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(54) **Title:** CELL

(57) **Abstract:** The present invention relates to a cell which comprises a chimeric antigen receptor (CAR) and a signal transduction modifying protein, selected from one of the following: (i) a truncated protein which comprises an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based activation motif (ITAM), but lacks a kinase domain; (ii) a truncated protein which comprises an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based inhibition motif (ITIM) but lacks a phosphatase domain; (iii) a fusion protein which comprises (a) an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based activation motif (ITAM) or from a protein which binds a phosphorylated immunoreceptor tyrosine-based inhibition motif (ITIM); and (ii) a heterologous domain.



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## FIELD OF THE INVENTION

The present invention relates to fusion proteins and truncated proteins which enable the signalling pathways which are propagated following immune cell activation to be manipulated or modulated.

## BACKGROUND TO THE INVENTION

Adoptive immunotherapy with autologous T cells involves the isolation of T cells from the patient followed by their stimulation, modification and/or expansion *ex vivo* in order to generate a population of T cells which display anti-tumour specificities. Once re-infused into the patient these cells are capable of recognizing tumour-expressed antigens and mediating tumour rejection.

This approach has already been shown in a number of trials in different settings to have the potential to be a powerful, effective and long-lasting treatment for cancer. For instance, EBV-driven tumours, such as lymphoproliferative disease following solid organ transplant can be effectively treated by *ex vivo* expanded EBV specific T-cells.

A similar therapy for non-viral malignancies involves tumour infiltrating lymphocytes (TILs) which are isolated from resected fragments of tumour and then subjected to stimulation and expansion with autologous tumour samples. Expanded T cell cultures which show tumour reactivity can then be re-infused into the patient.

Rather than selecting and refining T cell specificities with repeated exposure to antigens, the desired anti-tumour specificity can be conferred onto the T cells through gene modification and the introduction of either a tumour-specific T cell receptor (TCR) or a chimeric antigen receptor (CAR). These cells are expanded *ex vivo* in order to produce sufficient numbers of cells to achieve meaningful clinical responses within the patient.

However, the approaches detailed above have limitations. For instance, adoptively transferred T-cells may show limited persistence and expansion *in vivo* due to insufficient signalling, lack of IL2 or differentiation. By way of further example, adoptively transferred T-cells may succumb to inhibitory stimuli within the tumour microenvironment. For example they may become exhausted, undergo activation induced cell death consequent to over activation, or may cause on-target off-tumour effects.

Another promising approach to activating therapeutic anti-tumour immunity is the blockade of immune checkpoints. Immune checkpoints refer to the various inhibitory pathways of the immune system that are important for maintaining self-tolerance and modulating the duration and amplitude of physiological immune responses in peripheral tissues.

It is known that tumours exploit certain immune-checkpoint pathways as a major mechanism of immune resistance, particularly against T cells that are specific for tumour antigens. Many of the immune checkpoints are initiated by ligand–receptor interactions, meaning that they can be blocked by antibodies or modulated by recombinant forms of ligands or receptors. Cytotoxic T-lymphocyte-associated antigen 4 (CTLA4) antibodies were the first of this class of immunotherapeutics to achieve US Food and Drug Administration (FDA) approval. More recently, blockers of additional immune-checkpoint proteins, such as programmed cell death protein 1 (PD1), have been developed and shown to enhance anti-tumour immunity.

One problem with the use of immune checkpoint inhibitors is that there are a multitude of inhibitory pathways triggered by a multitude of ligand:receptor interactions. The use of an antibody or a recombinant form of the ligand/receptor will only block one such inhibitory pathway, leaving the possibility open that the tumour can compensate for the specific immune checkpoint block using other molecules.

## SUMMARY OF ASPECTS OF THE INVENTION

The present inventors have developed a system for modulating and/or manipulating signal transduction pathways in immune cells, such as T cells and natural killer (NK) cells.

Intracellular signalling pathways are initiated and controlled by the reversible post-translational modification of proteins. The present inventors have determined that activating and inhibitory signalling pathways in T cells can be modulated and/or manipulated by fusion proteins or truncated proteins comprising SH2 domains from immediate T-cell signal transduction proteins. In other words, activating and inhibitory signalling pathways in T cells can be modulated and/or manipulated by fusion proteins or truncated proteins comprising SH2 domains from proteins which are capable of binding phosphorylated immunoreceptor tyrosine-based activation motifs (ITAM) or phosphorylated immunoreceptor tyrosine-based inhibition motifs (ITIM).

Thus in a first aspect, the present invention provides a cell which comprises a chimeric antigen receptor (CAR) and a signal transduction modifying protein, selected from one of the following:

- (i) a truncated protein which comprises an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based activation motif (ITAM), but lacks a kinase domain;
- (ii) a truncated protein which comprises an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based inhibition motif (ITIM) but lacks a phosphatase domain;
- (iii) a fusion protein which comprises (a) an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based activation motif (ITAM) or from a protein which binds a phosphorylated immunoreceptor tyrosine-based inhibition motif (ITIM); and (ii) a heterologous domain.

The signal transduction modifying protein may be a truncated protein which comprises a ZAP70 SH2 domain but lacks a ZAP70 kinase domain.

The signal transduction modifying protein may be a truncated protein which comprises an PTPN6 SH2 but lacks a PTPN6 phosphatase domain.

The signal transduction modifying protein may be a truncated protein which comprises a SHP-2 SH2 domain but lacks a SHP-2 phosphatase domain.

The signal transduction modifying protein may be a fusion protein which comprises (i) an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based activation motif (ITAM); and (ii) a phosphatase domain.

The fusion protein may, for example, comprise a ZAP70 SH2 domain, a PTPN6 or an SHP-2 phosphatase domain.

The signal transduction modifying protein may be a fusion protein which comprises (i) an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based inhibition motif (ITIM); and (ii) a kinase domain.

The fusion protein may comprise an SH2 domain from PTPN6 or SHP-2.

The fusion protein may comprise a Zap70 kinase domain

The fusion protein may comprise an AKT or JAK kinase domain.

The signal transduction modifying protein may be a fusion protein which comprises (i) an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based activation motif (ITAM) or from a protein which binds a phosphorylated immunoreceptor tyrosine-based inhibition motif (ITIM); and (ii) a heterologous signalling domain.

The fusion protein may comprise an SH2 domain from ZAP70, PTPN6 or SHP-2.

The heterologous signalling domain may be from a signalling molecule which is not usually activated by an ITAM or ITIM containing receptor.

The heterologous signalling domain may be a co-stimulatory domain. In this respect, the fusion protein may comprise a CD28, OX40 or 41BB co-stimulatory domain.

The heterologous signalling domain may be an inhibitory domain. In this respect, the inhibitory domain may be or comprise the endodomain of CD148 or CD45. Alternatively, the heterologous signalling domain is or comprises the endodomain of ICOS, CD27, BTLA, CD30, GITR or HVEM.

The signal transduction modifying protein may be a fusion protein which comprises (i) an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based activation motif (ITAM); and (ii) an ITAM-containing domain.

The fusion protein may comprises a ZAP70 SH2 domain.

The ITAM-containing domain may be or comprise the endodomain of CD3-Zeta.

The signal transduction modifying protein may be a fusion protein which comprises (i) an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based inhibition motif (ITIM); and (ii) an ITIM-containing domain.

The fusion protein may comprise an SH2 domain from PTPN6 or SHP-2.

The ITIM-containing domain may be or comprise the endodomain from PD1, PDCD1, BTLA4, LILRB1, LAIR1, CTLA4, KIR2DL1, KIR2DL4, KIR2DL5, KIR3DL1 or KIR3DL3.

The signal transduction modifying protein may be a fusion protein which comprises (i) an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based activation

motif (ITAM) or from a protein which binds a phosphorylated immunoreceptor tyrosine-based inhibition motif (ITIM); and (ii) a protease domain.

The fusion protein may comprise an SH2 domain from ZAP70, PTPN6 or SHP-2.

The protease domain may be or comprise Tobacco Etch Virus Protease (TeV).

The cell may also comprises a membrane-tethered transcription factor having a protease cleavage site. Cleavage at the protease cleavage site may release the transcription factor leading to increased expression of a target gene.

The target gene encodes a cytokine, for example a cytokine selected from the following group: IL-2, IL-7, IL-15 and IL-12.

In this embodiment, the chimeric antigen receptor (CAR) may be a target CAR which comprises an intracellular protease cleavage site.

The target CAR may comprise an activatory or co-stimulatory endodomain and cleavage at the protease cleavage site removes the endodomain from the target CAR.

Alternatively, the target CAR may comprise an inhibitory endodomain and cleavage at the protease cleavage site removes the inhibitory endodomain from the target CAR. The inhibitory endodomain may comprise a CD148 or CD45 endodomain.

The cell of the present invention may comprise two CARs: an activating CAR comprising an ITAM-containing endodomain; and a target CAR as defined above.

Alternatively, the cell of the present invention may comprise two CARs: an inhibitory CAR comprising an ITIM-containing endodomain; and a target CAR as defined above.

In a second aspect, the present invention provides a nucleic acid construct, which comprises:

a first nucleic acid sequence encoding a chimeric antigen receptor; and

a second nucleic acid sequence encoding a truncated protein or a fusion protein as defined in connection with the first aspect of the invention.

The nucleic acid construct may also comprise a third nucleic acid sequence encoding a membrane-tethered transcription factor as defined above.

The nucleic acid construct may also comprise a third nucleic acid sequence encoding a target CAR as defined above.

The nucleic acid construct may also comprise a fourth nucleic acid sequence encoding an activating CAR or an inhibitory CAR as defined above.

In a third aspect, the vector which comprises a nucleic acid construct according to the second aspect of the invention or first and second, and optionally third and/or fourth, nucleic acid sequences as defined above.

There is also provided a set of vectors which comprises first and second, and optionally third and/or fourth, nucleic acid sequences as defined above.

The vector or set of vectors may be retroviral or lentiviral vector(s).

In a fourth aspect, there is provided a pharmaceutical composition comprising a plurality of cells according to the first aspect of the invention.

In a fifth aspect, there is provided a pharmaceutical composition according to the fourth aspect of the invention for use in treating and/or preventing a disease.

In a sixth aspect, there is provided method for treating and/or preventing a disease, which comprises the step of administering a pharmaceutical composition according to the fourth aspect of the invention to a subject.

The method may comprise the following steps:

- (i) isolation of a cell containing sample from a subject;
- (ii) transduction or transfection of the cells with a nucleic acid construct according to the second aspect of the invention, a vector or set of vectors according to the third aspect of the invention; and
- (iii) administering the cells from (ii) to the subject.

In a seventh aspect there is provided the use of a pharmaceutical composition according to the fourth aspect of the invention in the manufacture of a medicament for the treatment and/or prevention of a disease.

The disease may be cancer.

In an eighth aspect, there is provided a method for making a cell according to the first aspect of the invention, which comprises the step of introducing: a nucleic acid construct according to the second aspect of the invention, a vector or set of vectors according to the third aspect of the invention, into the cell.

The cell may be from a sample isolated from a subject.

In a first further aspect, the present invention also provides a fusion protein which comprises: (i) a ZAP70 or PTPN6 SH2 domain; and (ii) a heterologous domain.

The fusion protein may comprise a ZAP70 SH2 domain and an ITAM-containing domain. The ITAM-containing domain may be or comprise the endodomain of CD3-Zeta.

The fusion protein may comprise a PTPN6 SH2 domain and an ITIM-containing domain. The ITIM-containing domain may be or comprise the endodomain from PDCD1, BTLA4, LILRB1, LAIR1, CTLA4, KIR2DL1, KIR2DL4, KIR2DL5, KIR3DL1 or KIR3DL3.

The fusion protein may comprise a PTPN6 SH2 domain and fused to a ZAP70 kinase domain.

The fusion protein may comprise a ZAP70 SH2 domain fused to a PTPN6 kinase domain.

The fusion protein may comprise: (i) a ZAP70 or PTPN6 SH2 domain; and (ii) a heterologous signalling domain.

The heterologous signalling domain may be from a signalling molecule which is not usually activated by an ITAM containing receptor. The heterologous signalling domain may be or comprise the endodomain of CD28, 41BB or OX40. The heterologous signalling domain may be or comprise the endodomain of ICOS, CD27, BTLA, CD30, GITR or HVEM.

The fusion protein may comprise: (i) a ZAP70 or PTPN6 SH2 domain; and (ii) a kinase domain.

The kinase domain may be or comprise an AKT or JAK kinase domain.

The fusion protein may comprise: (i) a ZAP70 or PTPN6 SH2 domain; and (ii) a protease domain.



The protease domain may be or comprise Tobacco Etch Virus Protease (TeV).

In a second further aspect the present invention provides a truncated protein which comprises the ZAP70 SH2 domain but lacks the ZAP70 kinase domain.

In a third further aspect the present invention provides a truncated protein which comprises the PTPN6 SH2 domain but lacks the PTPN6 kinase domain.

The present invention also provides a signalling system comprising:

- (i) a receptor comprising an antigen-binding domain, a transmembrane domain and an intracellular signalling domain which comprises a CD3 zeta endodomain; and
- (ii) a fusion protein according to the first further aspect of the invention which comprises a ZAP70 SH2 domain; or a truncated protein according to the second further aspect of the invention;

wherein binding of antigen to the antigen-binding domain results in binding between the CD3 zeta endodomain and the fusion/truncated protein.

The present invention also provides a signalling system comprising:

- (i) a receptor comprising an antigen-binding domain, a transmembrane domain and an intracellular signalling domain which comprises a PTPN6 binding domain; and
- (ii) a fusion protein according to the first further aspect of the invention which comprises a PTPN6 SH2 domain; or a truncated protein according to the third further aspect of the invention

wherein binding of antigen to the antigen-binding domain results in binding between the PTPN6 binding domain and the fusion/truncated protein.

The receptor may be a T-cell receptor (TCR) or a chimeric antigen receptor (CAR).

In a fourth further aspect the present invention provides a nucleic acid which encodes a fusion protein according to the first further aspect of the present invention or a truncated protein according to the second or third further aspects of the present invention.

In a fifth further aspect the present invention provides a nucleic acid construct which comprises a nucleic acid sequence encoding a fusion protein which comprises (i) a ZAP70 or PTPN6 SH2 domain; and (ii) a protease domain (e.g. a TeV domain) and a nucleic acid sequence encoding a membrane tethered transcription factor which comprises:

- (i) a membrane tether;
- (ii) a protease recognition site; and
- (iii) a transcription factor.

In a sixth further aspect the present invention provides a nucleic acid construct which comprises

(a) a nucleic acid sequence encoding a fusion protein according to the first further aspect of the present invention which comprises a PTPN6 SH2 domain, or a truncated protein according to the third further aspect of the present invention; and

(b) a nucleic acid sequence encoding a receptor comprising an ITIM containing endodomain.

In a seventh further aspect the present invention provides a nucleic acid construct which comprises a nucleic acid sequence encoding a fusion protein which comprises (i) a ZAP70 or PTPN6 SH2 domain; and (ii) a protease domain (e.g. a TeV domain) and a nucleic acid sequence encoding a receptor which comprises a protease cleavage site.

In an eighth further aspect the present invention provides a nucleic acid construct which comprises:

(a) a nucleic acid sequence encoding a fusion protein which comprises (i) a PTPN6 SH2 domain; and (ii) a protease domain (e.g. a TeV domain);

(b) a nucleic acid sequence encoding a receptor which comprises a protease cleavage site; and

(c) a nucleic acid sequence encoding a receptor comprising an ITIM containing endodomain.

The receptor may be a T-cell receptor (TCR) or a chimeric antigen receptor (CAR).

Suitably, in the nucleic acid construct according to the eighth aspect of the present invention, the nucleic acid sequence (b) may be a T-cell receptor (TCR) or a chimeric antigen receptor (CAR) which comprises:

(i) a protease cleavage site between a transmembrane domain and an activating endodomain; or

(ii) an activating endodomain fused to an inhibitory endodomain via a protease cleavage site.

In a ninth further aspect the present invention provides a vector comprising a nucleic acid according to the fourth further aspect of the present invention or a nucleic acid construct according to any of fifth to the ninth further aspects of the present invention.

The vector may be a retroviral vector or a lentiviral vector.

In a tenth further aspect the present invention provides a cell comprising a fusion protein according to the first further aspect of the present invention or a truncated protein according to the second or third further aspects of the present invention.

In an eleventh further aspect the present invention provides a cell which comprises (a) a fusion protein according to the first further aspect of the present invention which comprises a PTPN6 SH2 domain, or a truncated protein according to the third further aspect of the present invention; and (b) a receptor comprising an ITIM containing endodomain.

The cell may be an immune cell, such as a T cell or a natural killer (NK) cell.

In a twelfth further aspect the present invention provides a cell which comprises a fusion protein which comprises (i) a ZAP70 or PTPN6 SH2 domain; and (ii) a protease domain(e.g. a TeV domain) and a receptor which comprises a protease cleavage site.

In a thirteenth further aspect the present invention provides a cell which comprises:

- (a) a fusion protein which comprises (i) a PTPN6 SH2 domain; and (ii) a protease domain (e.g. a TeV domain);
- (b) a receptor which comprises a protease cleavage site; and
- (c) a receptor comprising an ITIM containing endodomain.

The receptor may be a T-cell receptor (TCR) or a chimeric antigen receptor (CAR).

The receptor (b) may be a T-cell receptor (TCR) or a chimeric antigen receptor (CAR) which comprises:

- (i) a protease cleavage site between a transmembrane domain and an activating endodomain; or
- (ii) an activating endodomain fused to an inhibitory endodomain via a protease cleavage site.

In a fourteenth further aspect the present invention provides a cell which comprises a nucleic acid according to the fourth further aspect of the present invention or a nucleic acid construct according to any of the fifth to the ninth further aspects of the present invention.

In a fifteenth further aspect the present invention provides a pharmaceutical composition comprising a plurality of cells according to any of the tenth to the fourteenth further aspects of the present invention.

In a sixteenth further aspect the present invention provides a pharmaceutical composition according to the fifteenth further aspect of the present invention for use in treating and/or preventing a disease.

In a seventeenth further aspect the present invention relates to a method for treating and/or preventing a disease, which comprises the step of administering a pharmaceutical composition according the fifteenth further aspect to a subject.

The method may comprise the following steps:

- (i) isolation of a T cell or NK cell containing sample from a subject;
- (ii) transduction or transfection of the T cells or NK cells with a nucleic acid according to any of the fourth to the ninth further aspects of the present invention or a vector according to the tenth further aspect of the present invention; and
- (iii) administering the T cells or NK cells from (ii) to the subject.

In an eighteenth further aspect the present invention relates to the use of a pharmaceutical composition according to the fifteenth further aspect of the present invention in the manufacture of a medicament for the treatment and/or prevention of a disease.

The disease may be cancer.

In a nineteenth further aspect the present invention provides a kit which comprises a nucleic acid according to the fourth further aspect of the present invention or a nucleic acid construct according to any of the fifth to the eighth further aspects of the present invention or a vector according to the ninth further aspect of the present invention.

In a twentieth further aspect the present invention relates to a kit which comprises a cell according to any of the tenth to the fourteenth further aspects of the present invention.

In a twenty-first further aspect the present invention relates to a method for making a cell according to any of the tenth to the fourteenth further aspects of the present invention, which comprises the step of introducing: a nucleic acid sequence according to any of the fourth to the eighth further aspects of the present invention or the vector according to the ninth further aspect of the present invention, into the cell.

The cell may be from a sample isolated from a subject.

Yet further aspect of the invention are summarised in the following paragraphs:

A1. A truncated protein which comprises an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based activation motif (ITAM) but lacks a kinase domain.

A2. A truncated protein according to paragraph A1, which comprises the ZAP70 SH2 domain but lacks the ZAP70 kinase domain.

B1. A truncated protein which comprises an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based inhibition motif (ITIM) but lacks a phosphatase domain.

B2. A truncated protein according to paragraph B1, which comprises the PTPN6 SH2 domain but lacks the PTPN6 phosphatase domain.

B3. A truncated protein according to paragraph B1, which comprises the SHP-2 SH2 domain but lacks the SHP-2 phosphatase domain.

C1. A fusion protein which comprises (i) an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based activation motif (ITAM); and (ii) a phosphatase domain.

C2. A fusion protein according to paragraph C1, which comprises a ZAP70 SH2 domain.

C3. A fusion protein according to paragraph C1 or C2, which comprises a PTPN6 or SHP-2 phosphatase domain.

- D1. A fusion protein which comprises (i) an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based inhibition motif (ITIM); and (ii) a kinase domain.
- D2. A fusion protein according to paragraph D1, which comprises an SH2 domain from PTPN6 or SHP-2.
- D3. A fusion protein according to paragraph D1 or D2, which comprises a Zap70 kinase domain
- D4. A fusion protein according to paragraph D1 or D2, which comprises an AKT or JAK kinase domain.
- E1. A fusion protein which comprises (i) an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based activation motif (ITAM) or from a protein which binds a phosphorylated immunoreceptor tyrosine-based inhibition motif (ITIM); and (ii) a heterologous signalling domain.
- E2. A fusion protein according to paragraph E1, which comprises an SH2 domain from ZAP70, PTPN6 or SHP-2.
- E3. A fusion protein according to paragraph E1 or E2, wherein the heterologous signalling domain is from a signalling molecule which is not usually activated by an ITAM or ITIM containing receptor.
- E4. A fusion protein according to paragraph E1, E2 or E3, wherein the heterologous signalling domain is a co-stimulatory domain.
- E5. A fusion protein according to paragraph E4 which comprises a CD28, OX40 or 41BB co-stimulatory domain.
- E6. A fusion protein according to paragraph E1, E2 or E3, wherein the co-stimulatory domain is an inhibitory domain.
- E7. A fusion protein according to paragraph E6, wherein the inhibitory domain comprises the endodomain of CD148 or CD45.

E8. A fusion protein according to paragraph E6, wherein the heterologous signalling domain is or comprises the endodomain of ICOS, CD27, BTLA, CD30, GITR or HVEM.

F1. A fusion protein which comprises (i) an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based activation motif (ITAM); and (ii) an ITAM-containing domain.

F2. A fusion protein according to paragraph F1, which comprises a ZAP70 SH2 domain.

F3. A fusion protein according to paragraph F1 or F2, wherein the ITAM-containing domain is or comprises the endodomain of CD3-Zeta.

G1. A fusion protein which comprises (i) an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based inhibition motif (ITIM); and (ii) an ITIM-containing domain.

G2. A fusion protein according to paragraph G1, which comprises an SH2 domain from PTPN6 or SHP-2.

G3. A fusion protein according to paragraph G1 or G2, wherein the ITIM-containing domain is or comprises the endodomain from PD1, PDCD1, BTLA4, LILRB1, LAIR1, CTLA4, KIR2DL1, KIR2DL4, KIR2DL5, KIR3DL1 or KIR3DL3.

H1. A fusion protein which comprises (i) an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based inhibition motif (ITIM) or from a protein which binds a phosphorylated immunoreceptor tyrosine-based inhibition motif (ITIM); and (ii) a protease domain.

H2. A fusion protein according to paragraph H1, which comprises an SH2 domain from ZAP70, PTPN6 or SHP-2.

H3. A fusion protein according to paragraph H1 or H2, wherein the protease domain is or comprises Tobacco Etch Virus Protease (TeV).

I1. A nucleic acid sequence which encodes a truncated protein according to any of paragraphs A or B, or a fusion protein according to any of paragraphs C, D, E, F, G or H.

- J1. A nucleic acid construct which comprises a nucleic acid sequence according to paragraph I and a nucleic acid sequence encoding a chimeric antigen receptor
- J2. A nucleic acid construct which comprises a nucleic acid sequence according to paragraph I and a nucleic acid sequence encoding a membrane-tethered transcription factor having a protease cleavage site.
- J3. A nucleic acid construct which comprises a nucleic acid sequence according to paragraph I and a nucleic acid sequence encoding a target CAR which comprises an intracellular protease cleavage site.
- K1. A vector comprising a nucleic acid sequence according to paragraph I or a nucleic acid construct according to paragraphs J.
- L1. A cell which comprises a truncated protein according to any of paragraphs A or B, or a fusion protein according to any of paragraphs C, D, E, F, G or H.
- M1. A cell which comprises a fusion protein according to any of paragraphs H and a membrane-tethered transcription factor with a protease cleavage site.
- M2. A cell according to paragraph M1, wherein cleavage at the protease cleavage site releases the transcription factor leading to increased expression of a target gene.
- M3. A cell according to paragraph M2, wherein the target gene encodes a cytokine.
- M4. A cell according to paragraph M3, wherein the cytokine is selected from the following group: IL-2, IL-7, IL-15 and IL-12.
- M5. A cell which comprises a fusion protein according to any of paragraphs H and a target receptor (CAR) which comprises an intracellular protease cleavage site.
- M6. A cell according to claim M5, wherein the target CAR comprises an activatory or co-stimulatory endodomain and cleavage at the protease cleavage site removes the endodomain from the target CAR.



M7. A cell according to claim M5, wherein the target CAR comprises an inhibitory endodomain and cleavage at the protease cleavage site removes the inhibitory endodomain from the target CAR.

M8. A cell according to paragraph M7, wherein the inhibitory endodomain comprises a CD148 or CD45 endodomain.

M9. A cell which comprises a fusion protein according to any of paragraphs H and two CARs: an activating CAR comprising an ITAM-containing endodomain; and a target CAR as defined in any of paragraphs M5 to M8.

M10. A cell which comprises a fusion protein according to any of paragraphs H and two CARs: an inhibitory CAR comprising an ITIM-containing endodomain; and a target CAR as defined in any of paragraphs M5 to M8.

The aspects of the present invention described above enable T cell signalling pathways to be modulated and altered by, for example, the mechanisms described in Table 1. Table 1 : Application of signal modulation

<b>Type</b>	<b>Mechanism</b>	<b>Application</b>
<b>Blocking signal</b>	ZAP70, SHP-2 or PTPN6 are truncated - keeping SH2 domain alone	Truncated ZAP70, SHP-2 or PTPN6 competes with wild-type full-length ZAP70, SHP-2 or PTPN6. Since this does not signal, it will inhibit activation. Applications include, for example, with ZAP70 when a very strong activation signal is deleterious, or with PTPN6 or SHP-2 when the effect of an inhibitory signal e.g. PD1/PDL1 needs to be reduced.
<b>Crosswire signal</b>	ZAP70 SH2 fused to PTPN6/SHP-2 phosphatase, or PTPN6/SHP-2 SH2 fused to ZAP70 kinase for instance.	In this embodiment, a ZAP70 SH2 is fused to the phosphatase from PTPN6/SHP-2, or the other way round, i.e. the PTPN6/SHP-2 SH2 domain is fused with the ZAP70 kinase domain. When the T-cell receives an inhibitory signal, it interprets it as an excitatory signal or vice versa.
<b>Amplified signal</b>	ZAP70 fused to further ITAM domains or PTPN6/SHP-2 fused to further ITIM domains.	A single phospho-ITAM or ITIM leads to a concatenation of ITAMs or ITIMs leading to augmented signal or

		increased sensitivity to antigen.
<b>Bypass signal</b>	ZAP70 SH2 or PTPN6/SHP-2 SH2 fused with e.g. CD28, 41BB endodomains or AKT kinase domain, a JAK kinase domain etc.	In this embodiment, a “non-physiological” signal can be attached to the ITAM/ITM pathway. In this way an ITAM/ITIM signal can lead to a co-stimulatory signal, or a signal such as AKT or a cytokine type signal
<b>Transcriptional signal</b>	ZAP70 SH2 or PTPN6/SHP-2 SH2 fused to protease domain along with co-expression of a membrane tethered transcription factor with a liberating protease cleavage site	In this embodiment, a transcriptional signal is transmitted upon immune receptor activation or inhibition. Such a signal can, for example, result in the expression of a particular cytokine upon T-cell activation or inhibition.
<b>Castration signal</b>	ZAP70 SH2 domain or PTPN6/SHP-2 SH2 domain fused to a protease domain; a reciprocal receptor has a protease cleavage site	In this embodiment, activation or inhibition of a receptor results in inhibition or activation of another receptor

## DESCRIPTION OF THE FIGURES

**Figure 1 (a)** – Diagram of immediate T-cell activation pathways. T-cell receptor activation results in phosphorylation of ITAMs. Phosphorylated ITAMs are recognized by the ZAP70 SH2 domains. Upon recognition, ZAP70 is recruited to the juxta-membrane region and its kinase domain subsequently phosphorylates LAT. Phosphorylated LAT is subsequently recognized by the SH2 domains of GRAP, GRB2 and PLC- $\gamma$ . (b) – Diagram of immediate T-cell inhibition pathways. Activation of an inhibitory immune-receptor such as PD1 results in phosphorylation of ITIM domains. These are recognized by the SH2 domains of PTPN6. Upon recognition, PTPN6 is recruited to the juxta-membrane region and its phosphatase domain subsequently de-phosphorylates ITAM domains inhibiting immune activation.

**Figure 2** – Diagram of a blocking signal system - a) A truncated ZAP70 which does not comprise a kinase domain is over-expressed. Consequently, it competes with full-length ZAP70 for ITAMs and reduces ITAM signalling. (b) A truncated PTPN6 which does not comprise a phosphatase domain is over-expressed, competing for full-length PTPN6 reducing ITIM signalling.

**Figure 3** – Diagram of a crosswire signal system: (a) ZAP70 SH2 is fused to PTPN6 phosphatase, hence acts to dampen ITAM phosphorylation; (b) PTPN6 SH2 is fused to ZAP70 kinase resulting in paradoxical activation in response to an inhibitory signal.

**Figure 4** – Diagram of an amplified signal system: (a) full-length ZAP70 has a CD3 Zeta endodomain attached to its amino terminus so a cascade of ITAMs assembles. (b) full-length PTPN6 has PD1 endodomain attached to its amino terminus so a cascade of ITIMs assembles.

**Figure 5** – Diagram of examples of a bypass signal system: (a) ZAP70 fused with CD28 endodomain; (b) ZAP70 fused with 41BB endodomain; (c) ZAP70 fused with AKT kinase; (d) PTPN6 SH2 domain is fused with 41BB endodomain

**Figure 6** – Diagram of an illustrative transcriptional signal system: a) A ZAP-TeV fusion is co-expressed with a membrane-tethered transcription factor which can be released from the membrane by cleavage of its TeV recognition motif. This is shown co-expressed with a CD19 CAR. Hence, upon recognition of CD19 on a target cell, the T-cell becomes activated and in addition, the transcription factor becomes active. (b) An alternative system using a PTPN6-TeV fusion instead. Here the CAR consists of an ITIM-bearing endodomain. Hence, upon recognition of CD19 by the CAR, the transcription factor becomes active but this is independent of T-cell activation.

**Figure 7** – Diagram of a castration signal system: two CARs are shown – one which recognizes CD19 and is activating and one which recognizes CD33 and is inhibiting - these specificities are for illustration only (a) AND NOT signal castration; here an SH2-TeV fusion protein is recruited to activated ITIM CAR upon its activation. This results in cleavage of ITAMs from an activating CAR which is constructed such that a TeV cleavage site connects the transmembrane-domain to the ITAM domain. Hence, the activating CAR is inhibited. (b) AND signal castration: Here, an SH2-TeV fusion protein is recruited to an ITIM CAR upon its activation. This results in release of a phosphatase domain from an activating CAR which is constructed so that a phosphatase is connected to its carboxy-terminus via a TeV cleavage domain. This results in release of constitutive inhibition, allowing the CAR to activate in the presence of cognate antigen.

**Figure 8** – Several fusions of different SH2 domains and AKT kinase domain were constructed: ZAP-AKT, GRAP-AKT, GRB-AKT and PLC- $\gamma$ .

**Figure 9** - (a) Phospho-AKT staining of T-cells transduced with the different SH2/AKT fusions with and without activation with the mitogenic antibody OKT3. (b) Phospho-AKT staining of T-cells transduced with ZAP-AKT fusion, an improved ZAP-AKT fusion where ZAP and AKT are connected via a flexible linker, and a control ZAP-AKT where R190K substitution removes ability of ZAP to bind ITAMs. T-cells were either stimulated with OKT3 or not-stimulated with OKT3. The facs plots are overlaid over that of non-transduced T-cells.

**Figure 10** - (a) Phospho-AKT blot of T-cells activated with increasing amounts of OKT3. (b) Microscopy of ZAP-AKT or control T-cells unstimulated, stimulated with just OKT3 or stimulated with both OKT3 and IL-2. ZAP-AKT T-cells stimulated with just OKT3 resemble non-transduced T-cells stimulated with both OKT3 and IL2.

**Figure 11** - (a) Implementation of direct TeV transcriptional switch. A CD19 CAR's endodomain is replaced with the TeV protease. A membrane tethered VP16/GAL4 transcription factor is also co-expressed. A Luciferase reporter detects VP16/GAL5 activity. (b) Implementation with ZAP-TeV. A standard CD19 CAR is co-expressed with ZAP-TeV fusion along with the membrane tethered transcription factor.

**Figure 12** - Activity of ZAP-TeV based transcriptional switches and control expressing T-cells after exposure to CD19 negative (left), or CD19 positive (right) targets. Activity is measured by light output after adding Luciferase. In order the conditions tested are: (a) aCD19 CAR co-expressed with ZAP-TeV; (b) aCD19 CAR co-expressed with inactive (R190K); (c) aCD19 CAR co-expressed with ZAP-TeV and the membrane tethered transcription factor; (d) aCD19 CAR co-expressed with inactive (R190K) ZAP-TEV co-expressed with the membrane tethered transcription factor; (e) aCD19 CAR / TeV fusion co-expressed with the membrane-tethered transcription factor; (f) constitutively active GAL4/VP16 transcription factor.

**Figure 13** - (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 14** - Illustrative protein sequences of the present invention

**Figure 15** – PD-1 signal blockade using truncated SHP-1 (PTPN6) or truncated SHP-2  
PBMC cells were cotransduced with PD1 and either CAR alone (FMC63); or a bicistronic construct containing CAR and truncated SHP-1, or CAR and truncated SHP-2. These cells were co-cultured for 48 hours with SupT1 cells transduced with CD19, PDL1 or both and IFNγ release measured by ELISA.

**Figure 16** – PD-1 signal hijack using a fusion of SHP-2 SH2 domains and Zap70 kinase

PBMC cells were cotransduced with PD1 and either CAR alone (FMC63); or a bicistronic construct containing CAR and a fusion protein comprising SHP-2 SH2 domains and the ZAP70 kinase. These cells were co-cultured in a 1:1 ratio for 24 hours with SupT1 cells transduced with CD19 or PDL1. IFN $\gamma$  release was measured by ELISA (A) and killing of SupT1 cells was quantified by FACS (B).

## DETAILED DESCRIPTION

### PROTEIN

The present invention provides a truncated protein which comprises an SH2 domain.

The present invention also provides a fusion protein comprising (i) an SH2 domain; and (ii) a heterologous domain.

The SH2 domain may be from a protein which binds a phosphorylated immunoreceptor tyrosine-based activation motif (ITAM) or from a protein which binds a phosphorylated immunoreceptor tyrosine-based inhibition motif (ITIM).

An example of a protein which binds an ITAM is ZAP70. Examples of proteins which bind ITIMs include PTPN6 and SHP-2

The fusion protein of the invention therefore comprises an SH2 domain and at least one further domain which is not present in a wild-type protein from which the SH2 domain was derived.

### SRC HOMOLOGY 2 (SH2) DOMAIN

Intracellular signalling pathways are initiated and controlled by the reversible post-translational modification of proteins including phosphorylation, ubiquitinylation and acetylation.

SH2 domains are modular protein domains that serve as adaptors and mediate protein-protein interactions by binding to phosphorylated peptides in their respective protein binding partners, often cell surface receptors. SH2 domains typically bind a phosphorylated tyrosine residue in the context of a longer peptide motif within a target protein, and SH2 domains represent the largest class of known pTyr-recognition domains

Although SH2 domains lack any intrinsic catalytic activity they are frequently coupled to independent catalytic domains and thus, in response to a specific input signal, serve to localize

these catalytic domains so particular sub-cellular locations or to the vicinity of appropriate substrates, activators or inhibitors. In addition SH2 domains can also be found linked to adaptor protein domains and so can serve in the formation of large multi-protein complexes.

#### ZETA-CHAIN-ASSOCIATED PROTEIN KINASE 70 (ZAP70)

ZAP70 is a protein normally expressed near the surface membrane of T cells and natural killer cells. It is part of the T cell receptor (TCR), and plays a critical role in T-cell signalling. Its molecular weight is 70 kDa, and is composed of 2 N-terminal SH2 domains and a C-terminal kinase domain. It is a member of the protein-tyrosine kinase family.

The earliest step in T cell activation is the recognition of a peptide MHC-complex on the target cell by the TCR. This initial event causes the close association of Lck kinase with the cytoplasmic tail of CD3-zeta in the TCR complex. Lck then phosphorylates tyrosine residues in the cytoplasmic tail of CD3-zeta which allows the recruitment of ZAP70. ZAP70 is an SH2 containing kinase that plays a pivotal role in T cell activation following engagement of the TCR. Tandem SH2 domains in ZAP70 bind to the phosphorylated CD3 resulting in ZAP70 being phosphorylated and activated by Lck or by other ZAP70 molecules in trans. Active ZAP70 is then able to phosphorylate downstream membrane proteins, key among them the linker of activated T cells (LAT) protein. LAT is a scaffold protein and its phosphorylation on multiple residues allows it to interact with several other SH2 domain-containing proteins including Grb2, PLC-g and Grap which recognize the phosphorylated peptides in LAT and transmit the T cell activation signal downstream ultimately resulting in a range of T cell responses. This process is summarized in Figure 1.

Human ZAP70 protein has the UniProtKB accession number P43403. This sequence is 619 amino acids in length and is shown as SEQ ID NO: 1.

#### ZAP70 amino acid sequence (SEQ ID NO: 1)

```
MPDPAAHL PFFYGSISR AEEHLKLAGMADGLFLLRQCL RSLGGYVLSLVHDVRFHHFP IERQLNGTYA
IAGGKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQPGVFDCLRDAMVRDYVRQTWKLEGEALEQ
AIIISQAPQVEKLIATTAHERMPWYHSSLTREEAERKLYSGAQTGDKFLLRPRKEQGTYSLSLIYGKTVYH
YLISQDKAGKYCIPEGTKFDTLWQLVEYLLKLKADGLIYCLKEACPNSSASNASGAAAPTLPAPSTLTTHP
QRRIDTLNSDGYTPEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKFLKRDNLLIADIELGCGNFG
SVRQGVYRMRKKQIDVAIKVLKQGTEKADTEEMMREAQIMHQLDNPYIVRLIGVCQAEALMLVMEMAGGG
PLHKFLVGKREEIPVSNVAELLHQVSMGMKYLEEKNFVHRDLAARNVLLVNRHYAKISDFGLSKALGADD
SYYTARSAGKWPLKWYAPECINFRKFSSRSDVWSYGVMTWEALSYGQKPKMKMGPEVMAFIEQGKRMEC
PPECPELYALMSDCWIYKWEDRPDFTLVEQRM RACYYS LASKVEGPPGSTQKAEAAACA
```

The fusion protein of the invention may comprise a ZAP70 SH2 domain. The truncated protein of the invention may comprise or consist of a ZAP70 SH2 domain. In this respect, the fusion or truncated protein may comprise or consist of the sequence shown as SEQ ID NO: 2.

ZAP70 complete SH2 domain (SEQ ID NO: 2)

MPDPAAHLPPFFYGSISRAEAEHLKLAGMADGLFLLRQCLRSLSGGYVLSLVHDVRFHHFPIERQLNGTYA  
IAGGKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQPGVFDCLRDAMVRDYVRQTWKLEGEALEQ  
AIIISQAPQVEKLIATTAHERMPWYHSSLTREEAERKLYSGAQTDGKFLLRPRKEQGTYSLSIYGKTVYH  
YLISQDKAGKYCIEPGTKFDTLWQLVEYLKLDGLIYCLKEACPNSSASNASGAAAPTLPAPSTLTHP

ZAP70 has two SH2 domains at the N-terminal end of the sequence, at residues 10-102 and 163-254 of the sequence shown as SEQ ID No. 1. The truncated protein or fusion protein of the invention may therefor comprise one or both of the sequences shown as SEQ ID No. 3 and 4.

ZAP70 SH2 1 (SEQ ID NO: 3)

FFYGSISRAEAEHLKLAGMADGLFLLRQCLRSLSGGYVLSLVHDVRFHHFPIERQLNGTYA  
IAGGKAHCGPAELCEFYSRDPDGLPCNLRKPC

ZAP70 SH2 2 (SEQ ID NO: 4)

WYHSSLTREEAERKLYSGAQTDGKFLLRPRKEQGTYSLSIYGKTVYHYLISQDKAGKYCIEPGTKFDTL  
WQLVEYLKLDGLIYCLKEAC

The fusion protein may comprise a variant of SEQ ID NO: 2, 3 or 4 having at least 80, 85, 90, 95, 98 or 99% sequence identity, provided that the variant sequence is a SH2 domain sequence has the required properties. In other words, the variant sequence should be capable of binding to the phosphorylated tyrosine residues in the cytoplasmic tail of CD3-zeta which allow the recruitment of ZAP70.

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](http://www.ebi.ac.uk/Tools/psa/emboss_needle/nucleotide.html)).

In certain embodiments, the fusion protein may comprise the ZAP70 SH2 domain and the ZAP70 kinase domain. For example, the fusion protein may comprise the sequence shown as SEQ ID NO: 1 or a variant thereof having at least 80, 85, 90, 95, 98 or 99% sequence identity.

#### TYROSINE-PROTEIN PHOSPHATASE NON-RECEPTOR TYPE 6 (PTPN6)

PTPN6 is also known as Src homology region 2 domain-containing phosphatase-1 (SHP-1). It is a member of the protein tyrosine phosphatase family.

The N-terminal region of PTPN6 contains two tandem SH2 domains which mediate the interaction of PTPN6 and its substrates. The C-terminal region contains a tyrosine-protein phosphatase domain.

PTPN6 is capable of binding to, and propagating signals from, a number of inhibitory immune receptors or ITIM containing receptors. Examples of such receptors include, but are not limited to, PD1, PDCD1, BTLA4, LILRB1, LAIR1, CTLA4, KIR2DL1, KIR2DL4, KIR2DL5, KIR3DL1 and KIR3DL3.

Human PTPN6 protein has the UniProtKB accession number P29350. This sequence is 595 amino acids in length and is shown as SEQ ID NO: 5.

#### PTPN6 amino acid sequence (SEQ ID NO: 5)

```
MVRWFHRDL SGLDAETLLKGRGVHGSFLARPSRKNQGDFSLSVRVGDQVTHIRIQNSGDFYDLYGGEKFA
TLTELVEYYTQQQGV LQDRDGTIIHLKYP LNCSDPTSERWYHGHMSGGQAETLLQAKGEPWTF LVRRESLS
QPGDFVLSVLS DQPKAGPGSPLRVTHIKVMCEGGRYTVGGLET FDSLTDLVEHF KKTGIEEASGAFVYLR
QPYATRVNAADIENRVLELNKKQESED TAKAGFWEEFESLQKQEVKNLHQRLLEGQRPENKGKNRYKNIL
PFDHSRVILQGRDSNIPGSDYINANYIKNQL LGPDENAKTYIASQG CLEATVNDFWQMAWQENSRVIVMT
TREVEKGRNKCVPYWPEVGMQRAYGPYSVTNCGEHDTTEYKLRTLQVSPLDNGDLIREIWHYQYLSWPDH
GVPSEPGGVLSFLDQINQRQESLPHAGPIIVHCSAGIGRTGTIIVIDMLMENISTKGLDCDIDIQKTIQM
VRAQRSGMVQTEAQYKFIYVAIAQFIETTKKKLEVLQSQKGQSEYGNITYPPAMKNAHAKASRTSSKHK
EDVYENLHTKNKREEKVKKQRSADKEKSKGSLKRK
```

The fusion protein of the invention may comprise a PTPN6 SH2 domain. The truncated protein of the invention may comprise or consist of a PTPN6 SH2 domain. In this respect, the fusion or truncated protein may comprise or consist of the sequence shown as SEQ ID NO: 6.

#### PTPN6 SH2 complete domain (SEQ ID NO: 6)



MVRWFHRDL SGLDAETLLKGRGVHGSFLARPSRKNQGDFSLSVRVGDQVTHIRIQNSGDFYDLYGGEKFA  
 TLTELVEYYTQQQGV LQDRDGTIIHLKYPLNCSDPTSERWYHGHMSGGQAETLLQAKGEPWTF LVRSL S  
 QPGDFVLSVLS DQPKAGPGSPLRVTHIKVMCEGGRYTVGGLET FDSLTDLVEHFKKTGIEEASGAFVYLR  
 QPYY

PTPN6 has two SH2 domains at the N-terminal end of the sequence, at residues 4-100 and 110-213 of the sequence shown as SEQ ID No. 5. The truncated protein or fusion protein of the invention may therefor comprise one or both of the sequences shown as SEQ ID No. 3 and 4.

#### PTPN6 SH2 1 (SEQ ID NO: 7)

WFHRDL SGLDAETLLKGRGVHGSFLARPSRKNQGDFSLSVRVGDQVTHIRIQNSGDFYDLYGGEKFATLT  
 ELVEYYTQQQGV LQDRDGTIIHLKYPL

#### PTPN6 SH2 2 (SEQ ID No. 8)

WYHGHMSGGQAETLLQAKGEPWTF LVRSL S QPGDFVLSVLS DQPKAGPGSPLRVTHIKVMCEGGRYTVG  
 GLET FDSLTDLVEHFKKTGIEEASGAFVYLRQPY

The fusion protein may comprise a variant of SEQ ID NO: 6, 7 or 8 having at least 80, 85, 90, 95, 98 or 99% sequence identity, provided that the variant sequence is a SH2 domain sequence has the required properties. In other words, the variant sequence should be capable of binding to the phosphorylated tyrosine residues in the cytoplasmic tail of at least one of PD1, PDCD1, BTLA4, LILRB1, LAIR1, CTLA4, KIR2DL1, KIR2DL4, KIR2DL5, KIR3DL1 or KIR3DL3 which allow the recruitment of PTPN6.

In certain embodiments, the fusion protein may comprise the PTPN6 SH2 domain and the PTPN6 phosphatase domain. For example, the fusion protein may comprise the sequence shown as SEQ ID NO: 5 or a variant thereof having at least 80, 85, 90, 95, 98 or 99% sequence identity.

#### SHP-2

SHP-2, also known as PTPN11, PTP-1D and PTP-2C is a member of the protein tyrosine phosphatase (PTP) family. Like PTPN6, SHP-2 has a domain structure that consists of two tandem SH2 domains in its N-terminus followed by a protein tyrosine phosphatase (PTP) domain. In the inactive state, the N-terminal SH2 domain binds the PTP domain and blocks access of potential substrates to the active site. Thus, SHP-2 is auto-inhibited. Upon binding to target phospho-tyrosyl residues, the N-terminal SH2 domain is released from the PTP domain, catalytically activating the enzyme by relieving the auto-inhibition.

Human SHP-2 has the UniProtKB accession number P35235-1. This sequence is 597 amino acids in length and is shown as SEQ ID NO: 9.

**SHP-2 amino acid sequence (SEQ ID NO: 9)**

MTSRWFHPNITGVEAENLLLTRGVDGSFLARPSKSNPGDFTLSVRRNGAVTHIKIQNTGDYYDLYGGEK  
FATLAELVQYYMEHHGQLKEKNGDVIELKYPLNCADPTSERWFHGHLSGKEAEKLLTEKGKHGSFLVRES  
QSHPGDFVLSVRTGDDKGESNDGKSKVTHVMIRCQELKYDVGGGERFDSLTDLVEHYKKNPMVETLGTVL  
QLKQPLNTRINAAEIESRVRELSKLAETTDKVKQGFWEFETLQQQECKLLYSRKEGQRQENKNKNRYK  
NILPFDHTRVVLHDGDPNEPVSDYINANIIMPEFETKCNNSPKPSYIATQGCLQNTVNDFWRMVVFQENS  
RVIVMTTKEVERGKSKCVKYWPDEYALKEYGVMVRNVKESAAHDYTLRELKLSKVGQALLQGNTERTVW  
QYHFRTWPDHGVPSDPGGVLDLFLEEVHHKQESIVDAGPVVVHCSAGIGRTGTFIVIDILIDIIREKGVDC  
DIDVPKTIQMVRSQRSGMVQTEAQYRFIYMAVQHYIETLQRRIEEEQKSKRKGHEYTNIKYSLVDQTS  
QSPPLPPCTPTPPCAEMREDSARVYENVGLMQQQRFR

The fusion protein of the invention may comprise a SHP-2 SH2 domain. The truncated protein of the invention may comprise or consist of a SHP-2 SH2 domain. In this respect, the fusion or truncated protein may comprise or consist of the first SH2 domain of SHP-2, for example comprising amino acids 6-102 of SEQ ID NO. 9 or the second SH2 domain of SHP-2, for example comprising amino acids 112-216 of SHP-2. The fusion or truncated protein may comprise or consist of the sequence shown as SEQ ID NO: 10, 11 or 12.

**SHP-2 first SH2 domain (SEQ ID NO: 10)**

WFHPNITGVEAENLLLTRGVDGSFLARPSKSNPGDFTLSVRRNGAVTHIKIQNTGDYYDLYGGEKFATLA  
ELVQYYMEHHGQLKEKNGDVIELKYPL

**SHP-2 second SH2 domain (SEQ ID No. 11)**

WFHGHLSGKEAEKLLTEKGKHGSFLVRESQSHPGDFVLSVRTGDDKGESNDGKSKVTHVMIRCQELKYDV  
GGGERFDSLTDLVEHYKKNPMVETLGTVLQLKQPL

**SHP-2 both SH2 domains (SEQ ID No. 12)**

WFHPNITGVEAENLLLTRGVDGSFLARPSKSNPGDFTLSVRRNGAVTHIKIQNTGDYYDLYGGEKFATLA  
ELVQYYMEHHGQLKEKNGDVIELKYPLNCADPTSERWFHGHLSGKEAEKLLTEKGKHGSFLVRESQSHPG  
DFVLSVRTGDDKGESNDGKSKVTHVMIRCQELKYDVGGGERFDSLTDLVEHYKKNPMVETLGTVLQLKQPL

The fusion protein may comprise a variant of SEQ ID NO: 10, 11 or 12 having at least 80, 85, 90, 95, 98 or 99% sequence identity, provided that the variant sequence is a SH2 domain sequence capable of binding an ITIM-containing domain. For example, the variant sequence

may be capable of binding to the phosphorylated tyrosine residues in the cytoplasmic tail of PD1, PDCD1, BTLA4, LILRB1, LAIR1, CTLA4, KIR2DL1, KIR2DL4, KIR2DL5, KIR3DL1 or KIR3DL3.

## HETEROLOGOUS DOMAIN

As used herein, the term 'heterologous domain' refers to any protein domain which is not present in:

- i) wild type ZAP70 (see SEQ ID NO: 1) for fusion proteins comprising a ZAP70 SH2 domain;
- ii) wild type PTPN6 (see SEQ ID NO: 5) for fusion proteins comprising a PTPN6 SH2 domain; or
- iii) wild-type SHP-2 (see SEQ ID No. 9) for fusion proteins comprising a SHP-2 SH2 domain.

The heterologous domain may be or be derivable from (e.g. part of) a different protein from ZAP70, SHP-2 or PTPN6.

Alternatively the fusion protein may comprise a fusion of ZAP70 SH2 domain and a domain from PTPN6, such as the PTPN6 kinase domain. By the same token the fusion protein may comprise a fusion of PTPN6 SH2 domain and a domain from ZAP70, such as the ZAP70 kinase domain.

## AMPLIFIED SIGNAL

The present invention provides a fusion protein which comprises: an SH2 domain from an ITAM-binding protein; and an ITAM-containing domain.

The present invention also provide a fusion protein which comprises: an SH2 domain from an ITIM-binding protein; and an ITIM-containing domain.

These "amplified" signalling molecules will amplify an excitatory or inhibitory signal inside an immune cell such as a T cell.

As shown in Figure 4, the presence of such molecules will lead to a concatenation of either ITAMs or ITIMs leading to an augmented activatory or inhibitory signal, respectively.

Amplification of an activatory signal is useful in situations where it is desirable to increase the sensitivity of the immune cell (such as a CAR-T cell) to antigen. This may be the case when, for example, the target antigen is expressed at low levels on the target cells.

Amplification of an inhibitory systems in situations where it is desirable to reduce or prevent T cell activation. WO2015/075469 describes a panel of “logic gate” 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 A and B). The “AND NOT gate” described in this application comprises a pair of CARs such that the T cell triggers only when antigen A but not antigen B is present on the target cell. In this AND NOT gate, one CAR (recognising antigen A) has an activating endodomain comprising an ITAM, whereas the other CAR (recognising antigen B) has an inhibitory endodomain which may comprise an ITIM. In the presence of antigen A alone, the presence of unligated inhibitory CAR is insufficient to prevent T cell activation, so activation occurs. However, in the presence of both antigens, areas of membrane form with high concentrations of both activatory and inhibitory CARs. Since both endodomains are concentrated, T-cell activation is prevented or reduced.

Amplification of the inhibitory signal using an amplified signalling molecule of the present invention could be used in an AND gate to reduce or remove any residual signalling which occurs in the presence of both antigens i.e. from incomplete inhibition of the activatory CAR by the inhibitory CAR.

#### ITAM-CONTAINING DOMAIN

In one embodiment, the fusion protein comprises a ZAP70 SH2 domain and an immunoreceptor tyrosine-based activation motif (ITAM)-containing domain.

A fusion of full-length ZAP70 with an ITAM containing domain results in a structure which amplifies an activating immune signal. Here, the fusion protein is recruited to a phospho-ITAM immune-receptor endodomain. ZAP70 functions normally to propagate the signal but also provides another set of ITAMs which become phosphorylated and recruit more ZAP70. This may be useful to increase signal strength and may increase sensitivity to low-density antigens, for example. In some embodiments, the fusion may include only the ZAP70 SH2 domain with an ITAM containing endodomain (e.g. the fusion does not contain a ZAP70 kinase domain). In other embodiments, the ratio of ZAP70 catalytic domains (kinase domains) with ITAMs may be varied to affect the kinetics of activation in response to dynamics of the activating receptor interactions with cognate target.

An ITAM is a conserved sequence of four amino acids that is repeated twice in the cytoplasmic tails of certain cell surface proteins of the immune system. The motif contains a tyrosine separated from a leucine or isoleucine by any two other amino acids, giving the signature YxxL/I. Two of these signatures are typically separated by between 6 and 8 amino acids in the tail of the molecule (YxxL/Ix(6-8)YxxL/I).

ITAMs are important for signal transduction in immune cells. Hence, they are found in the tails of important cell signalling molecules such as the CD3 and  $\zeta$ -chains of the T cell receptor complex, the CD79-alpha and -beta chains of the B cell receptor complex, and certain Fc receptors. The tyrosine residues within these motifs become phosphorylated following interaction of the receptor molecules with their ligands and form docking sites for other proteins involved in the signalling pathways of the cell.

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 ITAM-containing domain may be or comprise a CD3-zeta endodomain. Suitably, the ITAM-containing domain may comprise the sequence shown as SEQ ID NO: 13 or a variant thereof having at least 80, 85, 90, 95, 98 or 99% sequence identity which retains the capacity to be phosphorylated and recruit ZAP70.

SEQ ID NO: 13 (CD3-zeta endodomain)

RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKPNPQEGLYNELQKDKMAEA  
YSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

By way of example, the fusion protein may be or comprise the sequence shown as SEQ ID NO: 14, which contains a ZAP70-SH2 domain fused to a CD3-zeta endodomain.

SEQ ID NO: 14

MRRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMA  
 EAYSEIGMKGERRRRGKGDGLYQGLSTATKDTYDALHMQALPPRSGGGGSGGGGSGGGGSGGGGSGMPDPA  
 AHLPPFFYGSISRAEAEHLKLAGMADGLFLLRQCLRSLGGYVLSLVHDVRFHHFPIERQLNGTYAIAGGK  
 AHC GPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQPGVFDCLRDAMVRDYVRQTWKLEGEALEQAIISQ  
 APQVEKLIATTAHERMPWYHSSLTREEAERKLYSGAQTGKFLLRPRKEQGTALSLIYGKTVYHYLISQ  
 DKAGKYCIPEGTKFDTLWQLVEYLKLDGLIYCLKEACPNSSASNASGAAAPTLPAPSTLTHPQRRID  
 TLNSDGYTPEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKFLKRDNLLIADIELGCGNFGSVRQG  
 VYRMRKKQIDVAIKVLKQGTEKADTEEMMREAQIMHQLDNPYIVRLIGVCQAEALMLVMEMAGGGPLHKF  
 LVGKREEIPVSNVAELLHQVSMGMKYLEEKNFVHRDLAARNVLLVNRHYAKISDFGLSKALGADDSYYTA  
 RSAGKWPLKWYAPPECINFRKFSSRSDVWSYGVTMWEALSYGQKPYKKMKGPVMAFIEQGRMECPPECP  
 PELYALMSDCWIYKWEDRPDFTLVEQRM RACYYS LASKVEGPPGSTQKAEAAACA

Suitably, the fusion protein may comprise the sequence shown as SEQ ID NO: 14 or a variant thereof having at least 80, 85, 90, 95, 98 or 99% sequence identity.

#### ITIM-CONTAINING DOMAIN

In one embodiment, the fusion protein comprises a PTPN6 SH2 domain and an immunoreceptor tyrosine-based inhibition motif (ITIM)-containing domain

A fusion of full-length PTPN6 with an ITIM containing domain results in a structure which amplifies an inhibitory immune signal. Here, the fusion protein is recruited to a phospho-ITIM immune-receptor endodomain. PTPN6 functions normally to propagate the signal but also provides another set of ITIMs which become phosphorylated and recruit more PTPN6. In some embodiments, the fusion may include only the PTPN6 SH2 domain with an ITIM containing endodomain (e.g. the fusion does not contain a PTPN6 phosphatase domain). In other embodiments, the ratio of PTPN6 catalytic domains (phosphatase domains) with ITIMs may be varied to affect the kinetics of activation in response to dynamics of the inhibitory receptor interactions with cognate target.

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. After ITIM-possessing inhibitory receptors interact with their ligand, their ITIM motif becomes phosphorylated by enzymes of the Src kinases, allowing them to recruit PTPN6 via interactions between the PTPN6 SH2 domain and the phosphorylated ITIM domains.

ITIM containing endodomains include those from CD22, LAIR-1, the Killer inhibitory receptor family (KIR), LILRB1, CTLA4, PD-1, BTLA, for example.

ITIM endodomains from PDCD1, BTLA4, LILRB1, LAIR1, CTLA4, KIR2DL1, KIR2DL4, KIR2DL5, KIR3DL1 and KIR3DL3 are shown in SEQ ID NO: 15 to 24 respectively

**SEQ ID NO: 15 PD CD1 endodomain**

CSRAARGTIGARRTGQPLKEDPSAVPVFSVDYGELDFQWREKTPEPPVPCVPEQTEYATI  
VFPSGMTSSPARRGSADGPRSAQPLRPEDGHCSWPL

**SEQ ID NO: 16 BTLA4**

KLQRRWKRTQSQQGLQENSSGQSFFVRNKKVRRAPLSEGPLSLGCYNPMMEDGISYTTLRFPENIIPRTG  
DAESSEMQRPPDCDDTVTYSALHKRQVGDIENVIPDFPEDEGIHYSELI  
QFGVGERPQAQENVYVILKH

**SEQ ID NO: 17 LILRB1**

LRHRRQGKHWTSTQRKADFQHPAGAVGPEPTDRGLQWRSSPAADAQEENLYAAVKHTQPEDGVEMDTRSP  
HDEDPAVTYAEVKHSRPRREMASPPSPLSGEFLDTKDRQAEEDRQMDTEAAASEAPQDVTYAQLHSLTL  
RREATEPPPSQEGPSPAVPSIYATLAIH

**SEQ ID NO: 18 LAIR1**

HRQNQIKQGPPRSKDEEQKPQQRPD LAVDVLER TADKATVNGLP EK DRETDT SALAAGSSQEV TYAQLDH  
WALTQRTARAVSPQSTKPMASITYA AVARH

**SEQ ID NO: 19 CTLA4**

FLLWILAAVSSGLFFYSFLLTAVSLSKMLKKRSPLTTGVYVKMPPTPEPECEKQFQPYFIPIN

**SEQ ID NO: 20 KIR2DL1**

GNSRHLHVLIGTSVVIIPFAILLFLLHRWCANKKNAVMDQEPAGNRTVNREDSDEQDPQEV TYTQLNH  
CVFTQRKITRPSQRPKTPPTDIIVYTELPNAESRSKV VSCP

**SEQ ID NO: 21 KIR2DL4**

GIARHLHAVIRYSVAIILFTILPFFLLHRWCSKKKENAAVMNQEPAGHRTVNREDSDEQDPQEV TYAQLD  
HCIFTQRKITGPSQRSKRPSTDTSVCIELPNAEPRALSPAHEHHSQALMGSSRETTALSQTQLASSNVPA  
AGI

**SEQ ID NO: 22 KIR2DL5**

TGIRRLHILIGTSVAIILFIILFFLLHCCCSNKKNAAVMDQEPAGDRTVNREDSDDQDPQEV TYAQLD  
HCVFTQTKITSPSQRPKTPPTDTTMYMELPNAKPRSLSPA HKHHSQALRGSSRETTALSQNRVASSH VPA  
AGI

**SEQ ID NO: 23 KIR3DL1**

KDPRHLHILIGTSVVIILFILLFLLHLWCSNKKNAAVMDQEPAGNRTANSEDSDEQDP EEV TYAQLDH  
CVFTQRKITRPSQRPKTPPTDTILYTELPNAKPRSKV VSCP

**SEQ ID NO: 24 KIR3DL3**

KDPGNSRHLHVLIGTSVVIIPFAILLFLLHRWCANKKNAVMDQEPAGNRTVNREDSDEQDPQEV TYAQ  
LNHCVFTQRKITRPSQRPKTPPTDTSV

The ITIM-containing domain may be or comprise a PDCD1, BTLA4, LILRB1, LAIR1, CTLA4, KIR2DL1, KIR2DL4, KIR2DL5, KIR3DL1 or KIR3DL3 endodomain. Suitably, the ITIM-containing domain may comprise the sequence shown any of SEQ ID NO: 15 to 24 or a variant thereof having at least 80, 85, 90, 95, 98 or 99% sequence identity which retains the capacity to be phosphorylated by Src kinases and amplify an inhibitory immune signal.

By way of example, the fusion protein may be or comprise the sequence shown as SEQ ID NO: 25, which contains a PTPN6-SH2 domain fused to a PD1 endodomain.

#### SEQ ID NO: 25

```
MTGQPLKEDPSAVPVFSVDYGELDFQWREKTPEPPVPCVPEQTEYATIVFPSGMGTSSPARRGSADGPRS
AQPLRPEDGHCSWPLSGGGGSGGGGSGGGGSGGGGSMVRWFHRDLSGLDAETLLKGRGVHGSFLARPSRK
NQGDFSLSVRVGDQVTHIRIQNSGDFYDLYGGEKFATLTELVEYYTQQQGVLQDRDGTIIHLKYP LNCS
PTSERWYHGHMSGGQAETLLQAKGEPWTF LVRESLSQPGDFVLSVLSQPKAGPGSPLRVTHIKVMCEGG
RYTVGGLETFDLTDLVEHFKKTGIEEASGAFVYLRQPYATRVNAADIENRVLELNKKQSEDTAKAGF
WEEFESLQKQEVKNLHQRLEGQRPENKGKNRYKNILPFDHSRVILQGRDSNIPGSDYINANYIKNQLLGP
DENAITYIASQGCLEATVNDWFQMAWQENSRVIVMTTREVEKGRNKCVPYWPEVGMQRAYGPYSVTNCGE
HDTTEYKLRTLQVSPLDNGDLIREIWHYQYLSWPDHGVPSPEGGVLSFLDQINQRQESLPHAGPIIVHCS
AGIGRTGTIIVIDMLMENISTKGLDCDIDIQKTIQMVRAQRSGMVQTEAQYKFIYVAIAQFIETTKKKLE
VLQSQKGQSEYGNITYPPAMKNAHAKASRTSSKHKEDVYENLHTKNKREEKVKKQRSADKEKSKGSLKR
K
```

Suitably, the fusion protein may comprise the sequence shown as SEQ ID NO: 25 or a variant thereof having at least 80, 85, 90, 95, 98 or 99% sequence identity

#### CROSSWIRE SIGNAL

The present invention provides a fusion protein which comprises: an SH2 domain from an ITAM-binding protein; and a phosphatase domain.

The present invention also provide a fusion protein which comprises: an SH2 domain from an ITIM-binding protein; and a kinase domain.

These “crosswire” signalling molecules will reverse an excitatory or inhibitory signal inside an immune cell such as a T cell. When a T-cell receives an excitatory signal, for example following recognition of a target antigen by a CAR, or MHC:peptide by a TCR, the presence of the first type of crosswire molecule will result in the cell interpreting the excitatory signal as an inhibitory signal.



Dampening down or revising T-cell activation may be useful in a variety of situations, for example, it may be used for CAR-expressing T cells where there is a high level of expression of the target antigen on the target cell. It may be used to prevent T-cell over-activation which may lead to T cell exhaustion and/or activation-induced cell death. Preventing a T-cell becoming activated too much or too quickly may also prevent or reduce pathological side effects of CAR-T cell treatment such as cytokine release syndrome (CRS).

The reverse situation is when a T-cell receives an inhibitory signal, for example following ligation of PD1, and the presence of the second type of crosswire molecule results in the cell interpreting the inhibitory signal as an excitatory signal.

Reducing or reversing T-cell inhibition will help the cell overcome the inhibitory stimuli within the hostile tumour microenvironment and should therefore increase T-cell persistence and expansion in vivo.

In one embodiment, the fusion protein comprises a PTPN6 SH2 domain and a ZAP70 kinase domain. In another embodiment the present fusion protein comprises a ZAP70 SH2 domain fused to a PTPN6 kinase domain.

In embodiments relating to a ZAP70 SH2 domain fused to the phosphatase domain from PTPN6, when the T cell receives an excitatory signal it interprets it as an inhibitory signal because the PTPN6 phosphatase domain is recruited to the activated ITAM via the ZAP70 SH2 domain.

In embodiments relating to a PTPN6 SH2 domain fused to the kinase domain from ZAP70, when the T cell receives an inhibitory signal it interprets it as an excitatory signal because the ZAP70 kinase domain is recruited to the activated ITIM via the PTPN6 domain. A fusion between PTPN6 SH2 domain and ZAP70 kinase domain will result in competition for phosphorylated ITIMs by wild-type PTPN6 blocking inhibitory signals, but in addition will transmit a paradoxical activation signal. This may have application in over-coming checkpoint blockade signals in a tumour microenvironment.

The sequence of human ZAP70 kinase, PTPN6 phosphatase and SHP-2 phosphatase domains are shown as SEQ ID NO: 26, 27 and 28 respectively.

SEQ ID NO: 26 – ZAP70 kinase domain

DPEELKDKKLFLKRDNLLIADIELGCGNFGSVRQGVYRMRKKQIDVAIKVLKQGTEKADTEEMMREAQIM  
HQLDNPYIVRLIGVCQAEALMLVMEMAGGGPLHKFLVGKREEIPVSNVAELLHQVSMGMKYLEEKNFVHR  
DLAARNVLLVNRHYAKISDFGLSKALGADDSYYTARSAGKWPLKWYAPECINFRKFSSRSVWSYGVTMW  
EALSYGQKPYKKMKGPVMAFIEQGKRMECPPECPELYALMSDCWIYKWEDRPDLTVEQRMRACTYSL  
ASKVEGPPGSTQKAEACA

#### SEQ ID NO: 27 – PTPN6 phosphatase domain

FWEEFESLQKQEVKNLHQRLLEGQRPENKGNRYKNILPFDHSRVILQGRDSNIPGSDYINANYIKNQLLG  
PDENAKTYIASQGCEATVNDFWQMAWQENSRVIVMTTREVKEGRNKCVPYWPVEVGMQRAYGPYSVTNCG  
EHDTEYKLRTLQVSPDLNGLIREIWHYQYLSWPDHGVPSEPGGVLSFLDQINQRQESLPHAGPIIVHC  
SAGIGRTGTIIVIDMLMENISTKGLDCDIDIQKTIQMVRAQRSGMVQTEAQYKFIYVAIAQFIETTKKKL

#### SEQ ID NO: 28 – SHP-2 phosphatase domain

WEEFETLQQQECKLLYSRKEGQRQENKNKNRYKNILPFDHTRVVLHDGDPNEPVSDYINANII  
MPEFETKCNNSPKKSYIATQGCLQNTVNDFWRMVFQENSRVIVMTTKEVERGKSKCVKYWPDEYALKE  
YGVMRVRNVKESAAHDYTLRELKLSKVGQALLQGNTERTVWQYHFRTWPDHGVPSPDGGVLDLEEYH  
HKQESIMDAGPVVVHCSAGIGRTGTIFIVIDLIDIIREKGVDCDIDVPKTIQMVRSQRSGMVQTEAQYRFIYM  
A

The ZAP70 kinase domain, PTPN6 phosphatase domain or SHP-2 phosphatase domain may be or comprise the sequence shown as SEQ ID NO: 26, SEQ ID NO: 27 or SEQ ID NO: 28, respectively; or a variant thereof having at least 80, 85, 90, 95, 98 or 99% sequence identity which retains the capacity to phosphorylate or dephosphorylate downstream proteins in the same manner as the wild-type kinase/phosphatase domains.

Examples of fusion protein comprising a PTPN6 SH2 domain fused to a ZAP70 kinase domain; a ZAP70 SH2 domain fused to a PTPN6 kinase domain; and a SHP-2 SH2 domain fused to a ZAP70 kinase domain are shown as SEQ ID NO: 29, SEQ ID NO: 30 and SEQ ID No. 61, respectively.

#### SEQ ID NO: 29 – PTPN6 SH2 domain fusion: ZAP70 kinase domain

MVRWFHRDLISGLDAETLLKGRGVHGSFLARPSRKNQGFSLSVRVGDQVTHIRIQNSGDFYDLYGGEKFA  
TLTELVEYYTQQQGVLDQDRDGTIIHLKYPLNCSDPTSERWYHGHMSGGQAEATLLQAKGEPWTFVRESLS  
QPGDFVLSVLSQDPKAGPGSPLRVTHIKVMCEGGRYTVGGLETFDSLTDLVEHFKKTGIEEASGAFVYLR  
QPYYSGGGGS DPEELKDKKLFLKRDNLLIADIELGCGNFGSVRQGVYRMRKKQIDVAIKVLKQGTEKADT  
EEMMREAQIMHQLDNPYIVRLIGVCQAEALMLVMEMAGGGPLHKFLVGKREEIPVSNVAELLHQVSMGMK  
YLEEKNFVHRDLAARNVLLVNRHYAKISDFGLSKALGADDSYYTARSAGKWPLKWYAPECINFRKFSSRS  
DVWSYGVTMWEALSYGQKPYKKMKGPVMAFIEQGKRMECPPECPELYALMSDCWIYKWEDRPDLTVE  
QRMRACTYSLASKVEGPPGSTQKAEACA

#### SEQ ID NO: 30 – ZAP70 SH2 domain fusion: PTPN6 phosphatase domain

MPDPAHLPPFFYGSISRAEAEHLKLAGMADGLFLLRQCLRSLLGGYVLSLVHDVRFHHFPIERQLNGTYA  
IAGGKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQPGVFDCLRDAMVRDYVRQTWKLEGEALEQ  
AIIISQAPQVEKLIATTAHERMPWYHSSLTREEAERKLYSGAQTGKFLLRPRKEQGTALSLIYGKTVYH  
YLISQDKAGKYCIPEGTKFDTLWQLVEYLKLDGLIYCLKEACPNSSASNASGAAAPTLPAHPSTLTHP  
SGGGSGGGSGGGSGGGSGGGSWEEFESLQKQEVKNLHQRLLEGQRPENKGNRYKNILPFDHSRVILQGR  
DSNIPGSDYINANYIKNQLLGPDENAKTYIASQGCEATVNDFWQMAWQENSRVIVMTTREVKEGRNKC  
VPYWPVEVGMQRAYGPYSVTNCGEHDTEYKLRTLQVSPDLNGLIREIWHYQYLSWPDHGVPSEPGGVLSF

LDQINQRQESLPHAGPIIVHCSAGIGRTGTIIVIDMLMENISTKGLDCDIDIQKTIQMVRAQRSGMVQTE  
AQYKFIIYVAIAQFIETTKKL

#### SEQ ID NO. 61 – dual SH2 domains from SHP-2 fused to ZAP70 kinase domain

WFHPNITGVEAENLLLTRGVDGSFLARPSKSNPGDFTLSVRRNGAVTHIKIQNTGDYYDLYGGEKFATLA  
ELVQYYMEHHGQLKEKNGDVIELKYPLNCADPTSERWFHGHLSGKEAEKLLTEKGKHGSFLVRESQSHPG  
DFVLSVRTGDDKGESNDGKSKVTHVMIRCQELKYDVGGGERFDSLTDLVEHYKKNPMVETLGTVLQLKQP  
LNTTRINPNSSASNASGAAAPTLPAPSTLTTHPQRRIDTLNSDGYTPEPARITSPDKPRPMPMDTSVYES  
PYSDPEELKDKKLFLKRDNLLIADIELGCGNFGSVRQGVYRMKKQIDVAIKVLKQGTEKADTEEMMREA  
QIMHQLDNPYIVRLIGVCQAEALMLVMEMAGGGPLHKFLVGKREEIPVSNVAELLHQVSMGMKYLEEKNF  
VHRDLAARNVLLVNRHYAKISDFGLSKALGADDSYYTARSAGKWPLKWYAPECINFRKFSSRSDVWSYGV  
TMWEALSYGQKPYKKMKGPEVMAFIEQGKRMECPPECPELYALMSDCWIYKWEDRPDFLTVEQRMRACTY  
YSL

The fusion protein may be or comprise the sequence shown as SEQ ID NO: 29, SEQ ID NO: 30 or SEQ ID No. 61 or a variant thereof having at least 80, 85, 90, 95, 98 or 99% sequence identity.

#### HETEROLOGOUS SIGNALLING DOMAIN

The present fusion protein may comprise (i) a ZAP70, PTPN6 or SHP-2 SH2 domain; and (ii) a heterologous signalling domain.

As used herein, the term “heterologous signalling domain” refers to a signalling domain which is not present in the wild type ZAP70, PTPN6 or SHP-2 protein. As such, where the fusion protein comprises a ZAP70 SH2 domain, it comprises a signalling domain which is not the ZAP70 kinase domain. Alternatively, where the fusion protein comprises a PTPN6 SH2 domain, it comprises a signalling domain which is not the PTPN6 phosphatase domain.

#### BYPASS SIGNAL

The heterologous signalling domain may be from a signalling molecule which is not usually activated by an ITAM containing receptor. In other words, the heterologous signalling domain may be from a signalling molecule which is not involved in the propagation of immunological signal 1 following the binding of antigen to the TCR. Immunological signal 1 is sufficient to trigger T-cell killing of cognate target cells but does not fully activate the T-cell to proliferate and survive.

In one embodiment of this aspect of the invention, the present invention provides a fusion protein which comprises (i) an SH2 domain from a protein which binds an ITAM; and (ii) a heterologous signalling domain.

A fusion between, for example, ZAP70 and another signaling molecule not typically activated with an ITAM containing receptor may act to bypass signal from one pathway into another. One example is co-stimulation. A fusion between ZAP70 and the endodomain of CD28 may transmit a CD28 co-stimulatory signal as well as an ITAM activatory signal. Similarly, a fusion between ZAP70 and the endodomain of 41BB or OX40 may transmit a 41BB or OX40 co-stimulatory signal. Other pathways may also be recruited, for instance a fusion between ZAP70 and AKT kinase domain may result in transmission of an AKT signal upon ITAM phosphorylation. Other examples might include Kinase domain from JAK. In this way, a T-cell may interpret a simple antigen recognition signal as transmitting a co-stimulatory or even a cytokine type signal.

Such fusion proteins may be useful, for example, in approaches where repeated *ex vivo* stimulations of T cells can result in populations which lack costimulatory surface antigens and which have limited proliferative capacity *in vivo* resulting in limited persistence and efficacy. The loss of costimulatory surface antigens leading to activation of T cells solely through the TCR has been linked to a greater degree of activation induced cell death which would negatively impact *in vivo* efficacy and persistence. The effect can be reversed by the activation of surface-expressed 4-1BB and OX40 demonstrating that costimulation can prevent activation induced cell death and can support greater expansion of tumour specific T cells.

In another embodiment of this aspect of the invention, the present invention provides a fusion protein which comprises (i) an SH2 domain from a protein which binds an ITIM; and (ii) a heterologous signalling domain.

For example, a PTPN6 SH2 domain or SHP-2 SH2 domain may be fused to a co-stimulatory endodomain so a T-cell interprets an inhibitory signal as a co-stimulatory one.

The heterologous signalling domain may be from, for example, CD28, 41BB or OX40.

CD28 provides a potent co-stimulatory signal - namely immunological signal 2, which triggers T-cell proliferation. CD28 is the receptor for CD80 (B7.1) and CD86 (B7.2) proteins.

41BB (CD137) is a type 2 transmembrane glycoprotein belonging to the TNF superfamily, expressed on activated T cells. Crosslinking of 41BB enhances T cell proliferation, IL-2 secretion survival and cytolytic activity.

OX40 (CD134) is a secondary co-stimulatory molecule, expressed after 24 to 72 hours following activation; its ligand, OX40L, is also not expressed on resting antigen presenting cells, but is following their activation. Expression of OX40 is dependent on full activation of the T cell; without CD28, expression of OX40 is delayed and of fourfold lower levels. Signalling through OX40 is required for prolonged T cell survival following initial activation and proliferation.

The CD28, 41BB and OX40 signalling domains (endodomains) are shown as SEQ ID NO: 31, 32 and 33, respectively.

SEQ ID NO: 31 – CD28 endodomain

MRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRS

SEQ ID NO: 32 – 41BB endodomain

MKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL

SEQ ID NO: 33 – OX40 endodomain

MRDQRLPPDAHKPPGGSFRTPIQEEQADAHSTLAKI

The heterologous signalling domain may be or comprise the sequence shown as SEQ ID NO: 31; SEQ ID NO: 32 or SEQ ID NO: 33, respectively, or a variant thereof having at least 80, 85, 90, 95, 98 or 99% sequence identity.

The heterologous signalling domain may be or comprise an inhibitory signalling domain.

For example, the inhibitory signalling domain 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 PLC $\gamma$ 1 and LAT.

CD45 present on all hematopoietic cells, is a protein tyrosine phosphatase which is capable of regulating signal transduction and functional responses, again by phosphorylating PLC  $\gamma$ 1.

An inhibitory signalling domain may comprise all or part of a receptor-like tyrosine phosphatase. The phosphatase may interfere with the phosphorylation and/or function of elements involved in T-cell signalling, such as PLC $\gamma$ 1 and/or LAT.

The inhibitory signalling domain may be or comprise the endodomain of ICOS, CD27, BTLA, CD30, GITR or HVEM.

The inhibitory signalling domain may comprise the sequence shown as SEQ ID NO: 34 to 39 or a variant thereof having at least 80% sequence identity.

**SEQ ID NO: 34 - ICOS endodomain**

CWLTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTL

**SEQ ID NO: 35 - CD27 endodomain**

QRRKYRSNKGESPVEPAEPCHYSCPREEEGSTIPIQEDYRKPEPACSP

**SEQ ID NO: 36 - BTLA endodomain**

RRHQGKQNELSDTAGREINLVDAHLKSEQTEASTRQNSQVLLSETGIYDNDPDLCFRMQEGSEVYSNPCL  
EENKPGIVYASLNHVSIGPNSRLARNVKEAPTEYASICVRS

**SEQ ID NO: 37 - CD30 endodomain**

HRRACRKRIRQKLHLCPVQTSQPKLELVDSRPRRSSTQLRSGASVTEPVAEERGLMSQPLMETCHSVGA  
AYLESPLQDASPAGGPSSPRDLPEPRVSTEHTNNKIEKIYIMKADTVIVGTVKAELPEGRGLAGPAEPE  
LEEELEADHTPHYPEQETEPPLGSCSDVMLSVEEEGKEDPLPTAASGK

**SEQ ID NO: 38 - GITR endodomain**

QLGLHIWQLRSQCMWPRETQLLLEVPSTEDARSCQFPPEERGERSAEEKGRLGDLWV

**SEQ ID NO: 39 - HVEM endodomain**

CVKRRKPRGDVVKVIVSVQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH

A variant sequence may have at least 80%, 85%, 90%, 95%, 98% or 99% sequence identity to SEQ ID NO: 34 to 39 provided that the sequence provides an effective intracellular signalling domain.

Suitably, the fusion protein may be or comprise any of the sequences shown as SEQ ID NOs: 40 to 45.

**(SEQ ID NO: 40) - CD28 endodomain fused to amino-terminus of full-length ZAP**

MRSKRSRLLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSSGGGGSGGGGSGGGGSGGGGSMPPDAAH  
LPFFYGSISRAEAEHLKLAGMADGLFLLRQCLRSLGGYVLSLVHDVRFHHFPIERQLNGTYAIAGGKAH  
CGPAELCFEYSRDPDGLPCNLRKPCNRPSGLEPQPGVFDCLRDAMVRDYVRQTWKLEGEALEQAIISQAP  
QVEKLIATTATHERMPWYHSSLTREEAERKLYSGAQTGKFLLRPRKEQGTYSLSLIYGKTVYHYLISQDK  
AGKYCIPEGTKFDTLWQLVEYLLKLKADGLIYCLKEACPNSASNASGAAAPTLPAPHPSTLTHPQRRIDTL  
NSDGYTPEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKFLKRDNLLIADIELGCGNFGSVRQGVY  
RMRKKQIDVAIKVLKQGTEKADTEEMMREAQIMHQLDNPIVRLIGVCQAEALMLVMEMAGGGPLHKFLV  
GKREEIPVSNVAELLHQVSMGMKYLEEKNFVHRDLAARNVLLVNRHYAKISDFGLSKALGADDSYYTARS

AGKWPLKWYAPECINFRKFSSRSVDVWSYGVMTWEALSYGQKPYKKMKGPVMAFIEQGKRMECPPECPP  
 LYALMSDCWIYKWEDRPDLTVEQMRACYYSLASKVEGPPGSTQKAEAAACA

**(SEQ ID NO: 41) - 41BB endodomain fused to amino-terminus of full-length ZAP**

MKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCESLGGGGSGGGGSGGGGSGGGGSMPPDPA  
 HLPFFYGSISRAEAEHLKLAGMADGLFLLRQCLRLGGYVLSLVHDVRFHHFPIERQLNGTYAIAAGKA  
 HCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQPGVFDCLRDAMVRDYVRQTWKLEGEALEQAIISQA  
 PQVEKLIATTATHERMPWYHSSLTREEAERKLYSGAQTGDKFLLRPRKEQGTYSLSLIYGKTVYHYLISQD  
 KAGKYCIPEGTKFDTLWQLVEYLKLLKADGLIYCLKEACPNSSASNASGAAAPTLPAPHPSTLTHPQRRIDT  
 LNSDGYTPEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLFLKRDNLLIADIELGCGNFGSVRQGV  
 YRMRKKQIDVAIKVLKQGTEKADTEEMMREAQIMHQLDNPIVRLIGVCQAEALMLVMEMAGGGPLHKFL  
 VGKREEIPVSNVAELLHQVSMGMKYLEEKNFVHRDLAARNVLLVNRHYAKISDFGLSKALGADDSYYTAR  
 SAGKWPLKWYAPECINFRKFSSRSVDVWSYGVMTWEALSYGQKPYKKMKGPVMAFIEQGKRMECPPECPP  
 ELYALMSDCWIYKWEDRPDLTVEQMRACYYSLASKVEGPPGSTQKAEAAACA

**(SEQ ID NO: 42) - OX40 endodomain fused to amino-terminus of full-length ZAP**

MRDQRLPPDAHKKPPGGGSFRTPIQEEQADAHSTLAKISGGGGSGGGGSGGGGSGGGGSMPPDPAHLPPFFY  
 GSISRAEAEHLKLAGMADGLFLLRQCLRLGGYVLSLVHDVRFHHFPIERQLNGTYAIAAGKAHCGPAE  
 LCEFYSRDPDGLPCNLRKPCNRPSGLEPQPGVFDCLRDAMVRDYVRQTWKLEGEALEQAIISQAPQVEKL  
 IATTATHERMPWYHSSLTREEAERKLYSGAQTGDKFLLRPRKEQGTYSLSLIYGKTVYHYLISQDKAGKYC  
 IPEGTKFDTLWQLVEYLKLLKADGLIYCLKEACPNSSASNASGAAAPTLPAPHPSTLTHPQRRIDTLNSDGY  
 TPEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLFLKRDNLLIADIELGCGNFGSVRQGVYRMRKK  
 QIDVAIKVLKQGTEKADTEEMMREAQIMHQLDNPIVRLIGVCQAEALMLVMEMAGGGPLHKFLVGKREE  
 IPVSNVAELLHQVSMGMKYLEEKNFVHRDLAARNVLLVNRHYAKISDFGLSKALGADDSYYTARSAGKW  
 PLKWYAPECINFRKFSSRSVDVWSYGVMTWEALSYGQKPYKKMKGPVMAFIEQGKRMECPPECPP  
 ELYALMSDCWIYKWEDRPDLTVEQMRACYYSLASKVEGPPGSTQKAEAAACA

**(SEQ ID NO: 43) - CD28 endodomain fused to the amino-terminus of PTPN6 SH2 domain.**

MRSKRSRLLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSSGGGGSGGGGSGGGGSGGGGSMVRWFHR  
 DLSGLDAETLLKGRGVHGSFLARPSRKNQGDFSLSVRVGDQVTHIRIQNSGDFYDLYGGEKFATLTELVE  
 YYTQQQGVLDQDRDGTIIHLKYPLNCSDPTSERWYHGHMSGGQAETLLQAKGEPWTFVRESLSQPGDFVL  
 SVLSDQPKAGPGSPLRVTHIKVMCEGGRYTVGGLETFDLSLTDLVEHFKKTGIEEASGAFVYLRQPY

**(SEQ ID NO: 44) - 41BB endodomain fused to the amino-terminus of PTPN6 SH2 domain**

MKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCESLGGGGSGGGGSGGGGSGGGGSMVRWFH  
 RDLSGLDAETLLKGRGVHGSFLARPSRKNQGDFSLSVRVGDQVTHIRIQNSGDFYDLYGGEKFATLTELVE  
 YYTQQQGVLDQDRDGTIIHLKYPLNCSDPTSERWYHGHMSGGQAETLLQAKGEPWTFVRESLSQPGDFVL  
 LSVLSDQPKAGPGSPLRVTHIKVMCEGGRYTVGGLETFDLSLTDLVEHFKKTGIEEASGAFVYLRQPY

**(SEQ ID NO: 45) - OX40 endodomain fused to the amino-terminus of PTPN6 SH2 domain**

MRDQRLPPDAHKKPPGGGSFRTPIQEEQADAHSTLAKISGGGGSGGGGSGGGGSGGGGSMVRWFHRDL  
 SGLDAETLLKGRGVHGSFLARPSRKNQGDFSLSVRVGDQVTHIRIQNSGDFYDLYGGEKFATLTELVEYYTQQ  
 QGVLDQDRDGTIIHLKYPLNCSDPTSERWYHGHMSGGQAETLLQAKGEPWTFVRESLSQPGDFVL  
 SVLSDQPKAGPGSPLRVTHIKVMCEGGRYTVGGLETFDLSLTDLVEHFKKTGIEEASGAFVYLRQPY

Suitably, the fusion protein may comprise the sequence shown as any of SEQ ID NOs: 40 to 45  
 or a variant thereof having at least 80, 85, 90, 95, 98 or 99% sequence identity

KINASE DOMAIN

The heterologous signalling domain may be a kinase domain. For example, the heterologous signalling domain may comprise an AKT kinase domain or a JAK kinase domain.

Akt, also known as protein kinase B (PKB), is a serine/threonine-specific protein kinase that plays a key role in multiple cellular processes such as glucose metabolism, apoptosis, cell proliferation, transcription and cell migration.

Following activation of the TCR, T cells secrete IL2 which supports survival and proliferation. However this secretion is transient and T cells that are activated and expanded *in vitro* become dependent on exogenous IL2 for survival. By increasing AKT phosphorylation following ITAM phosphorylation associated with TCR or CAR activation, the dependence of activated T cells on exogenous IL2 may be reduced or removed and their proliferation and survival enhanced.

The Akt kinase domain is shown as SEQ ID NO: 46.

#### SEQ ID NO: 46 – Akt kinase domain

```
AEEMEVS LAKPKHRVTMNEFEY LKLLGKGT FGKVI LVKEKATGRYYAMKILKKEVIVAKDEVAHTLTENR
VLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVFSEDRARFYGAIEIVSALDYLHSEKNV
VYRDLKLENLMLDKDGHIKITDFGLCKEGIKDGATMKTFCGTPEYLAPEVLEDNDYGRAVDWWGLGVVMY
EMMCGRLPFYNQDHEKLFELILMEEIRFPRTLGP EAKSLLSGLLKKDPKQRLGGGSEDAKEIMQHRFFAG
IVWQH VYEKKLSPPFKPQVTSETDTRYFDEEFTAQMITITPPDQDDSMECVDSERRPHFPQFSY SASGTA
```

The heterologous signalling domain may be or comprise the sequence shown as SEQ ID NO: 46, or a variant thereof having at least 80, 85, 90, 95, 98 or 99% sequence identity provided that the sequence provides an effective kinase domain.

By way of example, the fusion protein may be or comprise the any of the sequences shown as SEQ ID NO: 47 to 49 and 62 which contain a ZAP70-SH2 domain fused directly to an Akt kinase domain, a ZAP70-SH2 domain fused to an Akt kinase domain via a linker a ZAP70 mutated to be non-functional and fused to an Akt kinase domain; and a dual SHP-2 SH2 domain fused to an Akt kinase domain, respectively.

#### SEQ ID NO: 47 - ZAP70-SH2 domain fused directly to an Akt kinase domain

```
MPDPA AHL PFFYGSISR AEAEHLKLAGMADGLFLLRQCLRS LGGYVLSLVHDVRFHHFP IERQLNGTYA
IAGGKAHCGPAELCEFYSRDPDGLPCNL RKPCNRPSGLEPQPGVFDCLRDAMVRDYVRQ TWKLEGEALEQ
AIISQAPQVEKLIATTAHERMPWYHSSLTREEAERKLYSGAQTDGKFLLRPRKEQGT YALSLIYGKTVYH
YLISQDKAGKYCIPEGTKFDTLWQLVEY LKLLKADGLIYCLKEACPNSSASNASGAAAPTLP AHPSTLT HP
AEEMEVS LAKPKHRVTMNEFEY LKLLGKGT FGKVI LVKEKATGRYYAMKILKKEVIVAKDEVAHTLTENR
VLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVFSEDRARFYGAIEIVSALDYLHSEKNV
VYRDLKLENLMLDKDGHIKITDFGLCKEGIKDGATMKTFCGTPEYLAPEVLEDNDYGRAVDWWGLGVVMY
```



EMMCGRLPFYNQDHEKLFELILMEEIRFPRTLGPPEAKSLLSGLLKDPKQRLGGGSEDAKEIMQHRFFAG  
IVWQHVEKKLSPPFKPQVTSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRPHFPQFSYSASGTA

#### SEQ ID NO: 48 - ZAP70-SH2 domain fused to an Akt kinase domain via a linker

MPDPAHLPPFFYGSISRAEAEHLKLAGMADGLFLLRQCLRSLLGGYVLSLVHDVRFHHFPIERQLNGTYA  
IAGGKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSPGLEPQPGVFDCLRDAMVRDYVRQTWKLEGEALEQ  
AIIISQAPQVEKLIATTAHERMPWYHSSLTREEAERKLYSGAQTGKFLLRPRKEQGTYALSIIYGKTVYH  
YLISQDKAGKYCIPEGTKFDTLWQLVEYLKLLKADGLIYCLKEACPNSSASNASGAAAPTLPAPSTLTTHP  
SGGGGSGGGGSGGGGSGGGGSAEEMEVSALAKPKHRVTMNEFEYLKLLGKGTFGKVILVKEKATGRYYAMK  
ILKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVFSEDR  
ARFYGAEIVSALDYLHSEKNVYRDLKLENLMLDKDGHIKITDFGLCKEGIKDGATMKTFCGTPEYLAPE  
VLEDNDYGRAVDWWGLGVVYEMMCGRLPFYNQDHEKLFELILMEEIRFPRTLGPPEAKSLLSGLLKDPK  
QRLGGGSEDAKEIMQHRFFAGIVWQHVEKKLSPPFKPQVTSETDTRYFDEEFTAQMITITPPDQDDSM  
CEVDSERRPHFPQFSYSASGTA

#### SEQ ID NO: 49 - ZAP70 mutated to be non-functional and fused to an Akt kinase domain

MPDPAHLPPFFYGSISRAEAEHLKLAGMADGLFLLRQCLRSLLGGYVLSLVHDVRFHHFPIERQLNGTYA  
IAGGKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSPGLEPQPGVFDCLRDAMVRDYVRQTWKLEGEALEQ  
AIIISQAPQVEKLIATTAHERMPWYHSSLTREEAERKLYSGAQTGKFLLRPRKEQGTYALSIIYGKTVYH  
YLISQDKAGKYCIPEGTKFDTLWQLVEYLKLLKADGLIYCLKEACPNSSASNASGAAAPTLPAPSTLTTHP  
AEEMEVSALAKPKHRVTMNEFEYLKLLGKGTFGKVILVKEKATGRYYAMKILKKEVIVAKDEVAHTLTENR  
VLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVFSEDRARFYGAEIVSALDYLHSEKNV  
YRDLKLENLMLDKDGHIKITDFGLCKEGIKDGATMKTFCGTPEYLAPEVLEDNDYGRAVDWWGLGVVY  
EMMCGRLPFYNQDHEKLFELILMEEIRFPRTLGPPEAKSLLSGLLKDPKQRLGGGSEDAKEIMQHRFFAG  
IVWQHVEKKLSPPFKPQVTSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRPHFPQFSYSASGTA

#### SEQ ID No. 62 - dual SHP-2 SH2 domain fused to an Akt kinase domain

WFHPNITGVEAENLLLTRGVDGSFLARPSKSNPGDFTLSVRRNGAVTHIKIQNTGDYYDLYGGEKFATLA  
ELVQYYMEHHGQLKEKNGDVIELKYPLNCADPTSERWFHGLSGKEAEKLLTEKGKHSFLVRESQSHPG  
DFVLSVRTGDDKGESNDGKSKVTHVMIRCQELKYDVGGGERFDSLTDLVEHYKKNPMVETLGTVLQLKQP  
LNTTRINAEEMEVSALAKPKHRVTMNEFEYLKLLGKGTFGKVILVKEKATGRYYAMKILKKEVIVAKDEVA  
HTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVFSEDRARFYGAEIVSALDYL  
HSEKNVYRDLKLENLMLDKDGHIKITDFGLCKEGIKDGATMKTFCGTPEYLAPEVLEDNDYGRAVDWW  
GLGVVYEMMCGRLPFYNQDHEKLFELILMEEIRFPRTLGPPEAKSLLSGLLKDPKQRLGGGSEDAKEIM  
QHRFFAGIVWQHVEKKLSPPFKPQVTSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRPHFPQFS  
YSASGTA

The fusion protein may comprise the sequence shown as any of SEQ ID NO: 47 to 49 or 62 or a variant thereof having at least 80, 85, 90, 95, 98 or 99% sequence identity.

Janus kinase (JAK) is a family of intracellular, nonreceptor tyrosine kinases that transduce cytokine-mediated signals via the JAK-STAT pathway. The four JAK family members are: Janus kinase 1 (JAK1); Janus kinase 2 (JAK2); Janus kinase 3 (JAK3); and Tyrosine kinase 2 (TYK2).

#### SEQ ID NO: 50 – Kinase containing domain of JAK2

RNEDLIFNESLGQGTFTKIFKGVRRVGDYGQLHETEVLLKVLDAHRNYSSEFFEAASMSKLSHKHLV  
LNYGVCVCGDENILVQEFVKFGSLDYLKKNKNCINILWKLEVAKQLAWAMHFLEENTLIHGNVCAKNIL  
LIREEDRKTGNPPFIKLSDPGISITVLPKDILQERIPWVPPECIENPKNLNLATDKWSFGTTLWEICSGG

DKPLSALDSQRKLQFYEDRHQLPAPKWAE LANLINNCMDYEPDFRPSFRAIIRDLSLFTPDYELLTEND  
MLPNMRIGALGFSGAFEDRDPTQFEERHLKFLQQLGKGNFGSVEMCRYDPLQDNTGEVVAVKKLQHSTEE  
HLRDFEREIEILKSLQHDNIVKYKVCYSAGRNLKLIMEYLPYGSLRDY LQKHKERIDHIKLLQYTSQI  
CKGMEYLGTKRYIHRDLATRNLIVENENRVKIGDFGLTKVLPQDKEYYKVKEPGESPIFWYAPESLTESK  
FSVASDVWSFGVVLYELFTYIEKSKSPAEFMRMIGNDKQGQMIVFHLIELLKNNGRLPRPDGCPDEIYM  
IMTECWNNNVNQRP SFRDLALRVDQIRDNM

## PROTEASE DOMAIN

The present invention also provides a fusion protein which comprises (i) an SH2 domain from a protein which binds an ITAM or ITIM-containing protein and (ii) a protease domain.

The protease domain may be any protease which is capable of cleaving at a specific recognition sequence. As such the protease domain may be any protease which enables the separation of a single target polypeptide into two distinct polypeptides via cleavage at a specific target sequence.

The protease domain may be a Tobacco Etch Virus (TeV) protease domain.

TeV protease is a highly sequence-specific cysteine protease which is chymotrypsin-like proteases. It is very specific for its target cleavage site and is therefore frequently used for the controlled cleavage of fusion proteins both in vitro and in vivo. The consensus TeV cleavage site is ENLYFQ\S (where '\ ' denotes the cleaved peptide bond). Mammalian cells, such as human cells, do not express endogenous TeV protease.

Accordingly, the TeV cleavage recognition site is shown as SEQ ID NO: 51.

SEQ ID NO: 51 – Tev cleavage site

ENLYFQS

The TeV protease domain is shown as SEQ ID NO: 52.

## SEQ ID NO: 52

SLFKGPRDYNPISSSTICHLTNESDGHTTSLYGIGFGPFIITNKHLFRNNGTLLVQSLHGVFKVKNTTTTL  
QQHLIDGRDMIIRMPKDFPPFPQKLKFREPQREERICLVTTNFQTKSMSSMVSDTSCTFPSSDGI FWKH  
WIQTKDGQCGSPLVSTRDGFIVGIHSASNFTNTNNYFTSVPKNFMELLTNQEAQQWVSGWRLNADSVLWG  
GHKVFM SKPEEPFQPVKEATQLMNELVYSQ

Accordingly, the protease domain may be or comprise the sequence shown as SEQ ID NO: 52, or a variant thereof having at least 80, 85, 90, 95, 98 or 99% sequence identity provided that the sequence provides an effective protease function.

By way of example, the fusion protein may be or comprise the sequence shown as SEQ ID NO: 53 or 54, which contains a ZAP70-SH2 domain fused to a TEV protease sequence or a PTPN6-SH2 domain fused to a TEV protease sequence; respectively.

#### SEQ ID NO: 53

```
MPDFAAHLPPFFYGSISRAEAEHLKLAGMADGLFLLRQCLRSLGGYVLSLVHDVRFHHFPIERQLNGTYA
IAGGKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQPGVFDCLRDAMVRDYVRQTWKLEGEALEQ
AIISQAPQVEKLIATTAHERMPWYHSSLTREEAERKLYSGAQTGKFLLRPRKEQGTYALSLIYGKTVYH
YLISQDKAGKYCIPEGTKFDTLWQLVEYLKLLKADGLIYCLKEACPNSSASNASGAAAPTLPAPSTLTHP
SGGGGSGGGGSGGGGSGGGGSSLFKGPDRYNPISSTICHLTNESDGHTTSLYGIGFGPFIITNKHLFRRN
NGTLLVQSLHG VFKVKN TTTLQQHLIDGRD MIIIRMPKDFPPFPQKLKFREPQREERICLVTTNFQTKSM
SSMVSDTSCTFPSSDGI FWKHWIQTKDGQCGSPLVSTRDGFIVGIIHSASNFTNTNNYFTSVPKNFMELLT
NQEAQQWVSGWRLNADSVLWGGHKVFMSKPEEPFQPVKEATQLMNELVYSQ
```

#### SEQ ID NO: 54

```
MVRWFHRDL SGLDAETLLKGRGVHGSFLARPSRKNQGDFSLSVRVGDQVTHIRIQNSGDFYDLYGGEKFA
TLTELVEYYTQQQGV LQDRDGTIIHLKYPLNCSDPTSERWYHGHMSGGQAETLLQAKGEPWTFVRESLS
QPGDFVLSVLSDQPKAGPGSPLRVTHIKVMCEGGRYTVGGLETFDSLTDLVEHFKKTGIEEASGA FVYLR
QPYYSGGGGSSLFKGPDRYNPISSTICHLTNESDGHTTSLYGIGFGPFIITNKHLFRRNNGTLLVQSLHG
VFKVKN TTTLQQHLIDGRD MIIIRMPKDFPPFPQKLKFREPQREERICLVTTNFQTKSMSSMVSDTSCTF
PSSDGI FWKHWIQTKDGQCGSPLVSTRDGFIVGIIHSASNFTNTNNYFTSVPKNFMELLTNQEAQQWVSGW
RLNADSVLWGGHKVFMSKPEEPFQPVKEATQLMNELVYSQ
```

The fusion protein may comprise the sequence shown as SEQ ID NO: 53 or 54; or a variant thereof having at least 80, 85, 90, 95, 98 or 99% sequence identity.

The SH2 domain and heterologous domain of the fusion protein may be separated by a linker in order to spatially separate the SH2 domain and the heterologous domain.

#### TRANSCRIPTIONAL SIGNAL

A fusion protein which comprises a protease, as described in the previous section, may be co-expressed in a cell with a membrane-tethered protein having a protease cleavage site. Cleavage of the membrane-tethered protein at the protease site will release the membrane-distal part of the protein.

The membrane tethered protein may, for example, be a membrane-tethered transcription factor. When cleavage occurs, the transcription is released from its tether and free to transit to the nucleus.

A fusion between ZAP70 SH2 or PTPN6 SH2 domain and a protease domain will result in membrane-proximal recruitment of the protease following ITAM or ITIM phosphorylation, respectively.

Phosphorylation of ITAM or ITIM domains results in recruitment of the ZAP70 SH2 or PTPN6 SH2 fused with the protease domain, respectively, to the membrane-proximal area. This results in the transcription factor being cleaved from its tether and transferred to the nucleus. This may have many applications: for example upon activation the T-cell may be programmed to express transcription factors which act to prevent the T-cell from differentiating. For instance, upon activation the T-cell may be programmed to express a cytokine such as IL2, IL7 or IL15 which may act to stimulate proliferation and survival of the T-cell, or IL12 which may convert a hostile tumour microenvironment to one which more favours immune rejection of a tumour.

In particular, there is provided a cell which co-expresses:

- (i) a fusion protein comprising an SH2 domain from a protein which binds a phosphorylated ITAM; and

- (ii) a membrane tethered transcription factor

wherein the transcription factor, when released from the membrane tether, increases the expression of IL2, IL7 and/or IL15 in the cell.

There is also provided a cell which co-expresses:

- (i) a fusion protein comprising an SH2 domain from a protein which binds a phosphorylated ITIM; and

- (ii) a membrane tethered transcription factor

wherein the transcription factor, when released from the membrane tether, increases the expression of IL12 in the cell.

Protease recognition site

The protease recognition site may be any amino acid sequence which enables the protease domain of the fusion protein to specifically cleave the membrane tethered transcription factor between the membrane tether and the transcription factor. For example, in one embodiment

the protease domain is a TeV protease domain and the protease recognition site is a TeV protease recognition site.

#### Membrane tether

The membrane tether may be any sequence, signal or domain which is capable of localising the transcription factor and protease recognition site proximal to a membrane. For example, the membrane tether may be a myristylation signal or a transmembrane domain.

Suitably, 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. 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 stability.

#### Transcription factor

The transcription factor may be any transcription factor chosen to stimulate a desired response following phosphorylation of the relevant ITAM or ITIM motifs.

The transcription factor can be natural or artificial. Artificial transcription factors may be derived from, for example, TALENs, zinc-finger assemblies or CrispR/CAS9, the latter co-expressed with a guide mRNA.

Preferably, the transcription factor will contain a nuclear localization signal to aid its transportation to the nuclease following cleavage by the protease domain.

By way of example, nucleic acid sequence (ii) (which encodes a protein comprising a membrane tethered transcription factor which comprises: (i) a membrane tether; (ii) a protease recognition site; and (iii) a transcription factor) may encode a protein which consists of or comprises the sequence shown as SEQ ID NO: 55, which contains a RQR8 domain; a CD4-

Endotoxin1 transmembrane domain, a TEV protease recognition site and a VP16-GAL4 transcription factor.

#### SEQ ID NO: 55

```
MGTSLLCWMALCLLGADHADACPYSNPSLCSGGGGSELPTQGTFSNVSTNVSPAKPTTTACPYSNPSLCS
GGGGSPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDMALIVLGGVAGLLLFIGLGIFFC
VRCRHRRRQAERMAQIKRVVSEKKTAQAPHRFQKTCSPISGGGGSENLYFQMPKKKRKVAPPTDVSLGDE
LHLGDGEDVAMAHADALDDFDLMDLGDGDSPPGPGFTPHDSAPYGALDMADFEFEQMFTDALGIDEYGGSGG
GSMQILVASDATMKLLSSIEQACDICRLKKLKCSKEKPKCAKCLKNNWECRYSPKTKRSPLTRAHLTEVE
SRLEERLEQLFLLIFPREDLDMILKMDSLQDIKALLTGLFVQDNVNKDAVTDRLASVETDMPLTLRQHRIS
ATSSSEESSNKGQRQLTV
```

Suitably, the protein may comprise the sequence shown as SEQ ID NO: 55; or a variant thereof having at least 80, 85, 90, 95, 98 or 99% sequence identity

#### RECEPTOR

The present invention further provides a nucleic acid construct which comprises (a) a nucleic acid sequence encoding a fusion protein according to the first aspect of the present invention which comprises a PTPN6 SH2 domain, or a truncated protein according to the third aspect of the present invention; and (b) a nucleic acid sequence encoding a receptor comprising an ITIM containing endodomain.

#### CASTRATION SIGNAL

A fusion protein which comprises a protease, as described above, may be co-expressed in a cell with a target receptor which comprises an intracellular protease cleavage site. Cleavage of the target receptor at the protease site will release an intracellular, membrane-distal part of the target receptor.

The target receptor may, for example, be a T-cell receptor (TCR), or a chimeric antigen receptor (CAR).

The receptor may comprise an activatory or co-stimulatory endodomain positioned at the end of the intracellular part of the protein. Cleavage at the protease cleavage site then removes the activatory or co-stimulatory endodomain from the target CAR, reducing or preventing target receptor-mediated T cell activation.

Alternatively, the target receptor may comprise an inhibitory endodomain positioned at the end of the intracellular part of the protein. Cleavage at the protease cleavage site then removes the inhibitory endodomain from the target CAR, "switching-on" the potential for target receptor mediated T cell activation.

The inhibitory endodomain may, for example, comprise a CD148 or CD45 endodomain or an ITIM-containing endodomain from a protein such as PD1, PDCD1, BTLA4, LILRB1, LAIR1, CTLA4, KIR2DL1, KIR2DL4, KIR2DL5, KIR3DL1 or KIR3DL3.

By way of example, the target receptor may comprise the sequence shown as SEQ ID NO: 56, which contains a CAR against CD33 containing an ITIM endodomain from PD-1.

#### SEQ ID NO: 56

```
MAVPTQVLGLLLLWLTDARCDIQMTQSPSSLSASVGDRVTITCRASEDIYFNLVWYQQKPGKAPKLLIYD
TNRLADGVPSRFSGSGSGTQYTLTISSLPEDFATYYCQHYKNYPLTFGQGTKLEIKRSGGGGSGGGGSG
GGGSGGGGSRSEVQLVESGGGLVQPGGSLRLSCAASGFTLSNYGMHWIRQAPGKLEWVSSISLNGGSTY
YRDSVKGRFTISRDNASTLYLQMNSLRAEDTAVYYCAAQDAYTGGYFDYWGQGLTVTVSSMDPATTTKP
VLRTSPSPVHPTGTSQPQRPEDCRPRGSGVSGTGLDFACDIYGVGVGGLLGSLLVLLVWVLAVICSRARGTI
GARRTGQPLKEDPSAVPVFSVDYGELDFQWREKTPEPPVPCVPEQTEYATIVFPSGMGTSSPARRGSDG
PRSAQPLRPEDGHCSWPL
```

Suitably, the protein may comprise the sequence shown as SEQ ID NO: 56; or a variant thereof having at least 80, 85, 90, 95, 98 or 99% sequence identity.

Where the receptor comprises a protease cleavage site between a transmembrane domain and an activating endodomain, the castration signal fusion protein may be used to inhibit the receptor. For instance, a first CAR might be constructed whereby its endodomain is separated from the transmembrane domain by a protease cleavage site. A second CAR recognizing a different antigen might comprise of an ITIM containing endodomain. Recognition of the cognate antigen of the second receptor would result in recruitment of the castration signal fusion protein to the membrane and subsequent cleavage at the protease recognition site. Such cleavage would separate the activating endodomain from the first receptor and prevent activation and signal propagation from said receptor.

This would result in an "AND NOT" type logic gate where a sustained signal would be transmitted only if the first CAR was activated in isolation (i.e. when the first CAR bound its cognate antigen but the second CAR did not bind its cognate antigen). Such 'logic gates' may be useful, for example, because it is relatively rare for the presence (or absence) of a single antigen to effectively describe a cancer, which can lead to a lack of specificity. Targeting antigen expression on normal cells leads to on-target, off-tumour toxicity. In some cancers, a

tumour is best defined by presence of one antigen (typically a tissue-specific antigen) and the absence of another antigen which is present on normal cells. For example, acute myeloid leukaemia (AML) cells express CD33. Normal stem cells express CD33 but also express CD34, while AML cells are typically CD34 negative. Targeting CD33 alone to treat AML is associated with significant toxicity as it depletes normal stem cells. However, specifically targeting cells which are CD33 positive but not CD34 positive would avoid this considerable off-target toxicity.

Potential pairs of antigens for such an 'AND NOT' gate are shown in Table 2.

**TABLE 2**

<b>Disease</b>	<b>TAA</b>	<b>Normal cell which expresses TAA</b>	<b>Antigen expressed by normal cell but not cancer cell</b>
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

By way of example, the receptor which comprises a protease cleavage site between a transmembrane domain and an activating endodomain may be the sequence shown as SEQ ID NO: 57, which contains a CAR against CD19 with a cleavable CD3-zeta endodomain.

**SEQ ID NO: 57**

MSLPVTALLLPLALLLHAARPDIQMTQTTSSLSASLGDRVITISCRASQDISKYLNWYQQKPDGTVKLLIY  
HTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTKLEITKAGGGSGGGGS  
GGGGSGGGGSEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSWIRQPPRKGLEWLGVWGSETTYYN  
SALKSRLTIKDNSKSQVFLKMNSLQTDDTAIYYCAKHYYYGGSYAMDYWGQGTSTVTVSSDPTTTPAPRP  
PTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDI FWVLVVVGGVLACYSLLVTVAFII FWVRCRHR  
RRQAERMAQIKRVVSEKKTAAQAPHRFQKTCSPISGGGSENLYFQMRRVKFSRSADAPAYQQGQNQLYNE  
LNLGRREEYDVLDKRRGRDPGEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGL  
STATKDTYDALHMQALPPR

Suitably, the receptor may comprise the sequence shown as SEQ ID NO: 57; or a variant thereof having at least 80, 85, 90, 95, 98 or 99% sequence identity.

Where the receptor comprises an activating endodomain fused to an inhibitory endodomain via a protease cleavage site, a castration signal fusion protein can be used to activate artificial signalling domains. For instance, a first CAR might be constructed whereby its endodomain



comprises an activating endodomain fused to an inhibitory endodomain via a protease cleavage site. A second CAR recognizing a different antigen might comprise of an ITIM containing endodomain. Recognition of the cognate antigen of the second receptor would result in recruitment of the castration signal fusion protein to the membrane and subsequent cleavage of inhibitory endodomain from the activating endodomain of the first receptor. Cleavage, and thus separation, of the inhibitory domain from the activating domain would allow activation of the first CAR following antigen binding and hence activation of signalling via the first receptor.

This would result in an "AND" type CAR logic gate where productive signalling would occur only if both the first and second receptors were activated. Such 'logic gates' are useful, for example, because 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 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.

Potential pairs of antigens for such an 'AND' logic gate are shown in Table 3.

**Table 3**

<i>Cancer Type</i>	<i>Antigens</i>
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)

By way of example, the receptor which comprises an activating endodomain fused to an inhibitory endodomain via a protease cleavage site may be the sequence shown as SEQ ID NO: 58, which contains a CAR against CD19 with a CD3-zeta endodomain and a cleavable CD148 endodomain.

## SEQ ID NO: 58

MSLPVTALLLPLALLLHAARPDIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDGTVKLLIY  
 HTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTKLEITKAGGGGSGGGGS  
 GGGGSGGGGSEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSWIRQPPRKGLEWLGVIWGSETTYYN  
 SALKSRLTIKDNSKSQVFLKMNSLQTDDTAIYYCAKHYYYGGSYAMDYWGQGTSVTVSSDPTTTPAPRP  
 PTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIFWVLVVGGVLACYSLLVTVAFIIFWVRRVKF  
 SRSADAPAYQQQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI  
 GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPRENLYFQMAVFGCIFGALVIVTVGGFI FWRKKR  
 KDAKNEVSFSQIKPKKSKLIRVENFEAYFKKQQADSNCGFAEEYEDLKLVGISQPKYAAELAENRGKNR  
 YNNVLPYDISRVKLSVQTHSTDDYINANYMPGYHKKDFIATQGPLPNTLKDFFWRMVWEKNVYAIIMLT  
 CVEQGRTKCEEYWPSKQAQDYGDITVAMTSEIVLPEWTIRDFTVKNIQTSESHPLRQFHFTSWPDHGV  
 PDDLLINFRYLVRDYMKSPPESPILVHCSAGVGRGTGTFAIDRLIYQIENENTVDVYGIYDLMHRPL  
 MVQTEDQYVFLNQCVLDIVRSQKDSKVDLIYQNTTAMTIYENLAPVTTFGKTNGLYIA

Suitably, the receptor may comprise the sequence shown as SEQ ID NO: 58; or a variant thereof having at least 80, 85, 90, 95, 98 or 99% sequence identity.

## BLOCKING SIGNAL

The present invention provides a truncated protein which comprises an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based activation motif (ITAM) but lacks a kinase domain

For example, the truncated protein may comprise the ZAP70 SH2 domain but lack the ZAP70 kinase domain. In other words, the present invention provides a truncated protein which: (i) comprises the sequence shown as SEQ ID NO: 2 but does not comprise the sequence shown as SEQ ID NO: 26.

Over-expression of the ZAP70 SH2 domain results in competition with full-length / wild-type ZAP70. Since the truncated ZAP70 cannot propagate signals, signal transmission is reduced in proportion to the ratio between wild-type ZAP70 and the truncated protein. This may be useful to reduce strength of T-cell activation for instance to prevent T-cell over-activation which can result in T-cell exhaustion, activation induced cell death and in a clinical setting can result in cytokine storms.

The present invention also provide a truncated protein which comprises an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based inhibition motif (ITIM) but lacks a phosphatase domain

For example, the truncated protein may comprise the PTPN6 SH2 domain but lack the PTPN6 phosphatase domain. In other words, the present invention provides a truncated protein which:

(i) comprises the sequence shown as SEQ ID NO: 6 but does not comprise the sequence shown as SEQ ID NO: 27.

In this case, ITIM signalling can be reduced in proportion to the ratio between wild-type PTPN6 and the truncated protein. This may be useful to reduce inhibitory signals such as PD1 signalling. This may have application when T-cells are targeting a tumour which over-expresses PDL1 (or similar inhibitory receptors) to evade immune rejection.

The use of a blocking signal or a cross-wire signal as described above, offers a significant advantage over traditional immune checkpoint blockade approaches which typically block a single ligand/receptor interaction, such as PD-L1/PD1, with an antibody. As explained above, the inhibitory immune receptor class contains many members with redundancies and expression patterns which fluctuate with T-cell state. The use of an antibody or a recombinant ligand/receptor may effectively block one inhibitory receptor, but will not affect inhibitory signals transmitted from the rest. Genomic editing of individual inhibitory receptors (Menger et al, Cancer Res. 2016 Apr 15;76(8):2087-93) has a similar limitation. Strategies of fusions between individual inhibitory receptors and co-stimulatory domains also suffer from similar limitations (Liu et al, Cancer Res. 2016 Mar 15;76(6):1578-90).

The method of the present invention will block (and depending on the strategy re-interpret) inhibitory signals transmitted via an ITIM. Hence an entire class of inhibitory signals are modulated. A list of inhibitory receptors which signal through ITIMs is provided in Table II of Odorizzi and Wherry (2012) J. Immunol. 188:2957-2965. They include: PD1, BTLA, 2B4, CTLA-4, GP49B, Lair-1, Pir-B, PECAM-1, CD22, Siglec 7, Siglec 9, KLRG1, ILT2, CD94-NKG2A and CD5.

## NUCLEIC ACID

In one aspect the present invention provides a nucleic acid which encodes a fusion protein or a truncated protein according to the present invention.

As used herein, the terms “polynucleotide”, “nucleotide”, and “nucleic acid” are intended to be synonymous with each other.

It will be understood by a skilled person that numerous different polynucleotides and nucleic acids can encode the same polypeptide as a result of the degeneracy of the genetic code. In addition, it is to be understood that skilled persons may, using routine techniques, make

nucleotide substitutions that do not affect the polypeptide sequence encoded by the polynucleotides described here to reflect the codon usage of any particular host organism in which the polypeptides are to be expressed.

Nucleic acids according to the invention may comprise DNA or RNA. They may be single-stranded or double-stranded. They may also be polynucleotides which include within them synthetic or modified nucleotides. A number of different types of modification to oligonucleotides are known in the art. These include methylphosphonate and phosphorothioate backbones, addition of acridine or polylysine chains at the 3' and/or 5' ends of the molecule. For the purposes of the use as described herein, it is to be understood that the polynucleotides may be modified by any method available in the art. Such modifications may be carried out in order to enhance the *in vivo* activity or life span of polynucleotides of interest.

The terms “variant”, “homologue” or “derivative” in relation to a nucleotide sequence include any substitution of, variation of, modification of, replacement of, deletion of or addition of one (or more) nucleic acid from or to the sequence.

#### NUCLEIC ACID CONSTRUCT

In one aspect the present invention provides a nucleic acid construct which co-expresses a truncated protein or fusion protein of the present invention with another protein. The nucleic acid construct may comprise: a nucleic acid sequence encoding a truncated protein or a fusion protein of the present invention; and a nucleic acid encoding another protein.

The present invention provides a nucleic acid construct which co-expresses a truncated protein or fusion protein of the present invention with a chimeric antigen receptor. The nucleic acid construct may comprise: (i) a nucleic acid sequence encoding a truncated protein or a fusion protein of the present invention; and (ii) a nucleic acid encoding a chimeric antigen receptor.

The chimeric antigen receptor (CAR) may be an activatory CAR comprising an ITAM-containing endodomain, such as CD3 zeta. The CAR may be an inhibitory CAR comprising a “ligation-off” endodomain, as described in WO2015/075469 which may comprise all or part of the endodomain from a receptor-like tyrosine phosphatase, such as CD148 or CD45. The CAR may be an inhibitory CAR comprising a “ligation-on” endodomain, as described in WO2015/075470 which may comprise an ITIM domain.

The fusion proteins and truncated proteins of the invention may be used together with a cell expressing a “logic gate” combination of two or more CARs. An OR gate comprises two activatory CARs as described in WO2015/075468. An AND gate comprises an activatory CAR and a “ligation off” inhibitory CAR, as described in WO2015/075469. An AND not comprises an activatory CAR and a “ligation on” inhibitory CAR, as described in WO2015/075470.

Thus the present invention provides a nucleic acid construct which comprises:

- (i) a nucleic acid sequence encoding a truncated protein or fusion protein of the invention;
- (ii) a first chimeric antigen receptor (CAR); and
- (iii) a second chimeric antigen receptor.

With reference to the transcription signal aspect of the invention, there is provided a nucleic acid construct which comprises (i) a nucleic acid sequence encoding a fusion protein comprising a SH2 domain; and a protease domain; and (ii) a nucleic acid sequence encoding a membrane tethered transcription factor which comprises: a membrane tether; a protease recognition site; and a transcription factor.

With reference to the castration signal aspect of the invention, there is provided a nucleic acid construct which comprises (i) a nucleic acid sequence encoding a fusion protein which comprises an SH2 domain and a protease domain (e.g. a TeV domain); and (ii) a nucleic acid sequence encoding a receptor which comprises a protease cleavage site.

For example, the present invention provides a nucleic acid construct which comprises: (a) a nucleic acid sequence encoding a fusion protein which comprises (i) PTPN6 SH2 domain; and (ii) a protease domain (e.g. a TeV domain); (b) a nucleic acid sequence encoding a receptor which comprises a protease cleavage site; and (c) a nucleic acid sequence encoding a receptor comprising an ITIM containing endodomain.

The receptor may be a T-cell receptor (TCR) or a chimeric antigen receptor (CAR).

Suitably, the protein encoded by nucleic acid sequence (b) may be a T-cell receptor (TCR) or a chimeric antigen receptor (CAR) which comprises: (i) a protease cleavage site between a transmembrane domain and an activating endodomain; or (ii) an activating endodomain fused to an inhibitory endodomain via a protease cleavage site.

Where the nucleic acid construct of the invention, produces discrete polypeptides, such when it coexpresses a fusion protein of the invention and a CAR, it may also comprise a nucleic acid sequence enabling expression of both proteins. For example, it may comprise a sequence encoding a cleavage site between the two nucleic acid sequences. The cleavage site may be self-cleaving, such that when the nascent polypeptide is produced, it is immediately cleaved into the two proteins 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:

SEQ ID NO: 59

RAEGRGSLLTCTGDVEENPGP

or

SEQ ID NO: 60

QCTNYALLKLAGDVESNPGP

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

#### CHIMERIC ANTIGEN RECEPTOR (CAR)

CARs, which are shown schematically in Figure 13, 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 CD8 $\alpha$  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  $\gamma$  chain of the Fc $\epsilon$ R1 or CD3 $\zeta$ . 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 CD3 $\zeta$  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.

CARs typically therefore comprise: (i) an antigen-binding domain; (ii) a spacer; (iii) a transmembrane domain; and (iii) an intracellular domain which comprises or associates with a signalling domain.

#### 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.

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 aspects of the present invention which require two CARs, the first and second CARs may 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.

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.

Since CARs are typically homodimers (see Figure 13a), 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 "AND" and "AND NOT" gates described above, the spacer of the first CAR may be sufficiently different from the spacer of the second CAR in order to avoid cross-pairing but 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 are shown in the following Table:

<b>Stimulatory CAR spacer</b>	<b>Inhibitory CAR spacer</b>
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

## 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. It may be part of or associate with the intracellular domain 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 a CAR comprises 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. Suitable endodomains which contain an ITAM motif are described herein.

## INHIBITORY DOMAIN

In embodiments referred to above as the “AND” gate, the first CAR may comprise an activating endodomain fused to an inhibitory endodomain via a protease cleavage site. As such the inhibitory endodomain inhibits T-cell activation by the first CAR in the absence of activation of the second CAR. Upon activation of the second CAR, the ITIM in the endodomain of the second CAR is phosphorylated and the PTPN6/protease domain fusion protein is recruited to the membrane. This results in cleavage of the first CAR between the activating endodomain and inhibitory endodomain, thus enabling T-cell activation.

The inhibitory endodomains may comprise any sequence which inhibits T-cell signalling by the activating CAR when it is in the same endodomain.

The 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 co-localised with the activating endodomain of the CAR. 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 co-localised with the activating endodomain of the CAR.

## VECTOR

The present invention also provides a vector, or kit of vectors which comprises one or more nucleic acid sequence(s) or construct(s) according to the present invention. Such a vector may be used to introduce the nucleic acid sequence(s) or construct(s) into a host cell so that it expresses the proteins encoded by the nucleic acid sequence or construct.

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.

## CELL

The present invention also relates to an immune cell comprising the fusion protein, truncated protein, nucleic acid and/or nucleic acid construct of the present invention.

The cell may be a cytolytic immune cell.

Cytolytic immune cells can be T cells or T lymphocytes which 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.

Cytolytic 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<sup>+</sup>CD25<sup>+</sup>FoxP3<sup>+</sup> Treg cells) arise in the thymus and have been linked to interactions between developing T cells with both myeloid (CD11c<sup>+</sup>) and plasmacytoid (CD123<sup>+</sup>) 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.

Natural Killer Cells (or NK cells) are a type of cytolytic cell which form 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 cells of the invention may be any of the cell types mentioned above.

T or NK cells expressing the molecules of the invention 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).

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

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

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

The T or NK cell of the invention may be made by:

- (i) isolation of a T or NK cell-containing sample from a subject or other sources listed above; and
- (ii) transduction or transfection of the T or NK cells with one or more a nucleic acid sequence(s) according to the invention.

The T or NK cells may then be purified, for example, selected on the basis of expression of the antigen-binding domain of the antigen-binding polypeptide.

The present invention also provides a cell which comprises a fusion protein or a truncated protein of the invention and a chimeric antigen receptor (CAR).

The chimeric antigen receptor (CAR) may be an activatory CAR comprising an ITAM-containing endodomain, such as CD3 zeta. The CAR may be an inhibitory CAR comprising a "ligation-off" endodomain, as described in WO2015/075469 which may comprise all or part of the endodomain from a receptor-like tyrosine phosphatase, such as CD148 or CD45. The CAR may be an inhibitory CAR comprising a "ligation-on" endodomain, as described in WO2015/075470 which may comprise an ITIM domain.

The fusion proteins and truncated proteins of the invention may be used together with a cell expressing a "logic gate" combination of two or more CARs. An OR gate comprises two activatory CARs as described in WO2015/075468. An AND gate comprises an activatory CAR and a "ligation off" inhibitory CAR, as described in WO2015/075469. An AND not comprises an activatory CAR and a "ligation on" inhibitory CAR, as described in WO2015/075470.

Thus the present invention provides a cell which comprises:

- (i) a nucleic acid sequence encoding a truncated protein or fusion protein of the invention;
- (ii) a first chimeric antigen receptor (CAR); and
- (iii) a second chimeric antigen receptor.

With reference to the transcription signal aspect of the invention, there is provided a cell which comprises (i) a fusion protein comprising an SH2 domain and a protease; and (ii) a membrane tethered transcription factor which comprises: a membrane tether, a protease recognition site; and a transcription factor.

With reference to the castration signal aspect of the invention there is provided a cell which comprises (i) a fusion protein comprising an SH2 domain and a protease; and (ii) receptor which comprises a protease cleavage site.

The receptor may, for example be a T-cell receptor (TCR) or a chimeric antigen receptor (CAR) which comprises: (i) a protease cleavage site between a transmembrane domain and an activating endodomain; or (ii) an activating endodomain fused to an inhibitory endodomain via a protease cleavage site.

## COMPOSITION

The present invention also relates to a pharmaceutical composition containing a plurality of cells 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 cells of the present invention may be capable of killing target cells, such as cancer cells.

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

The 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.

The 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.

The 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 uterus or bladder; brain cancers including gliomas, glioblastoma multiforme and medulloblastomas; 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 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 – Subjugation of the T cell activation pathway to augmented or non-physiological signals**

A number of SH2 domains involved in early T cell signal activation were tested to determine whether T cell activation signals could be subjugated or “hijacked”, such that when a T cell was activated the signal could be modulated or re-transmitted.

The inventors generated several chimeric AKT constructs by linking the kinase domain of AKT to SH2 domains from Zap70, Grap, Grb2 and PLCγ (Figure 8).

In non-transduced (NT) T cells, very low levels of phosphorylation of the endogenous AKT were detectable following treatment with OKT3 to induce cross-linking and activation of the TCR

(Figure 10b:top panel). However, in cells expression the Zap-AKT construct, significant levels of phospho-AKT were observed (Figure 10b:bottom panel).

Linker for activation of T cell (LAT) is a downstream target of ZAP70 and is bound by several SH2-containing proteins, such as Grb2, Grap and PLC $\gamma$ . It was anticipated that the SH2 domains from each of these LAT-binders would also allow the activation signal from CD3-zeta to be hijacked. However, this was not the case.

No TCR-dependent phosphorylation of the AKT kinase domain was observed above levels observed for NT T cells when the AKT kinase domain was linked to the SH2 domains from Grb2, Grap or PLC $\gamma$  (Figure 9a).

This demonstrates that this system of T cell signalling hijacking specifically requires the tandem SH2 domain from a very early T cell signalling molecule, such as Zap70 or Tyrosine-protein phosphatase non-receptor type 6 (PTPN6).

### **Example 2 – Transcriptional Control**

The TeV protease was fused to the Zap70 SH2 domain. A membrane-bound transcription factor was also generated as follows: RQR8 was cloned in frame with the VP16/GAL4 transcription factor separated by a TeV cleavage site. This fusion protein allows release of the VP16/GAL4 transcription factor (which contains a nuclear localizing signal) upon TeV cleavage.

These proteins were both expressed in a T-cell which also expressed a CD19-specific chimeric antigen receptor. To demonstrate that the ZAP70-TeV approach is needed, the transcription factor was co-expressed with a CD19 CAR whose endodomain was replaced by TeV (Figure 11).

T-cells were exposed to CD19 negative and positive targets. Transcriptional activation was measured by a Luciferase cassette responsive to GALv/VP16. Only the condition where a standard CD19 CAR was co-expressed with ZAP-TeV and the membrane tethered transcription factor resulted in selective transcriptional activation upon CD19 recognition. The CD19 CAR fused directly to TeV resulted in constitutive transcriptional activation (Figure 12).

### **Example 3 - PD-1 signal blockade using truncated SHP-1 (PTPN6) or truncated SHP-2**

PBMC cells were transduced as shown in the following table:



<b>Name on Figure 15 key</b>	<b>Description</b>	<b>Construct(s)</b>
NT	Untransduced	-
FMC63	Transduced with CD19 CAR only	SFG.aCD19_fmc63-HCH2CH3w-CD28tmZw
PD1	Transduced with PD1 only	pDual-PD1-GFP
FMC63+PD1	Co-transduced with CD19CAR and PD1	SFG.aCD19_fmc63-HCH2CH3w-CD28tmZw and pDual-PD1-GFP
FMC63-SHP1+PD1	Co-transduced with a) bicistronic construct encoding CD19CAR and truncated SHP1, and b) PD1	SFG.aCD19_fmc63-HCH2CH3w-CD28tm-Zeta_w-2A-dualSH2_SHP-1 and pDual-PD1-GFP
FMC63-SHP2+PD1	Co-transduced with a) bicistronic construct encoding CD19CAR and truncated SHP1, and b) PD1	SFG.aCD19_fmc63-HCH2CH3w-CD28tm-Zeta_w-2A-dualSH2_SHP-2 and pDual-PD1-GFP

The cells were co-cultured for 48 hours with SupT1 cells transduced with CD19, PDL1 or both and IFN $\gamma$  release measured by ELISA. The results are shown in Figure 15.

The presence of PDL1 on SupT1 target cells caused a reduction in IFN $\gamma$  release. There was increased IFN $\gamma$  release with PBMC which expressed CAR together with the truncated SHP-1 or truncated SHP-2 construct compared with those which expressed CAR alone. This indicates that the truncated SHp-1 and SHP-2 constructs successfully inhibited the PDL1 inhibitory signal from the target cells.

#### **Example 4 – PD-1 signal hijack using a fusion of SHP-2 SH2 domains and Zap70 kinase**

PBMC cells were transduced as shown in the following table:

<b>Name on Figure 16 key</b>	<b>Description</b>	<b>Construct(s)</b>
NT	Untransduced	-
FMC63	Transduced with CD19 CAR only	SFG.aCD19_fmc63-HCH2CH3w-CD28tmZw
PD1	Transduced with PD1 only	pDual-PD1-GFP
FMC63+PD1	Co-transduced with CD19CAR	SFG.aCD19_fmc63-HCH2CH3w-

	and PD1	CD28tmZw and pDual-PD1-GFP
FMC63-SHP2Zap70+PD1	Co-transduced with a) bicistronic construct encoding CD19CAR and fusion of SHP2 SH2domains and Zap70 kinase, and b) PD1	SFG.aCD19_fmc63-HCH2CH3w-CD28tm-Zeta_w-2A-dualSH2_SHP-2-Zap70_Kinase and pDual-PD1-GFP

The cells were co-cultured in a 1:1 ratio for 24 hours with SupT1 cells transduced with CD19 or PDL1. IFN $\gamma$  release was measured by ELISA (Figure 16A). An increase in IFN- $\gamma$  production in was seen co-cultures of CAR-SHP2.Zap70 + PD1 transduced T cells with PDL1 SupT1 target cells compared with CAR + PD1 transduced T cells.

A cytotoxicity assay was also conducted in which killing of SupT1 cells was quantified by FACS (Figure 16B). Near complete killing of PDL1 SupT1 targets was observed in co-cultures of PDL1 positive target cells with CAR-SHP2.Zap70 + PD1 transduced T cells. By contrast, killing was not seen with CAR + PD1 alone construct. This indicated that replacing the phosphatase domain of SHP2 with the kinase domain of Zap70 successfully converted the inhibitory PD1 signal to an activatory signal. The SHP-2-Zap70kinase fusion protein therefore successfully hijacked the inhibitory PDL1-PD1 signal and turned it into a T-cell activation signal.

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, cellular immunology or related fields are intended to be within the scope of the following claims.

CLAIMS

1. A cell which comprises a chimeric antigen receptor (CAR) and a signal transduction modifying protein, selected from one of the following:
  - (i) a truncated protein which comprises an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based activation motif (ITAM), but lacks a kinase domain;
  - (ii) a truncated protein which comprises an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based inhibition motif (ITIM) but lacks a phosphatase domain;
  - (iii) a fusion protein which comprises (a) an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based activation motif (ITAM) or from a protein which binds a phosphorylated immunoreceptor tyrosine-based inhibition motif (ITIM); and (ii) a heterologous domain.
2. A cell according to claim 1, wherein the signal transduction modifying protein is a truncated protein which comprises a ZAP70 SH2 domain but lacks a ZAP70 kinase domain.
3. A cell according to claim 1, wherein the signal transduction modifying protein is a truncated protein which comprises an PTPN6 SH2 but lacks a PTPN6 phosphatase domain.
4. A cell according to claim 1, wherein the signal transduction modifying protein is a truncated protein which comprises a SHP-2 SH2 domain but lacks a SHP-2 phosphatase domain.
5. A cell according to claim 1, wherein the signal transduction modifying protein is a fusion protein which comprises (i) an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based activation motif (ITAM); and (ii) a phosphatase domain.
6. A cell according to claim 5, wherein the fusion protein comprises a ZAP70 SH2 domain.
7. A cell according to claim 5 or 6, wherein the fusion protein comprises a PTPN6 or SHP-2 phosphatase domain.
8. A cell according to claim 1, wherein the signal transduction modifying protein is a fusion protein which comprises (i) an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based inhibition motif (ITIM); and (ii) a kinase domain.

9. A cell according to claim 8, wherein the fusion protein comprises an SH2 domain from PTPN6 or SHP-2.
10. A cell according to claim 8 or 9, wherein the fusion protein comprises a Zap70 kinase domain
11. A cell according to claim 8 or 9, wherein the fusion protein comprises an AKT or JAK kinase domain.
12. A cell according to claim 1, wherein the signal transduction modifying protein is a fusion protein which comprises (i) an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based activation motif (ITAM) or from a protein which binds a phosphorylated immunoreceptor tyrosine-based inhibition motif (ITIM); and (ii) a heterologous signalling domain.
13. A cell according to claim 12, wherein the fusion protein comprises an SH2 domain from ZAP70, PTPN6 or SHP-2.
14. A cell according to claim 12 or 13, wherein the heterologous signalling domain is from a signalling molecule which is not usually activated by an ITAM or ITIM containing receptor.
15. A cell according to claim 12, 13 or 14, wherein the heterologous signalling domain is a co-stimulatory domain.
16. A cell according to claim 15 wherein the fusion protein comprises a CD28, OX40 or 41BB co-stimulatory domain.
17. A cell according to claim 12, 13 or 14, wherein the heterologous signalling domain is an inhibitory domain.
18. A cell according to claim 17, wherein the inhibitory domain comprises the endodomain of CD148 or CD45.
19. A cell according to claim 17, wherein the heterologous signalling domain is or comprises the endodomain of ICOS, CD27, BTLA, CD30, GITR or HVEM.

20. A cell according to claim 1, wherein the signal transduction modifying protein is a fusion protein which comprises (i) an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based activation motif (ITAM); and (ii) an ITAM-containing domain.
21. A cell according to claim 20, wherein the fusion protein comprises a ZAP70 SH2 domain.
22. A cell according to claim 20 or 21, wherein the ITAM-containing domain is or comprises the endodomain of CD3-Zeta.
23. A cell according to claim 1, wherein the signal transduction modifying protein is a fusion protein which comprises (i) an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based inhibition motif (ITIM); and (ii) an ITIM-containing domain.
24. A cell according to claim 23, wherein the fusion protein comprises an SH2 domain from PTPN6 or SHP-2.
25. A cell according to claim 23 or 24, wherein the ITIM-containing domain is or comprises the endodomain from PD1, PDCD1, BTLA4, LILRB1, LAIR1, CTLA4, KIR2DL1, KIR2DL4, KIR2DL5, KIR3DL1 or KIR3DL3.
26. A cell according to claim 1, wherein the signal transduction modifying protein is a fusion protein which comprises (i) an SH2 domain from a protein which binds a phosphorylated immunoreceptor tyrosine-based activation motif (ITAM) or from a protein which binds a phosphorylated immunoreceptor tyrosine-based inhibition motif (ITIM); and (ii) a protease domain.
27. A cell according to claim 26, wherein the fusion protein comprises an SH2 domain from ZAP70, PTPN6 or SHP-2.
28. A cell according to claim 26 or 27, wherein the protease domain is or comprises Tobacco Etch Virus Protease (TeV).
29. A cell according to any of claims 26 to 28, which also comprises a membrane-tethered transcription factor having a protease cleavage site.
30. A cell according to claim 29, wherein cleavage at the protease cleavage site releases the transcription factor leading to increased expression of a target gene.

31. A cell according to claim 30, wherein the target gene encodes a cytokine.
32. A cell according to claim 31, wherein the cytokine is selected from the following group: IL-2, IL-7, IL-15 and IL-12.
33. A cell according to any of claims 26 to 28 wherein the chimeric antigen receptor (CAR) is a target CAR which comprises an intracellular protease cleavage site.
34. A cell according to claim 33, wherein the target CAR comprises an activatory or co-stimulatory endodomain and cleavage at the protease cleavage site removes the endodomain from the target CAR.
35. A cell according to claim 33, wherein the target CAR comprises an inhibitory endodomain and cleavage at the protease cleavage site removes the inhibitory endodomain from the target CAR.
36. A cell according to claim 35, wherein the inhibitory endodomain comprises a CD148 or CD45 endodomain.
37. A cell according to claim 1 which comprises two CARs: an activating CAR comprising an ITAM-containing endodomain; and a target CAR as defined in any of claims 33 to 36.
38. A cell according to claim 1, which comprises two CARs: an inhibitory CAR comprising an ITIM-containing endodomain; and a target CAR as defined in any of claims 33 to 36.
39. A nucleic acid construct, which comprises:
  - a first nucleic acid sequence encoding a chimeric antigen receptor; and
  - a second nucleic acid sequence encoding a truncated protein or a fusion protein as defined in any preceding claim.
40. A nucleic acid construct according to claim 39 which also comprises a third nucleic acid sequence encoding a membrane-tethered transcription factor as defined in any of claims 29 to 32.
41. A nucleic acid construct according to claim 39 which also comprises a third nucleic acid sequence encoding a target CAR as defined in any of claims 33 to 36.

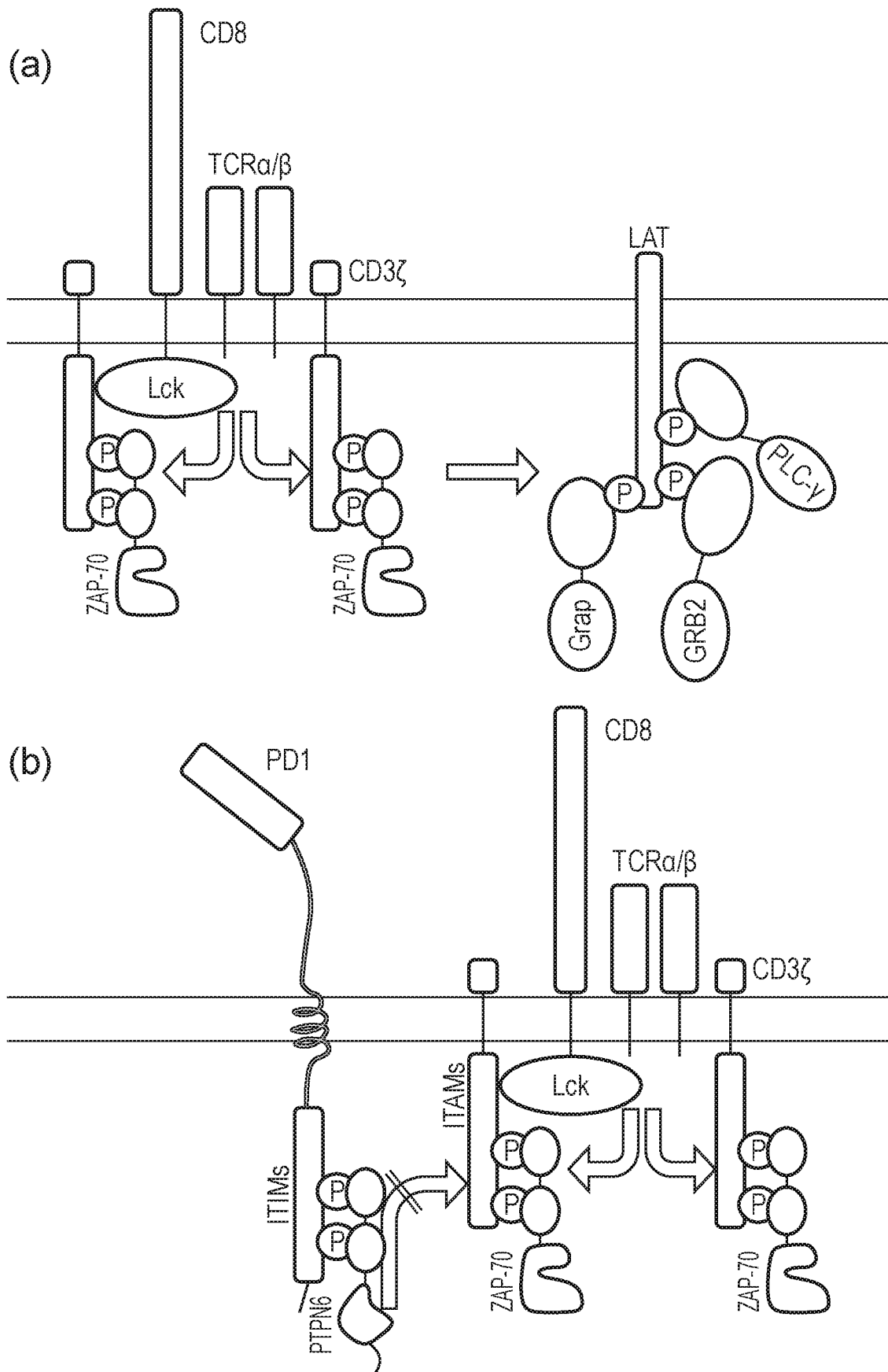
42. A nucleic acid construct according to claim 41 which also comprises a fourth nucleic acid sequence encoding an activating CAR as defined in claim 37 or an inhibitory CAR as defined in claim 38.
43. A vector which comprises a nucleic acid construct according to any of claims 39 to 42 or first and second, and optionally third and/or fourth, nucleic acid sequences as defined in any of claims 39 to 42.
44. A set of vectors which comprises first and second, and optionally third and/or fourth, nucleic acid sequences as defined in any of claims 39 to 42.
45. A vector or set of vectors according to claim 43 or 44, which is/are retroviral or lentiviral vector(s).
46. A pharmaceutical composition comprising a plurality of cells according to any of claims 1 to 38.
47. A pharmaceutical composition according to claim 46 for use in treating and/or preventing a disease.
48. A method for treating and/or preventing a disease, which comprises the step of administering a pharmaceutical composition according to claim 46 to a subject.
49. A method according to claim 48, which comprises the following steps:  
(i) isolation of a cell containing sample from a subject;  
(ii) transduction or transfection of the cells with a nucleic acid construct according to claim 41 or 42, a vector or set of vectors according to any of claims 43 to 45; and  
(iii) administering the cells from (ii) to the subject.
50. The use of a pharmaceutical composition according to claim 46 in the manufacture of a medicament for the treatment and/or prevention of a disease.
51. A pharmaceutical composition for use according to claim 47 or a method according to claim 48 or 49 or a use according to claim 50, wherein the disease is cancer.

52. A method for making a cell according to any of claims 1 to 38, which comprises the step of introducing: a nucleic acid construct according to claim 41 or 42, a vector or set of vectors according to any of claims 43 to 45, into the cell.

53. A method according to claim 52, wherein the cell is from a sample isolated from a subject.



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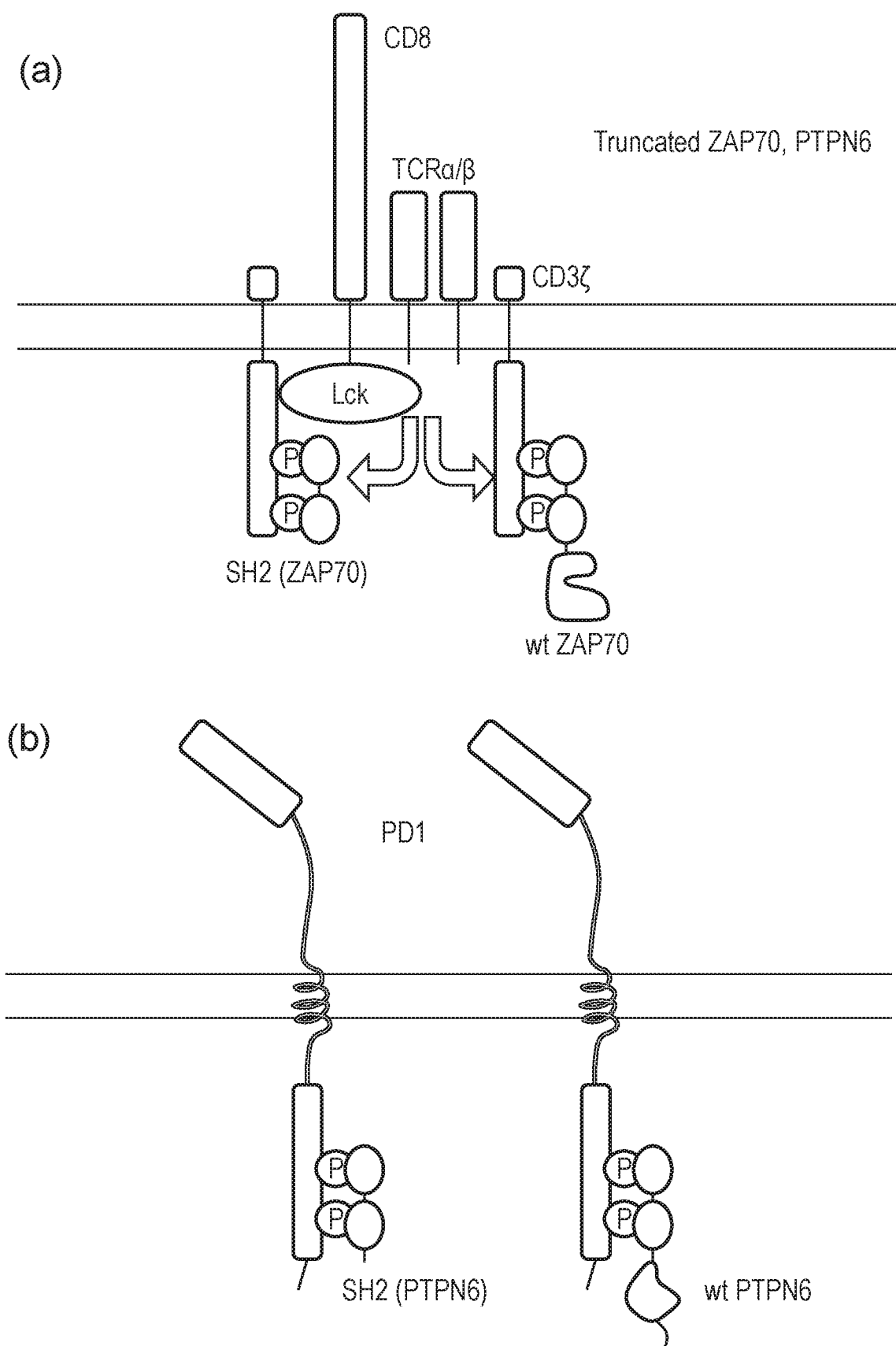


FIG. 2

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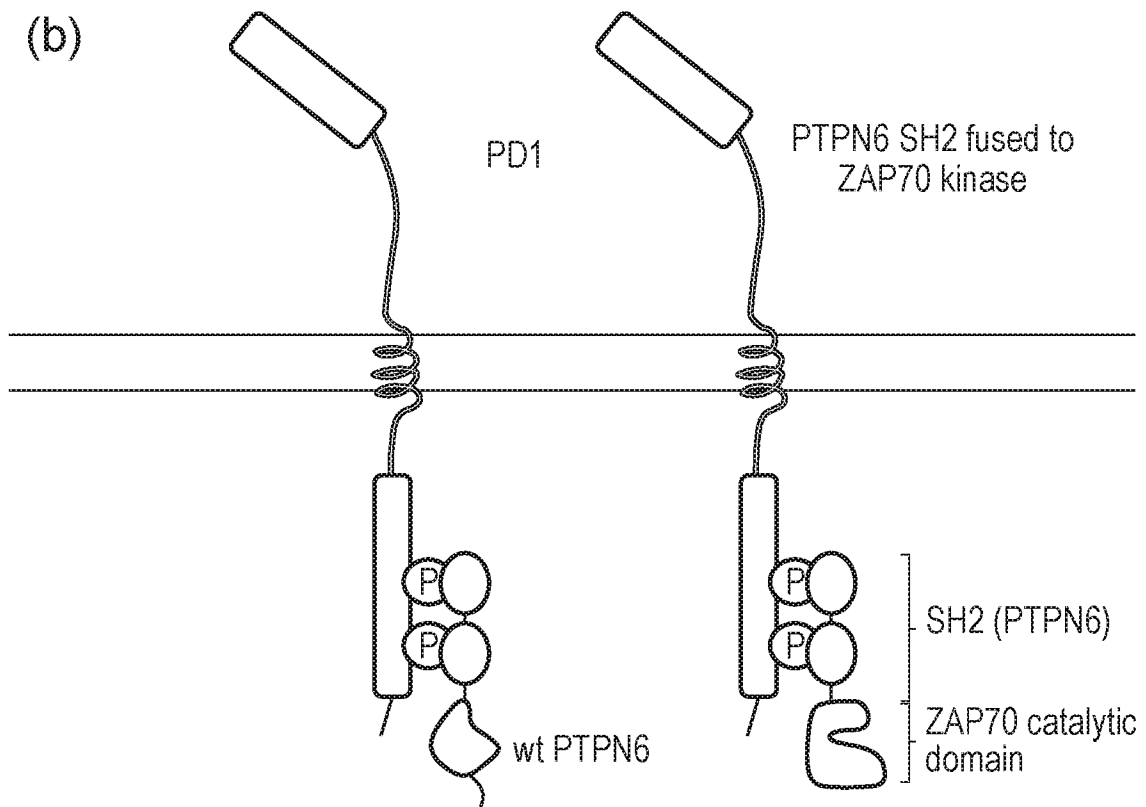
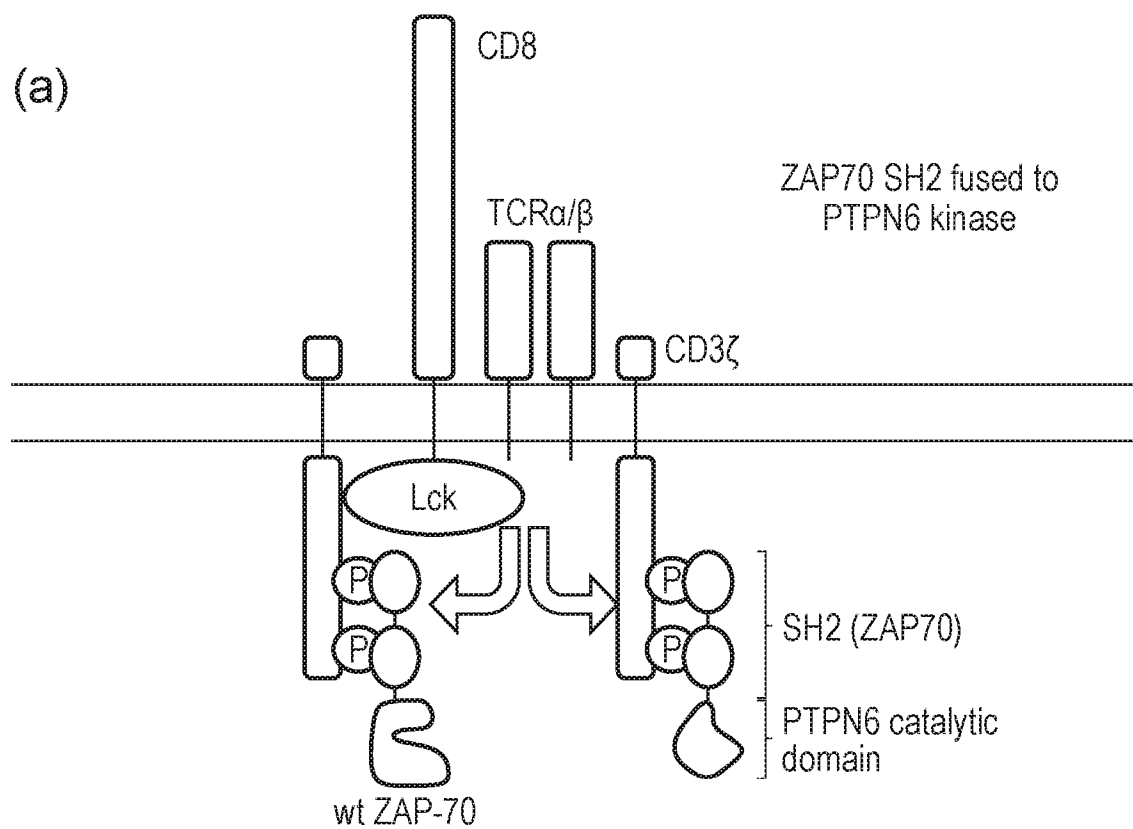


FIG. 3

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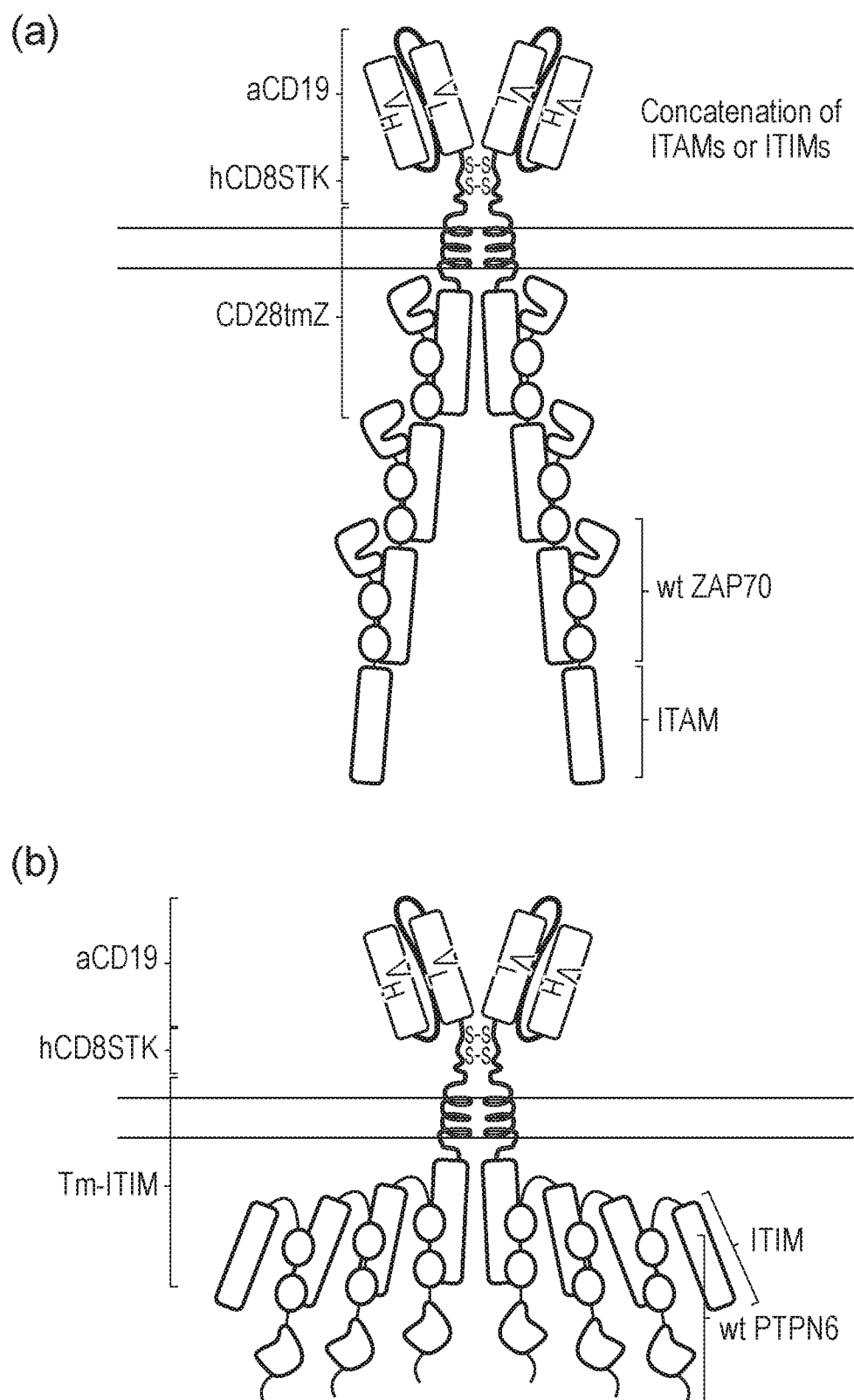


FIG. 4

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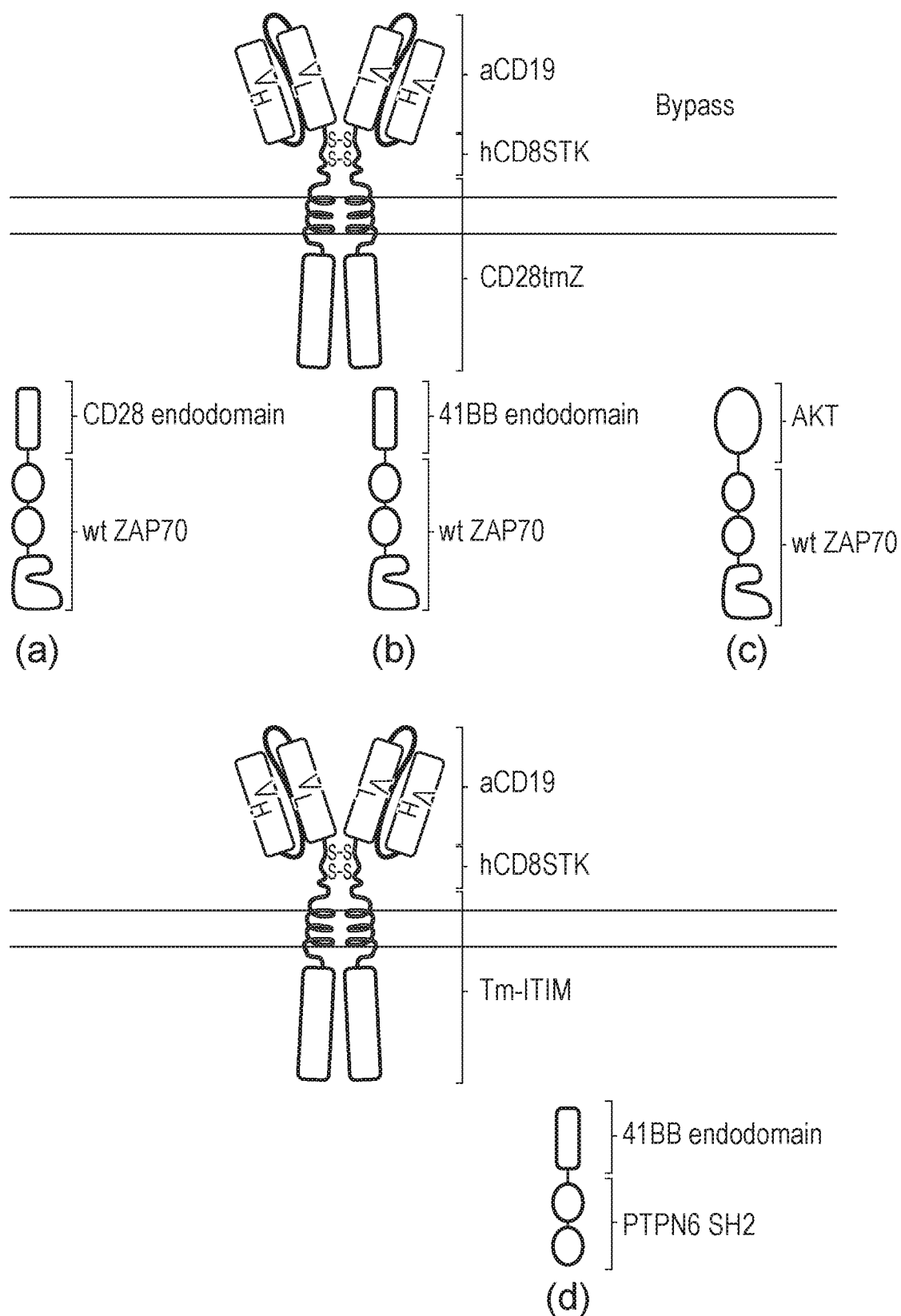


FIG. 5

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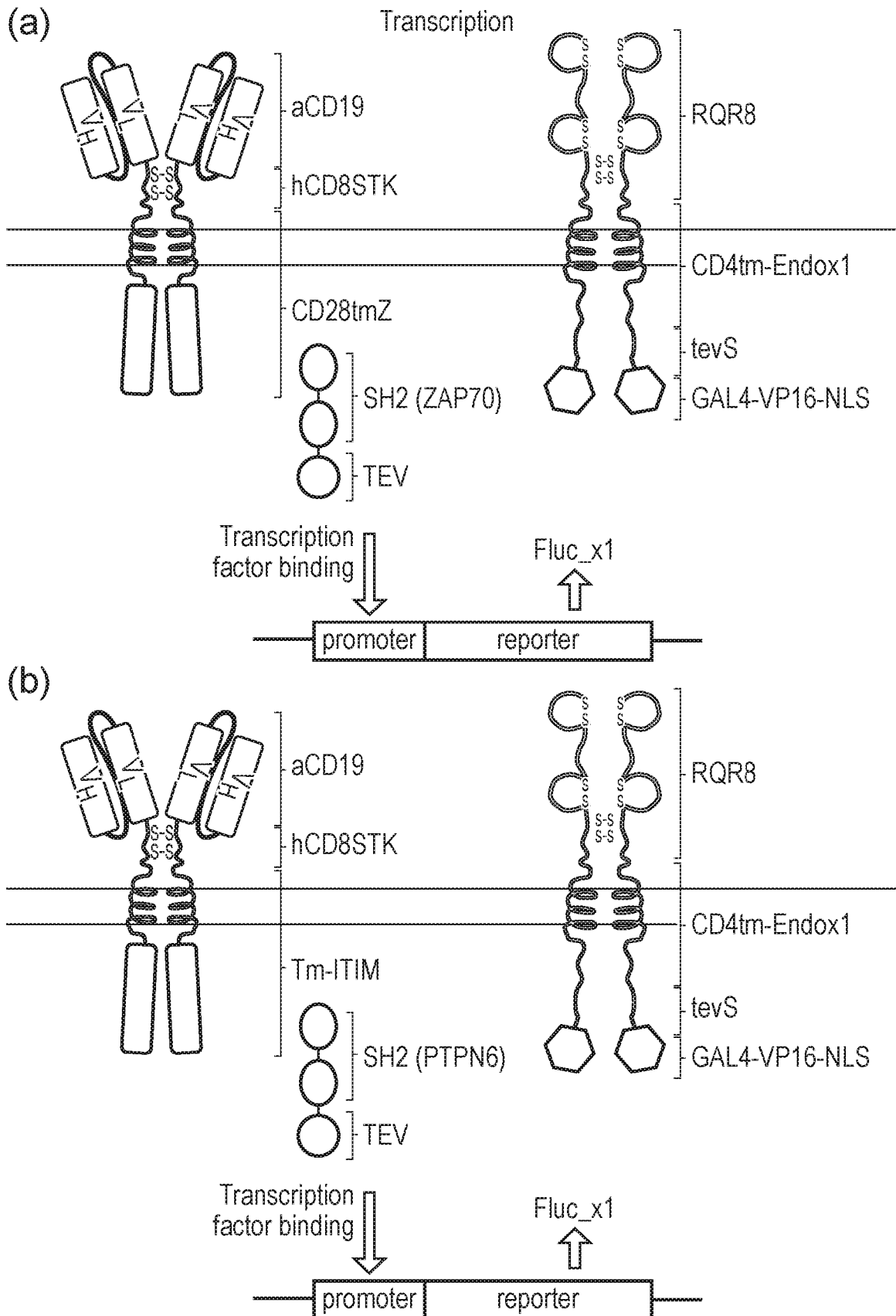


FIG. 6

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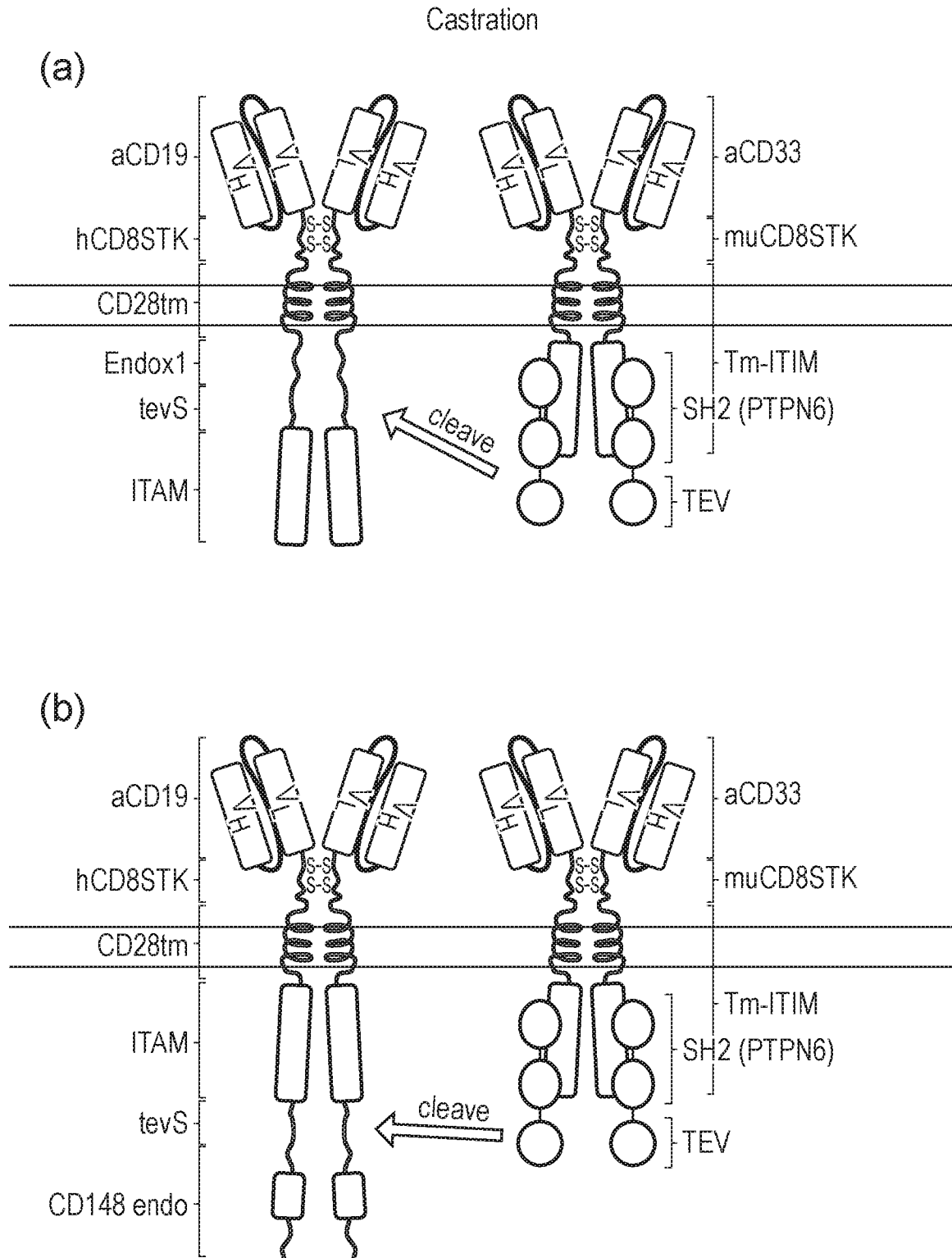


FIG. 7

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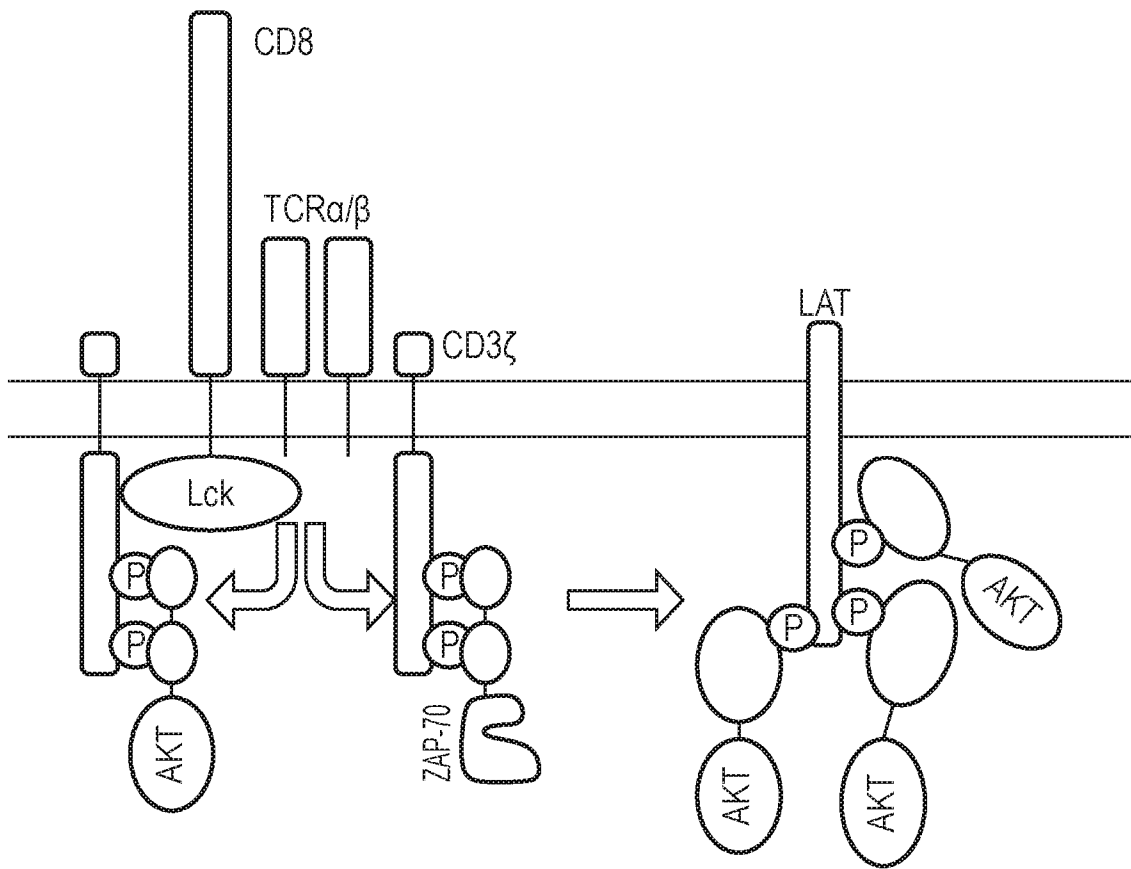


FIG. 8



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(a)

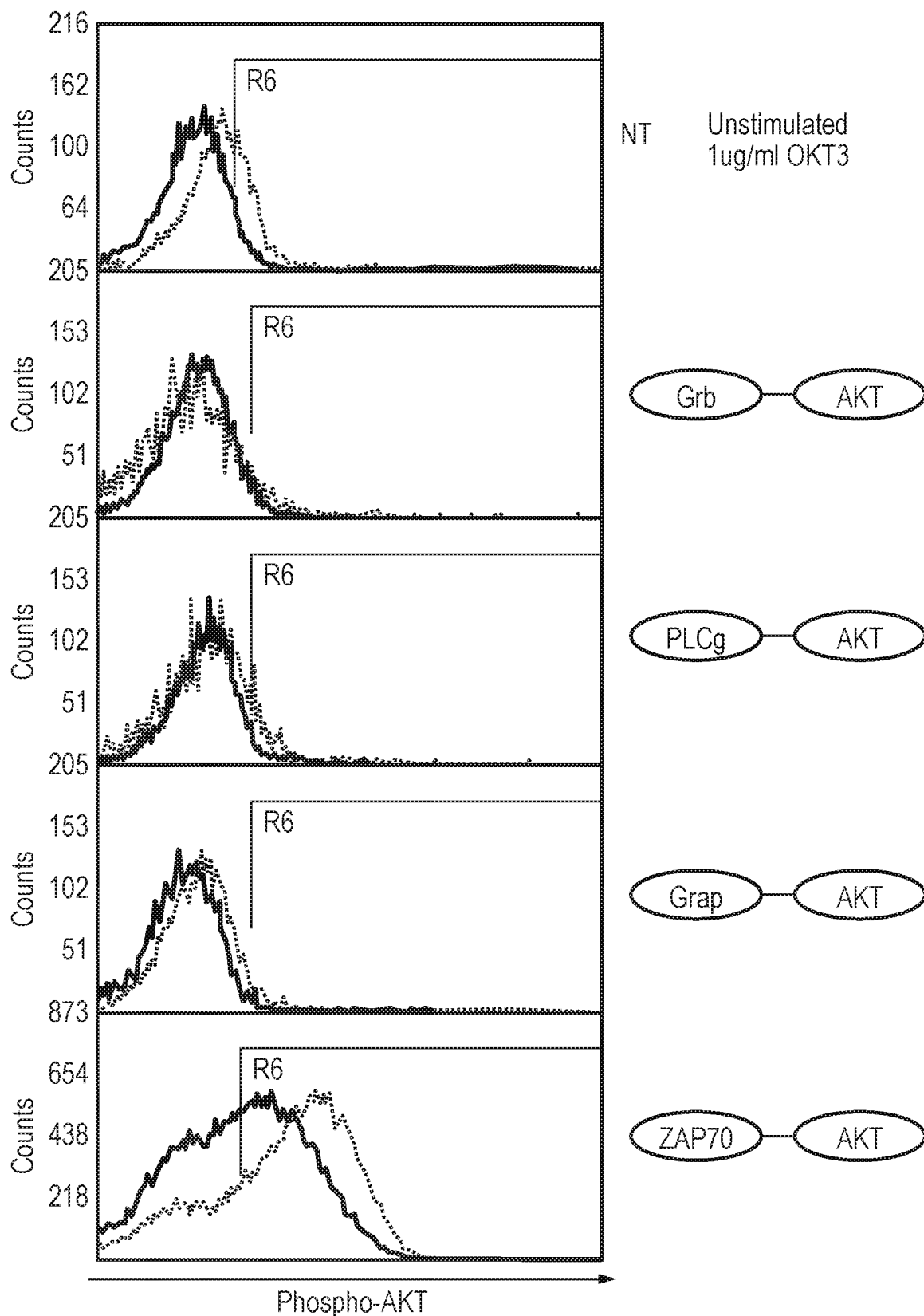


FIG. 9

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(b)

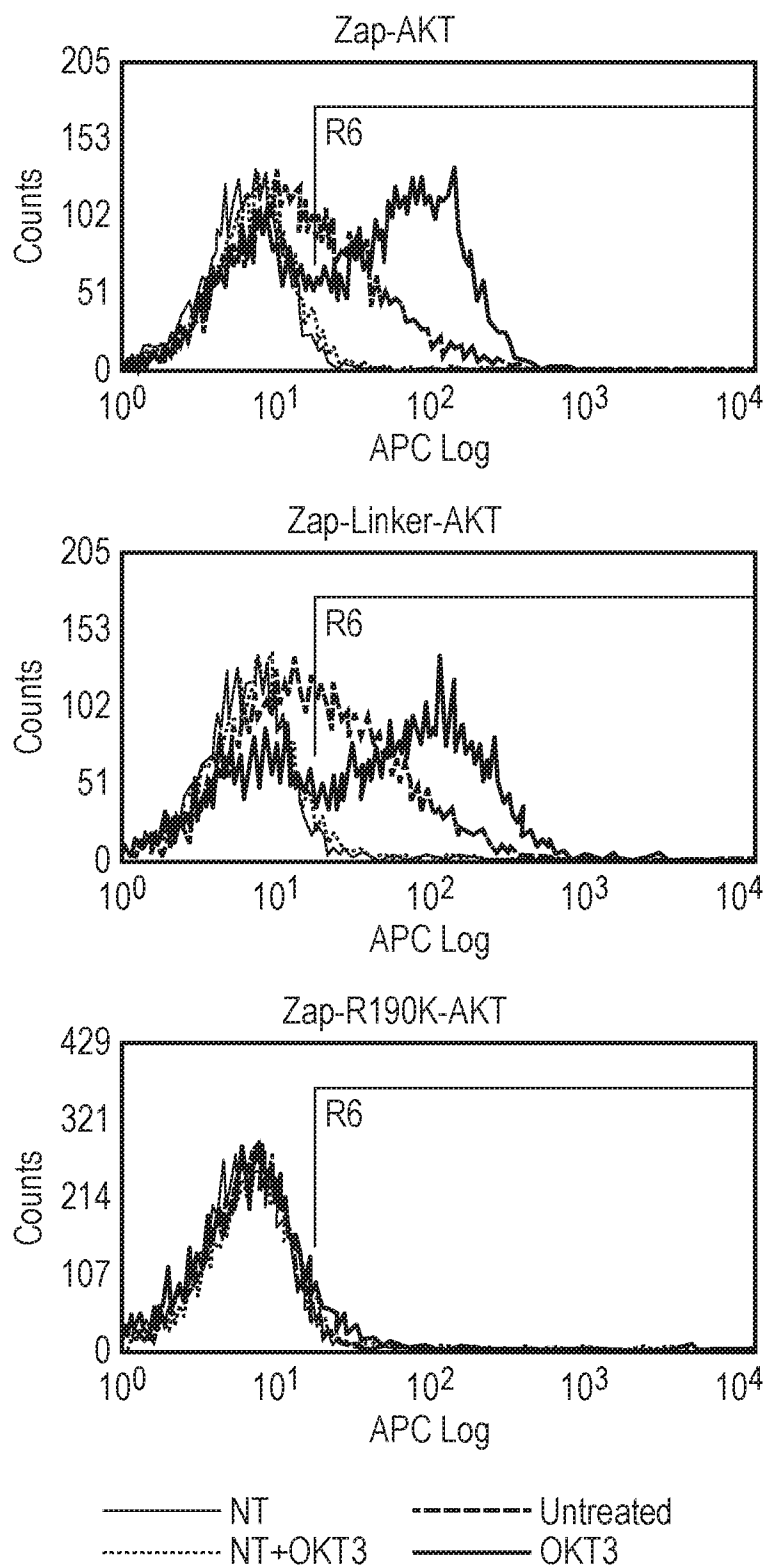
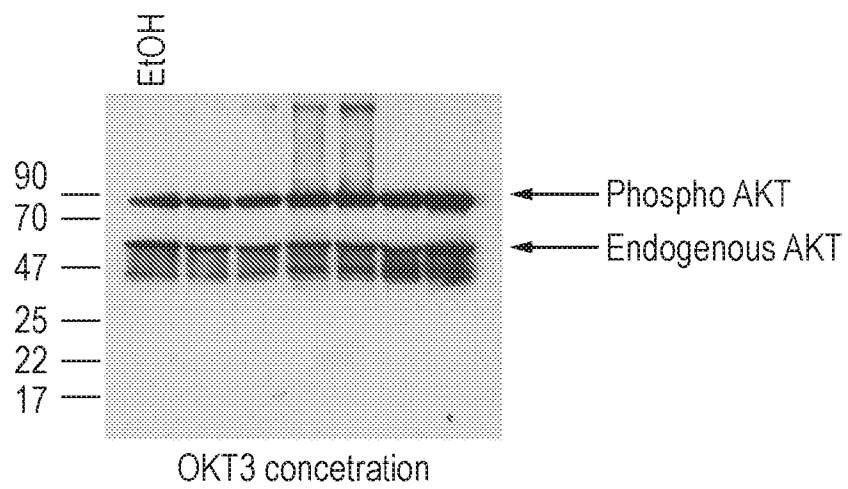


FIG. 9 (Continued)

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(a)



(b)

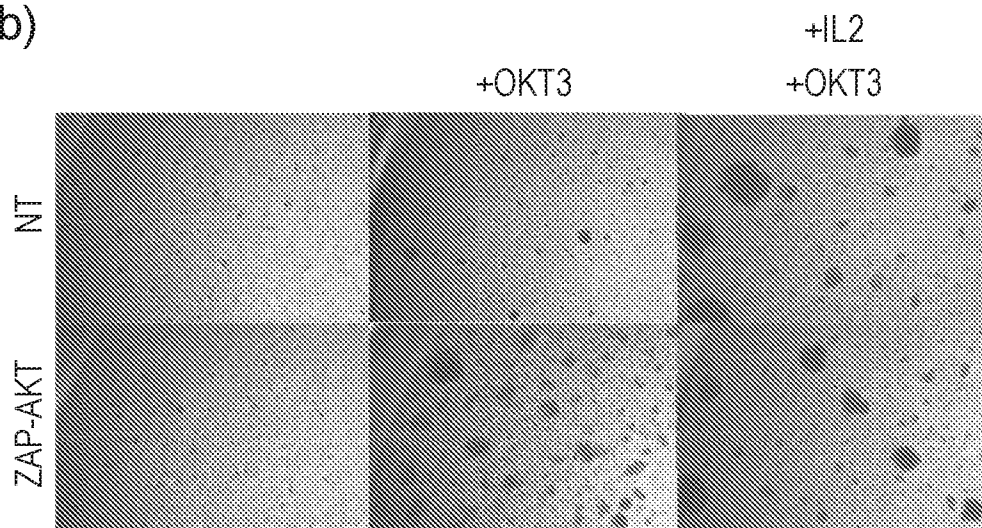


FIG. 10

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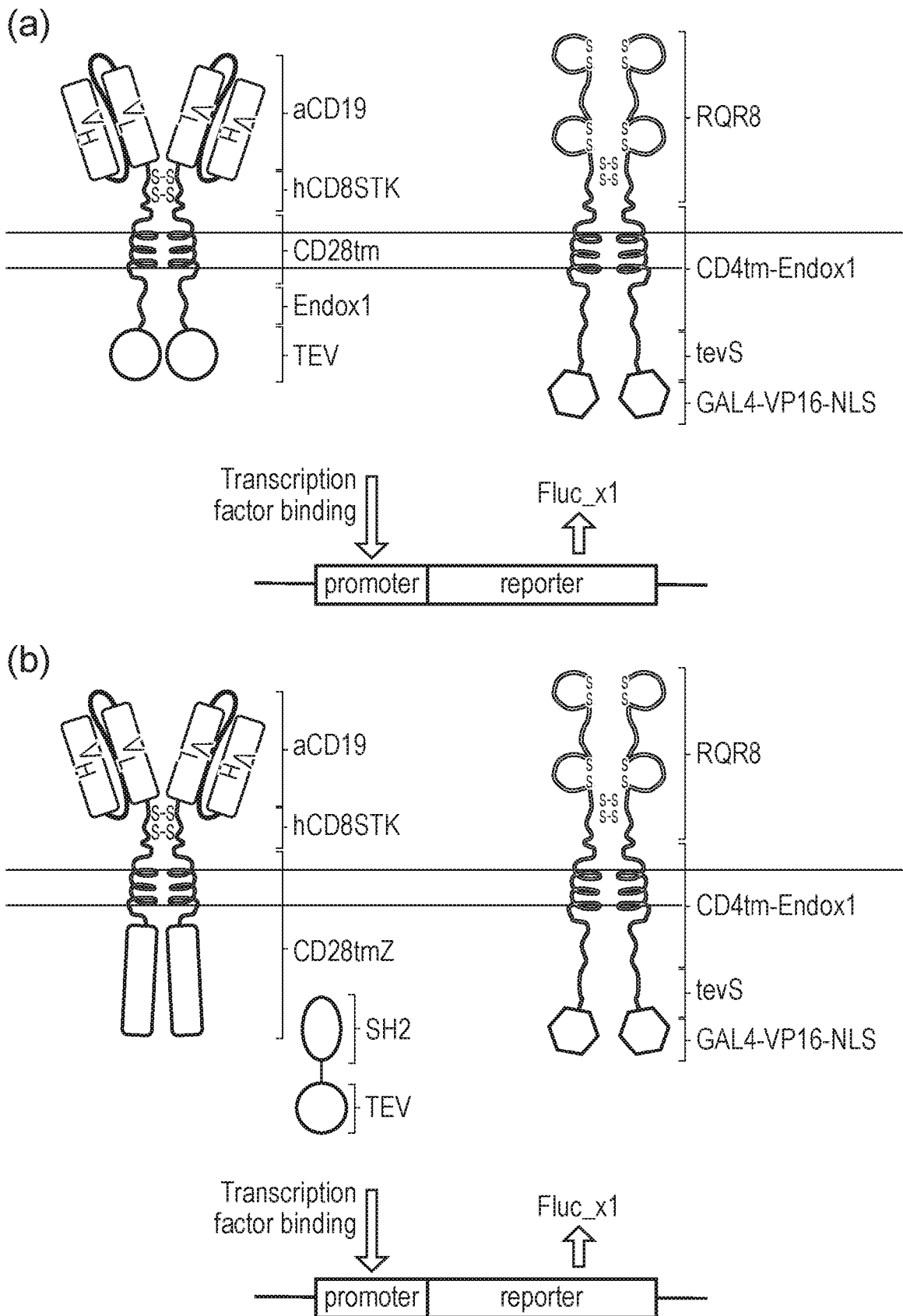


FIG. 11

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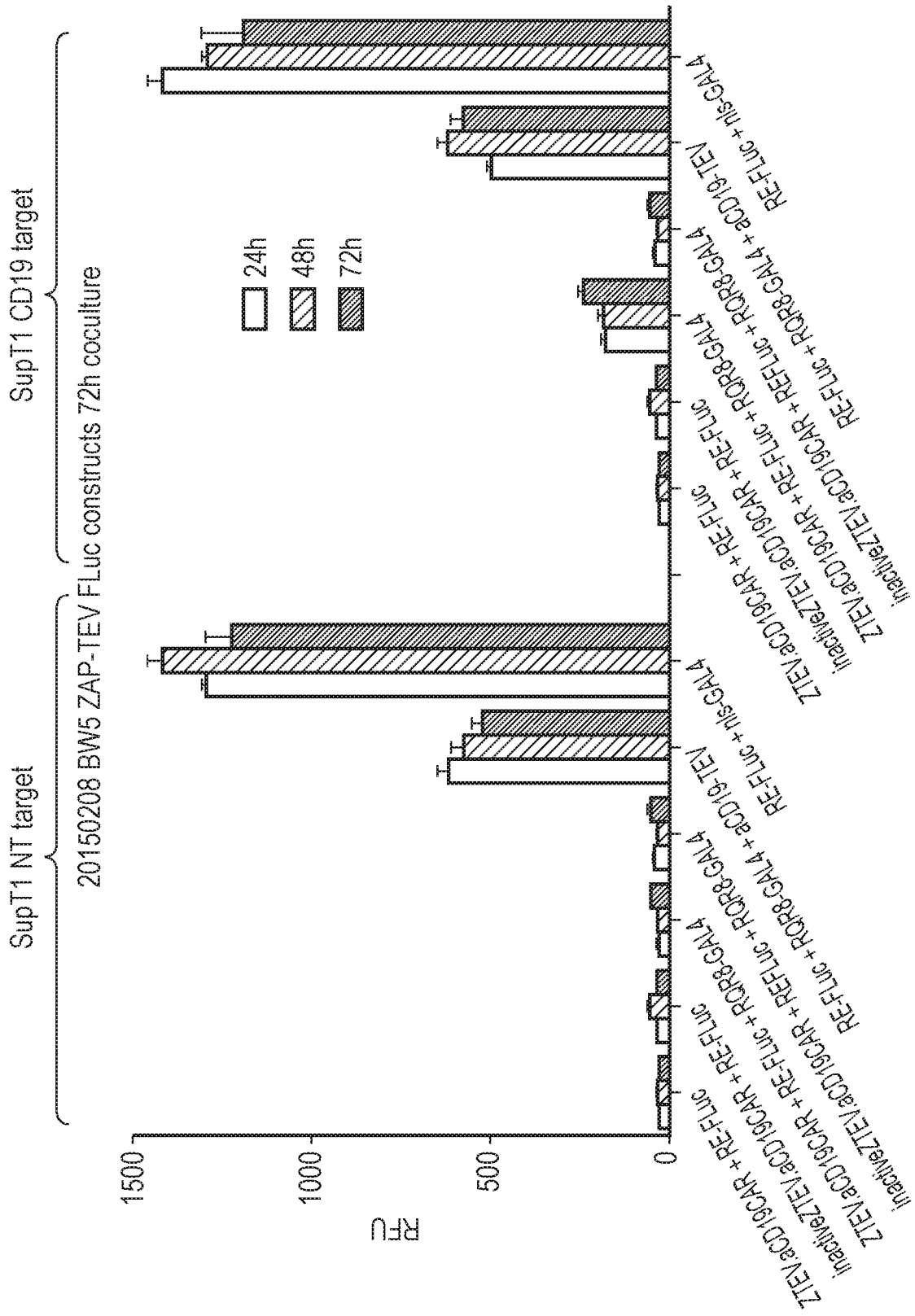


FIG. 12

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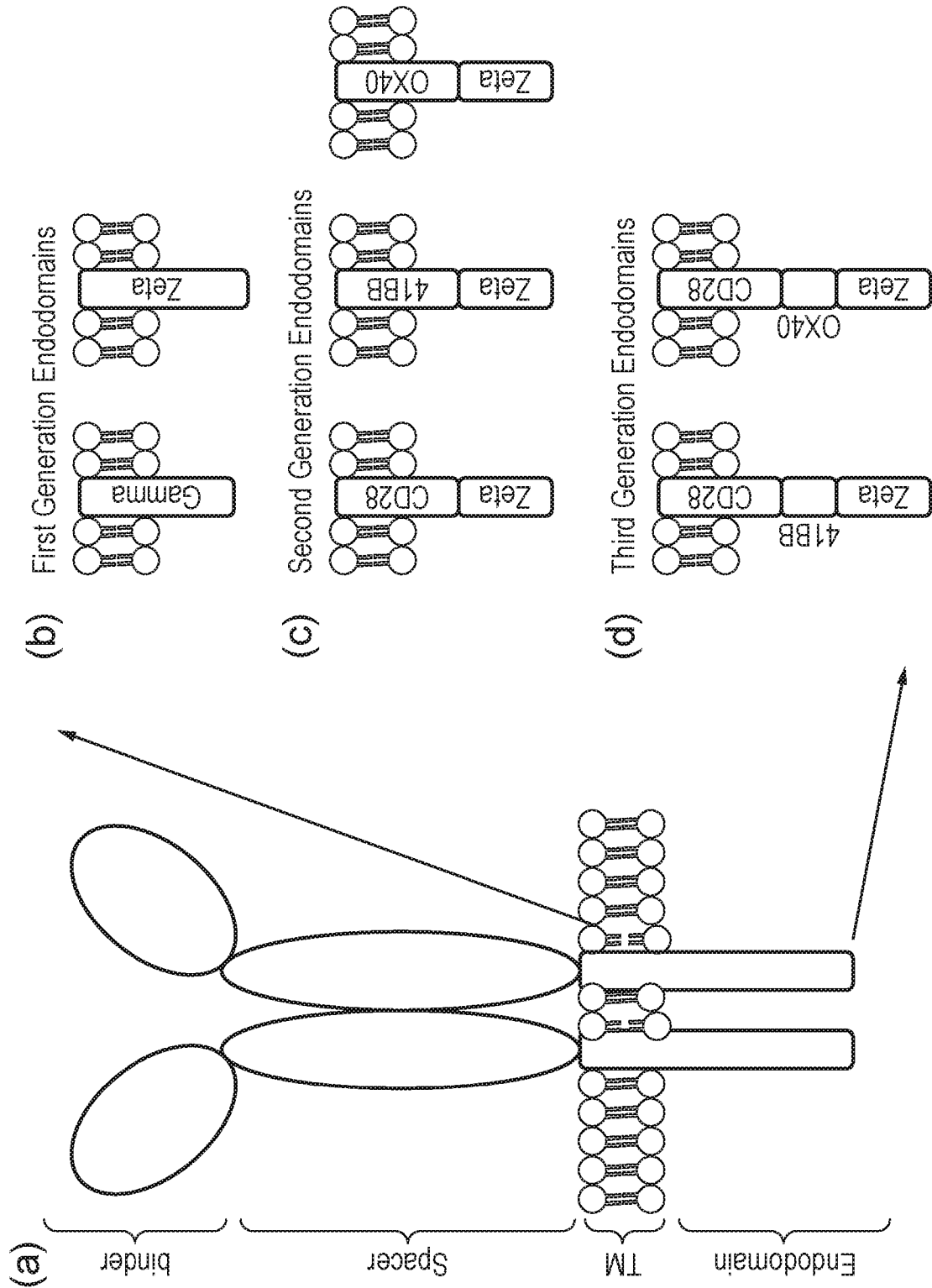


FIG. 13

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&gt;dZAP\_SH2 (SEQ ID No. 2)

```

MPDPAAHLPFFYGSISRAEAEHLKLAGMADGLFLLRQCLSLGGYVLSLVHDVRFHHFPIERQLNGTYA
AGGKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQPGVDFCLRDAMVRDYVRQTWKLEGEALE
QAIISQAPQVEKLIATTAHERMPWYHSSLTREEAERKLYSGAOTDQKFLLRPRKEQGTIALSLIYGKTVYHY
LISQDKAGKYCIPEGTKFDTLWQLVEYLKLLKADGLIYCLKEACPNSSASNASGAAAPTLPAPSTLTHP

```

MPD – ZAP70 SH2 domain

&gt;dPTPN6\_SH2 (SEQ ID No. 6)

```

MVRWFHRDLISGLDAETLLKGRGVHGSFLARPSRKNOGDFSLSVRVGDQVTHIRIQNSGDFYDLYGGEKE
ATLTTELVEYYTQQQGVLDQDRDGTIIHLKYPLNCSDPTSERWYHGHMSGGQAETLLOAKGEPWTFVLRES
LSQPGDFVLSVLSQPKAGPGSPLRVTHIKVMCEGGRYTVGGLETDFSLDLEHFKKTGIEEASGAFVYL
RQPY

```

MVR – PTPN6 SH2 domain

&gt;ZAP\_SH2-PTPN6 (SEQ ID No. 30)

```

MPDPAAHLPFFYGSISRAEAEHLKLAGMADGLFLLRQCLSLGGYVLSLVHDVRFHHFPIERQLNGTYA
AGGKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQPGVDFCLRDAMVRDYVRQTWKLEGEALE
QAIISQAPQVEKLIATTAHERMPWYHSSLTREEAERKLYSGAOTDQKFLLRPRKEQGTIALSLIYGKTVYHY
LISQDKAGKYCIPEGTKFDTLWQLVEYLKLLKADGLIYCLKEACPNSSASNASGAAAPTLPAPSTLTHP
GGSGGGSGGGSGGGSGGGSGGFEWEEFESLQKQEVKNLHORLEGQRPENKGKNRYKNILPFDHSRVILOGRD
SNIPGSDYINANYIKNOLLGPDENAKTYIASQGCEATVNDFWQMAWQENS RVIVMTTREV EKG R NKC
VPYWPVEVGMQRAYGPYSVTNCGEHDTEYKLR TLQVSP LDNGDLREIWHYQYLSWPDHGV PSEPGGV
LSFLDQINQRQESLPHAGPIIVHCSAGIGRTGTIIVIDMLMENISTKGLDCDIDIQKTQM VRAQRSGMVC
TEAQYKFIYVAIAQFIETTKK

```

MPD – ZAP70 SH2 domain

SGG - Linker

FEW - PTPN6 kinase

&gt;PTPN6\_SH2-ZAP (SEQ ID No. 29)

```

MVRWFHRDLISGLDAETLLKGRGVHGSFLARPSRKNOGDFSLSVRVGDQVTHIRIQNSGDFYDLYGGEKE
ATLTTELVEYYTQQQGVLDQDRDGTIIHLKYPLNCSDPTSERWYHGHMSGGQAETLLOAKGEPWTFVLRES
LSQPGDFVLSVLSQPKAGPGSPLRVTHIKVMCEGGRYTVGGLETDFSLDLEHFKKTGIEEASGAFVYL
RQPYSGGGSGDPEELKDKKFLKRDNLLIADIELGCGNFGSVRQGVYRMKKQIDVAIKVLKQGTEKAD
TEEMMREAQIMHQLDNPYIVRLIGVCQAEALMLVMEMAGGGPLHKFLVGKREEIPVS NVAELLHOVS
MGMKYLEEKNFVHRDLAARNVLLVNRHYAKISDFGLSKALGADDSY TARSAGKWPLK WYAP ECINFRK
FSSRSDVWSYGV TMWEALSYGOKPYKKMKGPVMAFIEQGKRMECPPECPELYALMSDCWYIKWED
RPDFLTVEQRM RACYSLASKVEGPPGSTQKAEAA

```

MVR – PTPN6 SH2 domain

SGG - Linker

FIG. 14

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DPE - ZAP70 kinase

&gt;ZETA-ZAP (SEQ ID No. 14)

```

MRRVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDRRGRDPENMGGKPRRKNPQEGLYNELQKD
KMAEAYSEIGMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPRSGGGGSGGGGSGGGGSGGG
GSMPPDPAHLPPFFYGSISRAEAEHLKLAGMADGLFLLRQCLSLGGYVLSLVHDVRFHHFPIERQLNGTY
AIAGGKAHCGPAELCEFYSRDPDGLPCNLKPCNRPSPGLEPQPGVDFCLRDAMVRDYVRQTWKLEGEAL
EQAIISQAPQVEKLIATTATHERMPWYHSSLTREEAERKLYSGAQTGDKFLLRPRKEQGTALSLIYGKTVYH
YLISQDKAGKYCIPEGTKFDTLWQLVEYLKLLKADGLIYCLKEACPNSSASNASGAAAPTLPAPSTLTHPQR
RIDTLNSDGYTPEPARITSPDKPRMPMDTSVYESPYSDPEELKDKKFLKRDNLLIADIELGCGNFGSVRO
GVYRMRKQIDVAIKVLKQGTAKADTEEMMREAQIMHQLDNPIYVRLIGVCQAEALMLVMEMAGGGP
LHKFLVGKREEIPVSNVAELLHQVSMGMKYLEEKNFVHRDLAARNVLLVNRHYAKISDFGLSKALGADDS
YYTARSAGKWPLKWAYPECINFRKFSSRSDVWSYGVTMWEALSYGQPKYKMKKGPEVMAFIEQGGRM
ECPECEPELYALMSDCWIYKWEDRPDLTVEQMRACYSLASKVEGPPGSTQKAEAAACA

```

MRR - CD3Zeta endodomain

SGG - Linker

MPD - full-length ZAP70

&gt;PD1\_endo-PTPN6 (SEQ ID No. 25)

```

MTGOPLKEDPSAVPVFSVDYGELDFQWREKTPEPPVPCVPEQTEYATIVFPSGMGTSSPARRGSADGPR
SAQPLRPEDGHCSWPLSGGGGSGGGGSGGGGSGGGGSMVRWFHRDLGLDAETLLKGRGVHGSFLA
RPSRKNOGDFLSVRVGDQVTHIRIONSGDFYDLYGGEKFATLTVEYYTQQQGVLDQDRDGTIIHLKYP
NCSDPTSERWYHGHMSGGQAETLLQAKGEPWTFVLRESLSQPGDFVLSVLSQPKAGPGSPLRVTHIKV
MCEGGRYTVGGLETDFSLTDLVEHFKKTGIEEASGAFVYLRQPYATRVNAADIENRVLELNKKQESD
KAGFWEEFESLQKQEVKNLHQRLEGQRPENKGNRYKNILPFDHSRVILQGRDSNIPGSDYINANYIKNO
LLGPDENAKTYIASOGCLEATVNDFWQMAWQENS RVIVMTT REVEKGRNKCVPYWPVEVGMQRAYGP
YSVTNCGEHDTEYKLRITLQVSPLDNGDLIREIWHYQYLSWPDHGVPSEPGGVLSFLDQINQROESLPH
GPIIVHCSAGIGRTGTIIVIDMLMENISTKGLDCDIDIQTIQMVRAQRSGMVQTEAQYKFIYVAIAQFIET
KKKLEVLQSQKGQSEYGNITYPPAMKNAHAKASRTSSKHKEDVYENLHTKNKREEKVKKQRSADKEKSK
GSLKRK

```

MTG - PD1 endodomain

SGG - Linker

MVR - full length PTPN6

&gt;CD28-ZAP (SEQ ID No. 40)

```

MRSKRSLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSGGGGSGGGGSGGGGSGGGGSMPD
PAHLPPFFYGSISRAEAEHLKLAGMADGLFLLRQCLSLGGYVLSLVHDVRFHHFPIERQLNGTYAIAGG
KAHCGPAELCEFYSRDPDGLPCNLKPCNRPSPGLEPQPGVDFCLRDAMVRDYVRQTWKLEGEALEQAIIS
QAPQVEKLIATTATHERMPWYHSSLTREEAERKLYSGAQTGDKFLLRPRKEQGTALSLIYGKTVYHYLISQ
DKAGKYCIPEGTKFDTLWQLVEYLKLLKADGLIYCLKEACPNSSASNASGAAAPTLPAPSTLTHPQRIDTL
NSDGYTPEPARITSPDKPRMPMDTSVYESPYSDPEELKDKKFLKRDNLLIADIELGCGNFGSVROGVYR
MRKKQIDVAIKVLKQGTAKADTEEMMREAQIMHQLDNPIYVRLIGVCQAEALMLVMEMAGGGPLHKF
LVGKREEIPVSNVAELLHQVSMGMKYLEEKNFVHRDLAARNVLLVNRHYAKISDFGLSKALGADDSYYTA

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FIG. 14 (continued)



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RSAGKWPLKWYAPECINFRKFSSRSVDVWSYGVTMWEALSYGQKPYKKMKGPVMAFIEQGKRMECPP  
 ECPPELYALMSDCWIYKWEDRPDLTVEQMRACYYSLASKVEGPPGSTQKAEAAACA

MRS - CD28 endodomain

SGG - Linker

MPD - full-length ZAP70

>41BB-ZAP (SEQ ID No. 41)

MKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELSGGGGSGGGGSGGGGSGGGGSGMPD  
 PAAHLPPFFYGSISRAEAEHLKLAGMADGLFLLRQCLRSLGGYVLSLVHDVRFHHFPIERQLNGTYAIAGG  
 KAHC GPAELCEFYSRDPDGLPCNLKPCNRPSGLEPQPGVDFCLRDAMVRDYVRQTWKLEGEALEQAIIS  
 QAPQVEKLIATTAHERMPWYHSSLTREEAERKLYSGAQTGKFLRPRKEQGTALSLIYGKTVYHYLISQ  
 DKAGKYCIPEGTKFDTLWQLVEYLKADGLIYCLKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTL  
 NSDGYTPEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLFKLRDNLIIADIELGCGNFGSVRQGVYR  
 MRKKQIDVAIKVLKOGTEKADTEEMMREAQIMHQLDNPYIVRLIGVCQAEALMLVMEMAGGGPLHKF  
 LVGKREEIPVSNVAELLHQVSMGMKYLEEKNFVHRDLAARNVLLVNRHYAKISDFGLSKALGADDSYTTA  
 RSAGKWPLKWYAPECINFRKFSSRSVDVWSYGVTMWEALSYGQKPYKKMKGPVMAFIEQGKRMECPP  
 ECPPELYALMSDCWIYKWEDRPDLTVEQMRACYYSLASKVEGPPGSTQKAEAAACA

MKR - 41BB endodomain

SGG - Linker

MPD - full-length ZAP70

>OX40-ZAP (SEQ ID No. 42)

MRDQRLPPDAHKKPPGGGSFRTPIQEEQADAHSTLAKSGGGGSGGGGSGGGGSGGGGSGMPDPAHL  
 FFYGSISRAEAEHLKLAGMADGLFLLRQCLRSLGGYVLSLVHDVRFHHFPIERQLNGTYAIAGGKAHC  
 GAELCEFYSRDPDGLPCNLKPCNRPSGLEPQPGVDFCLRDAMVRDYVRQTWKLEGEALEQAIISQAPQV  
 EKLIATTAHERMPWYHSSLTREEAERKLYSGAQTGKFLRPRKEQGTALSLIYGKTVYHYLISQDKAGKY  
 CIPEGTKFDTLWQLVEYLKADGLIYCLKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTLNSDGYT  
 PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLFKLRDNLIIADIELGCGNFGSVRQGVYRMRKKQ  
 IDVAIKVLKOGTEKADTEEMMREAQIMHQLDNPYIVRLIGVCQAEALMLVMEMAGGGPLHKFLVGKRE  
 EIPVSNVAELLHQVSMGMKYLEEKNFVHRDLAARNVLLVNRHYAKISDFGLSKALGADDSYTTARSAGK  
 WPLKWYAPECINFRKFSSRSVDVWSYGVTMWEALSYGQKPYKKMKGPVMAFIEQGKRMECPP  
 ECPPELYALMSDCWIYKWEDRPDLTVEQMRACYYSLASKVEGPPGSTQKAEAAACA

MRD - OX40 endodomain

SGG - Linker

MPD - full-length ZAP70

>CD28-PTPN6\_SH2 (SEQ ID No. 43)

MRSKRSLLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRSSGGGGSGGGGSGGGGSGGGGSGMVR  
 WFHRDLGLDAETLLKGRGVHGSFLARPSRKNQGDLSVRVGQVTHIRIQNSGDFDYLGGEKFATLT  
 ELVEYYTQQQGVLOQDRDGTIIHLKYPLNCSDPTSERWYHGHMSGGQAETLLQAKGEPWTFVRESLSQ  
 GDFVLSVLSQPKAGPGSPLRVTHIKVMCEGGRYTVGGLETDFSLTDLVEHFKKTGIEEASGAFVYLRQPY

FIG. 14 (continued)

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MRS - CD28 endodomain

SGG - Linker

MVR - amino-terminus of PTPN6 SH2 domain

&gt;41BB-PTPN6\_SH2 (SEQ ID No. 44)

MKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELSGGGGSGGGGSGGGGSGGGGS  
 MVRW  
 WFHRDLSGLDAETLLKGRGVHGSFLARPSRKNQGDLSVRVGDQVTHIRIQNSGDFYDLYGGEKFATLT  
 ELVEYYTQQQGVLDQDRDGTIIHLKYPLNCSDPTSERWYHGHMSGGQAETLLQAKGEPWTFVRESLSQP  
 GDFVLSVLSQPKAGPGSPLRVTHIKVMCEGGRYTVGGLETDFSLTDLVEHFKKTGIEEASGAFVYLROPY

MKR - 41BB endodomain

SGG - Linker

MVR - amino-terminus of PTPN6 SH2 domain

&gt;OX40-PTPN6\_SH2 (SEQ ID No. 45)

MRDQRLPPDAHKKPPGGGSFRTPIQEEQADAHSTLAKISGGGGSGGGGSGGGGSGGGGS  
 MVRW  
 WFHRDLSGLDAETLLKGRGVHGSFLARPSRKNQGDLSVRVGDQVTHIRIQNSGDFYDLYGGEKFATLT  
 ELVEYYTQQQGVLDQDRDGTIIHLKYPLNCSDPTSERWYHGHMSGGQAETLLQAKGEPWTFVRESLSQP  
 GDFVLSVLSQPKAGPGSPLRVTHIKVMCEGGRYTVGGLETDFSLTDLVEHFKKTGIEEASGAFVYLROPY

MRD - OX40 endodomain

SGG - Linker

MVR - amino-terminus of PTPN6 SH2 domain

&gt;ZAP\_SH2-AKT (SEQ ID No. 47)

MPDPAAHLPPFFYGSISRAEAEHLKLAGMADGLFLLRQCLRSLGGYVLSLVHDVRFHHFPIERQLNGTYAE  
 AGGKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQPGVFDCLRDAMVRDYVRQTWKLEGEALE  
 QAIISQAPQVEKLIATTAHERMPWYHSSLTREEAERKLYSGAQTGDKFLLRPRKEQGTAYLSLIYGKTVYHY  
 LISQDKAGKYCIPEGTKFDTLWQLVEYLKLGKADGLIYCLKEACPNSSASNASGAAAPTLPAPSTLTHPAEE  
 MEVSLAKPKHRVTMNEFEYLKLLGKGTFGKVILVKEKATGRYYAMKILKEVIVAKDEVAHSLTENRVLQN  
 SRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLRERVFSEDRARFYGAIEVSALDYHSEKNVVYRDLK  
 LENLMLDKDGHKIDTDFGLCKEGIKDGATMKTFCGTPEYLAPEVLEDNDYGRAVDWWGLGVVMYEMM  
 CGRLPFYNQDHEKLFELILMEEIRFPRTLGPPEAKSLLSGLLKKDPKQRLGGGSEDAKEIMQHRFFAGIVWQ  
 HVEYKKLSPPFKPQVTSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRPHFPQFSYSASGTA

MPD - ZAP70 SH2 domain

AEE - AKT kinase

&gt;ZAP\_SH2-L-AKT (SEQ ID No. 48)

fused with via a linker

MPDPAAHLPPFFYGSISRAEAEHLKLAGMADGLFLLRQCLRSLGGYVLSLVHDVRFHHFPIERQLNGTYAE  
 AGGKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQPGVFDCLRDAMVRDYVRQTWKLEGEALE  
 QAIISQAPQVEKLIATTAHERMPWYHSSLTREEAERKLYSGAQTGDKFLLRPRKEQGTAYLSLIYGKTVYHY  
 LISQDKAGKYCIPEGTKFDTLWQLVEYLKLGKADGLIYCLKEACPNSSASNASGAAAPTLPAPSTLTHPSGG  
 GGGGGGGGGGGGGGGGSAEEMEVSALAKPKHRVTMNEFEYLKLLGKGTFGKVILVKEKATGRYYAMKIL

FIG. 14 (continued)

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KKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVFSEDRARF  
 YGAEIVSALDYHSEKNVYRDLKENLMLDKDGHIKITDFGLCKEGIKDGATMKTFCGTPEYLAPEVLED  
 NDYGRAVDWWGLGVVMEYEMMCGRLPFYNQDHEKLFELILMEEIRFPRTLGPPEAKSLLSGLKKDPKQR  
 LGGGSEDAKEIMQHRFFAGIVWQHVEKKLSPPFKPQVTSETDTRYFDEEFTAQMITITPPDQDDSMEG  
 VDSERRPHFPQFSYSASGTA

MPD - ZAP70 SH2 domain

SGG - Linker

AEF - AKT kinase domain

>ZAPnf-AKT (SEQ ID No. 49)

MPDPAHLPPFFYGSISRAEAEHLKLAGMADGLFLLRQCLSLGGYVLSLVHDVRFHHFPIERQLNGTYAE  
 AGGKAHCGPAELCEFYSRDPDGLPCNLKPCNRPSGLEPQPGVDFCLRDAMVRDYVRQTWKLEGEALE  
 QAIISQAPQVEKLIATTAHERMPWYHSSLTREEAERKLYSGAQTGDKFLLKPRKEOGTYALSIIYGKTVYHY  
 LISQDKAGKYCIEPGTKFDTLWQLVEYLKADGLIYCLKEACPNSSASNASGAAAPTLPAHPSTLTHPAEF  
 MEVSLAKPKHRVTMNEFEYLKLLGKGTGKVLVKEKATGRYYAMKILKKEVIVAKDEVAHTLTENRVLQNS  
 RHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVFSEDRARFYGAEIVSALDYHSEKNVYRDLK  
 LENLMLDKDGHIKITDFGLCKEGIKDGATMKTFCGTPEYLAPEVLEDNDYGRAVDWWGLGVVMEYEMM  
 CGRLPFYNQDHEKLFELILMEEIRFPRTLGPPEAKSLLSGLKKDPKQRLGGGSEDAKEIMQHRFFAGIVWQ  
 HVYEKKLSPPFKPQVTSETDTRYFDEEFTAQMITITPPDQDDSMECVDSERRPHFPQFSYSASGTA

MPD - ZAP70 mutated to be non-functional

AEF - AKT kinase

>ZAP\_SH2-TEV (SEQ ID No. 53)

MPDPAHLPPFFYGSISRAEAEHLKLAGMADGLFLLRQCLSLGGYVLSLVHDVRFHHFPIERQLNGTYAE  
 AGGKAHCGPAELCEFYSRDPDGLPCNLKPCNRPSGLEPQPGVDFCLRDAMVRDYVRQTWKLEGEALE  
 QAIISQAPQVEKLIATTAHERMPWYHSSLTREEAERKLYSGAQTGDKFLLRPRKEOGTYALSIIYGKTVYHY  
 LISQDKAGKYCIEPGTKFDTLWQLVEYLKADGLIYCLKEACPNSSASNASGAAAPTLPAHPSTLTHPSGG  
 GGGGGGGGGGGGGGGGSLFKGPRDYNPISSSTICHTLTNESDGHTTSLYGIGFGPFIITNKHIFRRNNGTL  
 LVQSLHGVFVKNTTTLQQLIDGRDMIIRMPKDFPPFPQKLKFPREPQREERICLVTTNFQTKSMSSMVS  
 DTSCTFPSSDGIFWKHWIQTGQCGSPLVSTRDGFIVGIHSASNFTNTNNTYFTSVPKNFMELLTNQEAQ  
 QWVSGWRLNADSVLWGGGHKVFMSKPEEPFQPVKEATQLMNELVYSQ

MPD - ZAP70 SH2 domain

SLF - TEV protease

>PTPN6\_SH2-TEV (SEQ ID No. 54)

MVRWFHRDLGLDAETLLKGRGVHGSFLARPSRKNGQDFSLSVRVGDQVTHIRIQNSGDFYDLYGGEKR  
 ATLTELVEYYTQQQGVLDQDRDGTIIHLKYPLNCSDPTSERWYHGHMSGGQAETLLQAKGEPWTFVRES  
 LSQPGDFVLSVDQPKAGPGSPLRVTHIKVMCEGGRYTVGGLETDFSLDLVEHFKKTGIEEASGAFVYU  
 RQPYYSGGGGGSLFKGPRDYNPISSSTICHTLTNESDGHTTSLYGIGFGPFIITNKHIFRRNNGTLLVQSLHGVF  
 VKVNTTTLQQLIDGRDMIIRMPKDFPPFPQKLKFPREPQREERICLVTTNFQTKSMSSMVS DTSCTFPSS  
 DGIFWKHWIQTGQCGSPLVSTRDGFIVGIHSASNFTNTNNTYFTSVPKNFMELLTNQEAQQWVSGW  
 RLNADSVLWGGGHKVFMSKPEEPFQPVKEATQLMNELVYSQ

FIG. 14 (continued)

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MVR - PTPN6 SH2 domain

SGG - Linker

SLF - TEV protease

&gt;RQR8-CD4tm-Endox1-tevS-VP16-GAL4 (SEQ ID No. 55)

MGTSLLCWMALCLLGADHADACPYSNPSCSGGGGSELPTQGTFSNVSTNVSPAKPTTTACPYSNPSCG  
 SGGGGSPAPRPPTPAPTASQPLSLRPEACRPAAGGAVHTRGLDFACD MALIVLGGVAGLLFIGLGIFFC  
 MRCRHRRRQAERMAQIKRVVSEKKTAAQAPHRFQKTCSP SGGGGSENLYFQMPKKKRKVAPPTDVSLGD  
 ELHLDGEDVAMAHADALDDFDLMDLGDGDSPPGFTPHDSAPYGALDMADFEFEQMFTDALGIDEYG  
 SGGGSMQILVASDATMKLLSSIEQACDICRLKCLKSKEKPKCAKCLKNNWECRYSPKTKRSPLTRAHLT  
 EVESRLERLEQLFLIFPREDLDMILKMDSLQDIKALLTGLFVQDNVNKDAVTDRLASVETDMPLTLRQHR  
 SATSSSEESSNKGQRQLTM

MGT - RQR8 domain

RCR - CD4tm

SGG - Linker

ENL - TEV recognition site

PKK - VP16

MQI - GAL4

&gt;aCD33-muCD8STK-PD1\_tm\_endo (SEQ ID No. 56)

MAVPTQVLGLLLWLTDARCDIQMTQSPSSLSASVGDRVTITCRASEDIYFNLVWYQQKPGKAPKLLIYD  
 TNRLADGVPSRFSGSGSGTQYTLTISSLOPEDFATYYCQHYKNYPLTFGGGTKLEIKRSGGGGSGGGGSGG  
 GGGSGGGSRSEVQLVESGGGLVQPGGSLRLSCAASGFTLSNYGMHWIRQAPGKGLEWVSSISLNGGS  
 IYYRDSVKGRFTISRDNASTLYLQMNSLRAEDTAVYYCAAQDAYTGGYFDYWGGGTLTVTSSMDPAIT  
 TKPVLRTSPSPVHPTGTSQPQRPEDCRPRGSVKGTGLDFACDIYGVVGGLLGSLVLLVWVLAVICSRAAR  
 GTIGARRTGQPLKEDPSAVPVFSVDYGEIDFQWREKTPPEPPVPCVPEQTEYATIVFPSGMGTSSPARRGS  
 ADGPRSAQPLRPEDGHCSWPL

MAV - anti-CD33

ITTI - Mouse CD8alpha stalk

VGV - PD-1 endodomain

&gt;aCD19-hCD8STK-CD28tm-Endox1-tevS-Z (SEQ ID No. 57)

CAR against CD19 with cleavable Zeta endodomain

MSLPVTALLPLALLHAARPDIQMTQTSSLSASLGDRVTISCRASQDISKYNWYQQKPDGTVKLLIYHT  
 SRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTKLEITKAGGGGSGGGGSGGG  
 GSGGGGSEVKLQESGPGLVAPSQSLSVCTVSGVSLPDYGVSWIRQPPRKGLEWLGVIWGSETTYNSAL  
 KSRLTIKDNSKSQVFLKMNSLQDDTAIYYCAKHHYGGSYAMDYWGOGTSVTVSSDPTTTPAPRPPTP  
 APTIASQPLSLRPEACRPAAGGAVHTRGLDFACDI FWVLVVVGGVLACYSLLVTVAIFWVRCRHRRRQ  
 AERMAQIKRVVSEKKTAAQAPHRFQKTCSP SGGGGSENLYFQMRVKFSRSADAPAYQQGQNQLYNEI  
 NLGRREEYDVLDKRRGRDPEMGGKPRRKNPOEGLYNELOKDKMAEAYSEIGMKGERRRGKHDGLYC  
 GLSTATKDTYDALHMQALPPR

FIG. 14 (continued)

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MSL - anti-CD19  
 PTT - CD8alpha stalk  
 FWV - CD28 transmembrane domain  
 RCR - Endox1  
 ENL - TEV recognition site  
 RRV - CD3 zeta endodomain

>aCD19-hCD8STK-CD28tmZ-tevS-CD148endo (SEQ ID No. 58)

CAR against CD19 with Zeta endodomain and cleavable CD148 catalytic domain

MSLPVTALLPLALLHAARPDIQMTQTSSLSASLGDRVTISCRASQDISKYLNWYQOKPDGTVKLLIYHT  
 SRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQOQNTLPYTFGGGKLEITKAGGGGSGGGGSGGG  
 GSGGGGSEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSWIRQPPRKGLEWLGVIWGSETTYNSAL  
 KSRLTIKDNSKSQVFLKMNSLQTD DTAIYYCAHYYYGGSYAMDYWGQTSVTVSSDPTTTPAPRPPTP  
 APTIASQPLSLRPEACRPAAGGAVHTRGLDFACDFWVLVVVGGVLACYSLLVTVAFIIFWVRRVKFSRSA  
 DAPAYOQONQLYNELNLGRREYDVLDRRGRDPENMGKPRRNKPOEGLYNELOKDKMAEAYSEIG  
 MKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPRENLYFQMAVFGCIFGALVIVTVGGFIFWRKK  
 RKDAKNNEVSFSQIKPKSKLIRVENFEAYFKKQQADSNCGFAEYEDLKLVGISQPKYAAELAENRGKNR  
 YNNVLPYDISRVKLSVQTHSTDDYINANYMPGYHSHKDFIATQGPLPNTLKD FWRMVWEKNVYAIIMLT  
 KCVEQGRTKCEEYWPSKQAQDYGDITVAMTSEIVLPEWTIRDFTVKNIQTSESHPLRQFHFTSWPDHGV  
 PDTTDLLINFRYLVRDYMKQSPPEPILVHCSAGVGRTGTFAIDRLIYQIENENTVDVYGIVYDLRMHRPL  
 MVQTEDQYVFLNQCVLDIVRSQKDSKVDLIYQNTTAMTIYENLAPVTTFGKTNGYIA

MSL - anti-CD19  
 PTT - CD8alpha stalk  
 FWV - CD28 transmembrane domain  
 RRV - CD3 zeta endodomain  
 ENL - TEV recognition site  
 AVF - CD148 endodomain

>dualSH2 SHP-1-ZAP70 kinase (SEQ ID No. 61)

WFHPNITGVEAENLLLTRGVDGSFLARPSKSNPGDFILSVRRNGAVTHIKIONTGDDYYDLYG  
 GEKFATLAELVOYYMEHHGQLKEKNGDVIELKYPLNCADPTSERWFHGHLSGKEAEKLLTE  
 KGKHGSFLVRESQSHPGDFVLSVRTGDDKGESNDGKSKVTHVMIRCQELKYDVGGGERFD  
 SLTDLVEHYKKNPMVETLGTVLQKOPUNTRINPNSSASNASGAAAPTLPAPHPSTLTHPQR  
 RIDTLNSDGYTPEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKRLFLKRDNLADIELGC  
 GNFGSVROGVYRMRKKQIDVAIKVLKQTEKADTEEMMREAQIMHQLDNPYIVRLIGVCOAE  
 ALMLVMEAGGGPLHKFLVGKREEIPVSNVAELLHQVSMGMKYLEEKNEFVHRDLAARNVLI  
 VNRHYAKISDFGLSKALGADDSYTTARSAGKWPLKWWAPECINFRKFSSRSDDWSYGVTV  
 WEALSYGQKPKYKMKGPVMAFIEQGKRMECPPECPELYALMSDCWYKWEDRPDLTV  
 EQMRACYYSL

WFH - First SH2 domain from SHP-2  
 NCA - Linker  
 WFH - Second SH2 domain from SHP-2  
 NTT - Linker  
 LIA - Zap-70 protein kinase

>-dualSH2 SHP-2-Akt Kinase (SEQ ID No. 62)

WFHPNITGVEAENLLLTRGVDGSFLARPSKSNPGDFILSVRRNGAVTHIKIONTGDDYYDLYG  
 GEKFATLAELVOYYMEHHGQLKEKNGDVIELKYPLNCADPTSERWFHGHLSGKEAEKLLTE  
 KGKHGSFLVRESQSHPGDFVLSVRTGDDKGESNDGKSKVTHVMIRCQELKYDVGGGERFD

FIG. 14 (continued)

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SLTDLVEHYKKNPMVETLGTVLQLKQPLNTTIRINAEEMEVSLAKPKHRVTMNEFEYLKLLGK  
 GTFGKVLVKEKATGRYYAMKILKKEVIVAKDEVAHTLTENRVLONSRRHPFLTALKYSFQTHD  
 RLCFVMEYANGGELFFHLSRERVFSEDRARFYGAIEVSALDYHSEKNVVYRDLKLENMLD  
 KDGHKITDFGLCKEGIKDGATMKTFCGTPEYLAPEVLEDNDYGRAVDWWGLGVVMYEMMC  
 GRLPFYNQDHEKLFELILMEEIRFPRTLGPPEAKSLLSGLLKKDPKQRLGGGSEDAKEIMQHRF  
 FAGIVWQHVVYEKKLSPPFKPQVTSETDTRYFDEEFTAQMITITPPDQDDSMCEVDSERRPHF  
 PQFSYSASGTA

WFH - First SH2 domain from SHP-2

NCA - Linker

WFH - Second SH2 domain from SHP-2

NTT - Linker

FEY - AKT protein kinase

RFF - Linker

AGI - AKT AGC-kinase C-terminal

FIG. 14 (continued)

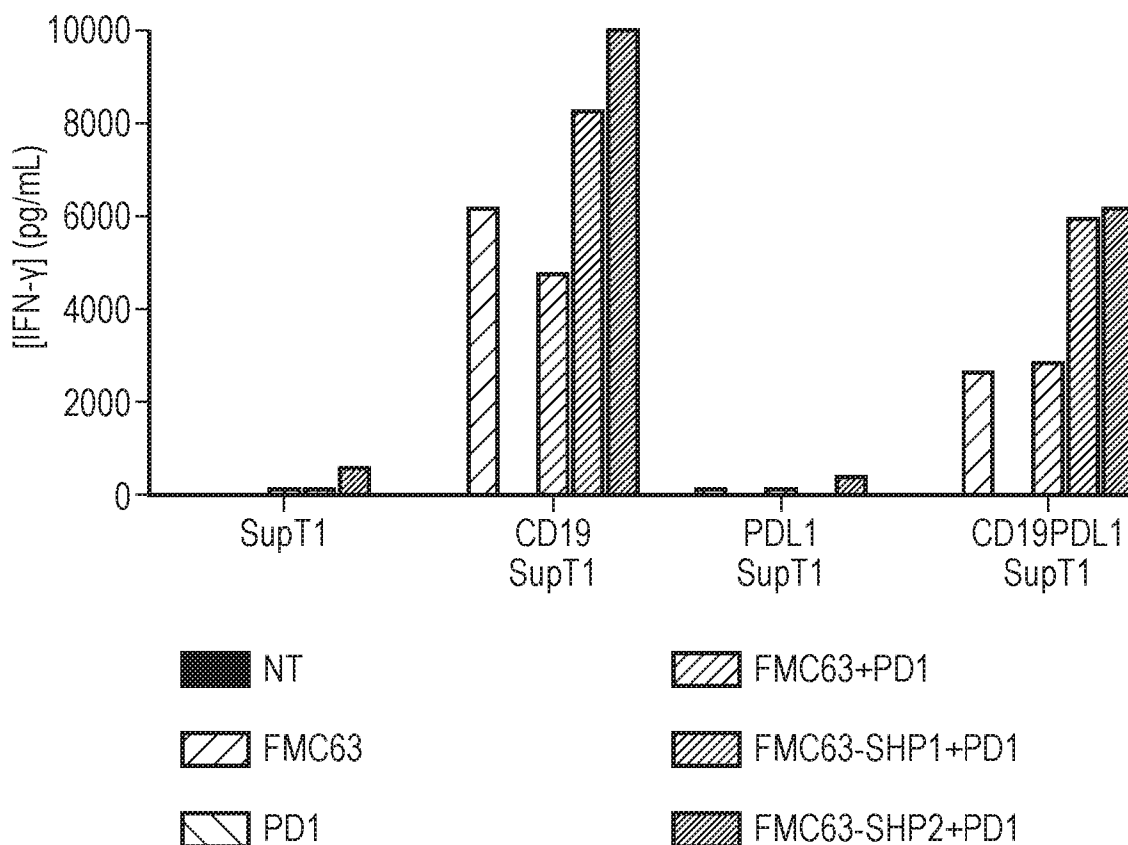


FIG. 15

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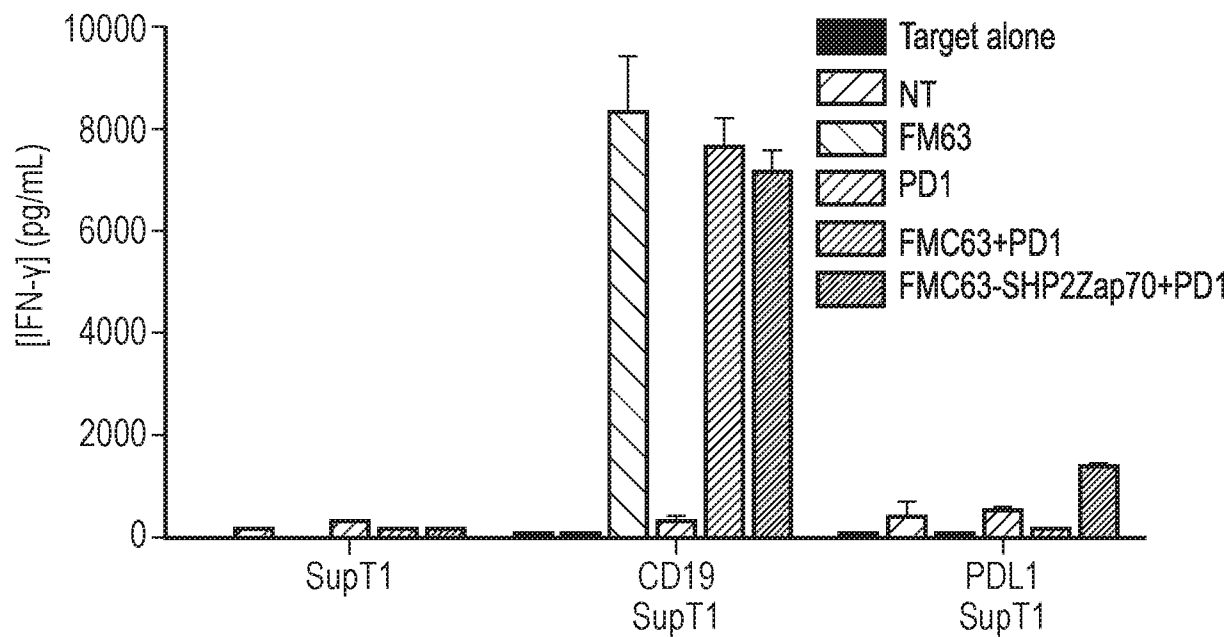


FIG. 16A

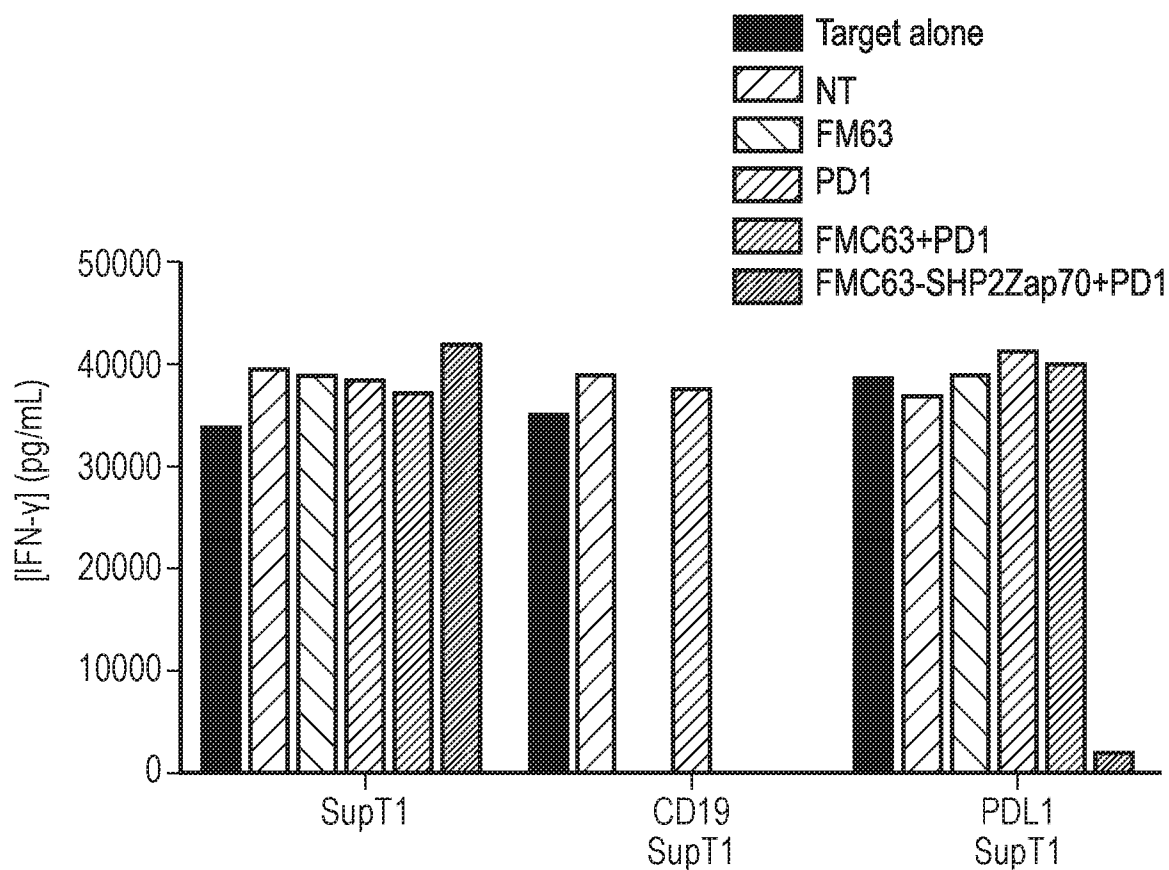


FIG. 16B

## INTERNATIONAL SEARCH REPORT

International application No

PCT/GB2016/051576

## A. CLASSIFICATION OF SUBJECT MATTER

INV. C12N5/0783 C12N15/63 C07K14/725  
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

C07K C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EPO-Internal, BIOSIS, EMBASE, WPI Data

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2015/075468 A1 (UCL BUSINESS PLC [GB]) 28 May 2015 (2015-05-28)	1, 3, 39, 43-53
Y	figure 13; example 7	1-11, 39-53
Y	----- WO 96/40199 A1 (UNIV PENNSYLVANIA [US]) 19 December 1996 (1996-12-19) page 19, line 7 - page 20, line 15	1-11, 39-53
Y	----- WO 97/31113 A1 (ARIAD PHARMA INC [US]; RICKLES RICHARD J [US]) 28 August 1997 (1997-08-28) page 20, line 3 - line 7 ----- -/-	1-11, 39-53



Further documents are listed in the continuation of Box C.



See patent family annex.

## \* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&amp;" document member of the same patent family

Date of the actual completion of the international search

12 July 2016

Date of mailing of the international search report

21/09/2016

Name and mailing address of the ISA/

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Authorized officer

Offermann, Stefanie



# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/GB2016/051576

## Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of additional fees.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

2-11(completely); 1, 39-53(partially)

### Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- ☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- ☐ No protest accompanied the payment of additional search fees.

## INTERNATIONAL SEARCH REPORT

International application No

PCT/GB2016/051576

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	<p>J P NORTHROP ET AL: "Characterization of the roles of SH2 domain-containing proteins in T-lymphocyte activation by using dominant negative SH2 domains.", MOLECULAR AND CELLULAR BIOLOGY., vol. 16, no. 5, 1 May 1996 (1996-05-01), pages 2255-2263, XP055287431, US</p> <p>ISSN: 0270-7306, DOI: 10.1128/MCB.16.5.2255</p> <p>the whole document</p> <p>-----</p>	<p>1-11, 39-53</p>

# INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No

PCT/GB2016/051576

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 2015075468	A1	28-05-2015	
		AU 2014351557 A1	26-05-2016
		AU 2014351558 A1	26-05-2016
		CA 2929984 A1	28-05-2015
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**FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210**

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 2-11(completely); 1, 39-53(partially)

a cell comprising a CAR and a signal transduction modifying protein comprising a SH2-domain from a protein binding to an ITAM/ITIM motif and a) lacking the corresponding kinase/phosphatase domain or b) comprising the kinase/phosphatase domain from an ITIM/ITAM-binding protein whereby e.g. the SH2-domain of a ITAM-binding kinase is linked to a phosphatase domain from a normally ITIM-binding phosphatase or vice versa;

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2. claims: 12-19(completely); 1, 39-53(partially)

a cell comprising a CAR and a signal transduction modifying protein comprising a SH2-domain from a protein binding to an ITAM/ITIM motif and a heterologous signalling domain which is preferably from a signalling molecule which is not usually activated by an ITAM/ITIM-containing receptor, such as a co-stimulatory domain like the CD28/OX40 or 41BB-co-stimulatory domain, or a inhibitory domain like the endodomain of CD148, CD45;

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3. claims: 20-25(completely); 1, 39-53(partially)

a cell comprising a CAR and a signal transduction modifying protein comprising a SH2-domain from a protein binding to an ITAM-motif and an ITAM-containing domain or comprising a SH2-domain from a protein binding to an ITIM-motif and an ITIM-containing domain;

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4. claims: 26-38(completely); 1, 39-53(partially)

a cell comprising one or two CARs and a signal transduction modifying protein comprising a SH2-domain from a protein binding to an ITAM/ITIM motif and, preferably, a protease-domain, such as from the Tobacco Etch Virus Protease (TeV). In the presence of two CARs, one of the CARs is a target CAR comprising an intracellular protease cleavage site.

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