            180                 185                 190

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr
        195                 200                 205

Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile Lys Asp Asn Ser
    210                 215                 220

Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr
225                 230                 235                 240

Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala
                245                 250                 255

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp Pro
            260                 265                 270

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
        275                 280                 285

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
    290                 295                 300

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Phe Trp
305                 310                 315                 320

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
                325                 330                 335

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Arg Val Lys Phe Ser Arg
            340                 345                 350

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
        355                 360                 365

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
    370                 375                 380

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
385                 390                 395                 400
```

```
Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
                405                 410                 415

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
            420                 425                 430

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
        435                 440                 445

Ala Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Glu Gly Arg Gly
    450                 455                 460

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Glu
465                 470                 475                 480

Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro Gly Ser
                485                 490                 495

Thr Gly Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Lys Pro
            500                 505                 510

Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser
        515                 520                 525

Thr Ser Gly Met Gly Val Gly Trp Ile Arg Gln Pro Ser Gly Lys Gly
    530                 535                 540

Leu Glu Trp Leu Ala His Ile Trp Trp Asp Asp Asp Val Tyr Tyr Asn
545                 550                 555                 560

Pro Ser Leu Lys Asn Gln Leu Thr Ile Ser Lys Asp Ala Ser Arg Asp
                565                 570                 575

Gln Val Phe Leu Lys Ile Thr Asn Leu Asp Thr Ala Asp Thr Ala Thr
            580                 585                 590

Tyr Tyr Cys Val Arg Arg Arg Ala Thr Gly Thr Gly Phe Asp Tyr Trp
        595                 600                 605

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
    610                 615                 620

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asn Ile Val Met Thr Gln Ser
625                 630                 635                 640

His Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Ala Cys
                645                 650                 655
```

```
Lys Ala Ser Gln Asp Val Gly Thr Ala Val Ala Trp Tyr Gln Gln Lys
            660                 665                 670

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg His
        675                 680                 685

Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
    690                 695                 700

Thr Leu Thr Ile Thr Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe
705                 710                 715                 720

Cys His Gln Tyr Asn Ser Tyr Asn Thr Phe Gly Ser Gly Thr Arg Leu
                725                 730                 735

Glu Leu Lys Arg Ser Asp Pro Ala Glu Pro Lys Ser Pro Asp Lys Thr
            740                 745                 750

His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
        755                 760                 765

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ala Arg Thr
    770                 775                 780

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
785                 790                 795                 800

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
                805                 810                 815

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
            820                 825                 830

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
        835                 840                 845

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
    850                 855                 860

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
865                 870                 875                 880

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
                885                 890                 895

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
            900                 905                 910
```

```
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
        915                 920                 925

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
    930                 935                 940

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
945                 950                 955                 960

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Lys
                965                 970                 975

Asp Pro Lys Ala Val Phe Gly Cys Ile Phe Gly Ala Leu Val Ile Val
            980                 985                 990

Thr Val Gly Gly Phe Ile Phe Trp  Arg Lys Lys Arg Lys  Asp Ala Lys
        995                 1000                1005

Asn Asn  Glu Val Ser Phe Ser  Gln Ile Lys Pro Lys  Lys Ser Lys
    1010                1015                1020

Leu Ile  Arg Val Glu Asn Phe  Glu Ala Tyr Phe Lys  Lys Gln Gln
    1025                1030                1035

Ala Asp  Ser Asn Cys Gly Phe  Ala Glu Glu Tyr Glu  Asp Leu Lys
    1040                1045                1050

Leu Val  Gly Ile Ser Gln Pro  Lys Tyr Ala Ala Glu  Leu Ala Glu
    1055                1060                1065

Asn Arg  Gly Lys Asn Arg Tyr  Asn Asn Val Leu Pro  Tyr Asp Ile
    1070                1075                1080

Ser Arg  Val Lys Leu Ser Val  Gln Thr His Ser Thr  Asp Asp Tyr
    1085                1090                1095

Ile Asn  Ala Asn Tyr Met Pro  Gly Tyr His Ser Lys  Lys Asp Phe
    1100                1105                1110

Ile Ala  Thr Gln Gly Pro Leu  Pro Asn Thr Leu Lys  Asp Phe Trp
    1115                1120                1125

Arg Met  Val Trp Glu Lys Asn  Val Tyr Ala Ile Ile  Met Leu Thr
    1130                1135                1140

Lys Cys  Val Glu Gln Gly Arg  Thr Lys Cys Glu Glu  Tyr Trp Pro
```

1145 1150 1155

Ser Lys Gln Ala Gln Asp Tyr Gly Asp Ile Thr Val Ala Met Thr
1160 1165 1170

Ser Glu Ile Val Leu Pro Glu Trp Thr Ile Arg Asp Phe Thr Val
1175 1180 1185

Lys Asn Ile Gln Thr Ser Glu Ser His Pro Leu Arg Gln Phe His
1190 1195 1200

Phe Thr Ser Trp Pro Asp His Gly Val Pro Asp Thr Thr Asp Leu
1205 1210 1215

Leu Ile Asn Phe Arg Tyr Leu Val Arg Asp Tyr Met Lys Gln Ser
1220 1225 1230

Pro Pro Glu Ser Pro Ile Leu Val His Cys Ser Ala Gly Val Gly
1235 1240 1245

Arg Thr Gly Thr Phe Ile Ala Ile Asp Arg Leu Ile Tyr Gln Ile
1250 1255 1260

Glu Asn Glu Asn Thr Val Asp Val Tyr Gly Ile Val Tyr Asp Leu
1265 1270 1275

Arg Met His Arg Pro Leu Met Val Gln Thr Glu Asp Gln Tyr Val
1280 1285 1290

Phe Leu Asn Gln Cys Val Leu Asp Ile Val Arg Ser Gln Lys Asp
1295 1300 1305

Ser Lys Val Asp Leu Ile Tyr Gln Asn Thr Thr Ala Met Thr Ile
1310 1315 1320

Tyr Glu Asn Leu Ala Pro Val Thr Thr Phe Gly Lys Thr Asn Gly
1325 1330 1335

Tyr Ile Ala
1340

<210> 44
<211> 4026
<212> DNA
<213> Artificial Sequence

<220>
<223> Single-chain variable fragment (scFv)
SFG.aCD19-CD8STK-CD28tmZ-2A-aCD5-HCH2CH3pvaa-dCD148

<400> 44
atgagcctgc ccgtgaccgc cctgctgctg cccctggccc tgctgctgca cgccgccaga 60

ccagacatcc agatgaccca gaccaccagc agcctgagcg ccagcctggg cgaccgggtg 120

accatcagct gcagagccag ccaggacatc agcaagtacc tgaactggta ccagcagaag 180

cccgacggca ccgtgaagct gctgatctac cacaccagcc ggctgcacag cggcgtgccc 240

agccggttca gcggcagcgg cagcggcacc gactacagcc tgaccatcag caacctggag 300

caggaggaca tcgccaccta cttctgccag cagggcaaca ccctgcccta caccttcgga 360

ggcggcacca agctggagat caccaaggcc ggaggcggag gctctggcgg aggcggctct 420

ggcggaggcg gctctggcgg aggcggcagc gaggtgaagc tgcaggagtc tggcccaggc 480

ctggtggccc caagccagag cctgagcgtg acctgcaccg tgagcggcgt gagcctgccc 540

gactacggcg tgagctggat caggcagccc ccacggaagg gcctggagtg gctgggcgtg 600

atctggggca gcgagaccac ctactacaac agcgccctga agagccggct gaccatcatc 660

aaggacaaca gcaagagcca ggtgttcctg aagatgaaca gcctgcagac cgacgacacc 720

gccatctact actgcgccaa gcactactac tatggcggca gctacgctat ggactactgg 780

ggccagggca ccagcgtgac cgtgagctca gatcccacca cgacgccagc gccgcgacca 840

ccaacaccgg cgcccaccat cgcgtcgcag cccctgtccc tgcgcccaga ggcgtgccgg 900

ccagcggcgg ggggcgcagt gcacacgagg gggctggact tcgcctgtga tatcttttgg 960

gtgctggtgg tggttggtgg agtcctggct tgctatagct tgctagtaac agtggccttt 1020

attattttct gggtgaggag agtgaagttc agcaggagcg cagacgcccc cgcgtaccag 1080

cagggccaga accagctcta taacgagctc aatctaggac gaagagagga gtacgatgtt 1140

ttggacaaga gacgtggccg ggaccctgag atgggggggaa agccgagaag gaagaaccct 1200

caggaaggcc tgtacaatga actgcagaaa gataagatgg cggaggccta cagtgagatt 1260

gggatgaaag gcgagcgccg gaggggcaag gggcacgatg gcctttacca gggtctcagt 1320

acagccacca aggacaccta cgacgccctt cacatgcagg ccctgcctcc tcgcagagcc 1380

gagggcaggg gaagtcttct aacatgcggg gacgtggagg aaaatcccgg gcccatggag 1440

accgacaccc tgctgctgtg ggtgctgctg ctgtgggtgc ccggcagcac cggccaggtg 1500

accctgaagg agagcggtcc cggcatcctg aagcccagcc agaccctgag cctgacctgc 1560

agcttcagcg gcttcagcct gagcaccagc ggcatgggcg tgggctggat tcggcagccc 1620

agcggcaagg gcctggagtg gctggcccac atctggtggg acgacgacgt gtactacaac 1680

cccagcctga agaaccagct gaccatcagc aaggacgcca gccgggacca ggtgttcctg 1740

aagatcacca acctggacac cgccgacacc gccacctact actgcgtgcg gcgccgggcc 1800

accggcaccg gcttcgacta ctggggccag ggcaccaccc tgaccgtgag cagcggtggc 1860

ggtggcagcg gcggcggcgg aagcggaggt ggtggcagca acatcgtgat gacccagagc 1920

cacaagttca tgagcaccag cgtgggcgac cgggtgagca tcgcctgcaa ggccagccag 1980

gacgtgggca ccgccgtggc ctggtaccag cagaagcctg gccagagccc caagctgctg 2040

atctactgga ccagcacccg gcacaccggc gtgcccgacc ggttcaccgg cagcggcagc 2100

ggcaccgact tcaccctgac catcaccaac gtgcagagcg aggacctggc cgactacttc 2160

tgccaccagt acaacagcta caacaccttc ggcagcggca cccggctgga gctgaagcgg 2220

tcggatcccg ccgagcccaa atctcctgac aaaactcaca catgcccacc gtgcccagca 2280

cctcccgtgg ccggcccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 2340

atcgcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 2400

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 2460

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 2520

tggctgaatg gcaaggagta caagtgcaag gtctccaaca aagccctccc agcccccatc 2580

gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 2640

ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 2700

tatcccagcg acatcgccgt ggagtgggag agcaatgggc aaccggagaa caactacaag 2760

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 2820

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggccctg 2880

cacaatcact atacccagaa atctctgagt ctgagcccag gcaagaagga ccccaaggcg 2940

gtttttggct gtatctttgg tgccctggtt attgtgactg tgggaggctt catcttctgg 3000

agaaagaaga ggaaagatgc aaagaataat gaagtgtcct tttctcaaat taaacctaaa 3060

aaatctaagt taatcagagt ggagaatttt gaggcctact tcaagaagca gcaagctgac 3120

tccaactgtg ggttcgcaga ggaatacgaa gatctgaagc ttgttggaat tagtcaacct 3180

aaatatgcag cagaactggc tgagaataga ggaaagaatc gctataataa tgttctgccc 3240

tatgatattt cccgtgtcaa actttcggtc cagacccatt caacggatga ctacatcaat 3300

gccaactaca tgcctggcta ccactccaag aaagatttta ttgccacaca aggaccttta 3360

ccgaacactt tgaaagattt ttggcgtatg gtttgggaga aaaatgtata tgccatcatt 3420

atgttgacta aatgtgttga acagggaaga accaaatgtg aggagtattg gccctccaag 3480

caggctcagg actatggaga cataactgtg gcaatgacat cagaaattgt tcttccggaa 3540

tggaccatca gagatttcac agtgaaaaat atccagacaa gtgagagtca ccctctgaga 3600

cagttccatt tcacctcctg gccagaccac ggtgttcccg acaccactga cctgctcatc 3660

aacttccggt acctcgttcg tgactacatg aagcagagtc ctcccgaatc gccgattctg 3720

gtgcattgca gtgctggggt cggaaggacg ggcactttca ttgccattga tcgtctcatc 3780

taccagatag agaatgagaa caccgtggat gtgtatggga ttgtgtatga ccttcgaatg 3840

cataggcctt taatggtgca gacagaggac cagtatgttt tcctcaatca gtgtgttttg 3900

gatattgtca gatcccagaa agactcaaaa gtagatctta tctaccagaa cacaactgca 3960

atgacaatct atgaaaacct tgcgcccgtg accacatttg gaaagaccaa tggttacatc 4020

gcctaa 4026

<210> 45
<211> 1342
<212> PRT
<213> Artificial Sequence

<220>
<223> Single-chain variable fragment (scFv)
SFG.aCD19-CD8STK-CD28tmZ-2A-aEGFRvIII-HCH2CH3pvaa-dCD148

<400> 45

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

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

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

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

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
85 90 95

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
115 120 125

Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser Gly Pro Gly
145 150 155 160

```
Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys Thr Val Ser Gly
                165                 170                 175

Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg
            180                 185                 190

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr
        195                 200                 205

Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile Lys Asp Asn Ser
    210                 215                 220

Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr
225                 230                 235                 240

Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala
                245                 250                 255

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp Pro
            260                 265                 270

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
        275                 280                 285

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
    290                 295                 300

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Phe Trp
305                 310                 315                 320

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
                325                 330                 335

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Arg Val Lys Phe Ser Arg
            340                 345                 350

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
        355                 360                 365

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
    370                 375                 380

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
385                 390                 395                 400

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
                405                 410                 415
```

```
Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
            420                 425                 430

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
        435                 440                 445

Ala Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Glu Gly Arg Gly
    450                 455                 460

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Glu
465                 470                 475                 480

Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro Gly Ser
                485                 490                 495

Thr Gly Gln Val Lys Leu Gln Gln Ser Gly Gly Gly Leu Val Lys Pro
            500                 505                 510

Gly Ala Ser Leu Lys Leu Ser Cys Val Thr Ser Gly Phe Thr Phe Arg
        515                 520                 525

Lys Phe Gly Met Ser Trp Val Arg Gln Thr Ser Asp Lys Arg Leu Glu
    530                 535                 540

Trp Val Ala Ser Ile Ser Thr Gly Gly Tyr Asn Thr Tyr Tyr Ser Asp
545                 550                 555                 560

Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn Thr
                565                 570                 575

Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu Tyr
            580                 585                 590

Tyr Cys Thr Arg Gly Tyr Ser Ser Thr Ser Tyr Ala Met Asp Tyr Trp
        595                 600                 605

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
    610                 615                 620

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser
625                 630                 635                 640

Pro Ala Ser Leu Ser Val Ala Thr Gly Glu Lys Val Thr Ile Arg Cys
                645                 650                 655

Met Thr Ser Thr Asp Ile Asp Asp Asp Met Asn Trp Tyr Gln Gln Lys
```

660 665 670

Pro Gly Glu Pro Pro Lys Phe Leu Ile Ser Glu Gly Asn Thr Leu Arg
675 680 685

Pro Gly Val Pro Ser Arg Phe Ser Ser Ser Gly Thr Gly Thr Asp Phe
690 695 700

Val Phe Thr Ile Glu Asn Thr Leu Ser Glu Asp Val Gly Asp Tyr Tyr
705 710 715 720

Cys Leu Gln Ser Phe Asn Val Pro Leu Thr Phe Gly Asp Gly Thr Lys
725 730 735

Leu Glu Ile Lys Arg Ser Asp Pro Ala Glu Pro Lys Ser Pro Asp Lys
740 745 750

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser
755 760 765

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ala Arg
770 775 780

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
785 790 795 800

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
805 810 815

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
820 825 830

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
835 840 845

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
850 855 860

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
865 870 875 880

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
885 890 895

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
900 905 910

```
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
        915                 920                 925

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
    930                 935                 940

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
945                 950                 955                 960

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                965                 970                 975

Lys Asp Pro Lys Ala Val Phe Gly Cys Ile Phe Gly Ala Leu Val Ile
            980                 985                 990

Val Thr Val Gly Gly Phe Ile Phe  Trp Arg Lys Lys Arg  Lys Asp Ala
        995                 1000                1005

Lys Asn  Asn Glu Val Ser Phe  Ser Gln Ile Lys Pro  Lys Lys Ser
    1010                1015                1020

Lys Leu  Ile Arg Val Glu Asn  Phe Glu Ala Tyr Phe  Lys Lys Gln
    1025                1030                1035

Gln Ala  Asp Ser Asn Cys Gly  Phe Ala Glu Glu Tyr  Glu Asp Leu
    1040                1045                1050

Lys Leu  Val Gly Ile Ser Gln  Pro Lys Tyr Ala Ala  Glu Leu Ala
    1055                1060                1065

Glu Asn  Arg Gly Lys Asn Arg  Tyr Asn Asn Val Leu  Pro Tyr Asp
    1070                1075                1080

Ile Ser  Arg Val Lys Leu Ser  Val Gln Thr His Ser  Thr Asp Asp
    1085                1090                1095

Tyr Ile  Asn Ala Asn Tyr Met  Pro Gly Tyr His Ser  Lys Lys Asp
    1100                1105                1110

Phe Ile  Ala Thr Gln Gly Pro  Leu Pro Asn Thr Leu  Lys Asp Phe
    1115                1120                1125

Trp Arg  Met Val Trp Glu Lys  Asn Val Tyr Ala Ile  Ile Met Leu
    1130                1135                1140

Thr Lys  Cys Val Glu Gln Gly  Arg Thr Lys Cys Glu  Glu Tyr Trp
    1145                1150                1155
```

```
Pro Ser  Lys Gln Ala Gln Asp  Tyr Gly Asp Ile Thr  Val Ala Met
    1160                1165                1170

Thr Ser  Glu Ile Val Leu Pro  Glu Trp Thr Ile Arg  Asp Phe Thr
    1175                1180                1185

Val Lys  Asn Ile Gln Thr Ser  Glu Ser His Pro Leu  Arg Gln Phe
    1190                1195                1200

His Phe  Thr Ser Trp Pro Asp  His Gly Val Pro Asp  Thr Thr Asp
    1205                1210                1215

Leu Leu  Ile Asn Phe Arg Tyr  Leu Val Arg Asp Tyr  Met Lys Gln
    1220                1225                1230

Ser Pro  Pro Glu Ser Pro Ile  Leu Val His Cys Ser  Ala Gly Val
    1235                1240                1245

Gly Arg  Thr Gly Thr Phe Ile  Ala Ile Asp Arg Leu  Ile Tyr Gln
    1250                1255                1260

Ile Glu  Asn Glu Asn Thr Val  Asp Val Tyr Gly Ile  Val Tyr Asp
    1265                1270                1275

Leu Arg  Met His Arg Pro Leu  Met Val Gln Thr Glu  Asp Gln Tyr
    1280                1285                1290

Val Phe  Leu Asn Gln Cys Val  Leu Asp Ile Val Arg  Ser Gln Lys
    1295                1300                1305

Asp Ser  Lys Val Asp Leu Ile  Tyr Gln Asn Thr Thr  Ala Met Thr
    1310                1315                1320

Ile Tyr  Glu Asn Leu Ala Pro  Val Thr Thr Phe Gly  Lys Thr Asn
    1325                1330                1335

Gly Tyr  Ile Ala
    1340


<210>  46
<211>  4029
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Single-chain variable fragment (scFv)
       SFG.aCD19-CD8STK-CD28tmZ-2A-aEGFRvIII-HCH2CH3pvaa-dCD148

<400>  46
```

atgagcctgc ccgtgaccgc cctgctgctg cccctggccc tgctgctgca cgccgccaga 60

ccagacatcc agatgaccca gaccaccagc agcctgagcg ccagcctggg cgaccgggtg 120

accatcagct gcagagccag ccaggacatc agcaagtacc tgaactggta ccagcagaag 180

cccgacggca ccgtgaagct gctgatctac cacaccagcc ggctgcacag cggcgtgccc 240

agccggttca gcggcagcgg cagcggcacc gactacagcc tgaccatcag caacctggag 300

caggaggaca tcgccaccta cttctgccag cagggcaaca ccctgcccta caccttcgga 360

ggcggcacca agctggagat caccaaggcc ggaggcggag gctctggcgg aggcggctct 420

ggcggaggcg gctctggcgg aggcggcagc gaggtgaagc tgcaggagtc tggcccaggc 480

ctggtggccc caagccagag cctgagcgtg acctgcaccg tgagcggcgt gagcctgccc 540

gactacggcg tgagctggat caggcagccc ccacggaagg gcctggagtg gctgggcgtg 600

atctggggca gcgagaccac ctactacaac agcgccctga agagccggct gaccatcatc 660

aaggacaaca gcaagagcca ggtgttcctg aagatgaaca gcctgcagac cgacgacacc 720

gccatctact actgcgccaa gcactactac tatggcggca gctacgctat ggactactgg 780

ggccagggca ccagcgtgac cgtgagctca gatcccacca cgacgccagc gccgcgacca 840

ccaacaccgg cgcccaccat cgcgtcgcag cccctgtccc tgcgcccaga ggcgtgccgg 900

ccagcggcgg ggggcgcagt gcacacgagg gggctggact tcgcctgtga tatcttttgg 960

gtgctggtgg tggttggtgg agtcctggct tgctatagct tgctagtaac agtggccttt 1020

attattttct gggtgaggag agtgaagttc agcaggagcg cagacgcccc cgcgtaccag 1080

cagggccaga accagctcta taacgagctc aatctaggac gaagagagga gtacgatgtt 1140

ttggacaaga gacgtggccg ggaccctgag atgggggggaa agccgagaag gaagaaccct 1200

caggaaggcc tgtacaatga actgcagaaa gataagatgg cggaggccta cagtgagatt 1260

gggatgaaag gcgagcgccg gaggggcaag gggcacgatg gcctttacca gggtctcagt 1320

acagccacca aggacaccta cgacgccctt cacatgcagg ccctgcctcc tcgcagagcc 1380

gagggcaggg gaagtcttct aacatgcggg gacgtggagg aaaatcccgg gcccatggag 1440

accgacaccc tgctgctgtg ggtgctgctg ctgtgggtgc ccggcagcac cggccaggtg 1500

aagctgcagc agagcggcgg aggcctggtg aagcccggcg ccagcctgaa gctgagctgc 1560

gtgaccagcg gcttcacctt ccggaagttc ggcatgagct gggtgcggca gaccagcgac 1620

aagcggctgg agtgggtggc cagcatcagc accggcggct acaacaccta ctacagcgac 1680

aacgtgaagg gccggttcac catcagccgg gagaacgcca agaacaccct gtacctgcag 1740

atgagcagcc tgaagagcga ggacaccgcc ctgtactact gcacccgggg ctacagcagc 1800

accagctacg ctatggacta ctggggccag ggcaccaccg tgacagtgag cagcggcgga 1860

ggaggcagtg gtgggggtgg atctggcgga ggtggcagcg acatcgagct gacccagagc 1920

cccgccagcc tgagcgtggc caccggcgag aaggtgacca tccggtgcat gaccagcacc 1980

gacatcgacg acgacatgaa ctggtaccag cagaagcccg gcgagccccc aaagttcctg 2040

atcagcgagg gcaacaccct gcggcccggc gtgcccagcc ggttcagcag cagcggcacc 2100

ggcaccgact tcgtgttcac catcgagaac accctgagcg aggacgtggg cgactactac 2160

tgcctgcaga gcttcaacgt gcccctgacc ttcggcgacg gcaccaagct ggagatcaag 2220

cggtcggatc ccgccgagcc caaatctcct gacaaaactc acacatgccc accgtgccca 2280

gcacctcccg tggccggccc gtcagtcttc ctcttccccc caaaacccaa ggacaccctc 2340

atgatcgccc ggacccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct 2400

gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgccaa gacaaagccg 2460

cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag 2520

gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cccagccccc 2580

atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg 2640

cccccatccc gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc 2700

ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggcaaccgga gaacaactac 2760

aagaccacgc ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc 2820

gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggcc 2880

ctgcacaatc actataccca gaaatctctg agtctgagcc caggcaagaa ggaccccaag 2940

gcggtttttg gctgtatctt tggtgccctg gttattgtga ctgtgggagg cttcatcttc 3000

tggagaaaga agaggaaaga tgcaaagaat aatgaagtgt ccttttctca aattaaacct 3060

aaaaaatcta agttaatcag agtggagaat tttgaggcct acttcaagaa gcagcaagct 3120

gactccaact gtgggttcgc agaggaatac gaagatctga agcttgttgg aattagtcaa 3180

cctaaatatg cagcagaact ggctgagaat agaggaaaga atcgctataa taatgttctg 3240

ccctatgata tttcccgtgt caaactttcg gtccagaccc attcaacgga tgactacatc 3300

aatgccaact acatgcctgg ctaccactcc aagaaagatt ttattgccac acaaggacct 3360

ttaccgaaca ctttgaaaga tttttggcgt atggtttggg agaaaaatgt atatgccatc 3420

attatgttga ctaaatgtgt tgaacaggga agaaccaaat gtgaggagta ttggccctcc 3480

aagcaggctc aggactatgg agacataact gtggcaatga catcagaaat tgttcttccg 3540

gaatggacca tcagagattt cacagtgaaa aatatccaga caagtgagag tcaccctctg 3600

agacagttcc atttcacctc ctggccagac cacggtgttc ccgacaccac tgacctgctc 3660

atcaacttcc ggtacctcgt tcgtgactac atgaagcaga gtcctcccga atcgccgatt 3720

ctggtgcatt gcagtgctgg ggtcggaagg acgggcactt tcattgccat tgatcgtctc 3780

atctaccaga tagagaatga gaacaccgtg gatgtgtatg ggattgtgta tgaccttcga 3840

atgcataggc ctttaatggt gcagacagag gaccagtatg ttttcctcaa tcagtgtgtt 3900

ttggatattg tcagatccca gaaagactca aaagtagatc ttatctacca gaacacaact 3960

gcaatgacaa tctatgaaaa ccttgcgccc gtgaccacat ttggaaagac caatggttac 4020

atcgcctaa 4029

<210> 47
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Immunoreceptor tyrosine-based inhibition motif (ITIM)

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa may be Ser, Ile, Val or Leu

<220>
<221> misc_feature
<222> (2)..(2)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (4)..(5)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa may be Ile, Val or Leu

<400> 47

Xaa Xaa Tyr Xaa Xaa Xaa
1 5

<210> 48
<211> 1114
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of a AND NOT gate (16076.SFG.aCD19fmc63-CD8STK-CD28tmZ-2A-aCD33glx-muCD8STK-tm-dPTPN6)

<400> 48

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

His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu

```
            20                  25                  30

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

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

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65                  70                  75                  80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
                85                  90                  95

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
            100                 105                 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
        115                 120                 125

Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser Gly Pro Gly
145                 150                 155                 160

Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys Thr Val Ser Gly
                165                 170                 175

Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg
            180                 185                 190

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr
        195                 200                 205

Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile Lys Asp Asn Ser
    210                 215                 220

Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr
225                 230                 235                 240

Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala
                245                 250                 255

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp Pro
            260                 265                 270
```

```
Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
        275                 280                 285

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
    290                 295                 300

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Phe Trp
305                 310                 315                 320

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
                325                 330                 335

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Arg Val Lys Phe Ser Arg
            340                 345                 350

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
        355                 360                 365

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
    370                 375                 380

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
385                 390                 395                 400

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
                405                 410                 415

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
            420                 425                 430

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
        435                 440                 445

Ala Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Glu Gly Arg Gly
    450                 455                 460

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala
465                 470                 475                 480

Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr Asp Ala
                485                 490                 495

Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
            500                 505                 510

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp Ile Tyr
        515                 520                 525
```

```
Phe Asn Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
    530                 535                 540

Leu Ile Tyr Asp Thr Asn Arg Leu Ala Asp Gly Val Pro Ser Arg Phe
545                 550                 555                 560

Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser Ser Leu
                565                 570                 575

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Lys Asn Tyr
            580                 585                 590

Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ser Gly
        595                 600                 605

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    610                 615                 620

Gly Gly Ser Arg Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
625                 630                 635                 640

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
                645                 650                 655

Thr Leu Ser Asn Tyr Gly Met His Trp Ile Arg Gln Ala Pro Gly Lys
            660                 665                 670

Gly Leu Glu Trp Val Ser Ser Ile Ser Leu Asn Gly Gly Ser Thr Tyr
        675                 680                 685

Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
    690                 695                 700

Lys Ser Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
705                 710                 715                 720

Ala Val Tyr Tyr Cys Ala Ala Gln Asp Ala Tyr Thr Gly Gly Tyr Phe
                725                 730                 735

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Met Asp Pro
            740                 745                 750

Ala Thr Thr Thr Lys Pro Val Leu Arg Thr Pro Ser Pro Val His Pro
        755                 760                 765

Thr Gly Thr Ser Gln Pro Gln Arg Pro Glu Asp Cys Arg Pro Arg Gly
    770                 775                 780
```

```
Ser Val Lys Gly Thr Gly Leu Asp Phe Ala Cys Asp Ile Tyr Trp Ala
785                 790                 795                 800

Pro Leu Ala Gly Ile Cys Val Ala Leu Leu Leu Ser Leu Ile Ile Thr
                805                 810                 815

Leu Ile Cys Tyr His Arg Ser Arg Lys Arg Val Cys Lys Ser Gly Gly
            820                 825                 830

Gly Ser Phe Trp Glu Glu Phe Glu Ser Leu Gln Lys Gln Glu Val Lys
        835                 840                 845

Asn Leu His Gln Arg Leu Glu Gly Gln Arg Pro Glu Asn Lys Gly Lys
    850                 855                 860

Asn Arg Tyr Lys Asn Ile Leu Pro Phe Asp His Ser Arg Val Ile Leu
865                 870                 875                 880

Gln Gly Arg Asp Ser Asn Ile Pro Gly Ser Asp Tyr Ile Asn Ala Asn
                885                 890                 895

Tyr Ile Lys Asn Gln Leu Leu Gly Pro Asp Glu Asn Ala Lys Thr Tyr
            900                 905                 910

Ile Ala Ser Gln Gly Cys Leu Glu Ala Thr Val Asn Asp Phe Trp Gln
        915                 920                 925

Met Ala Trp Gln Glu Asn Ser Arg Val Ile Val Met Thr Thr Arg Glu
    930                 935                 940

Val Glu Lys Gly Arg Asn Lys Cys Val Pro Tyr Trp Pro Glu Val Gly
945                 950                 955                 960

Met Gln Arg Ala Tyr Gly Pro Tyr Ser Val Thr Asn Cys Gly Glu His
                965                 970                 975

Asp Thr Thr Glu Tyr Lys Leu Arg Thr Leu Gln Val Ser Pro Leu Asp
            980                 985                 990

Asn Gly Asp Leu Ile Arg Glu Ile  Trp His Tyr Gln Tyr  Leu Ser Trp
        995                 1000                1005

Pro Asp  His Gly Val Pro Ser  Glu Pro Gly Gly Val  Leu Ser Phe
    1010                1015                1020

Leu Asp  Gln Ile Asn Gln Arg  Gln Glu Ser Leu Pro  His Ala Gly
```

1025 1030 1035

Pro Ile Ile Val His Cys Ser Ala Gly Ile Gly Arg Thr Gly Thr
1040 1045 1050

Ile Ile Val Ile Asp Met Leu Met Glu Asn Ile Ser Thr Lys Gly
1055 1060 1065

Leu Asp Cys Asp Ile Asp Ile Gln Lys Thr Ile Gln Met Val Arg
1070 1075 1080

Ala Gln Arg Ser Gly Met Val Gln Thr Glu Ala Gln Tyr Lys Phe
1085 1090 1095

Ile Tyr Val Ala Ile Ala Gln Phe Ile Glu Thr Thr Lys Lys Lys
1100 1105 1110

Leu

<210> 49
<211> 918
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of a AND NOT gate (MP16091.SFG.aCD19fmc63-CD8STK-CD28tmZ-2A-aCD33glx-muCD8STK-LAIR1 tm-endo)

<400> 49

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

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

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

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

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
85 90 95

```
Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
            100                 105                 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
        115                 120                 125

Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser Gly Pro Gly
145                 150                 155                 160

Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys Thr Val Ser Gly
                165                 170                 175

Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg
            180                 185                 190

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr
        195                 200                 205

Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile Lys Asp Asn Ser
    210                 215                 220

Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr
225                 230                 235                 240

Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala
                245                 250                 255

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp Pro
            260                 265                 270

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
        275                 280                 285

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
    290                 295                 300

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Phe Trp
305                 310                 315                 320

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
                325                 330                 335

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Arg Val Lys Phe Ser Arg
            340                 345                 350
```

```
Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
        355                 360                 365

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
    370                 375                 380

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
385                 390                 395                 400

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
                405                 410                 415

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
            420                 425                 430

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
        435                 440                 445

Ala Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Glu Gly Arg Gly
    450                 455                 460

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala
465                 470                 475                 480

Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr Asp Ala
                485                 490                 495

Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
            500                 505                 510

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp Ile Tyr
        515                 520                 525

Phe Asn Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
    530                 535                 540

Leu Ile Tyr Asp Thr Asn Arg Leu Ala Asp Gly Val Pro Ser Arg Phe
545                 550                 555                 560

Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser Ser Leu
                565                 570                 575

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Lys Asn Tyr
            580                 585                 590

Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ser Gly
        595                 600                 605
```

```
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    610                 615                 620

Gly Gly Ser Arg Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
625                 630                 635                 640

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
                645                 650                 655

Thr Leu Ser Asn Tyr Gly Met His Trp Ile Arg Gln Ala Pro Gly Lys
            660                 665                 670

Gly Leu Glu Trp Val Ser Ser Ile Ser Leu Asn Gly Gly Ser Thr Tyr
        675                 680                 685

Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
    690                 695                 700

Lys Ser Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
705                 710                 715                 720

Ala Val Tyr Tyr Cys Ala Ala Gln Asp Ala Tyr Thr Gly Gly Tyr Phe
                725                 730                 735

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Met Asp Pro
            740                 745                 750

Ala Thr Thr Thr Lys Pro Val Leu Arg Thr Pro Ser Pro Val His Pro
        755                 760                 765

Thr Gly Thr Ser Gln Pro Gln Arg Pro Glu Asp Cys Arg Pro Arg Gly
    770                 775                 780

Ser Val Lys Gly Thr Gly Leu Asp Phe Ala Cys Asp Ile Leu Ile Gly
785                 790                 795                 800

Val Ser Val Val Phe Leu Phe Cys Leu Leu Leu Leu Val Leu Phe Cys
                805                 810                 815

Leu His Arg Gln Asn Gln Ile Lys Gln Gly Pro Pro Arg Ser Lys Asp
            820                 825                 830

Glu Glu Gln Lys Pro Gln Gln Arg Pro Asp Leu Ala Val Asp Val Leu
        835                 840                 845

Glu Arg Thr Ala Asp Lys Ala Thr Val Asn Gly Leu Pro Glu Lys Asp
```

850 855 860

Arg Glu Thr Asp Thr Ser Ala Leu Ala Ala Gly Ser Ser Gln Glu Val
865 870 875 880

Thr Tyr Ala Gln Leu Asp His Trp Ala Leu Thr Gln Arg Thr Ala Arg
885 890 895

Ala Val Ser Pro Gln Ser Thr Lys Pro Met Ala Glu Ser Ile Thr Tyr
900 905 910

Ala Ala Val Ala Arg His
915

<210> 50
<211> 1362
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of a AND NOT gate
(MP16092.SFG.aCD19fmc63-CD8STK-CD28tmZ-2A-aCD33glx-muCD8STK-LAIR1
tm-endo-2A-PTPN6_SH2-dCD148)

<400> 50

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

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

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

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

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
85 90 95

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
115 120 125

```
Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser Gly Pro Gly
145                 150                 155                 160

Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys Thr Val Ser Gly
                165                 170                 175

Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg
            180                 185                 190

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr
        195                 200                 205

Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile Lys Asp Asn Ser
    210                 215                 220

Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr
225                 230                 235                 240

Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala
                245                 250                 255

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp Pro
            260                 265                 270

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
        275                 280                 285

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
    290                 295                 300

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Phe Trp
305                 310                 315                 320

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
                325                 330                 335

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Arg Val Lys Phe Ser Arg
            340                 345                 350

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
        355                 360                 365

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
    370                 375                 380
```

```
Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
385                 390                 395                 400

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
                405                 410                 415

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
            420                 425                 430

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
        435                 440                 445

Ala Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Glu Gly Arg Gly
    450                 455                 460

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala
465                 470                 475                 480

Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr Asp Ala
                485                 490                 495

Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
            500                 505                 510

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp Ile Tyr
        515                 520                 525

Phe Asn Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
    530                 535                 540

Leu Ile Tyr Asp Thr Asn Arg Leu Ala Asp Gly Val Pro Ser Arg Phe
545                 550                 555                 560

Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser Ser Leu
                565                 570                 575

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Lys Asn Tyr
            580                 585                 590

Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ser Gly
        595                 600                 605

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    610                 615                 620

Gly Gly Ser Arg Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
625                 630                 635                 640
```

```
Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
                645                 650                 655

Thr Leu Ser Asn Tyr Gly Met His Trp Ile Arg Gln Ala Pro Gly Lys
            660                 665                 670

Gly Leu Glu Trp Val Ser Ser Ile Ser Leu Asn Gly Gly Ser Thr Tyr
        675                 680                 685

Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
    690                 695                 700

Lys Ser Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
705                 710                 715                 720

Ala Val Tyr Tyr Cys Ala Ala Gln Asp Ala Tyr Thr Gly Gly Tyr Phe
                725                 730                 735

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Met Asp Pro
            740                 745                 750

Thr Thr Thr Lys Pro Val Leu Arg Thr Pro Ser Pro Val His Pro Thr
        755                 760                 765

Gly Thr Ser Gln Pro Gln Arg Pro Glu Asp Cys Arg Pro Arg Gly Ser
    770                 775                 780

Val Lys Gly Thr Gly Leu Asp Phe Ala Cys Asp Ile Leu Ile Gly Val
785                 790                 795                 800

Ser Val Val Phe Leu Phe Cys Leu Leu Leu Leu Val Leu Phe Cys Leu
                805                 810                 815

His Arg Gln Asn Gln Ile Lys Gln Gly Pro Pro Arg Ser Lys Asp Glu
            820                 825                 830

Glu Gln Lys Pro Gln Gln Arg Pro Asp Leu Ala Val Asp Val Leu Glu
        835                 840                 845

Arg Thr Ala Asp Lys Ala Thr Val Asn Gly Leu Pro Glu Lys Asp Arg
    850                 855                 860

Glu Thr Asp Thr Ser Ala Leu Ala Ala Gly Ser Ser Gln Glu Val Thr
865                 870                 875                 880

Tyr Ala Gln Leu Asp His Trp Ala Leu Thr Gln Arg Thr Ala Arg Ala
```

```
                885                 890                 895

Val Ser Pro Gln Ser Thr Lys Pro Met Ala Glu Ser Ile Thr Tyr Ala
            900                 905                 910

Ala Val Ala Arg His Arg Ala Glu Gly Arg Gly Ser Leu Leu Thr Cys
        915                 920                 925

Gly Asp Val Glu Glu Asn Pro Gly Pro Trp Tyr His Gly His Met Ser
    930                 935                 940

Gly Gly Gln Ala Glu Thr Leu Leu Gln Ala Lys Gly Glu Pro Trp Thr
945                 950                 955                 960

Phe Leu Val Arg Glu Ser Leu Ser Gln Pro Gly Asp Phe Val Leu Ser
                965                 970                 975

Val Leu Ser Asp Gln Pro Lys Ala Gly Pro Gly Ser Pro Leu Arg Val
            980                 985                 990

Thr His Ile Lys Val Met Cys Glu  Gly Gly Arg Tyr Thr  Val Gly Gly
        995                 1000                1005

Leu Glu  Thr Phe Asp Ser Leu  Thr Asp Leu Val Glu  His Phe Lys
    1010                1015                1020

Lys Thr  Gly Ile Glu Glu Ala  Ser Gly Ala Phe Val  Tyr Leu Arg
    1025                1030                1035

Gln Pro  Tyr Ser Gly Gly Gly  Gly Ser Phe Glu Ala  Tyr Phe Lys
    1040                1045                1050

Lys Gln  Gln Ala Asp Ser Asn  Cys Gly Phe Ala Glu  Glu Tyr Glu
    1055                1060                1065

Asp Leu  Lys Leu Val Gly Ile  Ser Gln Pro Lys Tyr  Ala Ala Glu
    1070                1075                1080

Leu Ala  Glu Asn Arg Gly Lys  Asn Arg Tyr Asn Asn  Val Leu Pro
    1085                1090                1095

Tyr Asp  Ile Ser Arg Val Lys  Leu Ser Val Gln Thr  His Ser Thr
    1100                1105                1110

Asp Asp  Tyr Ile Asn Ala Asn  Tyr Met Pro Gly Tyr  His Ser Lys
    1115                1120                1125
```

```
Lys Asp  Phe Ile Ala Thr Gln  Gly Pro Leu Pro Asn  Thr Leu Lys
    1130                1135                1140

Asp Phe  Trp Arg Met Val Trp  Glu Lys Asn Val Tyr  Ala Ile Ile
    1145                1150                1155

Met Leu  Thr Lys Cys Val Glu  Gln Gly Arg Thr Lys  Cys Glu Glu
    1160                1165                1170

Tyr Trp  Pro Ser Lys Gln Ala  Gln Asp Tyr Gly Asp  Ile Thr Val
    1175                1180                1185

Ala Met  Thr Ser Glu Ile Val  Leu Pro Glu Trp Thr  Ile Arg Asp
    1190                1195                1200

Phe Thr  Val Lys Asn Ile Gln  Thr Ser Glu Ser His  Pro Leu Arg
    1205                1210                1215

Gln Phe  His Phe Thr Ser Trp  Pro Asp His Gly Val  Pro Asp Thr
    1220                1225                1230

Thr Asp  Leu Leu Ile Asn Phe  Arg Tyr Leu Val Arg  Asp Tyr Met
    1235                1240                1245

Lys Gln  Ser Pro Pro Glu Ser  Pro Ile Leu Val His  Cys Ser Ala
    1250                1255                1260

Gly Val  Gly Arg Thr Gly Thr  Phe Ile Ala Ile Asp  Arg Leu Ile
    1265                1270                1275

Tyr Gln  Ile Glu Asn Glu Asn  Thr Val Asp Val Tyr  Gly Ile Val
    1280                1285                1290

Tyr Asp  Leu Arg Met His Arg  Pro Leu Met Val Gln  Thr Glu Asp
    1295                1300                1305

Gln Tyr  Val Phe Leu Asn Gln  Cys Val Leu Asp Ile  Val Arg Ser
    1310                1315                1320

Gln Lys  Asp Ser Lys Val Asp  Leu Ile Tyr Gln Asn  Thr Thr Ala
    1325                1330                1335

Met Thr  Ile Tyr Glu Asn Leu  Ala Pro Val Thr Thr  Phe Gly Lys
    1340                1345                1350

Thr Asn  Gly Tyr Ile Ala Ser  Gly Ser
    1355                1360
```

<210> 51
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> APRIL-based (A proliferation-inducing ligand-based) CAR, CD8 stalk APRIL CAR

<400> 51

```
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1               5                  10                  15

Gly Ser Thr Gly Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser
            20                  25                  30

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

Arg Gly Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp
    50                  55                  60

Ala Gly Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr
65                  70                  75                  80

Phe Thr Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu
                85                  90                  95

Thr Leu Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala
            100                 105                 110

Tyr Asn Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp
        115                 120                 125

Ile Leu Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser
    130                 135                 140

Pro His Gly Thr Phe Leu Gly Phe Val Lys Leu Ser Gly Gly Gly Ser
145                 150                 155                 160

Asp Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
                165                 170                 175

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
            180                 185                 190

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
        195                 200                 205
```

```
Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
    210                 215                 220

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
225                 230                 235                 240

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
                245                 250                 255

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
            260                 265                 270

Ala Tyr Arg Ser Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro
        275                 280                 285

Pro Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp
    290                 295                 300

Ala His Ser Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala
305                 310                 315                 320

Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
                325                 330                 335

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
            340                 345                 350

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
        355                 360                 365

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
    370                 375                 380

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
385                 390                 395                 400

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
                405                 410                 415

His Met Gln Ala Leu Pro Pro Arg
            420
```

<210> 52
<211> 398
<212> PRT
<213> Artificial Sequence

<220>

<223> APRIL-based (A proliferation-inducing ligand-based) CAR, APRIL IgG1 hinge based CAR

<400> 52

```
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1               5                  10                  15

Gly Ser Thr Gly Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser
            20                  25                  30

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

Arg Gly Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp
    50                  55                  60

Ala Gly Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr
65                  70                  75                  80

Phe Thr Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu
                85                  90                  95

Thr Leu Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala
            100                 105                 110

Tyr Asn Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp
        115                 120                 125

Ile Leu Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser
    130                 135                 140

Pro His Gly Thr Phe Leu Gly Phe Val Lys Leu Ser Gly Gly Gly Ser
145                 150                 155                 160

Asp Pro Ala Glu Pro Lys Ser Pro Asp Lys Thr His Thr Cys Pro Pro
                165                 170                 175

Cys Pro Lys Asp Pro Lys Phe Trp Val Leu Val Val Val Gly Gly Val
            180                 185                 190

Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp
        195                 200                 205

Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
    210                 215                 220

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
225                 230                 235                 240
```

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Asp Gln Arg Leu Pro
245 250 255

Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro Ile
260 265 270

Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile Arg Val
275 280 285

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
290 295 300

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
305 310 315 320

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
325 330 335

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
340 345 350

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
355 360 365

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
370 375 380

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
385 390 395

<210> 53
<211> 614
<212> PRT
<213> Artificial Sequence

<220>
<223> APRIL-based (A proliferation-inducing ligand-based) CAR, APRIL Fc-pvaa based CAR

<400> 53

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser
20 25 30

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

```
Arg Gly Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp
    50                  55                  60

Ala Gly Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr
65                  70                  75                  80

Phe Thr Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu
                85                  90                  95

Thr Leu Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala
            100                 105                 110

Tyr Asn Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp
        115                 120                 125

Ile Leu Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser
    130                 135                 140

Pro His Gly Thr Phe Leu Gly Phe Val Lys Leu Ser Gly Gly Gly Ser
145                 150                 155                 160

Asp Pro Ala Glu Pro Lys Ser Pro Asp Lys Thr His Thr Cys Pro Pro
                165                 170                 175

Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro
            180                 185                 190

Lys Pro Lys Asp Thr Leu Met Ile Ala Arg Thr Pro Glu Val Thr Cys
        195                 200                 205

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
    210                 215                 220

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
225                 230                 235                 240

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
                245                 250                 255

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
            260                 265                 270

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
        275                 280                 285

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
```

```
    290                 295                 300

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
305                 310                 315                 320

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
                325                 330                 335

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
            340                 345                 350

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
        355                 360                 365

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
    370                 375                 380

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Lys Asp Pro Lys Phe Trp
385                 390                 395                 400

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
                405                 410                 415

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu
            420                 425                 430

Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr
        435                 440                 445

Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr
    450                 455                 460

Arg Ser Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly
465                 470                 475                 480

Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His
                485                 490                 495

Ser Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
            500                 505                 510

Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
        515                 520                 525

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
    530                 535                 540
```

```
Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu
545                 550                 555                 560

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
                565                 570                 575

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
            580                 585                 590

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
        595                 600                 605

Gln Ala Leu Pro Pro Arg
    610
```