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(54) Title: CYCLIN A1 SPECIFIC T CELL RECEPTORS AND USES THEREOF

Cyclin A1 protein sequence

etc...
1 5 9 15 19 23 } 15mer design
1 MHCSNPKSGVVLATVARGPDACQILTRAPLGQDPPQRTVL
41 GLLTANGQYRRTCGQGITRIRCYSGSENAFPAGKKALPD
81 CGVQEPKQGFDIYMDELEQGDSDSCSVREGMAFEDVYEV
121 DTGTLKSDLHFLIDFNTVSPMLVDSLLSQSEDISSLGTD
161 VINVTEYAEELIYQYLREAEIRHRPKAHYMKKQPDITEGMR
201 TILVDWLVEVGEEYKLRAETLYLAVN**FLDRFLSCM**VLRG
241 KLQLVGTAAMLLASKYEEIYPFEVDEFVYITDDTYTKRQL
281 LKMEHLLKVLAFDLTVPTTNQFLLQYLRRQGVCVRTENL
321 AKYVAELSLLEADPFLKYL**SLTAAAFCL**NYTVNKHFW
361 PETLAAFTG**YSLSEIVPCL**SELHKAYLDIPHRPQQAIREK
401 YKASKYLCVSLMEPPAVLLQ

Lead HLA-A2 peptides

227-235 341-351 370-379

Library of 15mer peptides:
overlapping by 11 aa,
spanning the entire protein
421 aa -> 103 peptides

DCs + cyclin A1 peptide library
& CD8⁺ T cells co-cultured in
the presence of IL-21 &
expanded in IL-2, IL-7 & IL-15

3-4 rounds of stimulation
required to detect antigen-
specific responses by IFN- γ
production

FIG. 1

(57) Abstract: The present disclosure provides binding proteins, including TCRs, that specifically bind human cyclin A1 (CCNA1), host cells expressing such antigen specific binding proteins, nucleic acids encoding the same, and compositions for use in treating diseases or disorders in which cells overexpress CCNA1, such as in cancer.



TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW,
KM, ML, MR, NE, SN, TD, TG).

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CYCLIN A1 SPECIFIC T CELL RECEPTORS AND USES THEREOF

STATEMENT REGARDING SEQUENCE LISTING

The Sequence Listing associated with this application is provided in text format in lieu of a paper copy, and is hereby incorporated by reference into the specification.

- 5 The name of the text file containing the Sequence Listing is 360056_460WO_SEQUENCE_LISTING.txt. The text file is 269 KB, was created on February 10, 2019, and is being submitted electronically via EFS-Web.

BACKGROUND

- Adoptive immunotherapy involving *ex vivo* expansion and infusion of tumor-
10 reactive T-cells is an emerging treatment modality, especially in patients for whom conventional therapy fails (Stromnes *et al.*, *Immunol. Rev.* 257:145-64, 2014). In some cases, tumor-reactive T cells comprise an endogenous, exogenous, and/or engineered receptor specific for an antigen specific to or overexpressed on a tumor.

- Cancer-testes antigen cyclin A1 (CCNA1) is an alternative A-type cyclin and is
15 an attractive target for treatment of various cancers due its overexpression in acute myeloid leukemia (AML) and a number of epithelial cancers including testicular, endometrial, and ovarian cancer. Cyclin A1 is thought to promote cell proliferation and survival, has been shown to be leukemogenic in mice, and is detected in leukemic stem cells of more than 50% of AML patients.

- 20 Provided herein are methods for identifying tumor-reactive T cells reactive to cyclin A1, methods for identifying T-cell receptors (TCRs) specific for cyclin A1, as well as specific TCRs identified using the methods described herein.

BRIEF DESCRIPTION OF THE DRAWINGS

- Figure 1** depicts the Cyclin A1 TCR discovery scheme, targeting HLA-A2
25 restricted epitopes. Positions of lead HLA-A2 peptides 227-235 (SEQ ID NO:1), 341-351 (SEQ ID NO:2), and 370-379 (SEQ ID NO:3) on cyclin A1 protein sequence (SEQ ID NO:4) are shown.

Figure 2 shows that stimulating CD8⁺ T cells with a cyclin A1 overlapping peptide library resulted in the generation of antigen-specific lines.

Figures 3A-3B show that high affinity HLA-A2:01/cyclin A1 TCRs were identified by calculating tetramer dissociation constants (K_d) for individual T cell
5 clones.

Figure 4 shows a schematic for isolation, identification, and expression of high-affinity TCRs selected from high-avidity clones.

Figures 5A-5D show that HLA-A2:01/cyclin A1 TCRs recognized peptide pulsed targets and killed HLA-matched cyclin A1+ leukemia cell lines and primary
10 AML cells.

Figure 6 shows a schematic for murinization of top HLA-A2:01/cyclin A1 TCR candidates for *in vivo* safety testing.

DETAILED DESCRIPTION

In certain aspects, the present disclosure provides binding proteins (*e.g.*, T cell
15 receptors (TCRs)) specific for cyclin A1 associated with a major histocompatibility complex (MHC) (*e.g.*, human leukocyte antigen (HLA)), for use in, for example, adoptive immunotherapy to treat cancer.

The compositions and methods described herein will in certain embodiments have therapeutic utility for the treatment of diseases and conditions associated with
20 CCNA1 overexpression (*e.g.*, detectable CCNA1 expression at a level that is greater in magnitude, in a statistically significant manner, than the level of CCNA-1 expression that is detectable in a normal or disease-free cell). Such diseases include various forms of hyperproliferative disorders, such as acute myeloid leukemia. Non-limiting examples of these and related uses are described herein and include *in vitro*, *ex vivo* and
25 *in vivo* stimulation of CCNA1 antigen-specific T cell responses, such as by the use of recombinant T cells expressing a TCR specific for a CCNA1 peptide (*e.g.*, FLDRFLSCM (SEQ ID NO: 1), SLIAAAAFCLA (SEQ ID NO:2), or YSLSEIVPCL (SEQ ID NO:3)).

Prior to setting forth this disclosure in more detail, it may be helpful to an understanding thereof to provide definitions of certain terms to be used herein. Additional definitions are set forth throughout this disclosure.

In the present description, any concentration range, percentage range, ratio
5 range, or integer range is to be understood to include the value of any integer within the recited range and, when appropriate, fractions thereof (such as one tenth and one hundredth of an integer), unless otherwise indicated. Also, any number range recited herein relating to any physical feature, such as polymer subunits, size or thickness, are to be understood to include any integer within the recited range, unless otherwise
10 indicated. As used herein, the term "about" means $\pm 20\%$ of the indicated range, value, or structure, unless otherwise indicated. It should be understood that the terms "a" and "an" as used herein refer to "one or more" of the enumerated components. The use of the alternative (*e.g.*, "or") should be understood to mean either one, both, or any combination thereof of the alternatives. As used herein, the terms "include," "have" and
15 "comprise" are used synonymously, which terms and variants thereof are intended to be construed as non-limiting.

In addition, it should be understood that the individual compounds, or groups of compounds, derived from the various combinations of the structures and substituents described herein, are disclosed by the present application to the same extent as if each
20 compound or group of compounds was set forth individually. Thus, selection of particular structures or particular substituents is within the scope of the present disclosure.

The term "consisting essentially of" limits the scope of a claim to the specified materials or steps, or to those that do not materially affect the basic characteristics of a
25 claimed invention. For example, a protein domain, region, or module (*e.g.*, a binding domain, hinge region, linker module) or a protein (which may have one or more domains, regions, or modules) "consists essentially of" a particular amino acid sequence when the amino acid sequence of a domain, region, module, or protein includes extensions, deletions, mutations, or a combination thereof (*e.g.*, amino acids at the
30 amino- or carboxy-terminus or between domains) that, in combination, contribute to at most 20% (*e.g.*, at most 15%, 14%, 13%, 12%, 11%, 10%, 9%, 8%, 7%, 6%, 5%, 4%,

3%, 2% or 1%) of the length of a domain, region, module, or protein and do not substantially affect (*i.e.*, do not reduce the activity by more than 50%, such as no more than 40%, 30%, 25%, 20%, 15%, 10%, 5%, or 1%) the activity of the domain(s), region(s), module(s), or protein (*e.g.*, the target binding affinity of a binding protein).

5 As used herein, an "immune system cell" means any cell of the immune system that originates from a hematopoietic stem cell in the bone marrow, which gives rise to two major lineages, a myeloid progenitor cell (which give rise to myeloid cells such as monocytes, macrophages, dendritic cells, megakaryocytes and granulocytes) and a lymphoid progenitor cell (which give rise to lymphoid cells such as T cells, B cells and
10 natural killer (NK) cells). Exemplary immune system cells include a CD4⁺ T cell, a CD8⁺ T cell, a CD4⁻ CD8⁻ double negative T cell, a $\gamma\delta$ T cell, a regulatory T cell, a natural killer cell, and a dendritic cell. Macrophages and dendritic cells may be referred to as "antigen presenting cells" or "APCs," which are specialized cells that can activate T cells when a major histocompatibility complex (MHC) receptor on the surface of the
15 APC complexed with a peptide interacts with a TCR on the surface of a T cell.

 As used herein, a "hematopoietic progenitor stem cell" refers to undifferentiated hematopoietic cells that are capable of self-renewal either *in vivo*, essentially unlimited propagation *in vitro*, and capable of differentiation to other cell types including cells of the T cell lineage. Hematopoietic stem cells may be isolated, for example, but not
20 limited to, from fetal liver, bone marrow, cord blood.

 As used herein, a "hematopoietic progenitor cell" is a cell that can be derived from hematopoietic stem cells or fetal tissue and is capable of further differentiation into mature cells types (*e.g.*, immune system cells). Exemplary hematopoietic progenitor cells include those with a CD24^{Lo} Lin⁻ CD117⁺ phenotype or those found in
25 the thymus (referred to as progenitor thymocytes).

 As used herein, the term "host" refers to a cell (*e.g.*, T cell) or microorganism targeted for genetic modification with a heterologous or exogenous nucleic acid molecule to produce a polypeptide of interest (*e.g.*, high or enhanced affinity anti-CCNA-1 TCR). In certain embodiments, a host cell may optionally already possess or
30 be modified to include other genetic modifications that confer desired properties related or unrelated to biosynthesis of the heterologous or exogenous protein (*e.g.*, inclusion of

a detectable marker; deleted, altered or truncated endogenous TCR; increased co-stimulatory factor expression). In certain embodiments, a host cell is a human hematopoietic progenitor cell transduced with a heterologous or exogenous nucleic acid molecule encoding a TCR β , TCR α chain or both, specific for a CCNA-1 antigen peptide. In certain embodiments, a host cells are autologous, allogeneic or syngeneic to subject to receive the host cells containing a polynucleotide encoding a binding protein of this disclosure.

A "T cell" or "T lymphocyte" is an immune system cell that matures in the thymus and produces T cell receptors (TCRs), which can be obtained (enriched or isolated) from, for example, peripheral blood mononuclear cells (PBMCs) and are referred to herein as "bulk" T cells. After isolation of T cells, both cytotoxic (CD8+) and helper (CD4+) T cells can be sorted into naïve, memory, and effector T cell subpopulations, either before or after expansion. T cells can be naïve (not exposed to antigen; increased expression of CD62L, CCR7, CD28, CD3, CD127, and CD45RA, and decreased expression of CD45RO as compared to T_{CM}), memory T cells (T_M) (antigen-experienced and long-lived), and effector cells (antigen-experienced, cytotoxic). T_M can be further divided into subsets of central memory T cells (T_{CM}, increased expression of CD62L, CCR7, CD28, CD127, CD45RO, and CD95, and decreased expression of CD54RA as compared to naïve T cells) and effector memory T cells (T_{EM}, decreased expression of CD62L, CCR7, CD28, CD45RA, and increased expression of CD127 as compared to naïve T cells or T_{CM}). Effector T cells (T_E) refers to antigen-experienced CD8+ cytotoxic T lymphocytes that has decreased expression of CD62L, CCR7, CD28, and are positive for granzyme and perforin as compared to T_{CM}. Helper T cells (T_H) are CD4+ cells that influence the activity of other immune cells by releasing cytokines. CD4+ T cells can activate and suppress an adaptive immune response, and which action is induced will depend on presence of other cells and signals. T cells can be collected in accordance with known techniques, and the various subpopulations or combinations thereof can be enriched or depleted by known techniques, such as by affinity binding to antibodies, flow cytometry, or immunomagnetic selection. Other exemplary T cells include regulatory T cells, such as

CD4⁺ CD25⁺ (Foxp3⁺) regulatory T cells and Treg17 cells, as well as Tr1, Th3, CD8⁺CD28⁺, and Qa-1 restricted T cells.

"T cell receptor" (TCR) refers to an immunoglobulin superfamily member (having a variable binding domain, a constant domain, a transmembrane region, and a short cytoplasmic tail; *see, e.g., Janeway et al., Immunobiology: The Immune System in Health and Disease*, 3rd Ed., Current Biology Publications, p. 4:33, 1997) capable of specifically binding to an antigen peptide bound to a MHC receptor. A TCR can be found on the surface of a cell or in soluble form and generally is comprised of a heterodimer having α and β chains (also known as TCR α and TCR β , respectively), or γ and δ chains (also known as TCR γ and TCR δ , respectively). Like immunoglobulins, the extracellular portion of TCR chains (*e.g.,* α -chain, β -chain) contain two immunoglobulin domains, a variable domain (*e.g.,* α -chain variable domain or V α , β -chain variable domain or V β ; typically amino acids 1 to 116 based on Kabat numbering, Kabat *et al.*, "Sequences of Proteins of Immunological Interest, US Dept. Health and Human Services, Public Health Service National Institutes of Health, 1991, 5th ed.) at the N-terminus, and one constant domain (*e.g.,* α -chain constant domain or C α , typically amino acids 117 to 259 based on Kabat, β -chain constant domain or C β , typically amino acids 117 to 295 based on Kabat) adjacent to the cell membrane. Also like immunoglobulins, the variable domains contain complementary determining regions (CDRs) separated by framework regions (FRs) (*see, e.g., Jores et al., Proc. Nat'l Acad. Sci. U.S.A.* 87:9138, 1990; Chothia *et al., EMBO J.* 7:3745, 1988; *see also* Lefranc *et al., Dev. Comp. Immunol.* 27:55, 2003). In certain embodiments, a TCR is found on the surface of T cells (or T lymphocytes) and associates with the CD3 complex. The source of a TCR as used in the present disclosure may be from various animal species, such as a human, mouse, rat, rabbit or other mammals.

The term "variable region" or "variable domain" refers to the domain of a TCR α -chain or β -chain (or γ chain and δ chain for $\gamma\delta$ TCRs) that is involved in binding of the TCR to antigen. The variable domains of the α -chain and β -chain (V α and V β , respectively) of a native TCR generally have similar structures, with each domain comprising four conserved framework regions (FRs) and three CDRs. The V α domain is encoded by two separate DNA segments, the variable gene segment and the joining

gene segment (V-J); the V_β domain is encoded by three separate DNA segments, the variable gene segment, the diversity gene segment, and the joining gene segment (V-D-J). A single V_α or V_β domain may be sufficient to confer antigen-binding specificity. Furthermore, TCRs that bind a particular antigen may be isolated using a V_α or V_β domain from a TCR that binds the antigen to screen a library of complementary V_β or V_α domains, respectively.

The terms "complementarity determining region," and "CDR," which are synonymous with "hypervariable region" or "HVR," are known in the art to refer to non-contiguous sequences of amino acids within TCR variable regions, which confer antigen specificity and/or binding affinity. In general, there are three CDRs in each α -chain variable region (α CDR1, α CDR2, α CDR3) and three CDRs in each β -chain variable region (β CDR1, β CDR2, β CDR3). CDR3 is thought to be the main CDR responsible for recognizing processed antigen. CDR1 and CDR2 mainly interact with the MHC. However, the CDR1 loops of the alpha chain and beta chain have also been shown to interact with the N-terminal and C-terminal ends of the antigenic peptide, respectively, and may contribute to both peptide specificity and MHC binding.

As used herein, "TCR complex" refers to a complex formed by the association of CD3 with TCR. For example, a TCR complex can be composed of a CD3 γ chain, a CD3 δ chain, two CD3 ϵ chains, a homodimer of CD3 ζ chains, a TCR α chain, and a TCR β chain. Alternatively, a TCR complex can be composed of a CD3 γ chain, a CD3 δ chain, two CD3 ϵ chains, a homodimer of CD3 ζ chains, a TCR γ chain, and a TCR δ chain.

A "component of a TCR complex," as used herein, refers to a TCR chain (*i.e.*, TCR α , TCR β , TCR γ or TCR δ), a CD3 chain (*i.e.*, CD3 γ , CD3 δ , CD3 ϵ or CD3 ζ), or a complex formed by two or more TCR chains or CD3 chains (*e.g.*, a complex of TCR α and TCR β , a complex of TCR γ and TCR δ , a complex of CD3 ϵ and CD3 δ , a complex of CD3 γ and CD3 ϵ , or a sub-TCR complex of TCR α , TCR β , CD3 γ , CD3 δ , and two CD3 ϵ chains).

"Antigen" or "Ag" as used herein refers to an immunogenic molecule that provokes an immune response. This immune response may involve antibody production, activation of specific immunologically-competent cells (*e.g.*, T cells), or

both. An antigen (immunogenic molecule) may be, for example, a peptide, glycopeptide, polypeptide, glycopolypeptide, polynucleotide, polysaccharide, lipid or the like. It is readily apparent that an antigen can be synthesized, produced recombinantly, or derived from a biological sample. Exemplary biological samples that
5 can contain one or more antigens include tissue samples, tumor samples, cells, biological fluids, or combinations thereof. Antigens can be produced by cells that have been modified or genetically engineered to express an antigen. Exemplary antigens include CCNA-1.

The term "epitope" or "antigenic epitope" includes any molecule, structure,
10 amino acid sequence or protein determinant that is recognized and specifically bound by a cognate binding molecule, such as an immunoglobulin, T cell receptor (TCR), chimeric antigen receptor, or other binding molecule, domain or protein. Epitopic determinants generally contain chemically active surface groupings of molecules, such as amino acids or sugar side chains, and can have specific three dimensional structural
15 characteristics, as well as specific charge characteristics. For example, a CCNA-1 protein or fragment thereof may be an antigen that contains one or more antigenic epitopes.

"Major histocompatibility complex" (MHC) refers to glycoproteins that deliver peptide antigens to a cell surface. MHC class I molecules are heterodimers having a
20 membrane spanning α chain (with three α domains) and a non-covalently associated β 2 microglobulin. MHC class II molecules are composed of two transmembrane glycoproteins, α and β , both of which span the membrane. Each chain has two domains. MHC class I molecules deliver peptides originating in the cytosol to the cell surface, where a peptide:MHC complex is recognized by $CD8^+$ T cells. MHC class II
25 molecules deliver peptides originating in the vesicular system to the cell surface, where they are recognized by $CD4^+$ T cells. Human MHC is referred to as human leukocyte antigen (HLA).

A "binding domain" (also referred to as a "binding region" or "binding moiety"), as used herein, refers to a molecule or portion thereof (*e.g.*, peptide, oligopeptide,
30 polypeptide, protein) that possesses the ability to specifically and non-covalently associate, unite, or combine with a target (*e.g.*, CCNA-1, CCNA-1 peptide:MHC

complex). A binding domain includes any naturally occurring, synthetic, semi-synthetic, or recombinantly produced binding partner for a biological molecule, a molecular complex (*i.e.*, complex comprising two or more biological molecules), or other target of interest. Exemplary binding domains include single chain

- 5 immunoglobulin variable regions (*e.g.*, scTCR, scFv), receptor ectodomains, ligands (*e.g.*, cytokines, chemokines), or synthetic polypeptides selected for their specific ability to bind to a biological molecule, a molecular complex or other target of interest.

As used herein, "specifically binds" or "specific for" refers to an association or union of a binding protein (*e.g.*, TCR receptor) or a binding domain (or fusion protein
10 thereof) to a target molecule (*e.g.*, CCNA-1 peptide:HLA or a tetramer such as an HLA complex) with an affinity or K_a (*i.e.*, an equilibrium association constant of a particular binding interaction with units of $1/M$) equal to or greater than $10^5 M^{-1}$ (which equals the ratio of the on-rate [k_{on}] to the off-rate [k_{off}] for this association reaction), while not significantly associating or uniting with any other molecules or components in a
15 sample. Binding proteins or binding domains (or fusion proteins thereof) may be classified as "high affinity" binding proteins or binding domains (or fusion proteins thereof) or as "low affinity" binding proteins or binding domains (or fusion proteins thereof). "High affinity" binding proteins or binding domains refer to those binding proteins or binding domains having a K_a of at least $10^7 M^{-1}$, at least $10^8 M^{-1}$, at least
20 $10^9 M^{-1}$, at least $10^{10} M^{-1}$, at least $10^{11} M^{-1}$, at least $10^{12} M^{-1}$, or at least $10^{13} M^{-1}$. "Low affinity" binding proteins or binding domains refer to those binding proteins or binding domains having a K_a of up to $10^7 M^{-1}$, up to $10^6 M^{-1}$, up to $10^5 M^{-1}$. Alternatively, affinity may be defined as an equilibrium dissociation constant (K_d) of a particular binding interaction with units of M (*e.g.*, $10^{-5} M$ to $10^{-13} M$).

- 25 In certain embodiments, a receptor or binding domain may have "enhanced affinity," which refers to selected or engineered receptors or binding domains with stronger binding to a target antigen than a wild type (or parent) binding domain. For example, enhanced affinity may be due to a K_a (equilibrium association constant) for the target antigen that is higher than the wild type binding domain, due to a K_d
30 (dissociation constant) for the target antigen that is less than that of the wild type binding domain, due to an off-rate (k_{off}) for the target antigen that is less than that of the

wild type binding domain, or a combination thereof. In certain embodiments, enhanced affinity TCRs may be codon optimized to enhance expression in a particular host cell, such as T cells (Scholten *et al.*, *Clin. Immunol.* 119:135, 2006).

A variety of assays are known for identifying binding domains of the present disclosure that specifically bind a particular target, as well as determining binding domain or binding protein affinities, such as Western blot, ELISA, analytical ultracentrifugation, spectroscopy, surface plasmon resonance (Biacore®) analysis, MHC tetramer assay (*see, e.g.,* Scatchard *et al.*, *Ann. N.Y. Acad. Sci.* 51:660, 1949; Wilson, *Science* 295:2103, 2002; Wolff *et al.*, *Cancer Res.* 53:2560, 1993; Altman *et al.*, *Science* 274:94-96, 1996; and U.S. Patent Nos. 5,283,173, 5,468,614, or the equivalent).

The term "CCNA-1-specific binding protein" refers to a protein or polypeptide that specifically binds to CCNA-1 or a peptide or fragment thereof. In some embodiments, a protein or polypeptide binds to CCNA-1 or a peptide thereof, such as a CCNA-1 peptide in complexed with an MHC or HLA molecule, *e.g.*, on a cell surface, with at or at least about a particular affinity. In certain embodiments, a CCNA-1-specific binding protein binds a CCNA-1-derived peptide:HLA complex (or CCNA-1-derived peptide:MHC complex) with a K_d of less than about 10^{-8} M, less than about 10^{-9} M, less than about 10^{-10} M, less than about 10^{-11} M, less than about 10^{-12} M, or less than about 10^{-13} M, or with an affinity that is about the same as, at least about the same as, or is greater than at or about the affinity exhibited by an exemplary CCNA-1 specific binding protein provided herein, such as any of the CCNA-1-specific TCRs provided herein, for example, as measured by the same assay. In certain embodiments, a CCNA-1-specific binding protein comprises a CCNA-1-specific immunoglobulin superfamily binding protein or binding portion thereof.

Assays for assessing affinity or apparent affinity or relative affinity are known. In certain examples, apparent affinity for a TCR is measured by assessing binding to various concentrations of tetramers, for example, by flow cytometry using labeled tetramers. In some examples, apparent K_D of a TCR is measured using 2-fold dilutions of labeled tetramers at a range of concentrations, followed by determination of binding

curves by non-linear regression, apparent K_D being determined as the concentration of ligand that yielded half-maximal binding.

The term "CCNA-1 binding domain" or "CCNA-1 binding fragment" refers to a domain or portion of a CCNA-1-specific binding protein responsible for the specific CCNA-1 binding. A CCNA-1-specific binding domain alone (*i.e.*, without any other portion of a CCNA-1-specific binding protein) can be soluble and can bind to CCNA-1 with a K_d of less than about 10^{-8} M, less than about 10^{-9} M, less than about 10^{-10} M, less than about 10^{-11} M, less than about 10^{-12} M, or less than about 10^{-13} M. Exemplary CCNA-1-specific binding domains include CCNA-1-specific scTCR (*e.g.*, single chain $\alpha\beta$ TCR proteins such as $V\alpha$ -L- $V\beta$, $V\beta$ -L- $V\alpha$, $V\alpha$ -C α -L- $V\beta$, or $V\alpha$ -L- $V\beta$ -C β , wherein $V\alpha$ and $V\beta$ are TCR α and β variable domains respectively, C α and C β are TCR α and β constant domains, respectively, and L is a linker) and scFv fragments as described herein, which can be derived from an anti-CCNA-1 TCR or antibody.

Principles of antigen processing by antigen presenting cells (APC) (such as dendritic cells, macrophages, lymphocytes or other cell types), and of antigen presentation by APC to T cells, including major histocompatibility complex (MHC)-restricted presentation between immunocompatible (*e.g.*, sharing at least one allelic form of an MHC gene that is relevant for antigen presentation) APC and T cells, are well established (*see, e.g.*, Murphy, Janeway's Immunobiology (8th Ed.) 2011 Garland Science, NY; chapters 6, 9 and 16). For example, processed antigen peptides originating in the cytosol (*e.g.*, tumor antigen, intracellular pathogen) are generally from about 7 amino acids to about 11 amino acids in length and will associate with class I MHC molecules, whereas peptides processed in the vesicular system (*e.g.*, bacterial, viral) will vary in length from about 10 amino acids to about 25 amino acids and associate with class II MHC molecules.

"Cyclin-A1" or "CCNA-1" refers to a protein belonging to the cyclin family that is involved in cell cycle control of the male germline meiotic cell cycle. Cyclin A1 is minimally expressed in normal tissues, except the testis, and overexpressed in many cancers including acute myeloid leukemia (AML) and a number of epithelial cancers, including testicular, endometrial, and ovarian cancer. In certain embodiments, CCNA1 refers to isoform 3 of the protein, which differs from isoform 1 in that amino acids 1-44

are missing. In a particular embodiment, CCNA1 comprises an amino acid sequence set forth in SEQ ID NO:4.

"CCNA-1 antigen" or "CCNA-1 peptide antigen" refers to a naturally or synthetically produced portion of a CCNA-1 protein ranging in length from about 5 7 amino acids to about 15 amino acids, which can form a complex with a MHC (*e.g.*, HLA) molecule and such a complex can bind with a TCR specific for a CCNA-1 peptide:MHC (*e.g.*, HLA) complex. CCNA-1 antigen peptides are presented in the context of class I MHC. In particular embodiments, a CCNA-1 peptide is FLDRFLSCM (SEQ ID NO:1), SLIAAAAFCLA (SEQ ID NO:2), or YSLSEIVPCL 10 (SEQ ID NO:3), which associate with human class I HLA and, more specifically, associates with allele HLA-A*02:01.

A "linker" refers to an amino acid sequence that connects two proteins, polypeptides, peptides, domains, regions, or motifs and may provide a spacer function compatible with interaction of the two sub-binding domains so that the resulting 15 polypeptide retains a specific binding affinity (*e.g.*, scTCR) to a target molecule or retains signaling activity (*e.g.*, TCR complex). In certain embodiments, a linker is comprised of about two to about 35 amino acids, for instance, or about four to about 20 amino acids or about eight to about 15 amino acids or about 15 to about 25 amino acids.

"Junction amino acids" or "junction amino acid residues" refer to one or more 20 (*e.g.*, about 2-10) amino acid residues between two adjacent motifs, regions or domains of a polypeptide, such as between a binding domain and an adjacent constant domain or between a TCR chain and an adjacent self-cleaving peptide. Junction amino acids may result from the construct design of a binding protein (*e.g.*, amino acid residues resulting from the use of a restriction enzyme site during the construction of a nucleic acid 25 molecule encoding a binding protein).

An "altered domain" or "altered protein" refers to a motif, region, domain, peptide, polypeptide, or protein with a non-identical sequence identity to a wild type motif, region, domain, peptide, polypeptide, or protein (*e.g.*, a wild type TCR α chain, TCR β chain, TCR α constant domain, TCR β constant domain) of at least 85% (*e.g.*, 30 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.1%, 99.2%, 99.3%, 99.4%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, 100%) identity.

As used herein, "nucleic acid" or "nucleic acid molecule" refers to any of deoxyribonucleic acid (DNA), ribonucleic acid (RNA), oligonucleotides, polynucleotides, fragments thereof generated, for example, by the polymerase chain reaction (PCR) or by *in vitro* transcription, and also to fragments generated by any of ligation, scission, endonuclease action, or exonuclease action. In certain embodiments, the nucleic acids of the present disclosure are produced by PCR. Nucleic acids can be composed of monomers that are naturally occurring nucleotides (such as deoxyribonucleotides and ribonucleotides), analogs of naturally occurring nucleotides (*e.g.*, α -enantiomeric forms of naturally occurring nucleotides), or a combination of both. Modified nucleotides can have modifications in or replacement of sugar moieties, or pyrimidine or purine base moieties. Nucleic acid monomers can be linked by phosphodiester bonds or analogs of such linkages. Analogs of phosphodiester linkages include phosphorothioate, phosphorodithioate, phosphoroselenoate, phosphorodiselenoate, phosphoroanilothioate, phosphoranilidate, phosphoramidate, and the like. Nucleic acid molecules can be either single stranded or double stranded.

The term "isolated" means that the material is removed from its original environment (*e.g.*, the natural environment if it is naturally occurring). For example, a naturally occurring nucleic acid or polypeptide present in a living animal is not isolated, but the same nucleic acid or polypeptide, separated from some or all of the co-existing materials in the natural system, is isolated. Such a nucleic acid could be part of a vector and/or such nucleic acid or polypeptide could be part of a composition (*e.g.*, a cell lysate), and still be isolated in that such vector or composition is not part of the natural environment for the nucleic acid or polypeptide. The term "gene" means the segment of DNA involved in producing a polypeptide chain; it includes regions preceding and following the coding region ("leader and trailer") as well as intervening sequences (introns) between individual coding segments (exons).

The term "construct" refers to any polynucleotide that contains a recombinant nucleic acid molecule. A construct may be present in a vector (*e.g.*, a bacterial vector, a viral vector) or may be integrated into a genome.

A "vector" is a nucleic acid molecule that is capable of transporting another nucleic acid. Vectors may be, for example, plasmids, cosmids, viruses, phage, a RNA

vector, or a linear or circular DNA or RNA molecule that may include chromosomal, non-chromosomal, semi-synthetic or synthetic nucleic acid molecules. Exemplary vectors are those capable of autonomous replication (episomal vector) or expression of nucleic acid molecules to which they are linked (expression vectors).

5 "Retroviruses" are viruses having an RNA genome. "Gammaretrovirus" refers to a genus of the retroviridae family. Exemplary gammaretroviruses include mouse stem cell virus, murine leukemia virus, feline leukemia virus, feline sarcoma virus, and avian reticuloendotheliosis viruses.

 "Lentivirus" refers to a genus of retroviruses that are capable of infecting
10 dividing and non-dividing cells. Several examples of lentiviruses include HIV (human immunodeficiency virus: including HIV type 1, and HIV type 2); equine infectious anemia virus; feline immunodeficiency virus (FIV); bovine immune deficiency virus (BIV); and simian immunodeficiency virus (SIV).

 "Lentiviral vector," as used herein, means HIV-based lentiviral vectors for gene
15 delivery, which can be integrative or non-integrative, have relatively large packaging capacity, and can transduce a range of different cell types. Lentiviral vectors are usually generated following transient transfection of three (packaging, envelope and transfer) or more plasmids into producer cells. Like HIV, lentiviral vectors enter the target cell through the interaction of viral surface glycoproteins with receptors on the
20 cell surface. On entry, the viral RNA undergoes reverse transcription, which is mediated by the viral reverse transcriptase complex. The product of reverse transcription is a double-stranded linear viral DNA, which is the substrate for viral integration into the DNA of infected cells.

 The term "operably-linked" refers to the association of two or more nucleic acid
25 molecules on a single nucleic acid fragment so that the function of one is affected by the other. For example, a promoter is operably-linked with a coding sequence when it is capable of affecting the expression of that coding sequence (*i.e.*, the coding sequence is under the transcriptional control of the promoter). "Unlinked" means that the associated genetic elements are not closely associated with one another and the function
30 of one does not affect the other.

The term "expression", as used herein, refers to the process by which a polypeptide is produced based on the encoding sequence of a nucleic acid molecule, such as a gene. The process can include transcription, post-transcriptional control, post-transcriptional modification, translation, post-translational control, post translational
5 modification, or any combination thereof.

As used herein, "expression vector" refers to a DNA construct containing a nucleic acid molecule that is operably-linked to a suitable control sequence capable of effecting the expression of the nucleic acid molecule in a suitable host. Such control sequences include a promoter to effect transcription, an optional operator sequence to
10 control such transcription, a sequence encoding suitable mRNA ribosome binding sites, and sequences which control termination of transcription and translation. The vector may be a plasmid, a phage particle, a virus, or simply a potential genomic insert. Once transformed into a suitable host, the vector may replicate and function independently of the host genome, or may, in some instances, integrate into the genome itself. In the
15 present specification, "plasmid," "expression plasmid," "virus" and "vector" are often used interchangeably.

The term "introduced" in the context of inserting a nucleic acid molecule into a cell, means "transfection", or "transformation", or "transduction" and includes reference to the incorporation of a nucleic acid molecule into a eukaryotic or prokaryotic cell
20 wherein the nucleic acid molecule can be incorporated into the genome of a cell (*e.g.*, a chromosome, a plasmid, a plastid, or a mitochondrial DNA), converted into an autonomous replicon, or transiently expressed (*e.g.*, transfected mRNA).

As used herein, "heterologous" nucleic acid molecule, construct or sequence refers to a nucleic acid molecule or portion of a nucleic acid molecule that is not native
25 to a host cell, but can be homologous to a nucleic acid molecule or portion of a nucleic acid molecule from the host cell. The source of the heterologous nucleic acid molecule, construct or sequence can be from a different genus or species. In certain embodiments, a heterologous nucleic acid molecule is added (*i.e.*, not endogenous or native) to a host cell or host genome by, for example, conjugation, transformation, transfection,
30 transduction, electroporation, or the like, wherein the added molecule can integrate into the host genome or exist as extra-chromosomal genetic material (*e.g.*, as a plasmid or

other form of self-replicating vector), and can be present in multiple copies. In addition, "heterologous" refers to a non-native enzyme, protein or other activity encoded by a non-endogenous nucleic acid molecule introduced into the host cell, even if the host cell encodes a homologous protein or activity.

5 The term "homologous" or "homolog" refers to a molecule or activity found in or derived from a host cell, species or strain. For example, a heterologous molecule or gene encoding the molecule may be homologous to a native host or host cell molecule or gene that encodes the molecule, respectively, and may optionally have an altered structure, sequence, expression level or combinations thereof.

10 As used herein, the term "endogenous" or "native" refers to a gene, protein, compound, molecule or activity that is normally present in a host or host cell. Moreover, a gene, protein or activity that is mutated, overexpressed, shuffled, duplicated or otherwise altered as compared to a parent gene, protein or activity is still considered to be endogenous or native to that particular host cell. For example, an
15 endogenous control sequence from a first gene (*e.g.*, a promoter, translational attenuation sequences) can be used to alter or regulate expression of a second native gene or nucleic acid molecule, wherein the expression or regulation of the second native gene or nucleic acid molecule differs from normal expression or regulation in a parent cell.

20 As used herein, the term "engineered," "recombinant," "modified" or "non-natural" refers to an organism, microorganism, cell, nucleic acid molecule, or vector that has been modified by introduction of a heterologous nucleic acid molecule, or refers to a cell or microorganism that has been genetically engineered by human intervention—that is, modified by introduction of a heterologous nucleic acid
25 molecule, or refers to a cell or microorganism that has been altered such that expression of an endogenous nucleic acid molecule or gene is controlled, deregulated or constitutive, where such alterations or modifications can be introduced by genetic engineering. Human-generated genetic alterations can include, for example, modifications introducing nucleic acid molecules (which may include an expression
30 control element, such as a promoter) encoding one or more proteins, binding proteins, or enzymes, or other nucleic acid molecule additions, deletions, substitutions, or other

functional disruption of or addition to a cell's genetic material. Exemplary modifications include those in coding regions or functional fragments thereof heterologous or homologous polypeptides from a reference or parent molecule. Additional exemplary modifications include, for example, modifications in non-coding regulatory regions in which the modifications alter expression of a gene or operon.

As used herein, "mutation" refers to a change in the sequence of a nucleic acid molecule or polypeptide molecule as compared to a reference or wild-type nucleic acid molecule or polypeptide molecule, respectively. A mutation can result in several different types of change in sequence, including substitution, insertion or deletion of nucleotide(s) or amino acid(s).

A "conservative substitution" is recognized in the art as a substitution of one amino acid for another amino acid that has similar properties. Exemplary conservative substitutions are well known in the art (*see, e.g.*, WO 97/09433 at page 10; Lehninger, Biochemistry, 2nd Edition; Worth Publishers, Inc. NY, NY, pp.71-77, 1975; Lewin, Genes IV, Oxford University Press, NY and Cell Press, Cambridge, MA, p. 8, 1990).

"Sequence identity," as used herein, refers to the percentage of amino acid residues in one sequence that are identical with the amino acid residues in another reference polypeptide sequence after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. The percentage sequence identity values can be generated using the NCBI BLAST 2.0 software as defined by Altschul *et al.* (1997), *Nucl. Acids Res.* 25:3389-3402, with the parameters set to default values.

As used herein, "hyperproliferative disorder" refers to excessive growth or proliferation as compared to a normal or undiseased cell. Exemplary hyperproliferative disorders include tumors, cancers, hematological malignancies, neoplastic tissue, carcinoma, sarcoma, malignant cells, pre-malignant cells, as well as non-neoplastic or non-malignant hyperproliferative disorders (*e.g.*, adenoma, fibroma, lipoma, leiomyoma, hemangioma, fibrosis, restenosis, as well as autoimmune diseases such as rheumatoid arthritis, osteoarthritis, psoriasis, inflammatory bowel disease, or the like). In certain embodiments, a hyperproliferative disorder is acute myelogenous leukemia.

"Adoptive cellular immunotherapy" or "adoptive immunotherapy" refers to the administration of naturally occurring or genetically engineered, disease antigen-specific immune cells (*e.g.*, T cells). Adoptive cellular immunotherapy may be autologous (immune cells are from the recipient), allogeneic (immune cells are from a donor of the same species) or syngeneic (immune cells are from a donor genetically identical to the recipient).

"Treat" or "treatment" or "ameliorate" refers to medical management of a disease, disorder, or condition of a subject (*e.g.*, a human or non-human mammal, such as a primate, horse, dog, mouse, rat). In general, an appropriate dose or treatment regimen comprising a host cell expressing a CCNA1-specific binding protein of the present disclosure is administered in an amount sufficient to elicit a therapeutic or prophylactic benefit. Therapeutic or prophylactic/preventive benefit includes improved clinical outcome; lessening or alleviation of symptoms associated with a disease; decreased occurrence of symptoms; improved quality of life; longer disease-free status; diminishment of extent of disease, stabilization of disease state; delay of disease progression; remission; survival; prolonged survival; or any combination thereof.

A "therapeutically effective amount" or "effective amount" of a binding protein or cell expressing a binding protein of this disclosure refers to that amount of compound or cells sufficient to result in amelioration of one or more symptoms of the disease being treated in a statistically significant manner. When referring to an individual active ingredient or a cell expressing a single active ingredient, administered alone, a therapeutically effective dose refers to the effects of that ingredient or cell expressing that ingredient alone. When referring to a combination, a therapeutically effective dose refers to the combined amounts of active ingredients or combined adjunctive active ingredient with a cell expressing an active ingredient that results in a therapeutic effect, whether administered serially or simultaneously. Another combination may be a cell expressing more than one active ingredient, such as two different binding proteins, or other relevant therapeutic.

CCNA-1 Specific Binding Proteins

Cyclin A1 refers to a protein encoded by the *CCNA1* gene. CCNA1 is a member of the cyclin family, whose expression is normally limited to the testes, where

it is involved in regulating spermatogenesis. CCNA1 is highly expressed in leukemic cells and other malignancies and may promote cell proliferation and survival. Several peptides of the CCNA1 protein are known to be tumor-associated antigen peptides that are HLA A*02:01-restricted antigens. Due to these characteristics, the CCNA1 protein
 5 is an attractive target for clinical development.

In certain aspects, the present disclosure provides binding proteins (*e.g.*, an immunoglobulin superfamily binding protein or portion thereof) that specifically bind CCNA1 peptide FLDRFLSCM (SEQ ID NO:1), CCNA1 peptide SLIAAAAFCLA (SEQ ID NO:2), or CCNA1 peptide YSLSEIVPCL (SEQ ID NO:3).

10 In one aspect, the present disclosure provides a binding protein (*e.g.*, an immunoglobulin superfamily binding protein or portion thereof), comprising: (a) a T cell receptor (TCR) α chain variable (V_α) domain comprising a complementary determining region 3 (CDR3) amino acid sequence set forth in any one of SEQ ID NOS:5, 7, 9, 11, 13, 15, 17, and 19, or a CDR3 amino acid sequence set forth in any
 15 one of SEQ ID NOS: 5, 7, 9, 11, 13, 15, 17, and 19 with up to five amino acid substitutions, insertions and/or deletions, and a TCR β chain variable (V_β) domain; (b) TCR V_α domain, and a TCR V_β domain comprising a CDR3 amino acid sequence set forth in any one of SEQ ID NOS:6, 8, 10, 12, 14, 16, 18, 20, and 189, or a CDR3 amino acid sequence set forth in any one of SEQ ID NOS: 6, 8, 10, 12, 14, 16, 18, 20,
 20 and 189 with up to five amino acid substitutions, insertions and/or deletions; or (c) a V_α domain of (a) and a V_β of (b), wherein the binding protein is capable of specifically binding to a human cyclin A1 (CCNA1) peptide 227-235 FLDRFLSCM (SEQ ID NO:1):human leukocyte antigen (HLA) complex.

In certain embodiments, (a) the V_α domain comprises the CDR3 amino acid
 25 sequence of SEQ ID NO:5 and the V_β domain comprises the CDR3 amino acid sequence of SEQ ID NO:6; (b) the V_α domain comprises the CDR3 amino acid sequence of SEQ ID NO:7 and the V_β domain comprises the CDR3 amino acid sequence of SEQ ID NO:8; (c) the V_α domain comprises the CDR3 amino acid sequence of SEQ ID NO:9 and the V_β domain comprises the CDR3 amino acid
 30 sequence of SEQ ID NO:10; (d) the V_α domain comprises the CDR3 amino acid sequence of SEQ ID NO:11 and the V_β domain comprises the CDR3 amino acid

sequence of SEQ ID NO:12; (e) the V α domain comprises the CDR3 amino acid sequence of SEQ ID NO:13 and the V β domain comprises the CDR3 amino acid sequence of SEQ ID NO:14; (f) the V α domain comprises the CDR3 amino acid sequence of SEQ ID NO:15 and the V β domain comprises the CDR3 amino acid sequence of SEQ ID NO:16; (g) the V α domain comprises the CDR3 amino acid sequence of SEQ ID NO:17 and the V β domain comprises the CDR3 amino acid sequence of SEQ ID NO:18; (h) the V α domain comprises the CDR3 amino acid sequence of SEQ ID NO:19 and the V β domain comprises the CDR3 amino acid sequence of SEQ ID NO:20; or (i) the V α domain comprises the CDR3 amino acid sequence of SEQ ID NO:7 and the V β domain comprises the CDR3 amino acid sequence of SEQ ID NO:189.

In one aspect, the present disclosure provides a binding protein (*e.g.*, an immunoglobulin superfamily binding protein or portion thereof), comprising: (a) a T cell receptor (TCR) α chain variable (V α) domain comprising a complementary determining region 3 (CDR3) amino acid sequence set forth in any one of SEQ ID NOS: 89, 97, 105, 113, 119, 127, 133, and 137, or a CDR3 amino acid sequence set forth in any one of SEQ ID NOS: 89, 97, 105, 113, 119, 127, 133, and 137 with up to five amino acid substitutions, insertions and/or deletions, and a TCR β chain variable (V β) domain; (b) TCR V α domain, and a TCR V β domain comprising a CDR3 amino acid sequence set forth in any one of SEQ ID NOS: 93, 101, 109, 117, 123, 129, 140, and 190, or a CDR3 amino acid sequence set forth in any one of SEQ ID NOS: 93, 101, 109, 117, 123, 129, 140, and 190 with up to five amino acid substitutions, insertions and/or deletions; or (c) a V α domain of (a) and a V β of (b), wherein the binding protein is capable of specifically binding to a human cyclin A1 (CCNA1) peptide 227-235 FLDRFLSCM (SEQ ID NO:1):human leukocyte antigen (HLA) complex.

In certain embodiments, (a) the V α domain comprises the CDR3 amino acid sequence of SEQ ID NO:89 and the V β domain comprises the CDR3 amino acid sequence of SEQ ID NO:93; (b) the V α domain comprises the CDR3 amino acid sequence of SEQ ID NO:97 and the V β domain comprises the CDR3 amino acid sequence of SEQ ID NO:101; (c) the V α domain comprises the CDR3 amino acid sequence of SEQ ID NO:105 and the V β domain comprises the CDR3 amino acid

sequence of SEQ ID NO:109; (d) the $V\alpha$ domain comprises the CDR3 amino acid sequence of SEQ ID NO:113 and the $V\beta$ domain comprises the CDR3 amino acid sequence of SEQ ID NO:117; (e) the $V\alpha$ domain comprises the CDR3 amino acid sequence of SEQ ID NO:119 and the $V\beta$ domain comprises the CDR3 amino acid sequence of SEQ ID NO:123; (f) the $V\alpha$ domain comprises the CDR3 amino acid sequence of SEQ ID NO:127 and the $V\beta$ domain comprises the CDR3 amino acid sequence of SEQ ID NO:129; (g) the $V\alpha$ domain comprises the CDR3 amino acid sequence of SEQ ID NO:133 and the $V\beta$ domain comprises the CDR3 amino acid sequence of SEQ ID NO:129; (h) the $V\alpha$ domain comprises the CDR3 amino acid sequence of SEQ ID NO:137 and the $V\beta$ domain comprises the CDR3 amino acid sequence of SEQ ID NO:140; or (i) the $V\alpha$ domain comprises the CDR3 amino acid sequence of SEQ ID NO:97 and the $V\beta$ domain comprises the CDR3 amino acid sequence of SEQ ID NO:190.

Peptide-MHC complexes, such as CCNA1 peptide:MHC complexes, are recognized by and bound through the TCR $V\alpha$ and TCR $V\beta$ domains. During lymphocyte development, $V\alpha$ exons are assembled from different variable and joining gene segments (V-J), and $V\beta$ exons are assembled from different variable, diversity, and joining gene segments (V-D-J). The TCR α chromosomal locus has 70-80 variable gene segments and 61 joining gene segments. The TCR β chromosomal locus has 52 variable gene segments, and two separate clusters of each containing a single diversity gene segment, together with six or seven joining gene segments. Functional $V\alpha$ and $V\beta$ gene exons are generated by the recombination of a variable gene segment with a joining gene segment for $V\alpha$, and a variable gene segment with a diversity gene segment and a joining gene segment for $V\beta$.

The $V\alpha$ and $V\beta$ domains each comprise three hypervariable loops, also referred to as complementary determining regions (CDRs) that contact the peptide-MHC complex. CDR1 and CDR2 are encoded within the variable gene segment, whereas CDR3 is encoded by the region spanning the variable and joining segments for $V\alpha$, or the region spanning variable, diversity, and joining segments for $V\beta$. Thus, if the identity of the variable gene segment of a $V\alpha$ or $V\beta$ is known, the sequences of their corresponding CDR1 and CDR2 can be deduced. Compared with CDR1 and CDR2,

CDR3 is significantly more diverse because of the addition and loss of nucleotides during the recombination process.

TCR variable domain sequences can be aligned to a numbering scheme (International Immunogenetics Information System (IMGT) and Aho), allowing
 5 equivalent residue positions to be annotated and for different molecules to be compared using Antigen receptor Numbering And Receptor Classification (ANARCI) software tool (2016, Bioinformatics 15:298-300). A numbering scheme provides a standardized delineation of framework regions and CDRs in the TCR variable domains.

Table 1 provides the identities of the variable gene segment and joining gene
 10 segment for a TCR V α comprising a CDR3 comprising an amino acid sequence of any one of SEQ ID NOS:5, 7, 9, 11, 13, 15, 17, 19, 21, and 23, and the identities of the variable gene segment and joining gene segment for a TCR V β comprising a CDR3 comprising an amino acid sequence of any one of SEQ ID NOS:6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 189. Accordingly, the CDR1 and CDR2 sequences of the V α and V β
 15 domains may be deduced from the corresponding variable gene segments.

In some embodiments, (a) the V β domain comprises the CDR1 amino acid sequence encoded by a TRBV9*01 gene; and the V α domain comprises the CDR1 amino acid sequence encoded by a TRAV30*01 gene; (b) the V β domain comprises the CDR1 amino acid sequence encoded by a TRBV2*01 gene; and the V α domain
 20 comprises the CDR1 amino acid sequence encoded by a TRAV10*01 gene; (c) the V β domain comprises the CDR1 amino acid sequence encoded by a TRBV6-6*01 gene; and the V α domain comprises the CDR1 amino acid sequence encoded by a TRAV24*01 gene; (d) the V β domain comprises the CDR1 amino acid sequence encoded by a TRBV5-6*01 gene; and the V α domain comprises the CDR1 amino acid
 25 sequence encoded by a TRAV21*01 gene; (e) the V β domain comprises the CDR1 amino acid sequence encoded by a TRBV7-3*01 gene; and the V α domain comprises the CDR1 amino acid sequence encoded by a TRAV21*02 gene; (f) the V β domain comprises the CDR1 amino acid sequence encoded by a TRBV7-3*01 gene; and the V α domain comprises the CDR1 amino acid sequence encoded by a TRAV12-2*02 gene;
 30 (g) the V β domain comprises the CDR1 amino acid sequence encoded by a TRBV7-3*01 gene; and the V α domain comprises the CDR1 amino acid sequence encoded by a

TRAV17*01 gene; (h) the V β domain comprises the CDR1 amino acid sequence encoded by a TRBV7-2*01 gene; and the V α domain comprises the CDR1 amino acid sequence encoded by a TRAV17*01 gene; or (i) the V β domain comprises the CDR1 amino acid sequence encoded by a TRBV10-2*01 gene; and the V α domain comprises
5 the CDR1 amino acid sequence encoded by a TRAV10*01 gene.

In some embodiments, (a) the V β domain comprises the CDR1 amino acid sequence of SEQ ID NO:91 and the V α domain comprises the CDR1 amino acid sequence of SEQ ID NO:87; (b) the V β domain comprises the CDR1 amino acid sequence of SEQ ID NO:99 and the V α domain comprises the CDR1 amino acid
10 sequence of SEQ ID NO:95; (c) the V β domain comprises the CDR1 amino acid sequence of SEQ ID NO:107 and the V α domain comprises the CDR1 amino acid sequence of SEQ ID NO:103; (d) the V β domain comprises the CDR1 amino acid sequence of SEQ ID NO:115 and the V α domain comprises the CDR1 amino acid sequence of SEQ ID NO:111; (e) the V β domain comprises the CDR1 amino acid
15 sequence of SEQ ID NO:121 and the V α domain comprises the CDR1 amino acid sequence of SEQ ID NO:111; (f) the V β domain comprises the CDR1 amino acid sequence of SEQ ID NO:121 and the V α domain comprises the CDR1 amino acid sequence of SEQ ID NO:125; (g) the V β domain comprises the CDR1 amino acid sequence of SEQ ID NO:121 and the V α domain comprises the CDR1 amino acid
20 sequence of SEQ ID NO:131; or (h) the V β domain comprises the CDR1 amino acid sequence of SEQ ID NO:167 and the V α domain comprises the CDR1 amino acid sequence of SEQ ID NO:95.

In some embodiments, (a) the V β domain comprises the CDR2 amino acid sequence encoded by a TRBV9*01 gene; and the V α domain comprises the CDR2
25 amino acid sequence encoded by a TRAV30*01 gene; (b) the V β domain comprises the CDR2 amino acid sequence encoded by a TRBV2*01 gene; and the V α domain comprises the CDR2 amino acid sequence encoded by a TRAV10*01 gene; (c) the V β domain comprises the CDR2 amino acid sequence encoded by a TRBV6-6*01 gene; and the V α domain comprises the CDR2 amino acid sequence encoded by a
30 TRAV24*01 gene; (d) the V β domain comprises the CDR2 amino acid sequence encoded by a TRBV5-6*01 gene; and the V α domain comprises the CDR2 amino acid

sequence encoded by a TRAV21*01 gene; (e) the V β domain comprises the CDR2 amino acid sequence encoded by a TRBV7-3*01 gene; and the V α domain comprises the CDR2 amino acid sequence encoded by a TRAV21*02 gene; (f) the V β domain comprises the CDR2 amino acid sequence encoded by a TRBV7-3*01 gene; and the V α domain comprises the CDR2 amino acid sequence encoded by a TRAV12-2*02 gene; (g) the V β domain comprises the CDR2 amino acid sequence encoded by a TRBV7-3*01 gene; and the V α domain comprises the CDR2 amino acid sequence encoded by a TRAV17*01 gene; (h) the V β domain comprises the CDR2 amino acid sequence encoded by a TRBV7-2*01 gene; and the V α domain comprises the CDR2 amino acid sequence encoded by a TRAV17*01 gene; or (i) the V β domain comprises the CDR2 amino acid sequence encoded by a TRBV10-2*01 gene; and the V α domain comprises the CDR2 amino acid sequence encoded by a TRAV10*01 gene.

In some embodiments, (a) the V β domain comprises the CDR2 amino acid sequence of SEQ ID NO:92 and the V α domain comprises the CDR2 amino acid sequence of SEQ ID NO:88; (b) the V β domain comprises the CDR2 amino acid sequence of SEQ ID NO:100 and the V α domain comprises the CDR2 amino acid sequence of SEQ ID NO:96; (c) the V β domain comprises the CDR2 amino acid sequence of SEQ ID NO:108 and the V α domain comprises the CDR2 amino acid sequence of SEQ ID NO:104; (d) the V β domain comprises the CDR2 amino acid sequence of SEQ ID NO:116 and the V α domain comprises the CDR2 amino acid sequence of SEQ ID NO:112; (e) the V β domain comprises the CDR2 amino acid sequence of SEQ ID NO:122 and the V α domain comprises the CDR2 amino acid sequence of SEQ ID NO:112; (f) the V β domain comprises the CDR2 amino acid sequence of SEQ ID NO:122 and the V α domain comprises the CDR2 amino acid sequence of SEQ ID NO:126; (g) the V β domain comprises the CDR2 amino acid sequence of SEQ ID NO:122 and the V α domain comprises the CDR2 amino acid sequence of SEQ ID NO:132; (h) the V β domain comprises the CDR2 amino acid sequence of SEQ ID NO:129 and the V α domain comprises the CDR2 amino acid sequence of SEQ ID NO:132; or (i) the V β domain comprises the CDR2 amino acid sequence of SEQ ID NO:168 and the V α domain comprises the CDR2 amino acid sequence of SEQ ID NO:96.

Thus, in certain embodiments, (a) the V β domain comprises the CDR3 amino acid sequence of SEQ ID NO:6 or 93 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRBV9*01 gene; and the V α domain comprises the CDR3 amino acid sequence of SEQ ID NO:5 or 89 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRAV30*01 gene; (b) the V β domain comprises the CDR3 amino acid sequence of SEQ ID NO:8 or 190 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRBV2*01 gene; and the V α domain comprises the CDR3 amino acid sequence of SEQ ID NO:7 or 97 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRAV10*01 gene; (c) the V β domain comprises the CDR3 amino acid sequence of SEQ ID NO:10 or 109 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRBV6-6*01 gene; and the V α domain comprises the CDR3 amino acid sequence of SEQ ID NO:9 or 105 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRAV24*01 gene; (d) the V β domain comprises the CDR3 amino acid sequence of SEQ ID NO:12 or 117 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRBV5-6*01 gene; and the V α domain comprises the CDR3 amino acid sequence of SEQ ID NO:11 or 113 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRAV21*01 gene; (e) the V β domain comprises the CDR3 amino acid sequence of SEQ ID NO:14 or 123 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRBV7-3*01 gene; and the V α domain comprises the CDR3 amino acid sequence of SEQ ID NO:13 or 119 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRAV21*02 gene; (f) the V β domain comprises the CDR3 amino acid sequence of SEQ ID NO:16 or 129 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRBV7-3*01 gene; and the V α domain comprises the CDR3 amino acid sequence of SEQ ID NO:15 or 127 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRAV12-2*02 gene; (g) the V β domain comprises the CDR3 amino acid sequence of SEQ ID NO:18 or 129 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRBV7-3*01 gene; and the V α domain comprises the CDR3 amino acid sequence of SEQ ID NO:17 or 133 and a CDR1 amino acid sequence and a

CDR2 amino acid sequence encoded by a TRAV17*01 gene; (h) the V β domain comprises the CDR3 amino acid sequence of SEQ ID NO:20 or 140 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRBV7-2*01 gene; and the V α domain comprises the CDR3 amino acid sequence of SEQ ID NO:19 or 137 and
 5 a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRAV17*01 gene; or (i) the V β domain comprises the CDR3 amino acid sequence of SEQ ID NO:189 or 101 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRBV10-2*01 gene; and the V α domain comprises the CDR3 amino acid sequence of SEQ ID NO:7 or 97 and a CDR1 amino acid sequence and a
 10 CDR2 amino acid sequence encoded by a TRAV10*01 gene.

In certain embodiments, (a) the V β domain comprises the CDR1 amino acid sequence of SEQ ID NO: 91, the CDR2 amino acid sequence of SEQ ID NO:92, and the CDR3 amino acid sequence of SEQ ID NO:6 or 93; and the V α domain comprises the CDR1 amino acid sequence of SEQ ID NO:87, the CDR2 amino acid sequence of
 15 SEQ ID NO:88, and the CDR3 amino acid sequence of SEQ ID NO:5 or 89; (b) the V β domain comprises the CDR1 amino acid sequence of SEQ ID NO:99, the CDR2 amino acid sequence of SEQ ID NO:100, and the CDR3 amino acid sequence of SEQ ID NO:189 or 101; and the V α domain comprises the CDR1 amino acid sequence of SEQ ID NO:95, the CDR2 amino acid sequence of SEQ ID NO:96, and the CDR3 amino
 20 acid sequence of SEQ ID NO:7 or 97; (c) the V β domain comprises the CDR1 amino acid sequence of SEQ ID NO:107, the CDR2 amino acid sequence of SEQ ID NO:108, and the CDR3 amino acid sequence of SEQ ID NO:10 or 109; and the V α domain comprises the CDR1 amino acid sequence of SEQ ID NO: 103, the CDR2 amino acid sequence of SEQ ID NO:104, and the CDR3 amino acid sequence of SEQ ID NO:9 or
 25 105; (d) the V β domain comprises the CDR1 amino acid sequence of SEQ ID NO:115, the CDR2 amino acid sequence of SEQ ID NO:116, and the CDR3 amino acid sequence of SEQ ID NO:12 or 117; and the V α domain comprises the CDR1 amino acid sequence of SEQ ID NO:111, the CDR2 amino acid sequence of SEQ ID NO:112, and the CDR3 amino acid sequence of SEQ ID NO:11 or 113; (e) the V β domain
 30 comprises the CDR1 amino acid sequence of SEQ ID NO:121, the CDR2 amino acid sequence of SEQ ID NO:122, and the CDR3 amino acid sequence of SEQ ID NO:14 or

123; and the V α domain comprises the CDR1 amino acid sequence of SEQ ID NO:111, the CDR2 amino acid sequence of SEQ ID NO:112, and the CDR3 amino acid sequence of SEQ ID NO:13 or 119; (f) the V β domain comprises the CDR1 amino acid sequence of SEQ ID NO:121, the CDR2 amino acid sequence of SEQ ID NO:122, and the CDR3 amino acid sequence of SEQ ID NO:16 or 129; and the V α domain comprises the CDR1 amino acid sequence of SEQ ID NO:125, the CDR2 amino acid sequence of SEQ ID NO:126, and the CDR3 amino acid sequence of SEQ ID NO:15 or 127; (g) the V β domain comprises the CDR1 amino acid sequence of SEQ ID NO:121, the CDR2 amino acid sequence of SEQ ID NO:122, and the CDR3 amino acid sequence of SEQ ID NO:18 or 129; and the V α domain comprises the CDR1 amino acid sequence of SEQ ID NO:131, the CDR2 amino acid sequence of SEQ ID NO:132, and the CDR3 amino acid sequence of SEQ ID NO:17 or 133; (h) the V β domain comprises the CDR1 amino acid sequence of SEQ ID NO:121, the CDR2 amino acid sequence of SEQ ID NO:139, and the CDR3 amino acid sequence of SEQ ID NO:20 or 140; and the V α domain comprises the CDR1 amino acid sequence of SEQ ID NO:131, the CDR2 amino acid sequence of SEQ ID NO:132, and the CDR3 amino acid sequence of SEQ ID NO:19 or 137; or (i) the V β domain comprises the CDR1 amino acid sequence of SEQ ID NO:167, the CDR2 amino acid sequence of SEQ ID NO:168, and the CDR3 amino acid sequence of SEQ ID NO:8 or 190; and the V α domain comprises the CDR1 amino acid sequence of SEQ ID NO:95, the CDR2 amino acid sequence of SEQ ID NO:96, and the CDR3 amino acid sequence of SEQ ID NO:7 or 97; .

In certain embodiments, the binding protein comprises: (a) a V α domain that is at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the V α amino acid sequence contained in any one of SEQ ID NOS:36, 38, 40, 42, 44, 86, 49, 51, 53, 57, 59, 63, 65, 67, 81, and 83; (b) a V β domain that is at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the V β amino acid sequence contained in any one of SEQ ID NOS:36, 38, 40, 42, 46, 86, 49, 51, 55, 57, 61, 63, 67, 81, and 83; or (c) a V α domain of (a) and a V β of (b); wherein at least three or four of the CDRs have no mutations and the CDRs that do have mutations have three or less amino acid

substitutions, insertions, and/or deletions. Such variant V α and V β may be used in binding proteins described herein provided that the binding proteins retain or substantially retain the ability to specifically bind to CCNA1 peptide (SEQ ID NO:1):HLA complex.

- 5 In further embodiments, the binding protein comprises: (a) a V α domain comprising or consisting of the V α amino acid sequence contained in any one of SEQ ID NOS: 36, 38, 40, 42, 44, 86, 49, 51, 53, 57, 59, 63, 65, 67, 81, 83, 162, 165, 170, 172, 174, 176, 178, 180, and 186; (b) a V β domain comprising or consisting of the V β amino acid sequence contained in any one of SEQ ID NOS:36, 38, 40, 42, 46, 86, 49,
10 51, 55, 57, 61, 63, 67, 81, 83, 162, 165, 170, 172, 174, 176, 178, 180, and 186; or (c) a V α domain of (a) and a V β of (b).

- In some embodiments, the binding protein comprises: (a) a V α domain that is at least about 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ
15 ID NOS:90, 98, 106, 114, 120, 128, 134, and 138; (b) a V β domain that is at least about 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS:94, 102, 110, 118, 124, 130, 136, 141, and 166; or (c) a V α domain of (a) and a V β of (b), wherein at least three or four of the CDRs have no mutations and the CDRs
20 that do have mutations have three or less amino acid substitutions, insertions, and/or deletions. Such variant V α and V β may be used in binding proteins described herein provided that the binding proteins retain or substantially retain the ability to specifically bind to CCNA1 peptide (SEQ ID NO:1):HLA complex.

- In some embodiments, the binding protein comprises: (a) a V α domain
25 comprising or consisting of the amino acid sequence of any one of SEQ ID NOS:90, 98, 106, 114, 120, 128, 134, and 138; (b) a V β domain comprising or consisting of the V β amino acid sequence of any one of SEQ ID NOS:94, 102, 110, 118, 124, 130, 136, 141, and 166; or (c) a V α domain of (a) and a V β of (b).

- An exemplary binding protein comprises: (a) the V α domain comprising the V α
30 amino acid sequence contained in SEQ ID NO:36 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:36; (b) the V α domain comprising

- the V α amino acid sequence contained in SEQ ID NO:38 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:38; (c) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:40 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:40; (d) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:42 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:42; (e) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:44 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:46; (f) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:86 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:86; (g) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:49 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:49; (h) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:51 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:51; (i) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:53 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:55; (j) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:57 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:57; (k) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:59 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:61; (l) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:63 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:63; (m) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:65 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:67; (n) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:67 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:67; (o) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:81 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:81; (p) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:83 and the V β domain comprising the V β

- amino acid sequence contained in SEQ ID NO:83; (q) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:162 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:162; (r) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:165 and the V β
- 5 domain comprising the V β amino acid sequence contained in SEQ ID NO:165; (s) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:170 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:170; (t) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:172 and the V β domain comprising the V β amino acid sequence contained in SEQ
- 10 ID NO:172; (u) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:174 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:174; (v) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:176 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:176; (w) the V α domain comprising the V α amino
- 15 acid sequence contained in SEQ ID NO:178 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:178; (x) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:180 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:180; or (y) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:186 and the V β
- 20 domain comprising the V β amino acid sequence contained in SEQ ID NO:186.

- An exemplary binding protein comprises: (a) the V α domain comprising the amino acid sequence of SEQ ID NO:90 and the V β domain comprising the amino acid sequence of SEQ ID NO:94; (b) the V α domain comprising the amino acid sequence of SEQ ID NO:98 and the V β domain comprising the amino acid sequence of SEQ ID
- 25 NO:102; (c) the V α domain comprising the amino acid sequence of SEQ ID NO:106 and the V β domain comprising the amino acid sequence of SEQ ID NO:110; (d) the V α domain comprising the amino acid sequence of SEQ ID NO:114 and the V β domain comprising the amino acid sequence of SEQ ID NO:118; (e) the V α domain comprising the amino acid sequence of SEQ ID NO:120 and the V β domain comprising the amino
- 30 acid sequence of SEQ ID NO:124; (f) the V α domain comprising the amino acid sequence of SEQ ID NO:128 and the V β domain comprising the amino acid sequence

of SEQ ID NO:130; (g) the V α domain comprising the amino acid sequence of SEQ ID NO:134 and the V β domain comprising the amino acid sequence of SEQ ID NO:136; (h) the V α domain comprising the amino acid sequence of SEQ ID NO:138 and the V β domain comprising the amino acid sequence of SEQ ID NO:141; or (i) the V α domain
5 comprising the amino acid sequence of SEQ ID NO:98 and the V β domain comprising the amino acid sequence of SEQ ID NO:166.

In another aspect, the present disclosure provides a binding protein (*e.g.*, an immunoglobulin superfamily binding protein or portion thereof), comprising: (a) a T cell receptor (TCR) α chain variable (V α) domain comprising a complementary
10 determining region 3 (CDR3) amino acid sequence set forth in SEQ ID NO:21 or 143, or a CDR3 amino acid sequence set forth in SEQ ID NO:21 or 143 with up to five amino acid substitutions, insertions and/or deletions, and a TCR β chain variable (V β) domain; (b) a TCR V α domain, and a TCR V β domain comprising a CDR3 amino acid sequence set forth in SEQ ID NO:22 or 147, or a CDR3 amino acid sequence set forth
15 in SEQ ID NO:22 or 147 with up to five amino acid substitutions, insertions and/or deletions; or (c) a V α domain of (a) and a V β of (b), wherein the binding protein is capable of specifically binding to a human cyclin A1 (CCNA1) peptide 341-351 SLIAAAAFCLA (SEQ ID NO:2):human leukocyte antigen (HLA) complex. In specific embodiments, the V α domain comprises the CDR3 amino acid sequence of
20 SEQ ID NO:21 or 143 and the V β domain comprises the CDR3 amino acid sequence of SEQ ID NO:22 or 147.

In some embodiments, (a) the V β domain comprises the CDR1 amino acid sequence encoded by a TRBV19*01 gene; and the V α domain comprises the CDR1 amino acid sequence encoded by a TRAV24*01 gene. In some embodiments, (a) the
25 V β domain comprises the CDR1 amino acid sequence of SEQ ID NO:145 and the V α domain comprises the CDR1 amino acid sequence of SEQ ID NO:103.

In some embodiments, (a) the V β domain comprises the CDR2 amino acid sequence encoded by a TRBV19*01 gene; and the V α domain comprises the CDR2 amino acid sequence encoded by a TRAV24*01 gene. In some embodiments, (a) the
30 V β domain comprises the CDR2 amino acid sequence of SEQ ID NO:146 and the V α domain comprises the CDR2 amino acid sequence of SEQ ID NO:142.

In certain embodiments, the V β domain comprises: (a) the CDR3 amino acid sequence of SEQ ID NO:22 or 147 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRBV19*01 gene; (b) the V α domain comprises the CDR3 amino acid sequence of SEQ ID NO:21 or 143 and a CDR1 amino acid sequence
5 and a CDR2 amino acid sequence encoded by a TRAV24*01 gene; or both (a) and (b).

In certain embodiments, (a) the V β domain comprises the CDR1 amino acid sequence of SEQ ID NO: 145, the CDR2 amino acid sequence of SEQ ID NO:146, and the CDR3 amino acid sequence of SEQ ID NO:147; and the V α domain comprises the CDR1 amino acid sequence of SEQ ID NO:103, the CDR2 amino acid sequence of
10 SEQ ID NO:142, and the CDR3 amino acid sequence of SEQ ID NO:143.

In certain embodiments, the binding protein comprises (a) a V α domain that is at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the V α amino acid sequence of SEQ ID NO:69 or contained in SEQ ID NO:73 or 182; (b) a V β domain that is at least about 75%, 80%, 85%, 90%,
15 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the V β amino acid sequence of SEQ ID NO:71 or contained in SEQ ID NO:73 or 182; or (c) a V α domain of (a) and a V β of (b); wherein at least three or four of the CDRs have no mutations and the CDRs that do have mutations have three or less amino acid substitutions, insertions, and/or deletions. Such variant V α and V β domains may be
20 used in binding proteins described herein provided that the binding proteins retain or substantially retain the ability to specifically bind to CCNA1 peptide (SEQ ID NO:2):HLA complex.

In some embodiments, the binding protein comprises: (a) a V α domain that is at least about 75%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%,
25 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO:144; (b) a V β domain that is at least about 75%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO:148; or (c) a V α domain of (a) and a V β of (b).

In some embodiments, the binding protein comprises: (a) a V α domain
30 comprising or consisting of the amino acid sequence of SEQ ID NO:144; (b) a V β comprising or consisting of the amino acid sequence of SEQ ID NO:148; or (c) a V α

domain of (a) and a V β of (b). In some aspects, the exemplary binding protein comprises the V α domain comprising the amino acid sequence of SEQ ID NO:144 and the V β domain comprising the amino acid sequence of SEQ ID NO:148.

In certain embodiments, the binding protein comprises: (a) a V α domain
 5 comprising or consisting of the V α amino acid sequence of SEQ ID NO:69 or contained in SEQ ID NO:73; (b) a V β domain comprising or consisting of the V β amino acid sequence of SEQ ID NO:71 or contained in SEQ ID NO:73; or (c) a V α domain of (a) and a V β of (b). In specific embodiments, the binding protein comprises: (a) the V α domain comprising the V α amino acid sequence of SEQ ID NO:69 and the V β domain
 10 comprising the V β amino acid sequence of SEQ ID NO:71; or (b) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:73 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:73.

In another aspect, the present disclosure provides a binding protein (*e.g.*, an immunoglobulin superfamily binding protein or portion thereof), comprising: (a) a T
 15 cell receptor (TCR) α chain variable (V α) domain comprising a complementary determining region 3 (CDR3) amino acid sequence set forth in SEQ ID NO:23 or 151, or a CDR3 amino acid sequence set forth in SEQ ID NO:23 or 151 with up to five amino acid substitutions, insertions and/or deletions, and a TCR β chain variable (V β) domain; (b) a TCR V α domain, and a TCR V β domain comprising a CDR3 amino acid
 20 sequence set forth in SEQ ID NO:24 or 153, or a CDR3 amino acid sequence set forth in SEQ ID NO:24 or 153 with up to five amino acid substitutions, insertions and/or deletions; or (c) a V α domain of (a) and a V β of (b), wherein the binding protein is capable of specifically binding to a human cyclin A1 (CCNA1) peptide 370-379 YSLSEIVPCL (SEQ ID NO:3):human leukocyte antigen (HLA) complex.

25 In certain embodiments, the V α domain comprises the CDR3 amino acid sequence of SEQ ID NO:23 or 151 and the V β domain comprises the CDR3 amino acid sequence of SEQ ID NO:24 or 153.

In some embodiments, (a) the V β domain comprises the CDR1 amino acid sequence encoded by a TRBV5-6*01 gene; and the V α domain comprises the CDR1
 30 amino acid sequence encoded by a TRAV19*01 gene. In some embodiments, (a) the

V β domain comprises the CDR1 amino acid sequence of SEQ ID NO:115 and the V α domain comprises the CDR1 amino acid sequence of SEQ ID NO:149.

In some embodiments, (a) the V β domain comprises the CDR2 amino acid sequence encoded by a TRBV5-6*01 gene; and the V α domain comprises the CDR2 amino acid sequence encoded by a TRAV19*01 gene. In some embodiments, (a) the V β domain comprises the CDR2 amino acid sequence of SEQ ID NO:116 and the V α domain comprises the CDR2 amino acid sequence of SEQ ID NO:150.

In certain embodiments, (a) the V β domain comprises the CDR3 amino acid sequence of SEQ ID NO:24 or 153 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRBV5-6*01 gene; (b) the V α domain comprises the CDR3 amino acid sequence of SEQ ID NO:23 or 151 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRAV19*01 gene; or both (a) and (b).

In certain embodiments, (a) the V β domain comprises the CDR1 amino acid sequence of SEQ ID NO: 115, the CDR2 amino acid sequence of SEQ ID NO:116, and the CDR3 amino acid sequence of SEQ ID NO:153; and the V α domain comprises the CDR1 amino acid sequence of SEQ ID NO:149, the CDR2 amino acid sequence of SEQ ID NO:150, and the CDR3 amino acid sequence of SEQ ID NO:151.

In certain embodiments, the binding protein comprises: (a) a V α domain that is at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the V α amino acid sequence contained in SEQ ID NO:75, 79, or 184; (b) a V β domain that is at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the V β amino acid sequence contained in SEQ ID NO:77, 79, or 184; or (c) a V α domain of (a) and a V β of (b); wherein at least three or four of the CDRs have no mutations and the CDRs that do have mutations have three or less amino acid substitutions, insertions, and/or deletions. Such variant V α and V β domains may be used in binding proteins described herein provided that the binding proteins retain or substantially retain the ability to specifically bind to CCNA1 peptide (SEQ ID NO:3):HLA complex.

In some embodiments, the binding protein comprises: (a) a V α domain that is at least about 75%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%,

97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 152; (b) a V β domain that is at least about 75%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO:154; or (c) a V α domain of (a) and a V β of (b). In some embodiments, the binding protein comprises: (a) a V α domain comprising or consisting of the amino acid sequence of SEQ ID NO:152; (b) a V β domain comprising or consisting of the amino acid sequence of SEQ ID NO:154; or (c) a V α domain of (a) and a V β of (b). In some aspects, the exemplary binding protein comprises the V α domain comprising the amino acid sequence of SEQ ID NO:152 and the V β domain comprising the amino acid sequence of SEQ ID NO:154.

In certain embodiments, the binding protein comprises: (a) a V α domain comprising or consisting of the V α amino acid sequence contained in SEQ ID NO:75, 79, or 184; (b) a V β domain comprising or consisting of the V β amino acid sequence contained in SEQ ID NO:77, 79, or 184; or (c) a V α domain of (a) and a V β of (b). In specific embodiments, the binding protein comprises: (a) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:75 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:77; (b) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:79 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:79; or (c)) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:184 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:184.

In another aspect, the present disclosure provides binding proteins that are capable of specifically binding to a CCNA1 peptide YSLSEIVPCL (SEQ ID NO:3). In certain embodiments, the binding protein is capable of binding to CCNA1 peptide YSLSEIVPCL (SEQ ID NO:3):HLA complex.

Methods of identifying binding pairs of TCR V α and V β domains are known in the art and include, for example, PCT Patent Publication No. WO 2016/161273; Redmond et al., 2016, Genome Med. 8: 80; Munson et al., 2016, Proc. Natl. Acad. Sci. 113:8272-7; Kim et al., 2012, PLoS ONE 7:e37338 (each of the methods from which are incorporated by reference in its entirety). Accordingly, a V α domain for the

CCNA1-specific V β domains described herein (*e.g.*, a V β domain comprising CDR3 as set forth in any one of SEQ ID NOS: 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 93, 101, 109, 117, 123, 129, 140, 147, 153, 189, or 190), or vice versa (*e.g.*, a V α domain comprising CDR3 as set forth in any one of SEQ ID NOS: 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 89, 97, 105, 113, 119, 127, 133, 137, 143, or 151), may be identified using methods known in the art.

Conservative substitutions of amino acids are well known and may occur naturally or may be introduced when the binding protein or TCR is recombinantly produced. Amino acid substitutions, deletions, and additions may be introduced into a protein using mutagenesis methods known in the art (*see, e.g.*, Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, 3d ed., Cold Spring Harbor Laboratory Press, NY, 2001). Oligonucleotide-directed site-specific (or segment specific) mutagenesis procedures may be employed to provide an altered polynucleotide that has particular codons altered according to the substitution, deletion, or insertion desired. Alternatively, random or saturation mutagenesis techniques, such as alanine scanning mutagenesis, error prone polymerase chain reaction mutagenesis, and oligonucleotide-directed mutagenesis may be used to prepare immunogen polypeptide variants (*see, e.g.*, Sambrook *et al.*, *supra*).

A variety of criteria known to persons skilled in the art indicate whether an amino acid that is substituted at a particular position in a peptide or polypeptide is conservative (or similar). For example, a similar amino acid or a conservative amino acid substitution is one in which an amino acid residue is replaced with an amino acid residue having a similar side chain. Similar amino acids may be included in the following categories: amino acids with basic side chains (*e.g.*, lysine, arginine, histidine); amino acids with acidic side chains (*e.g.*, aspartic acid, glutamic acid); amino acids with uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine, histidine); amino acids with nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan); amino acids with beta-branched side chains (*e.g.*, threonine, valine, isoleucine), and amino acids with aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan). Proline, which is considered more difficult to classify, shares properties with amino

acids that have aliphatic side chains (*e.g.*, leucine, valine, isoleucine, and alanine). In certain circumstances, substitution of glutamine for glutamic acid or asparagine for aspartic acid may be considered a similar substitution in that glutamine and asparagine are amide derivatives of glutamic acid and aspartic acid, respectively. As understood in the art, "similarity" between two polypeptides is determined by comparing the amino acid sequence and conserved amino acid substitutes thereto of the polypeptide to the sequence of a second polypeptide (*e.g.*, using GENEWORKS, Align, the BLAST algorithm, or other algorithms described herein and practiced in the art).

In certain embodiments, the CCNA1-specific binding proteins provided in the present disclosure are capable of specifically binding a CCNA1 peptide in an HLA*02:01 restricted manner.

Exemplary binding proteins of the present disclosure include TCRs, antigen binding fragments of a TCR, and chimeric antigen receptors. Exemplary TCRs include $\alpha\beta$ TCR, $\gamma\delta$ TCR, single chain TCR (scTCR), soluble TCR, and single domain TCR. Binding proteins of the present disclosure may be chimeric, humanized, or human.

Another exemplary binding protein is a TCR-CAR. A TCR-CAR is a heterodimeric fusion protein generally comprising a soluble TCR (a $V\alpha C\alpha$ polypeptide chain and a $V\beta C\beta$ polypeptide chain) wherein the $V\beta C\beta$ polypeptide chain is linked to a transmembrane domain and an intracellular signaling component (*e.g.*, comprising an ITAM-containing T cell activating domain and optionally a costimulatory signaling domain) (*see, e.g.*, Walseng *et al.*, 2017 Scientific Reports 7:10713, incorporated by reference in its entirety).

In any of the embodiments described herein, binding proteins of the present disclosure, *e.g.*, TCRs, may further comprise a TCR constant domain, *e.g.*, joined to the C-terminus of a $V\alpha$ domain, a $V\beta$ domain, or both. A TCR β -chain constant domain may be encoded by a TRBC1 gene or TRBC2 gene. An exemplary TCR β -chain constant domain ($C\beta$) is a TRBC1 constant domain comprising at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the amino acid sequence of SEQ ID NO:34 or a TRBC2 constant domain comprising at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the amino acid sequence of SEQ ID NO:84. A TCR α -chain

constant domain (C α) may be encoded by a TRAC gene. An exemplary TCR α -chain constant domain is a TRAC constant domain comprising at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the amino acid sequence to SEQ ID NO:33, 156, or 157.

- 5 In certain embodiments, a TCR C α domain, a C β domain, or both comprises a cysteine substitution to create an interchain disulfide bond between the constant domain cysteine residues which is not present in native TCRs. In particular embodiments, a binding protein comprises: (a) a C α domain comprising a cysteine substitution at a position corresponding to position 49 of SEQ ID NO:33, at a position corresponding to
10 position 48 of SEQ ID NO: 156, at a position corresponding to position 47 of SEQ ID NO: 157 (Thr $\rightarrow$ Cys), (b) a C β domain comprising a cysteine substitution at a position corresponding to position 57 of SEQ ID NO:34 or position 56 of SEQ ID NO:84 (Ser $\rightarrow$ Cys), or (c) both (a) and (b).

- In any of the embodiments described herein, binding proteins of the present
15 disclosure, *e.g.*, TCRs, may further comprise a TCR constant domain, *e.g.*, joined to the C-terminus of a V α domain, a V β domain, or both. An exemplary TCR β -chain constant domain (C β) is a TRBC1 constant domain comprising at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the amino acid sequence of SEQ ID NO:155 or a TRBC2 constant domain comprising at least
20 about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the amino acid sequence of SEQ ID NO:135. A TCR α -chain constant domain (C α) may be encoded by a TRAC gene. An exemplary TCR α -chain constant domain is a TRAC constant domain comprising at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the amino acid
25 sequence to SEQ ID NO:158, 159, or 160.

- In certain embodiments, a TCR C α domain is a truncated TCR C α domain. In a particular embodiment, the truncated TCR α -chain constant domain is truncated at its C-terminus. In some embodiments, a truncated TCR α -chain constant domain can have truncations of 1, 2, 3, 4, or more amino acids at its C-terminus corresponding to the
30 amino acid sequence of SEQ ID NO:33. In a particular embodiment, the truncated TCR α -chain constant domain is truncated at its N-terminus. In some embodiments, a

truncated TCR α -chain constant domain can have truncations of 1, 2, 3, 4, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:33.

In certain embodiments, a TCR C β domain is a truncated TCR C β domain. In a particular embodiment, the truncated TCR β -chain constant domain is truncated at its C-terminus. In some embodiments, a truncated TCR α -chain constant domain can have truncations of 1, 2, 3, 4, or more amino acids at its C-terminus corresponding to the amino acid sequence of SEQ ID NO:34 or 84. In a particular embodiment, the truncated TCR β -chain constant domain is truncated at its N-terminus. In some
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embodiments, a truncated TCR β -chain constant domain can have truncations of 1, 2, 3, 4, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:34 or 84.

In some embodiments, a binding protein of the present disclosure is a TCR comprising: (a) an α chain comprising at least about 75%, 80%, 85%, 90%, 91%, 92%,
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93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the α chain amino acid sequence contained in any one of SEQ ID NOS:36, 38, 40, 42, 44, 86, 49, 51, 53, 57, 59, 63, 65, 67, 81, 83, 162, 165, 170, 172, 174, 176, 178, 180, and 186; (b) a β chain comprising at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the β chain amino acid sequence contained in any
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one of SEQ ID NOS:36, 38, 40, 42, 46, 86, 49, 51, 55, 57, 61, 63, 67, 81, 83, 162, 165, 170, 172, 174, 176, 178, 180, and 186; or (c) an α chain of (a) and a β chain of (b), wherein the binding protein is capable of specifically binding to human CCNA1 peptide FLDRFLSCM (SEQ ID NO:1):HLA complex.

Exemplary TCRs include a TCR comprising: (a) the TCR α chain comprising
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the α chain amino acid sequence contained in SEQ ID NO:36 and the TCR β chain comprising the β chain amino acid sequence of SEQ ID NO:36; (b) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:38 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:38; (c) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID
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NO:40 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:40; (d) the TCR α chain comprising the α chain amino acid sequence

- contained in SEQ ID NO:42 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:42; (e) the TCR α chain comprising the amino acid sequence of SEQ ID NO:44 and the TCR β chain comprising the amino acid sequence of SEQ ID NO:46; (f) the TCR α chain comprising the α chain amino acid sequence
- 5 contained in SEQ ID NO:86 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:86; (g) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:49 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:49; (h) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:51 and the TCR
- 10 β chain comprising the β chain amino acid sequence contained in SEQ ID NO:51; (i) the TCR α chain comprising the amino acid sequence of SEQ ID NO:53 and the TCR β chain comprising the amino acid sequence of SEQ ID NO:55; (j) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:57 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:57; (k)
- 15 the TCR α chain comprising the amino acid sequence of SEQ ID NO:59 and the TCR β chain comprising the amino acid sequence of SEQ ID NO:61; (l) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:63 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:63; (m) the TCR α chain comprising the amino acid sequence of SEQ ID NO:65 and the TCR β
- 20 chain comprising the β chain amino acid sequence contained in SEQ ID NO:67; (n) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:67 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:67; (o) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:81 and the TCR β chain comprising the β chain amino acid sequence
- 25 contained in SEQ ID NO:81; (p) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:83 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:83; (q) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:162 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:162; (r) the TCR
- 30 α chain comprising the α chain amino acid sequence contained in SEQ ID NO:165 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID

NO:165; (s) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:170 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:170; (t) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:172 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:172; (u) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:174 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:174; (v) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:176 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:176; (w) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:178 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:178; (x) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:180 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:180; or (y) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:186 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:186.

In further embodiments, a binding protein of the present disclosure is a TCR comprising: (a) an α chain comprising at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the amino acid sequence of SEQ ID NO:69 or the α chain amino acid sequence contained in SEQ ID NO:73 or 182; (b) a β chain comprising at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the amino acid sequence of SEQ ID NO:71 or the β chain amino acid sequence contained in SEQ ID NO:73 or 182; or (c) an α chain of (a) and a β chain of (b), wherein the binding protein is capable of specifically binding to human CCNA1 peptide SLIAAAAFCLA (SEQ ID NO:2):HLA complex.

An exemplary TCR comprises: (a) the TCR α chain comprising the amino acid sequence of SEQ ID NO:69 and the TCR β chain comprising the amino acid sequence of SEQ ID NO:71; (b) the TCR α chain comprising the amino acid sequence contained in SEQ ID NO:73 and the TCR β chain comprising the amino acid sequence contained in SEQ ID NO:73; or (c) the TCR α chain comprising the amino acid sequence

contained in SEQ ID NO:182 and the TCR β chain comprising the amino acid sequence contained in SEQ ID NO:182.

In yet further embodiments, a binding protein of the present disclosure is a TCR comprising: (a) an α chain comprising at least about 75%, 80%, 85%, 90%, 91%, 92%,
 5 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the amino acid sequence of SEQ ID NO:75 or the α chain amino acid sequence contained in SEQ ID NO:79 or 184;
 (b) a β chain comprising at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%,
 95%, 96%, 97%, 98%, 99%, or 100% identity to the amino acid sequence of SEQ ID
 NO:77 or a β chain amino acid sequence contained in SEQ ID NO:79 or 184; or (c) an
 10 α chain of (a) and a β chain of (b), wherein the binding protein is capable of specifically binding to human CCNA1 peptide YSLSEIVPCL (SEQ ID NO:3):HLA complex.

An exemplary TCR comprises: (a) the TCR α chain comprising the amino acid sequence of SEQ ID NO:75 and the TCR β chain comprising the amino acid sequence of SEQ ID NO:77; (b) the TCR α chain comprising the amino acid sequence contained
 15 in SEQ ID NO:79 and the TCR β chain comprising the amino acid sequence contained in SEQ ID NO:79; or (c) the TCR α chain comprising the amino acid sequence contained in SEQ ID NO:184 and the TCR β chain comprising the amino acid sequence contained in SEQ ID NO:184.

Polynucleotides, Vectors, and Host Cells

20 In certain aspects, nucleic acid molecules are provided that encode any one or more binding proteins described herein.

In another aspect, the present disclosure provides a polynucleotide encoding a binding protein that comprises a T cell receptor (TCR) α chain variable ($V\alpha$) domain and a TCR β chain variable ($V\beta$) domain, wherein the encoded binding protein is
 25 capable of specifically binding to a human cyclin A1 (CCNA1) peptide YSLSEIVPCL (SEQ ID NO:3), wherein the heterologous polynucleotide is codon optimized for expression in a host cell.

In certain embodiments, a polynucleotide encoding a TCR α -chain or portion thereof and a polynucleotide encoding a TCR β -chain or a portion thereof are contained
 30 in a single open reading frame comprised in the engineered host cell (e.g., immune cell), wherein the single open reading frame further comprises a polynucleotide

encoding a self-cleaving peptide disposed between the α -chain-encoding polynucleotide and the β -chain-encoding polynucleotide. In certain embodiments, a self-cleaving peptide is selected from internal ribosome entry sites (IRES), furin cleavage sites, viral 2A peptides, or any combination thereof. Exemplary viral self-cleaving polypeptides
5 include a viral 2A peptide from porcine teschovirus-1 (P2A), *Thosea asigna* virus (T2A), equine rhinitis A virus (E2A), foot-and-mouth disease virus (F2A), or variants thereof. In certain embodiments, an exemplary T2A peptide sequence comprises an amino acid sequence of SEQ ID NO:16. Further exemplary nucleic acid and amino acid sequences for 2A peptides are set forth in, for example, Kim *et al.* (*PLOS One*
10 6:e18556, 2011, which 2A nucleic acid and amino acid sequences are incorporated herein by reference in their entirety). An exemplary P2A peptide comprises an amino acid sequence of SEQ ID NO:29. An exemplary T2A peptide comprises an amino acid sequence of SEQ ID NO:30. An exemplary E2A peptide comprises an amino acid sequence of SEQ ID NO:31. An exemplary F2A peptide comprises an amino acid
15 sequence of SEQ ID NO:32.

A polynucleotide encoding a desired binding protein can be accomplished by using any suitable molecular biology engineering techniques known in the art, including the use of restriction endonuclease digestion, ligation, transformation, plasmid purification, and DNA sequencing as described in, for example, Sambrook *et al.* (1989
20 and 2001 editions; *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, NY) and Ausubel *et al.* (Current Protocols in Molecular Biology, 2003). Alternatively, a sequence of interest can be produced synthetically.

A nucleic acid of this disclosure may refer to a single- or a double-stranded DNA, cDNA or RNA in any form, and may include a positive and a negative strand of
25 the nucleic acid which complement each other, including anti-sense DNA, cDNA and RNA. Also included are siRNA, microRNA, RNA—DNA hybrids, ribozymes, and other various naturally occurring or synthetic forms of DNA or RNA.

In certain embodiments, a heterologous polynucleotide encoding a TCR α -chain and a heterologous polynucleotide encoding a TCR β -chain are contained in a single
30 open reading frame comprised in the engineered immune cell, wherein the single open reading frame further comprises a polynucleotide encoding a self-cleaving peptide

disposed between the α -chain-encoding polynucleotide and the β -chain-encoding polynucleotide.

In any of the embodiments described herein, a polynucleotide of the present disclosure may be codon optimized for efficient expression in a host cell, such as an
5 immune cell, containing the polynucleotide (*see, e.g.* Scholten *et al.*, *Clin. Immunol. 119*:135-145 (2006)). As used herein, a "codon optimized" polynucleotide comprises a heterologous polynucleotide having codons modified with silent mutations corresponding to the abundances of tRNA levels in a host cell of interest.

A single polynucleotide molecule may encode one, two, or more binding
10 proteins according to any of the embodiments disclosed herein. A polynucleotide encoding more than one transcript may comprise a sequence (*e.g.*, a viral 2A peptide) disposed between each transcript for multicistronic expression.

In certain embodiments, the binding proteins of the present disclosure may be operatively linked to certain elements of a vector. For example, polynucleotide
15 sequences that are needed to effect the expression and processing of coding sequences to which they are ligated may be operatively linked. Expression control sequences may include appropriate transcription initiation, termination, promoter and enhancer sequences; efficient RNA processing signals such as splicing and polyadenylation signals; sequences that stabilize cytoplasmic mRNA; sequences that enhance translation
20 efficiency (*i.e.*, Kozak consensus sequences); sequences that enhance protein stability; and possibly sequences that enhance protein secretion. Expression control sequences may be operatively linked if they are contiguous with the gene of interest and expression control sequences that act in *trans* or at a distance to control the gene of interest.

25 Certain embodiments include a polynucleotide of the present disclosure contained in a vector. One of skill in the art can readily ascertain suitable vectors for use with certain embodiments disclosed herein. An exemplary vector may comprise a nucleic acid molecule capable of transporting another nucleic acid molecule to which it has been linked, or which is capable of replication in a host organism. Some examples
30 of vectors include plasmids, viral vectors, cosmids, and others. Some vectors may be capable of autonomous replication in a host cell into which they are introduced (*e.g.*

bacterial vectors having a bacterial origin of replication and episomal mammalian vectors), whereas other vectors may be integrated into the genome of a host cell or promote integration of the polynucleotide insert upon introduction into the host cell and thereby replicate along with the host genome (*e.g.*, lentiviral vector)). Additionally, 5 some vectors are capable of directing the expression of genes to which they are operatively linked (these vectors may be referred to as "expression vectors"). According to related embodiments, it is further understood that, if one or more agents (*e.g.*, polynucleotides encoding binding proteins as described herein) is co-administered to a subject, that each agent may reside in separate or the same vectors, and multiple 10 vectors (each containing a different agent or the same agent) may be introduced to a cell or cell population or administered to a subject.

A vector may be, for example, a plasmid, cosmid, virus, a RNA vector, or a linear or circular DNA or RNA molecule that may include chromosomal, non-chromosomal, semi-synthetic or synthetic nucleic acid molecules. Exemplary vectors 15 are those capable of autonomous replication (episomal vector) or expression of nucleic acid molecules to which they are linked (expression vectors).

Viral vectors include retrovirus, adenovirus, parvovirus (*e.g.*, adeno-associated viruses), coronavirus, negative strand RNA viruses such as ortho-myxovirus (*e.g.*, influenza virus), rhabdovirus (*e.g.*, rabies and vesicular stomatitis virus), paramyxovirus 20 (*e.g.*, measles and Sendai), positive strand RNA viruses such as picornavirus and alphavirus, and double-stranded DNA viruses including adenovirus, herpesvirus (*e.g.*, Herpes Simplex virus types 1 and 2, Epstein-Barr virus, cytomegalovirus), and poxvirus (*e.g.*, vaccinia, fowlpox and canarypox). Other viruses include Norwalk virus, togavirus, flavivirus, reoviruses, papovavirus, hepadnavirus, and hepatitis virus, for 25 example. Examples of retroviruses include avian leukosis-sarcoma, mammalian C-type, B-type viruses, D type viruses, HTLV-BLV group, lentivirus, spumavirus (Coffin, J. M., *Retroviridae: The viruses and their replication*, In *Fundamental Virology*, Third Edition, B. N. Fields *et al.*, Eds., Lippincott-Raven Publishers, Philadelphia, 1996).

The viral vector can, in certain embodiments, be a gammaretrovirus, *e.g.*, 30 Moloney murine leukemia virus (MLV)-derived vectors. In other embodiments, the viral vector can be a more complex retrovirus-derived vector, *e.g.*, a lentivirus-derived

vector. HIV-1-derived vectors belong to this category. Other examples include lentivirus vectors derived from HIV-2, FIV, equine infectious anemia virus, SIV, and Maedi-Visna virus (ovine lentivirus). Methods of using retroviral and lentiviral viral vectors and packaging cells for transducing mammalian host cells with viral particles containing transgenes are known in the art and have been previously described, for example, in: U.S. Patent 8,119,772; Walchli *et al.*, *PLoS One* 6:327930, 2011; Zhao *et al.*, *J. Immunol.* 174:4415, 2005; Engels *et al.*, *Hum. Gene Ther.* 14:1155, 2003; Frecha *et al.*, *Mol. Ther.* 18:1748, 2010; and Verhoeyen *et al.*, *Methods Mol. Biol.* 506:97, 2009. Retroviral and lentiviral vector constructs and expression systems are also commercially available. Other viral vectors also can be used for polynucleotide delivery including DNA viral vectors, including, for example adenovirus-based vectors and adeno-associated virus (AAV)-based vectors; vectors derived from herpes simplex viruses (HSVs), including amplicon vectors, replication-defective HSV and attenuated HSV (Krisky *et al.*, *Gene Ther.* 5:1517, 1998).

Other vectors recently developed for gene therapy uses can also be used with the compositions and methods of this disclosure. Such vectors include those derived from baculoviruses and α -viruses. (Jolly, D J. 1999. Emerging Viral Vectors. pp 209-40 in Friedmann T. ed. The Development of Human Gene Therapy. New York: Cold Spring Harbor Lab), or plasmid vectors (such as sleeping beauty or other transposon vectors).

Construction of an expression vector that is used for genetically engineering and producing a binding protein of interest can be accomplished by using any suitable molecular biology engineering techniques known in the art. To obtain efficient transcription and translation, a polynucleotide in each recombinant expression construct includes at least one appropriate expression control sequence (also called a regulatory sequence), such as a leader sequence and particularly a promoter operably (*i.e.*, operatively) linked to the nucleotide sequence encoding the binding protein.

Markers are sometimes used to identify or monitor expression of a heterologous polynucleotide by a host cell transduced with the same, or to detect cells expressing a binding protein of interest. In certain embodiments, a polynucleotide further comprises a polynucleotide that encodes a marker. A marker may be a selection marker, which confers drug resistance, or a detectable marker, such as a fluorescent marker or cell

surface protein that can be detected by methods such as flow cytometry. In certain embodiments, the polynucleotide encoding the marker is located 3' of the polynucleotide encoding the binding protein. In other embodiments, the polynucleotide encoding the marker is located 5' of the polynucleotide encoding binding protein.

- 5 Exemplary markers include green fluorescent protein (GFP), an extracellular domain of human CD2, a truncated human EGFR (huEGFRt; *see* Wang *et al.*, *Blood* 118:1255 (2011)), a truncated human CD19 (huCD19t), a truncated human CD34 (huCD34t), or a truncated human NGFR (huNGFRt). In certain embodiments, the encoded marker comprises EGFRt, CD19t, CD34t, or NGFRt. An exemplary truncated human EGFR
- 10 sequence comprises an amino acid sequence of SEQ ID NO:85.

- In certain embodiments, the vector may further comprise a suicide gene, where expression of the suicide gene results in the death of the host cell comprising the vector. For example, in some instances, prolonged expression of the binding protein of the invention is not desirable. Inclusion of a suicide gene in the vector allows for finer
- 15 control of binding protein expression in a subject. In certain embodiments, expression of the suicide gene is inducible, for example with the use of an inducible promoter regulating suicide gene expression. In a specific embodiment, a suicide gene is an inducible caspase-9 gene (*see* U.S. Patent Publication No. 2013/0071414, incorporated by reference in its entirety).

- 20 When a viral vector genome comprises a plurality of polynucleotides within a single transgene to be expressed in a host cell as separate proteins, the viral vector may also comprise additional sequences between the two (or more) polynucleotides allowing for bicistronic or multicistronic expression. Examples of such sequences used in viral vectors include internal ribosome entry sites (IRES), furin cleavage sites, viral 2A
- 25 peptides, or any combination thereof.

- In any of the embodiments described herein, a polynucleotide can further comprise a polynucleotide that encodes a self-cleaving polypeptide, wherein the polynucleotide encoding the self-cleaving polypeptide is located between the polynucleotide encoding the binding protein and the polynucleotide encoding the
- 30 marker.

In certain embodiments, a self-cleaving polypeptide comprises a viral 2A peptide from porcine teschovirus-1 (P2A), *Thosea asigna* virus (T2A), equine rhinitis A virus (E2A), foot-and-mouth disease virus (F2A), or variant thereof. In certain embodiments, an exemplary T2A peptide sequence comprises an amino acid sequence of SEQ ID NO:16. Further exemplary nucleic acid and amino acid sequences the 2A peptides are set forth in, for example, Kim *et al.* (*PLOS One* 6:e18556, 2011, which 2A nucleic acid and amino acid sequences are incorporated herein by reference in their entirety). An exemplary P2A peptide comprises an amino acid sequence of SEQ ID NO:29. An exemplary T2A peptide comprises an amino acid sequence of SEQ ID NO:30. An exemplary E2A peptide comprises an amino acid sequence of SEQ ID NO:31. An exemplary F2A peptide comprises an amino acid sequence of SEQ ID NO:32.

Binding proteins of the present disclosure can, in certain aspects, be expressed on the surface of a host cell or be secreted by or isolated from a host cell. A host cell may include any individual cell or cell culture which may receive a vector or the incorporation of nucleic acids or express proteins. The term also encompasses progeny of the host cell, whether genetically or phenotypically the same or different. Suitable host cells may depend on the vector and may include mammalian cells, animal cells, human cells, simian cells, insect cells, yeast cells, and bacterial cells. These cells may be induced to incorporate the vector or other material by use of a viral vector, transformation via calcium phosphate precipitation, DEAE-dextran, electroporation, microinjection, or other methods. See, for example, Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual* 2d ed. (Cold Spring Harbor Laboratory, 1989).

In addition to vectors, certain embodiments relate to host cells modified (*i.e.*, genetically engineered) to contain a heterologous polynucleotide encoding a binding protein (*e.g.*, TCR) or a vector comprising a heterologous polynucleotide encoding a binding protein (*e.g.*, TCR) that are presently disclosed. A modified or genetically engineered host cell comprising a heterologous polynucleotide encoding at least one binding protein expresses on its cell surface at least one binding protein of the instant disclosure. A modified host cell may express a single type of binding protein or two or more different types of binding proteins of the present disclosure. Host cells can be

modified *ex vivo* or *in vivo*. A host cell may include any individual cell or cell culture that may receive a vector or the incorporation of a nucleic acid or protein, as well as any progeny cells. The term also encompasses progeny of the host cell, whether genetically or phenotypically the same or different. Suitable host cells may depend on the vector
5 and may include mammalian cells, animal cells, human cells, simian cells, insect cells, yeast cells, and bacterial cells. These cells may be induced to incorporate the vector or other material by use of a viral vector, transformation via calcium phosphate precipitation, DEAE-dextran, electroporation, microinjection, or other methods. *See*, for example, Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual* 2d ed. (Cold
10 Spring Harbor Laboratory, 1989). In any of the aforementioned embodiments, a host cell containing a polynucleotide encoding a binding protein of this disclosure are comprised of cells that are autologous, allogeneic or syngeneic to the subject receiving the modified host cells, such as in an adoptive immunotherapy procedure.

In certain embodiments, the host cell transduced to express a binding protein of the
15 present disclosure is a hematopoietic progenitor cell or a human immune system cell. As used herein, a "hematopoietic progenitor cell" is a cell that can be derived from hematopoietic stem cells or fetal tissue and is capable of further differentiation into mature cells types (*e.g.*, immune system cells). Exemplary hematopoietic progenitor cells include those with a CD24^{Lo} Lin⁻ CD117⁺ phenotype or those found in the thymus
20 (referred to as progenitor thymocytes).

In certain embodiments, the host cell is an immune system cell, including a B cell, a CD4⁺ T cell, a CD8⁺ T cell, a CD4⁻ CD8⁻ double negative T cell, a $\gamma\delta$ T cell, a regulatory T cell, a natural killer cell (*e.g.*, a NK cell or a NK-T cell), and a dendritic cell.

25 In certain embodiments, the host cell is a T cell. A T cell may be a naïve T cell, a memory T cell (T_M), a helper T cell (T_H), an effector T cell (T_E), a $\gamma\delta$ T cell, a regulatory T cell (Treg), natural killer T cell (NKT), or any combination thereof. T_M can be further divided into subsets of central memory T cells (T_{CM}, increased expression of CD62L, CCR7, CD28, CD127, CD45RO, and CD95, and decreased
30 expression of CD54RA as compared to naïve T cells) and effector memory T cells

(T_{EM}, decreased expression of CD62L, CCR7, CD28, CD45RA, and increased expression of CD127 as compared to naïve T cells or T_{CM}).

T cells can be collected using known techniques, and the various subpopulations or combinations thereof can be enriched or depleted by known techniques, such as by
5 affinity binding to antibodies, flow cytometry, or immunomagnetic selection.

Methods for transfecting/transducing T cells with desired nucleic acids have been described (e.g., U.S. Patent Application Pub. No. US 2004/0087025; U.S. Patent No. 6,410,319; PCT Publication No. WO 2014/031687; Brentjens *et al.*, 2007, *Clin. Cancer Res.* 13:5426) as have adoptive transfer procedures using T cells of desired
10 target-specificity (e.g., Schmitt *et al.*, *Hum. Gen.* 20:1240, 2009; Dossett *et al.*, *Mol. Ther.* 17:742, 2009; Till *et al.*, *Blood* 112:2261, 2008; Wang *et al.*, *Hum. Gene Ther.* 18:712, 2007; Kuball *et al.*, *Blood* 109:2331, 2007; US 2011/0243972; US 2011/0189141; Leen *et al.*, *Ann. Rev. Immunol.* 25:243, 2007; Kalos *et al.*, *Sci Transl. Med.* 3:95ra73, 2011; Porter *et al.*, 2011, *N. Engl. J. Med.* 365:725-33, 2011), such that
15 adaptation of these methodologies to the presently disclosed embodiments is contemplated, based on the teachings herein, including those directed to binding proteins of the present disclosure.

Eukaryotic host cells contemplated as an aspect of this disclosure when harboring a polynucleotide, vector, or protein according to this disclosure include, in
20 addition to a human immune cells (e.g., a human patient's own immune cells), VERO cells, HeLa cells, Chinese hamster ovary (CHO) cell lines (including modified CHO cells capable of modifying the glycosylation pattern of expressed multivalent binding molecules, see US Patent Application Publication No. 2003/0115614), COS cells (such as COS-7), W138, BHK, HepG2, 3T3, RIN, MDCK, A549, PC12, K562, HEK293
25 cells, HepG2 cells, N cells, 3T3 cells, *Spodoptera frugiperda* cells (e.g., Sf9 cells), *Saccharomyces cerevisiae* cells, and any other eukaryotic cell known in the art to be useful in expressing, and optionally isolating, a protein or peptide according to this disclosure. Also contemplated are prokaryotic cells, including *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, a Streptomycete, or any prokaryotic cell
30 known in the art to be suitable for expressing, and optionally isolating, a protein or peptide according to this disclosure. In isolating protein or peptide from prokaryotic

cells, in particular, it is contemplated that techniques known in the art for extracting protein from inclusion bodies may be used. Host cells that glycosylate the binding proteins of this disclosure are contemplated.

Transformed or transfected host cells are cultured according to conventional
5 procedures in a culture medium containing nutrients and other components required for the growth of the chosen host cells. A variety of suitable media, including defined media and complex media, are known in the art and generally include a carbon source, a nitrogen source, essential amino acids, vitamins and minerals. Media can also contain such components as growth factors or serum, as required. The growth medium will
10 generally select for cells containing the heterologous polynucleotide by, for example, drug selection or deficiency in an essential nutrient which is complemented by the selectable marker carried on the expression vector or co-transfected into the host cell.

In certain embodiments, a binding protein of the present disclosure is expressed on the surface of a host cell such that binding to a target antigen elicits an activity or
15 response from the host cell. Such expressed proteins may be functionally characterized according to any of a large number of art-accepted methodologies for assaying host cell (*e.g.*, T cell) activity, including determination of T cell binding, activation or induction and also including determination of T cell responses that are antigen-specific. Examples include determination of T cell proliferation, T cell cytokine release, antigen-
20 specific T cell stimulation, MHC restricted T cell stimulation, CTL activity (*e.g.*, by detecting ⁵¹Cr or Europium release from pre-loaded target cells), changes in T cell phenotypic marker expression, and other measures of T cell functions. Procedures for performing these and similar assays are may be found, for example, in Lefkovits (*Immunology Methods Manual: The Comprehensive Sourcebook of Techniques*, 1998).
25 *See, also, Current Protocols in Immunology*; Weir, *Handbook of Experimental Immunology*, Blackwell Scientific, Boston, MA (1986); Mishell and Shigii (eds.) *Selected Methods in Cellular Immunology*, Freeman Publishing, San Francisco, CA (1979); Green and Reed, *Science* 281:1309 (1998) and references cited therein.

Levels of cytokines may be determined according to methods described herein
30 and practiced in the art, including for example, ELISA, ELISPOT, intracellular cytokine staining, and flow cytometry and combinations thereof (*e.g.*, intracellular

cytokine staining and flow cytometry). Immune cell proliferation and clonal expansion resulting from an antigen-specific elicitation or stimulation of an immune response may be determined by isolating lymphocytes, such as circulating lymphocytes in samples of peripheral blood cells or cells from lymph nodes, stimulating the cells with antigen, and
5 measuring cytokine production, cell proliferation and/or cell viability, such as by incorporation of tritiated thymidine or non-radioactive assays, such as MTT assays and the like. The effect of an immunogen described herein on the balance between a Th1 immune response and a Th2 immune response may be examined, for example, by determining levels of Th1 cytokines, such as IFN- γ , IL-12, IL-2, and TNF- β , and Type
10 2 cytokines, such as IL-4, IL-5, IL-9, IL-10, and IL-13.

In other aspects, kits are provided comprising (a) a vector or an expression construct as described herein and optional reagents for transducing the vector or the expression construct into a host cell, and (b) (i) a binding protein, isolated polynucleotide, or expression vector as disclosed herein, and (ii) optional reagents for
15 transducing the polynucleotide or expression vector into a host cell, and (c) a host cell of this disclosure.

Methods of Use

In certain aspects, the compositions provided in the present disclosure may be used in methods for treating a hyperproliferative disorder or condition characterized by
20 overexpression of CCNA-1 comprising administering to a subject in need thereof a binding protein, a vector comprising a polynucleotide encoding a binding protein, a modified host cell expressing a binding protein, or a pharmaceutical composition thereof. In certain embodiments, the disease is a cancer.

As used, herein the term “cancer” includes solid tumors and hematological
25 malignancies (*e.g.*, leukemias). Exemplary cancers that may be treated include biliary cancer, bladder cancer, bone and soft tissue carcinoma, brain tumor, breast cancer, cervical cancer, colon cancer, colorectal adenocarcinoma, colorectal cancer, desmoid tumor, embryonal cancer, endometrial cancer, esophageal cancer, gastric cancer, gastric adenocarcinoma, glioblastoma multiforme, gynecological tumor, head and neck
30 squamous cell carcinoma, hepatic cancer, lung cancer, mesothelioma, malignant melanoma, osteosarcoma, ovarian cancer, pancreatic cancer, pancreatic ductal

adenocarcinoma, primary astrocytic tumor, primary thyroid cancer, prostate cancer, renal cancer, renal cell carcinoma, rhabdomyosarcoma, skin cancer, soft tissue sarcoma, testicular germ-cell tumor, urothelial cancer, uterine sarcoma, and uterine cancer.

Exemplary hematological malignancies include acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), chronic myelogenous leukemia (CML), chronic eosinophilic leukemia (CEL), myelodysplastic syndrome (MDS), Hodgkin's lymphoma, non-Hodgkin's lymphoma (NHL) (*e.g.*, follicular lymphoma, diffuse large B-cell lymphoma, or chronic lymphocytic leukemia), myeloma, and multiple myeloma (MM).

In certain embodiments, the subject is a human or non-human animal, such as a non-human primate, cow, horse, sheep, pig, cat, dog, goat, mouse, rat, rabbit, or guinea pig. In one embodiment, the subject is a human, such as a human adult, adolescent, child, or infant.

In certain embodiments, the modified host cells administered to the subject are autologous, allogeneic, or syngeneic.

The level of a CTL immune response may be determined by any one of numerous immunological methods described herein and routinely practice in the art. The level of a CTL immune response may be determined prior to and following administration of any one of the herein described CCNA1-specific binding proteins expressed by, for example, a T cell. Cytotoxicity assays for determining CTL activity may be performed using any one of several techniques and methods routinely practice in the art (*see, e.g.*, Henkart *et al.*, "Cytotoxic T-Lymphocytes" in *Fundamental Immunology*, Paul (ed.) (2003 Lippincott, Williams & Wilkins, Philadelphia, PA), pages 1127-50, and references cited therein).

Antigen-specific T cell can be determined by comparison of observed T cell responses according to any of the herein described T cell functional parameters (*e.g.*, proliferation, cytokine release, CTL activity, altered cell surface marker phenotype, etc.) that may be made between T cells that are exposed to a cognate antigen in an appropriate context (*e.g.*, the antigen used to prime or activate the T cells, when presented by immunocompatible antigen-presenting cells) and T cells from the same source population that are exposed instead to a structurally distinct or irrelevant control

antigen. A response to the cognate antigen that is greater, with statistical significance, than the response to the control antigen signifies antigen-specificity.

A biological sample may be obtained from a subject for determining the presence and level of an immune response to a disease antigen peptide. A "biological sample" as used herein may be a blood sample (from which serum or plasma may be prepared), biopsy specimen, body fluids (*e.g.*, lung lavage, ascites, mucosal washings, synovial fluid), bone marrow, lymph nodes, tissue explant, organ culture, or any other tissue or cell preparation from the subject or a biological source. Biological samples may also be obtained from the subject prior to receiving any immunogenic composition, which biological sample is useful as a control for establishing baseline (*i.e.*, pre-immunotherapy) data.

Binding proteins, polynucleotides, vectors, or modified host cells as described herein may be administered to a subject in a pharmaceutically or physiologically acceptable or suitable excipient or carrier. Pharmaceutically acceptable excipients are biologically compatible vehicles, *e.g.*, physiological saline, which are described in greater detail herein, that are suitable for administration to a human or other non-human mammalian subject. A therapeutically effective dose, in the context of adoptive cell therapy, is an amount of host cells (expressing a binding protein according to the present disclosure) used in adoptive transfer that is capable of producing a clinically desirable result (*e.g.*, a cytotoxic T cell response) in a statistically significant manner) in a treated human or non-human mammal. As is well known in the medical arts, the dosage for any one patient depends upon many factors, including the patient's size, weight, body surface area, age, the particular therapy to be administered, sex, time and route of administration, general health, and other drugs being administered concurrently. Doses will vary, but a preferred dose for administration of a host cell comprising a recombinant expression vector as described herein is about 10^7 cells/m², about 5×10^7 cells/m², about 10^8 cells/m², about 5×10^8 cells/m², about 10^9 cells/m², about 5×10^9 cells/m², about 10^{10} cells/m², about 5×10^{10} cells/m², or about 10^{11} cells/m².

Pharmaceutical compositions may be administered in a manner appropriate to the disease or condition to be treated (or prevented) as determined by persons skilled in

the medical art. An appropriate dose and a suitable duration and frequency of administration of the compositions will be determined by such factors as the health condition of the patient, size of the patient (*i.e.*, weight, mass, or body area), the type and severity of the patient's disease, the particular form of the active ingredient, and the method of administration. In general, an appropriate dose and treatment regimen provide the composition(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit (such as described herein, including an improved clinical outcome, such as more frequent complete or partial remissions, or longer disease-free and/or overall survival, or a lessening of symptom severity). For prophylactic use, a dose should be sufficient to prevent, delay the onset of, or diminish the severity of a disease associated with disease or disorder. Prophylactic benefit of the immunotherapeutic compositions administered according to the methods described herein can be determined by performing pre-clinical (including *in vitro* and *in vivo* animal studies) and clinical studies and analyzing data obtained therefrom by appropriate statistical, biological, and clinical methods and techniques, all of which can readily be practiced by a person skilled in the art.

The pharmaceutical compositions described herein may be presented in unit-dose or multi-dose containers, such as sealed ampoules or vials. Such containers may be frozen to preserve the stability of the formulation until use. In certain embodiments, a unit dose comprises a recombinant host cell as described herein at a dose of about 10^7 cells/ m^2 to about 10^{11} cells/ m^2 . The development of suitable dosing and treatment regimens for using the particular compositions described herein in a variety of treatment regimens, including *e.g.*, parenteral or intravenous administration or formulation, can be determined by a person skilled in the art.

If the subject composition is administered parenterally, the composition may also include sterile aqueous or oleaginous solution or suspension. Suitable non-toxic parenterally acceptable diluents or solvents include water, Ringer's solution, isotonic salt solution, 1,3-butanediol, ethanol, propylene glycol or polythethylene glycols in mixtures with water. Aqueous solutions or suspensions may further comprise one or more buffering agents, such as sodium acetate, sodium citrate, sodium borate or sodium tartrate. Of course, any material used in preparing any dosage unit formulation should

be pharmaceutically pure and substantially non-toxic in the amounts employed. In addition, the active compounds may be incorporated into sustained-release preparation and formulations. Dosage unit form, as used herein, refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit may contain a

- 5 predetermined quantity of recombinant cells or active compound calculated to produce the desired therapeutic effect in association with an appropriate pharmaceutical carrier.

In general, an appropriate dosage and treatment regimen provide the active molecules or cells in an amount sufficient to provide therapeutic or prophylactic benefit. Such a response can be monitored by establishing an improved clinical
10 outcome (*e.g.*, more frequent remissions, complete or partial, or longer disease-free survival) in treated subjects as compared to non-treated subjects. Increases in preexisting immune responses to a tumor protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples
15 obtained from a subject before and after treatment.

In certain embodiments, methods of treating a disease comprise administering modified immune cells in combination with one or more additional agents.

In certain embodiments, a modified immune cell of the present disclosure is administered to a subject with an inhibitor of an immune suppression component.

- 20 As used herein, the term "immune suppression component" or "immunosuppression component" refers to one or more cells, proteins, molecules, compounds or complexes providing inhibitory signals to assist in controlling or suppressing an immune response. For example, immune suppression components include those molecules that partially or totally block immune stimulation; decrease,
25 prevent or delay immune activation; or increase, activate, or up regulate immune suppression. Exemplary immunosuppression component targets are described in further detail herein and include immune checkpoint molecules, such as PD-1, PD-L1, PD-L2, CD80, CD86, B7-H3, B7-H4, HVEM, adenosine, GAL9, VISTA, CEACAM-1, PVRL2, CTLA-4, BTLA, KIR, LAG3, TIM3, A2aR, CD244/2B4, CD160, TIGIT,
30 LAIR-1, PVRIG/CD112R; metabolic enzymes, such as arginase, indoleamine

2,3-dioxygenase (IDO); immunosuppressive cytokines, such as IL-10, IL-4, IL-1RA, IL-35; T_{reg} cells, or any combination thereof.

An inhibitor of an immune suppression component may be a compound, an antibody, an antibody fragment or fusion polypeptide (*e.g.*, Fc fusion, such as CTLA4-Fc or LAG3-Fc), an antisense molecule, a ribozyme or RNAi molecule, or a low molecular weight organic molecule. In any of the embodiments disclosed herein, a method may comprise administering a modified immune cell with one or more inhibitor of any one of the following immune suppression components, singly or in any combination.

10 In certain embodiments, a modified immune cell is used in combination with a PD-1 inhibitor, for example a PD-1-specific antibody or binding fragment thereof, such as pidilizumab, nivolumab (Keytruda, formerly MDX-1106), pembrolizumab (Opdivo, formerly MK-3475), MEDI0680 (formerly AMP-514), AMP-224, BMS-936558 or any combination thereof.

15 In certain embodiments, a modified immune cell is used in combination with a PD-L1 specific antibody or binding fragment thereof, such as BMS-936559, durvalumab (MEDI4736), atezolizumab (RG7446), avelumab (MSB0010718C), MPDL3280A, or any combination thereof.

In certain embodiments, a modified immune cell is used in combination with a LAG3 inhibitor, such as LAG525, IMP321, IMP701, 9H12, BMS-986016, or any combination thereof.

In certain embodiments, a modified immune cell is used in combination with an inhibitor of CTLA4. In particular embodiments, a modified immune cell is used in combination with a CTLA4 specific antibody or binding fragment thereof, such as ipilimumab, tremelimumab, CTLA4-Ig fusion proteins (*e.g.*, abatacept, belatacept), or any combination thereof.

In certain embodiments, a modified immune cell is used in combination with a B7-H3 specific antibody or binding fragment thereof, such as enoblituzumab (MGA271), 376.96, or both.

30 In certain embodiments, a modified immune cell is used in combination with a B7-H4 specific antibody or binding fragment thereof, such as a scFv or fusion protein

thereof, as described in, for example, Dangaj *et al.*, *Cancer Res.* 73:4820, 2013, as well as those described in U.S. Patent No. 9,574,000 and PCT Patent Publication Nos. WO 2016/40724 and WO 2013/025779.

In some embodiments, a modified immune cell is used in combination with an
5 inhibitor of CD244.

In certain embodiments, a modified immune cell is used in combination with an inhibitor of BLTA, HVEM, CD160, or any combination thereof. Anti CD-160 antibodies are described in, for example, PCT Publication No. WO 2010/084158.

In more embodiments, a modified immune cell is used in combination with an
10 inhibitor of TIM3.

In still more embodiments, a modified immune cell is used in combination with an inhibitor of Gal9.

In certain embodiments, a modified immune cell is used in combination with an inhibitor of adenosine signaling, such as a decoy adenosine receptor.

15 In certain embodiments, a modified immune cell is used in combination with an inhibitor of A2aR.

In certain embodiments, a modified immune cell is used in combination with an inhibitor of KIR, such as lirilumab (BMS-986015).

In certain embodiments, a modified immune cell is used in combination with an
20 inhibitor of an inhibitory cytokine (typically, a cytokine other than TGF β) or Treg development or activity.

In certain embodiments, a modified immune cell is used in combination with an IDO inhibitor, such as levo-1-methyl tryptophan, epacadostat (INCB024360; *Liu et al.*, *Blood* 115:3520-30, 2010), ebselen (Terentis *et al.*, *Biochem.* 49:591-600, 2010),
25 indoximod, NLG919 (Mautino *et al.*, American Association for Cancer Research 104th Annual Meeting 2013; Apr 6-10, 2013), 1-methyl-tryptophan (1-MT)-tira-pazamine, or any combination thereof.

In certain embodiments, a modified immune cell is used in combination with an arginase inhibitor, such as N(omega)-Nitro-L-arginine methyl ester (L-NAME), N-
30 omega-hydroxy-nor-l-arginine (nor-NOHA), L-NOHA, 2(S)-amino-6-borono-hexanoic acid (ABH), S-(2-boronoethyl)-L-cysteine (BEC), or any combination thereof.

In certain embodiments, a modified immune cell is used in combination with an inhibitor of VISTA, such as CA-170 (Curis, Lexington, MA).

In certain embodiments, a modified immune cell is used in combination with a LAIR1 inhibitor.

5 In certain embodiments, a modified immune cell is used in combination with an inhibitor of CEACAM-1, CEACAM-3, CEACAM-5, or any combination thereof.

In certain embodiments, a modified immune cell is used in combination with an agent that increases the activity (*i.e.*, is an agonist) of a stimulatory immune checkpoint molecule. For example, a modified immune cell can be used in combination with a
10 CD137 (4-1BB) agonist (such as, for example, urelumab), a CD134 (OX-40) agonist (such as, for example, MEDI6469, MEDI6383, or MEDI0562), lenalidomide, pomalidomide, a CD27 agonist (such as, for example, CDX-1127), a CD28 agonist (such as, for example, TGN1412, CD80, or CD86), a CD40 agonist (such as, for example, CP-870,893, rhuCD40L, or SGN-40), a CD122 agonist (such as, for example,
15 IL-2), an agonist of GITR (such as, for example, humanized monoclonal antibodies described in PCT Patent Publication No. WO 2016/054638), an agonist of ICOS (CD278) (such as, for example, GSK3359609, mAb 88.2, JTX-2011, Icos 145-1, or Icos 314-8), or any combination thereof. In any of the embodiments disclosed herein, a method may comprise administering a modified immune cell with one or more agonists
20 of a stimulatory immune checkpoint molecule, including any of the foregoing, singly or in any combination.

In other embodiments, a method of this disclosure further comprises administering a secondary therapy comprising one or more of: an antibody or antigen binding fragment specific for a cancer antigen expressed by the cancer cell being
25 targeted; a chemotherapeutic agent; surgery; radiation therapy treatment; a cytokine; an RNA interference therapy, or any combination thereof.

Exemplary monoclonal antibodies useful in cancer therapies include, for example, monoclonal antibodies described in Galluzzi *et al.*, *Oncotarget* 5(24):12472-12508, 2014, which antibodies are incorporated by reference in their entirety.

30 In certain embodiments, a combination therapy method comprises administering a modified immune cell and further administering a radiation treatment or a surgery to a

subject. Radiation therapy includes X-ray therapies, such as gamma-irradiation, and radiopharmaceutical therapies. Surgeries and surgical techniques appropriate to treating a given cancer or non-inflamed solid tumor may be used in a subject in combination with a modified immune cell of this disclosure.

- 5 In certain embodiments, a combination therapy method comprises administering a modified immune cell and a chemotherapeutic agent to a subject. A chemotherapeutic agent includes, but is not limited to, an inhibitor of chromatin function, a topoisomerase inhibitor, a microtubule inhibiting drug, a DNA damaging agent, an antimetabolite (such as folate antagonists, pyrimidine analogs, purine analogs, and sugar-modified
- 10 analogs), a DNA synthesis inhibitor, a DNA interactive agent (such as an intercalating agent), and a DNA repair inhibitor. Illustrative chemotherapeutic agents include, without limitation, the following groups: anti-metabolites/anti-cancer agents, such as pyrimidine analogs (5-fluorouracil, floxuridine, capecitabine, gemcitabine and cytarabine) and purine analogs, folate antagonists and related inhibitors
- 15 (mercaptopurine, thioguanine, pentostatin and 2-chlorodeoxyadenosine (cladribine)); antiproliferative / antimitotic agents including vinca alkaloids (vinblastine, vincristine, and vinorelbine), microtubule disruptors such as taxane (paclitaxel, docetaxel), vincristin, vinblastin, nocodazole, epothilones and navelbine, epidipodophyllotoxins (etoposide, teniposide), DNA damaging agents (actinomycin, amsacrine,
- 20 anthracyclines, bleomycin, busulfan, camptothecin, carboplatin, chlorambucil, cisplatin, cyclophosphamide, cytoxan, dactinomycin, daunorubicin, doxorubicin, epirubicin, hexamethylmelamineoxaliplatin, iphosphamide, melphalan, merchloroethamine, mitomycin, mitoxantrone, nitrosourea, plicamycin, procarbazine, taxol, taxotere, temozolamide, teniposide, triethylenethiophosphoramidate and etoposide (VP 16));
- 25 antibiotics such as dactinomycin (actinomycin D), daunorubicin, doxorubicin (adriamycin), idarubicin, anthracyclines, mitoxantrone, bleomycins, plicamycin (mithramycin) and mitomycin; enzymes (L-asparaginase which systemically metabolizes L-asparagine and deprives cells which do not have the capacity to synthesize their own asparagine); antiplatelet agents; antiproliferative / antimitotic
- 30 alkylating agents such as nitrogen mustards (mechlorethamine, cyclophosphamide and analogs, melphalan, chlorambucil), ethylenimines and methylmelamines

(hexamethylmelamine and thiotepa), alkyl sulfonates -busulfan, nitrosoureas (carmustine (BCNU) and analogs, streptozocin), trazenes— dacarbazine (DTIC); antiproliferative/antimitotic antimetabolites such as folic acid analogs (methotrexate); platinum coordination complexes (cisplatin, carboplatin), procarbazine, hydroxyurea, 5 mitotane, aminoglutethimide; hormones, hormone analogs (estrogen, tamoxifen, goserelin, bicalutamide, nilutamide) and aromatase inhibitors (letrozole, anastrozole); anticoagulants (heparin, synthetic heparin salts and other inhibitors of thrombin); fibrinolytic agents (such as tissue plasminogen activator, streptokinase and urokinase), aspirin, dipyridamole, ticlopidine, clopidogrel, abciximab; antimigratory agents; 10 antisecretory agents (breveldin); immunosuppressives (cyclosporine, tacrolimus (FK-506), sirolimus (rapamycin), azathioprine, mycophenolate mofetil); anti-angiogenic compounds (TNP470, genistein) and growth factor inhibitors (vascular endothelial growth factor (VEGF) inhibitors, fibroblast growth factor (FGF) inhibitors); angiotensin receptor blocker; nitric oxide donors; anti-sense oligonucleotides; antibodies 15 (trastuzumab, rituximab); chimeric antigen receptors; cell cycle inhibitors and differentiation inducers (tretinoin); mTOR inhibitors, topoisomerase inhibitors (doxorubicin (adriamycin), amsacrine, camptothecin, daunorubicin, dactinomycin, eniposide, epirubicin, etoposide, idarubicin, irinotecan (CPT-11) and mitoxantrone, topotecan, irinotecan), corticosteroids (cortisone, dexamethasone, hydrocortisone, 20 methylprednisolone, prednisone, and prednisolone); growth factor signal transduction kinase inhibitors; mitochondrial dysfunction inducers, toxins such as Cholera toxin, ricin, Pseudomonas exotoxin, Bordetella pertussis adenylate cyclase toxin, or diphtheria toxin, and caspase activators; and chromatin disruptors.

Cytokines can be used to manipulate host immune response towards anticancer 25 activity. *See, e.g.,* Floros and Tarhini, *Semin. Oncol.* 42:539, 2015. Cytokines useful for promoting anticancer or antitumor response include, for example, IFN- α , IL-2, IL-3, IL-4, IL-10, IL-12, IL-13, IL-15, IL-16, IL-17, IL-18, IL-21, IL-24, and GM-CSF, singly or in any combination.

Another cancer therapy approach involves reducing expression of oncogenes 30 and other genes needed for growth, maintenance, proliferation, and immune evasion by cancer cells. RNA interference, and in particular the use of microRNAs (miRNAs)

small inhibitory RNAs (siRNAs) provides an approach for knocking down expression of cancer genes. *See, e.g., Larsson et al., Cancer Treat. Rev. 16:128, 2017.*

In any of the embodiments disclosed herein, any of the therapeutic agents (*e.g.*, a modified immune cell, an inhibitor of an immune suppression component, an agonist
5 of a stimulatory immune checkpoint molecule, a chemotherapeutic agent, a radiation therapy, a surgery, a cytokine, or an inhibitory RNA) may be administered once or more than once to the subject over the course of a treatment, and, in combinations, may be administered to the subject in any order (*e.g.*, simultaneously, concurrently, or in any sequence) or any combination. An appropriate dose, suitable duration, and frequency
10 of administration of the compositions will be determined by such factors as a condition of the patient; size, type, spread, growth, and severity of the tumor or cancer; particular form of the active ingredient; and the method of administration.

In certain embodiments, a plurality of doses of a modified immune cell as described herein is administered to the subject, which may be administered at intervals
15 between administrations of about two to about four weeks. In further embodiments, a cytokine (*e.g.*, IL-2, IL-15, IL-21) is administered sequentially, provided that the subject was administered the recombinant host cell at least three or four times before cytokine administration. In certain embodiments, a cytokine is administered concurrently with the host cell. In certain embodiments, a cytokine is administered
20 subcutaneously.

In still further embodiments, a subject being treated is further receiving immunosuppressive therapy, such as calcineurin inhibitors, corticosteroids, microtubule inhibitors, low dose of a mycophenolic acid prodrug, or any combination thereof. In yet further embodiments, a subject being treated has received a non-myeloablative or a
25 myeloablative hematopoietic cell transplant, wherein the treatment may be administered at least two to at least three months after the non-myeloablative hematopoietic cell transplant.

An effective amount of a therapeutic or pharmaceutical composition refers to an amount sufficient, at dosages and for periods of time needed, to achieve the desired
30 clinical results or beneficial treatment, as described herein. An effective amount may be delivered in one or more administrations. If the administration is to a subject already

known or confirmed to have a disease or disease-state, the term "therapeutic amount" may be used in reference to treatment, whereas "prophylactically effective amount" may be used to describe administering an effective amount to a subject that is susceptible or at risk of developing a disease or disease-state (*e.g.*, recurrence) as a
 5 preventative course.

EXAMPLES

EXAMPLE 1:

CYCLIN A1 TCRs

Human cyclin A1 isoform 3 protein sequence (SEQ ID NO:4), which is the most
 10 conserved of cyclin A1 isoforms, was selected to maximize the chance that a targeted epitope is expressed by cancers. Cyclin A1-specific TCRs were discovered by stimulating donor CD8⁺ T cells with a library of over-lapping peptides spanning the entire CCNA1 protein sequence and designed to cover all possible MHC-I epitopes. When reactive T cells were observed against the full peptide library after ~ 3 rounds of
 15 peptide stimulation, the minimal peptide epitope and presenting HLA allele were determined by screening with individual peptides and cell lines expressing single HLA alleles of interest (*see*, Figure 1).

Cyclin A1 (227-235)-specific T cell responses were detected after 3 rounds of stimulation of several different HLA-A2⁺ donor cells. Antigen-specific responses were
 20 detected by labelling with an HLA-A2/cyclin A1(227-235) fluorescently labelled multimer (first row of Figure 2). HLA-restriction and effector function were confirmed by incubating T cells together with 721.221 leukemia cell line transduced to express cyclin A1 as well as HLA-A1 as a negative control (2nd row of Figure 2) or HLA-A2 (3rd row of Figure 2). Free peptide was added to the T cells as a positive control (row 4
 25 of Figure 2). After a 4 hour co-incubation in the presence of golgi inhibitors, T cells were fixed and permeabilized before labelling with anti-IFN γ antibodies and analysis by flow cytometry. Several of the T cell lines demonstrated not only antigen-specificity (by tetramer binding) but effector function in response to both free peptide and

naturally processed peptide presented by a cell line expressing the correct combination of tumor antigen and HLA allele.

HLA-A2/cyclin A1 (227-235)-specific T cell lines were ranked by their tetramer binding affinity in order to select the highest affinity TCRs for further analysis. About 5 150 different T cell lines or clones were generated from 12 different donors in a series of separate experiments. A subset of these is shown in Figures 3A-3B. T cells were carefully counted and equal numbers of T cells from each T cell line were labelled with decreasing concentrations of a HLA-A2/cyclin A1(227-235) fluorescently labelled multimer. The mean fluorescence intensity of multimer staining for each line was 10 plotted against tetramer concentration (Figure 3A). From this graph a linear regression analysis was performed to determine the maximum binding coefficient, which was applied to the raw data to generate relative dissociation constants (Kd) for each line- the tetramer concentration that provides 50% maximal binding. These values were inversely related to TCR affinity, with the lowest Kd corresponding to the highest 15 predicted affinity (Figure 3B). There were a range of different affinities for the MHC-peptide multimer among the different donors and T cell lines tested. The 10 best candidates were selected for RACE PCR, TCR sequencing and generation of lentiviral TCR gene-transfer vectors.

Figure 4 shows a schematic of how TCRs from high avidity antigen-specific T 20 cell lines, predicted to have high affinity TCRs, were isolated, identified and expressed in donor CD8⁺ T cells, where they were functionally compared. Of the 10 HLA-A2/cyclin A1(227-235)-specific TCRs tested, 5 were successfully cloned into lentiviral vectors, expressed in CD8⁺ T cells and bind to the MHC-CCNA1 peptide multimer. A previously generated HLA-A2/cyclin A1(227-235)-specific TCR #4 was included for 25 comparison and two other TCRs specific for HLA-A2/cyclin A1(341-351), TCR #7, and HLA-A2/cyclin A1(370-379), TCR #8, were also cloned, expressed, and tested. Successfully transduced CD8⁺ T cells were sorted with the relevant MHC-peptide multimer and expanded before performing functional assays. CDR3 sequences, and T cell receptor α and β gene usage are provided in Table 1.

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Table 1. Cyclin A1 Specific TCRs

TCR Name	TCR α (TRA) gene	V α CDR3	TCR β (TRB) gene	V β CDR3
5	TRAV30*01 J20*01	CGTEEANDYKLSF (SEQ ID NO:5)	TRBV9*01 J2-7*01	CASSVGQGSSYEQYF (SEQ ID NO:6)
9	TRAV10*01 J34*01	CVVWGGDTDKLIF (SEQ ID NO:7)	TRBV2*01 J1-6*01	CAILDGEGSPLHF (SEQ ID NO:8)
6	TRAV24*01 J20*01	CALGPYNDYKLSF (SEQ ID NO:9)	TRBV6-6*01 J2-2*01	CASSDRSNTGELFF (SEQ ID NO:10)
1	TRAV21*01 J12*01	CAVEGDSSYKLIF (SEQ ID NO:11)	TRBV5-6*01 J2-5*01	CASSFFSQETQYF (SEQ ID NO:12)
2	TRAV21*02 J26*01	CAVIGEQNFVF (SEQ ID NO:13)	TRBV7-3*01 J2-6*01	CASSLSGLGSGANVLT (SEQ ID NO:14)
3	TRAV12-2*02 J13*02	CAVDSGGYQKVTF (SEQ ID NO:15)	TRBV7-3*01 J1-1*01	CASSLNMNTEAFF (SEQ ID NO:16)
10	TRAV17*01 J53*01	CATDESSNYKLTF (SEQ ID NO:17)	TRBV7-3*01 J1-1*01	CASSLNMNTEAFF (SEQ ID NO:18)
4	TRAV17*01 J48*01	CATDAWESNFGNEKLTF (SEQ ID NO:19)	TRBV7-2*01 J2-7*01	CASSLVVGSYEQYF (SEQ ID NO:20)
7	TRAV24*01 J49*01	CAYLGAGNQFYF (SEQ ID NO:21)	TRBV19*01 J1-2*01	CASSLNRGRYGYTF (SEQ ID NO:22)
8	TRAV19*01 J6*01	CALSELASGGSYIPTF (SEQ ID NO:23)	TRBV5-6*01 J2-3*01	CASSFRLAGGPSTDTQYF (SEQ ID NO:24)
11	TRAV10*01 J34*01	CVVWGGDTDKLIF (SEQ ID NO:7)	TRBV10-2*01 J2-7*01	CASSDGGGQYF (SEQ ID NO:189)

TCRs #5, 9, 6, 1, 2, 3, 10, 11, and 4 are specific for cyclin A1 (227-235) FLDRFLSCM peptide (SEQ ID NO:1) complexed with HLA*02:01. TCR #7 is specific for cyclin A1 (341-351) SLIAAAAFCLA (SEQ ID NO:2) complexed with HLA*02:01. TCR #8 is specific for cyclin A1 (370-379) complexed with HLA*02:01.

First T cells were incubated for 4 hr with different concentrations of their specific peptide ligand in the presence of golgi inhibitors before T cells were fixed and permeabilised and labelled with anti-IFN γ antibodies for analysis by flow cytometry (Figure 5A). The cytotoxic function of the TCR-transduced T cells was then tested by co-incubating the T cells at different ratios with HLA-A2+cyclin A1+ KCL22 leukemia cell targets. Targets were labelled with a fluorescent dye and mixed at an equal ratio with antigen-negative control cells (Figure 5B). At the end of a 6 hr incubation the

frequency of remaining labelled targets (relative to control cells) was determined by flow cytometry and from this data the % of antigen-specific killing was calculated. The binding strength of the different peptide epitopes to HLA-A2 and the likelihood that these epitopes would be result from proteosomal processing of the full length protein were predicted using several open-access online algorithms (Figure 5C). A second cytotoxicity assay was performed as in Figure 5B, but this time comparing the ability of the most promising cyclin A1(227-235)-specific TCR (#3) to kill peptide-loaded T2 target cells, an HLA-A2+cyclin A1+ AML cell line (ML1) and an HLA-A2+cyclin A1+ primary AML sample (Figure 5D). Untransduced T cells were incubated with the same targets in separate wells to control for specificity of killing.

Figure 5A shows that TCRs recognizing peptides 341 and 370 are superior to the 227-specific TCRs when stimulated with low doses of free peptide. In Figure 5B, the killing assay using target cells that endogenously express the cyclin A1 protein, which is proteosomally processed, loaded onto an MHC molecule and transported to the cell surface in order to be recognized by T cells shows superior killing by at least one of the 227-specific TCRs. This indicates that the 227 peptide may be processed more efficiently by the tumor cell line than the other epitopes, while the 341 and 370 may be more stable in solution or bind more strongly to MHC when introduced as free ligands, resulting in superior T cell function. Figure 5C shows that there is some bioinformatics data to suggest that peptide 370 indeed binds to HLA-A2 more strongly than peptide 227, but that 227 is the only one of the three CCNA1 peptides that is predicted to be cut by the general proteosomal processing machinery of the cell. This information is supportive of peptide 227 being a good target for cancer therapy. Figure 5D shows that the best performing 227 TCR candidate is able to kill peptide-loaded target cells, a cyclin A1 expressing AML cell line and a primary AML sample almost equally well, despite the fact that the peptide concentration on the surface of the tumor cells is likely to be much lower than in the case of peptide-loading.

As the cyclin A1 protein sequence is highly conserved in humans and mice and both mice and humans exhibit low levels of CCNA1 mRNA expression in the lungs and brain (by qPCR), the mouse is a good model to test the safety of cyclin A1-specific TCRs *in vivo*. In order for the human HLA*A02:01-restricted TCRs to recognize their

cognate antigen in the mice, transgenic mice that have been genetically engineered to express the HLA*A0:012 molecule are used for *in vivo* testing. The human TCR variable domains thus maintain their ability to recognize both the peptide and presenting MHC molecule. For effective expression of the human TCR on the surface of mouse T cells, the murine TCR constant domains have been engineered in place of the human TCR constant domains of the human TCR, thus allowing normal function in the mouse cells (*see*, Figure 6).

The various embodiments described above can be combined to provide further embodiments. All of the U.S. patents, U.S. patent application publications, U.S. patent applications, foreign patents, foreign patent applications and non-patent publications referred to in this specification and/or listed in the Application Data Sheet, including U.S. Provisional Patent Application No. 62/629,648 filed February 12, 2018, U.S. Provisional Patent Application No. 62/630,198 filed February 13, 2018, and U.S. Provisional Patent Application No. 62/667,207 filed May 4, 2018, are incorporated herein by reference, in their entirety. Aspects of the embodiments can be modified, if necessary to employ concepts of the various patents, applications and publications to provide yet further embodiments.

These and other changes can be made to the embodiments in light of the above-detailed description. In general, in the following claims, the terms used should not be construed to limit the claims to the specific embodiments disclosed in the specification and the claims, but should be construed to include all possible embodiments along with the full scope of equivalents to which such claims are entitled. Accordingly, the claims are not limited by the disclosure.

CLAIMS

What is claimed is:

1. A binding protein, comprising:
 - (a) a T cell receptor (TCR) α chain variable (V_α) domain comprising a complementary determining region 3 (CDR3) amino acid sequence set forth in any one of SEQ ID NOS: 5, 7, 9, 11, 13, 15, 17, and 19, or a CDR3 amino acid sequence set forth in any one of SEQ ID NOS: 5, 7, 9, 11, 13, 15, 17, and 19 with up to five amino acid substitutions, insertions and/or deletions, and a TCR β chain variable (V_β) domain;
 - (b) a TCR V_α domain, and a TCR V_β domain comprising a CDR3 amino acid sequence set forth in any one of SEQ ID NOS: 6, 8, 10, 12, 14, 16, 18, 20, and 189 or a CDR3 amino acid sequence set forth in any one of SEQ ID NOS: 6, 8, 10, 12, 14, 16, 18, 20, and 189 with up to five amino acid substitutions, insertions and/or deletions; or
 - (c) a V_α domain of (a) and a V_β of (b),wherein the binding protein is capable of specifically binding to a human cyclin A1 (CCNA1) peptide FLDRFLSCM (SEQ ID NO:1):human leukocyte antigen (HLA) complex.
2. The binding protein of claim 1, wherein:
 - (a) the V_α domain comprises the CDR3 amino acid sequence of SEQ ID NO:5 and the V_β domain comprises the CDR3 amino acid sequence of SEQ ID NO:6;
 - (b) the V_α domain comprises the CDR3 amino acid sequence of SEQ ID NO:7 and the V_β domain comprises the CDR3 amino acid sequence of SEQ ID NO:8;
 - (c) the V_α domain comprises the CDR3 amino acid sequence of SEQ ID NO:9 and the V_β domain comprises the CDR3 amino acid sequence of SEQ ID NO:10;
 - (d) the V_α domain comprises the CDR3 amino acid sequence of SEQ ID NO:11 and the V_β domain comprises the CDR3 amino acid sequence of SEQ ID NO:12;

(e) the $V\alpha$ domain comprises the CDR3 amino acid sequence of SEQ ID NO:13 and the $V\beta$ domain comprises the CDR3 amino acid sequence of SEQ ID NO:14;

(f) the $V\alpha$ domain comprises the CDR3 amino acid sequence of SEQ ID NO:15 and the $V\beta$ domain comprises the CDR3 amino acid sequence of SEQ ID NO:16;

(g) the $V\alpha$ domain comprises the CDR3 amino acid sequence of SEQ ID NO:17 and the $V\beta$ domain comprises the CDR3 amino acid sequence of SEQ ID NO:18;

(h) the $V\alpha$ domain comprises the CDR3 amino acid sequence of SEQ ID NO:19 and the $V\beta$ domain comprises the CDR3 amino acid sequence of SEQ ID NO:20; or

(i) the $V\alpha$ domain comprises the CDR3 amino acid sequence of SEQ ID NO:7 and the $V\beta$ domain comprises the CDR3 amino acid sequence of SEQ ID NO:189.

3. The binding protein of claim 1, wherein:

(a) the $V\beta$ domain comprises the CDR3 amino acid sequence of SEQ ID NO:6 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRBV9*01 gene; and the $V\alpha$ domain comprises the CDR3 amino acid sequence of SEQ ID NO:5 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRAV30*01 gene;

(b) the $V\beta$ domain comprises the CDR3 amino acid sequence of SEQ ID NO:8 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRBV2*01 gene; and the $V\alpha$ domain comprises the CDR3 amino acid sequence of SEQ ID NO:7 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRAV10*01 gene;

(c) the $V\beta$ domain comprises the CDR3 amino acid sequence of SEQ ID NO:10 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRBV6-6*01 gene; and the $V\alpha$ domain comprises the CDR3 amino acid sequence of

SEQ ID NO:9 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRAV24*01 gene;

(d) the V β domain comprises the CDR3 amino acid sequence of SEQ ID NO:12 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRBV5-6*01 gene; and the V α domain comprises the CDR3 amino acid sequence of SEQ ID NO:11 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRAV21*01 gene;

(e) the V β domain comprises the CDR3 amino acid sequence of SEQ ID NO:14 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRBV7-3*01 gene; and the V α domain comprises the CDR3 amino acid sequence of SEQ ID NO:13 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRAV21*02 gene;

(f) the V β domain comprises the CDR3 amino acid sequence of SEQ ID NO:16 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRBV7-3*01 gene; and the V α domain comprises the CDR3 amino acid sequence of SEQ ID NO:15 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRAV12-2*02 gene;

(g) the V β domain comprises the CDR3 amino acid sequence of SEQ ID NO:18 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRBV7-3*01 gene; and the V α domain comprises the CDR3 amino acid sequence of SEQ ID NO:17 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRAV17*01 gene;

(h) the V β domain comprises the CDR3 amino acid sequence of SEQ ID NO:20 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRBV7-2*01 gene; and the V α domain comprises the CDR3 amino acid sequence of SEQ ID NO:19 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRAV17*01 gene; or

(i) the V β domain comprises the CDR3 amino acid sequence of SEQ ID NO:189 or 101 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRBV10-2*01 gene; and the V α domain comprises the CDR3 amino acid

sequence of SEQ ID NO:7 or 97 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRAV10*01 gene.

4. The binding protein according to claim 1 or 2, wherein the binding protein comprises:

(a) a V α domain that is at least about 90% identical to the V α amino acid sequence contained in any one of SEQ ID NOS:36, 38, 40, 42, 44, 86, 49, 51, 53, 57, 59, 63, 65, 67, 81, 83, 162, 165, 170, 172, 174, 176, 178, 180, and 186;

(b) a V β domain that is at least about 90% identical to the V β amino acid sequence set contained in any one of SEQ ID NOS:36, 38, 40, 42, 46, 86, 49, 51, 55, 57, 61, 63, 67, 81, 83, 162, 165, 170, 172, 174, 176, 178, 180, and 186; or

(c) a V α domain of (a) and a V β of (b);

wherein at least three or four of the CDRs have no mutations and the CDRs that do have mutations have three or less amino acid substitutions, insertions, and/or deletions.

5. The binding protein of claim 4, wherein the binding protein comprises:

(a) a V α domain comprising or consisting of the V α amino acid sequence contained in any one of SEQ ID NOS:36, 38, 40, 42, 44, 86, 49, 51, 53, 57, 59, 63, 65, 67, 81, 83, 162, 165, 170, 172, 174, 176, 178, 180, and 186;

(b) a V β domain comprising or consisting of the V β amino acid sequence contained in any one of SEQ ID NOS:36, 38, 40, 42, 46, 86, 49, 51, 55, 57, 61, 63, 67, 81, 83, 162, 165, 170, 172, 174, 176, 178, 180, and 186; or

(c) a V α domain of (a) and a V β of (b).

6. The binding protein of claim 5, wherein the binding protein comprises:

(a) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:36 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:36;

(b) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:38 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:38;

(c) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:40 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:40;

(d) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:42 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:42;

(e) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:44 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:46;

(f) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:86 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:86;

(g) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:49 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:49;

(h) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:51 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:51;

(i) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:53 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:55;

(j) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:57 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:57;

(k) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:59 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:61;

(l) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:63 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:63;

(m) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:65 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:67;

(n) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:67 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:67;

(o) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:81 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:81; (p) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:83 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:83;

(q) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:162 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:162;

(r) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:165 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:165;

(s) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:170 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:170;

(t) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:172 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:172;

(u) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:174 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:174;

(v) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:176 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:176;

(w) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:178 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:178;

(x) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:180 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:180; or

(y) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:186 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:186.

7. A binding protein, comprising:

(a) a T cell receptor (TCR) α chain variable (V α) domain comprising a complementary determining region 3 (CDR3) amino acid sequence set forth in SEQ ID NO:21, or a CDR3 amino acid sequence set forth in SEQ ID NO:21 with up to five amino acid substitutions, insertions and/or deletions, and a TCR β chain variable (V β) domain;

(b) a TCR V α domain, and a TCR V β domain comprising a CDR3 amino acid sequence set forth in SEQ ID NO:22, or a CDR3 amino acid sequence set forth in SEQ ID NO:22 with up to five amino acid substitutions, insertions and/or deletions; or

(c) a V α domain of (a) and a V β of (b),

wherein the binding protein is capable of specifically binding to a human cyclin A1 (CCNA1) peptide SLIAAAAFCLA(SEQ ID NO:2):human leukocyte antigen (HLA) complex.

8. The binding protein of claim 7, wherein the V α domain comprises the CDR3 amino acid sequence of SEQ ID NO:21 and the V β domain comprises the CDR3 amino acid sequence of SEQ ID NO:22.

9. The binding protein of claim 7 or 8, wherein:

the V β domain comprises the CDR3 amino acid sequence of SEQ ID NO:22 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRBV19*01 gene; and

the V α domain comprises the CDR3 amino acid sequence of SEQ ID NO:21 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRAV24*01 gene.

10. The binding protein according to any one of claims 7-9, wherein the binding protein comprises:

(a) a V α domain that is at least about 90% identical to the V α amino acid sequence contained in SEQ ID NO:69 or 73;

(b) a V β domain that is at least about 90% identical to the V β amino acid sequence contained in SEQ ID NO:71 or 73; or

(c) a V α domain of (a) and a V β of (b);

wherein at least three or four of the CDRs have no mutations and the CDRs that do have mutations have three or less amino acid substitutions, insertions, and/or deletions.

11. The binding protein of claim 10, wherein the binding protein comprises:

(a) a V α domain comprising or consisting of the V α amino acid sequence contained in SEQ ID NO:69 or 73;

(b) a V β domain comprising or consisting of the amino acid sequence set forth in SEQ ID NO:71 or 73; or

(c) a V α domain of (a) and a V β of (b).

12. The binding protein of claim 11, wherein the binding protein comprises:

(a) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:69 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:71; or

(b) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:73 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:73.

13. A binding protein, comprising:

(a) a T cell receptor (TCR) α chain variable (V α) domain comprising a complementary determining region 3 (CDR3) amino acid sequence set forth in SEQ ID NO:23, or a CDR3 amino acid sequence set forth in SEQ ID NO:23 with up to five amino acid substitutions, insertions and/or deletions, and a TCR β chain variable (V β) domain;

(b) a TCR V α domain, and a TCR V β domain comprising a CDR3 amino acid sequence set forth in SEQ ID NO:24, or a CDR3 amino acid sequence set forth in SEQ ID NO:24 with up to five amino acid substitutions, insertions and/or deletions; or

(c) a V α domain of (a) and a V β of (b),

wherein the binding protein is capable of specifically binding to a human cyclin A1 (CCNA1) peptide YSLSEIVPCL (SEQ ID NO:3):human leukocyte antigen (HLA) complex.

14. The binding protein of claim 13, wherein the V α domain comprises the CDR3 amino acid sequence of SEQ ID NO:23 and the V β domain comprises the CDR3 amino acid sequence of SEQ ID NO:24.

15. The binding protein of claim 13 or 14, wherein:

the V β domain comprises the CDR3 amino acid sequence of SEQ ID NO:24 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRBV5-6*01 gene; and

the V α domain comprises the CDR3 amino acid sequence of SEQ ID NO:23 and a CDR1 amino acid sequence and a CDR2 amino acid sequence encoded by a TRAV19*01 gene.

16. The binding protein according to any one of claims 13-15, wherein the binding protein comprises:

(a) a V α domain that is at least about 90% identical to the V α amino acid sequence contained in SEQ ID NO:75 or 79;

(b) a V β domain that is at least about 90% identical to the V β amino acid sequence contained in SEQ ID NO:77 or 79; or

(c) a V α domain of (a) and a V β of (b);

wherein at least three or four of the CDRs have no mutations and the CDRs that do have mutations have three or less amino acid substitutions, insertions, and/or deletions.

17. The binding protein of claim 16, wherein the binding protein comprises:

(a) a V α domain comprising or consisting of the V α amino acid sequence contained in SEQ ID NO:75 or 79;

(b) a V β domain comprising or consisting of the V β amino acid sequence contained in SEQ ID NO:77 or 79; or

(c) a V α domain of (a) and a V β of (b).

18. The binding protein of claim 17, wherein the binding protein comprises:

(a) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:75 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:77; or

(b) the V α domain comprising the V α amino acid sequence contained in SEQ ID NO:79 and the V β domain comprising the V β amino acid sequence contained in SEQ ID NO:79.

19. The binding protein of any one of claims 1-18, wherein the binding protein is a TCR, an antigen binding fragment of a TCR, or a chimeric antigen receptor.

20. The binding protein of claim 19, wherein the antigen binding fragment of the TCR comprises a single chain TCR (scTCR).

21. The binding protein of claim 19, wherein the binding protein is a TCR.
22. The binding protein of claim 21, wherein the TCR comprises an α chain constant ($C\alpha$) domain comprising at least 90% sequence identity to the amino acid sequence of SEQ ID NO:33.
23. The binding protein of claim 22, wherein the $C\alpha$ domain comprises the amino acid sequence of SEQ ID NO:33.
24. The binding protein of claim 21, wherein the TCR comprises a truncated $C\alpha$ domain.
25. The binding protein of claim 24, wherein the truncated $C\alpha$ domain comprises truncations of 1, 2, 3, 4, or more amino acids at its N-terminus, C-terminus or both, corresponding to the amino acid sequence of SEQ ID NO:33.
26. The binding protein of any one of claims 19-25, wherein the TCR comprises a β chain constant ($C\beta$) domain comprising at least 90% sequence identity to the amino acid sequence of SEQ ID NO:34 or SEQ ID NO:84.
27. The binding protein of claim 26, wherein the $C\beta$ domain comprises the amino acid sequence of SEQ ID NO:34 or SEQ ID NO:84.
28. The binding protein of any one of claims 19-27, wherein the TCR comprises:
- (a) a $C\alpha$ domain comprising a cysteine substitution at position 49 of SEQ ID NO:33,
 - (b) a $C\beta$ domain comprising a cysteine substitution at a position corresponding to position 57 of SEQ ID NO:34 or position 56 of SEQ ID NO:84, or
 - (c) both (a) and (b).

29. The binding protein of claim 21, wherein the TCR comprises:

- (a) an α chain comprising at least 90% sequence identity to the α chain amino acid sequence contained in any one of SEQ ID NO:36, 38, 40, 42, 44, 86, 49, 51, 53, 57, 59, 63, 65, 67, 81, 83, 162, 165, 170, 172, 174, 176, 178, 180, and 186;
- (b) a β chain comprising at least 90% sequence identity to the β chain amino acid sequence contained in any one of SEQ ID NO: 36, 38, 40, 42, 46, 86, 49, 51, 55, 57, 61, 63, 67, 81, 83, 162, 165, 170, 172, 174, 176, 178, 180, and 186; or
- (c) an α chain of (a) and a β chain of (b).

30. The binding protein of claim 29, wherein the TCR comprises:

- (a) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:36 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:36;
- (b) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:38 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:38;
- (c) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:40 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:40;
- (d) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:42 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:42;
- (e) the TCR α chain comprising the amino acid sequence of SEQ ID NO:44 and the TCR β chain comprising the amino acid sequence of SEQ ID NO:46;
- (f) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:86 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:86;
- (g) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:49 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:49; or

(h) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:51 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:51;

(i) the TCR α chain comprising the amino acid sequence of SEQ ID NO:53 and the TCR β chain comprising the amino acid sequence of SEQ ID NO:55;

(j) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:57 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:57;

(k) the TCR α chain comprising the amino acid sequence of SEQ ID NO:59 and the TCR β chain comprises the amino acid sequence of SEQ ID NO:61;

(l) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:63 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:63;

(m) the TCR α chain comprising the amino acid sequence of SEQ ID NO:65 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:67;

(n) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:67 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:67;

(o) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:81 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:81;

(p) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:83 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:83;

(q) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:162 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:162;

(r) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:165 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:165;

(s) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:170 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:170;

(t) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:172 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:172;

(u) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:174 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:174;

(v) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:176 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:176;

(w) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:178 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:178;

(x) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:180 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:180; or

(y) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:186 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:186.

31. The binding protein of claim 21, wherein the TCR comprises:

(a) an α chain comprising at least 90% sequence identity to the amino acid sequence of SEQ ID NO:69 or the α chain amino acid sequence contained in SEQ ID NO:73;

(b) a β chain comprising at least 90% sequence identity to the amino acid sequence of SEQ ID NO:71 or the α chain amino acid sequence contained in SEQ ID NO:73; or

(c) an α chain of (a) and a β chain of (b).

32. The binding protein of claim 31, wherein the TCR comprises:

- (a) the TCR α chain comprising the amino acid sequence of SEQ ID NO:69 and the TCR β chain comprising the amino acid sequence of SEQ ID NO:71;
- (b) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:73 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:73; or
- (c) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:182 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:182.

33. The binding protein of claim 21, wherein the TCR comprises:

- (a) an α chain comprising at least 90% sequence identity to the amino acid sequence of SEQ ID NO:75 or the α chain amino acid sequence contained in SEQ ID NO:79;
- (b) a β chain comprising at least 90% sequence identity to the amino acid sequence of SEQ ID NO:77 or the α chain amino acid sequence contained in SEQ ID NO:79; or
- (c) an α chain of (a) and a β chain of (b).

34. The binding protein of claim 33, wherein the TCR comprises:

- (a) the TCR α chain comprising an amino acid sequence of SEQ ID NO:75 and the TCR β chain comprises an amino acid sequence of SEQ ID NO:77;
- (b) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:79 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:79; or
- (c) the TCR α chain comprising the α chain amino acid sequence contained in SEQ ID NO:184 and the TCR β chain comprising the β chain amino acid sequence contained in SEQ ID NO:184.

35. The binding protein of any one of claims 1-34, wherein the HLA comprises HLA-A*02:01.

36. The binding protein of any one of claims 1-35, wherein the binding protein is a chimeric, humanized, or human TCR, antigen-binding fragment of the TCR, or chimeric antigen receptor.

37. A polynucleotide encoding a binding protein that comprises a T cell receptor (TCR) α chain variable ($V\alpha$) domain and a TCR β chain variable ($V\beta$) domain, wherein the encoded binding protein is capable of specifically binding to a human cyclin A1 (CCNA1) peptide YSLSEIVPCL (SEQ ID NO:3), wherein the polynucleotide is codon optimized for expression in a host cell.

38. The polynucleotide of claim 37, wherein the encoded binding protein is capable of specifically binding CCNA1 peptide YSLSEIVPCL (SEQ ID NO:3):HLA complex.

39. The polynucleotide of claim 38, wherein the HLA comprises HLA-A*02:01.

40. A polynucleotide encoding a binding protein of any one of claims 1-36.

41. The polynucleotide of claim 40, wherein the polynucleotide encoding the binding protein is codon optimized for expression in a host cell of interest.

42. A vector comprising a polynucleotide of any one of claims 37-41.

43. The vector of claim 42, wherein the vector is a viral vector.

44. The vector of claim 43, wherein the viral vector is a lentiviral vector or a γ -retroviral vector.

45. A host cell comprising a polynucleotide of any one of claims 37-41 or a vector of any one of claims 42-44, wherein the host cell expresses on its cell surface a binding protein encoded by the polynucleotide.

46. The host cell of claim 45, wherein the host cell is a hematopoietic progenitor cell or an immune cell.

47. The host cell of claim 46, wherein the immune cell is a CD4⁺ T cell, a CD8⁺ T cell, a CD4-CD8⁻ T cell, a $\gamma\delta$ T cell, a natural killer cell, a dendritic cell, or any combination thereof.

48. The host cell of claim 46, wherein the immune cell is a T cell.

49. The host cell of claim 48, wherein the T cell is a naïve T cell, a central memory T cell, an effector memory T cell, or any combination thereof.

50. The host cell of any one of claims 45-49, wherein the host cell is human.

51. A composition comprising the host cell of any one of claims 45-50, and a pharmaceutically acceptable carrier, diluent, or excipient.

52. A method of treating a hyperproliferative disorder, comprising administering to a subject in need thereof a composition comprising a binding protein specific for a CCNA1 peptide according to any one of claims 1-36, a polynucleotide encoding a binding protein specific for a CCNA1 peptide according to any one of claims 37-41, the vector of any one of claims 42-44, the host cell of any one of claims 45-50, or the composition of claim 51.

53. The method of claim 52, wherein the hyperproliferative disorder is a hematological malignancy or a solid cancer.

54. The method of claim 53, wherein the hematological malignancy is selected from acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), chronic myelogenous leukemia (CML), chronic eosinophilic leukemia (CEL), myelodysplastic syndrome (MDS), non-Hodgkin's lymphoma (NHL), and multiple myeloma (MM).

55. The method of claim 53, wherein the solid cancer is selected from biliary cancer, bladder cancer, bone and soft tissue carcinoma, brain tumor, breast cancer, cervical cancer, colon cancer, colorectal adenocarcinoma, colorectal cancer, desmoid tumor, embryonal cancer, endometrial cancer, esophageal cancer, gastric cancer, gastric adenocarcinoma, glioblastoma multiforme, gynecological tumor, head and neck squamous cell carcinoma, hepatic cancer, lung cancer, mesothelioma, malignant melanoma, osteosarcoma, ovarian cancer, pancreatic cancer, pancreatic ductal adenocarcinoma, primary astrocytic tumor, primary thyroid cancer, prostate cancer, renal cancer, renal cell carcinoma, rhabdomyosarcoma, skin cancer, soft tissue sarcoma, testicular germ-cell tumor, urothelial cancer, uterine sarcoma, or uterine cancer.

56. The method of any one of claims 52-55, wherein the binding protein is capable of promoting an antigen-specific T cell response against a human cyclin A1 in a class I HLA-restricted manner.

57. The method of claim 56, wherein the antigen-specific T cell response comprises at least one of a CD4⁺ helper T lymphocyte (Th) response and a CD8⁺ cytotoxic T lymphocyte (CTL) response.

58. The method according to claim 57, wherein the CTL response is directed against a CCNA1-overexpressing cell.

59. The method according to any one of claims 52-58, wherein the host cell is administered parenterally.

60. The method according to any one of claims 52-59, wherein the method comprises administering a plurality of doses of the host cell to the subject.

61. The method according to claim 60, wherein the plurality of doses are administered at intervals between administrations of about two to about four weeks.

62. The method according to any one of claims 52-61, wherein the host cell is administered to the subject at a dose of about 10^7 cells/m² to about 10^{11} cells/m².

63. The method according to any one of claims 52-62, wherein the method further comprises administering a cytokine to the subject.

64. The method according to claim 63, wherein the cytokine is IL-2, IL-15, IL-21 or any combination thereof.

65. The method according to claim 64, wherein the cytokine is IL-2 and is administered concurrently or sequentially with the host cell.

66. The method according to claim 65, wherein the cytokine is administered sequentially, provided that the subject was administered the host cell at least three or four times before cytokine administration.

67. The method according to any one of claims 63-66, wherein the cytokine is IL-2 and is administered subcutaneously.

68. The method according to any one of claims 52-67, wherein the subject is further receiving an immunosuppressive therapy.

69. The method according to claim 68, wherein the immunosuppressive therapy is selected from calcineurin inhibitors, corticosteroids, microtubule inhibitors, low dose of a mycophenolic acid prodrug, or any combination thereof.

70. The method according to any one of claims 52-69, wherein the subject has received a non-myeloablative or a myeloablative hematopoietic cell transplant.

71. The method according to claim 70, wherein the subject is administered the host cell at least three months after the non-myeloablative hematopoietic cell transplant.

72. The method according to claim 71, wherein the subject is administered the host cell at least two months after the myeloablative hematopoietic cell transplant.

73. The method according to any one of claims 51-72, further comprising administering an inhibitor of an immune suppression agent to the subject.

74. The method according to claim 73, wherein the inhibitor of the immune suppression agent inhibits PD-1, PD-L1, PD-L2, LAG3, CTLA4, B7-H3, B7-H4, CD244/2B4, HVEM, BTLA, CD160, TIM3, GAL9, adenosine, A2aR, an immunosuppressive cytokine, IDO, arginase, VISTA, TIGIT, PVRIG, PVRL2, KIRs, LAIR1, CEACAM-1, CEACAM-3, CEACAM-5, CD160, Treg cells, or any combination thereof.

75. The method according to claim 73 or 74, wherein the inhibitor of the immune suppression agent is selected from the group consisting of an antibody or antigen binding fragment thereof, a fusion protein, a small molecule, an RNAi molecule, a ribozyme, an aptamer, an antisense oligonucleotide, or any combination thereof.

76. The method according to claim 75, wherein the inhibitor of the immune suppression agent comprises pidilizumab, nivolumab, pembrolizumab, MEDI0680, AMP-224, BMS-936558 BMS-936559, durvalumab, atezolizumab, avelumab, MPDL3280A, LAG525, IMP321, IMP701, 9H12, BMS-986016, ipilimumab, tremelimumab, abatacept, belatacept, enoblituzumab, 376.96, an anti-B7-H4 antibody

or antigen binding fragment, lirilumab, levo-1-methyl tryptophan, epacadostat, ebselen, indoximod, NLG919, 1-methyl-tryptophan (1-MT)-tira-pazamine, N(omega)-Nitro-L-arginine methyl ester (L-NAME), N-omega-hydroxy-nor-l-arginine (nor-NOHA), L-NOHA, 2(S)-amino-6-boronohexanoic acid (ABH), S-(2-boronoethyl)-L-cysteine (BEC), CA-170, COM902, COM701, or antigen binding fragments thereof, or any combination thereof.

77. The method according to any one of claims 52-76, further comprising administering to the subject a therapeutically effective amount of an agonist of a stimulatory immune checkpoint molecule.

78. The method according to claim 77, wherein the agonist is selected from urelumab, MEDI6469, MEDI6383, MEDI0562, lenalidomide, pomalidomide, CDX-1127, TGN1412, CD80, CD86, CP-870,893, rhuCD40L, SGN-40, IL-2, GSK3359609, mAb 88.2, JTX-2011, Icos 145-1, Icos 314-8, or any combination thereof.

79. The method according to any one of claims 52-78, further comprising administering to the subject one or more of: a therapeutic antibody, chemotherapy, radiation therapy, surgery, or any combination thereof.

80. The method according to any one of claims 52-79, wherein the subject is human.

81. A unit dose form comprising a host cell according to any one of claims 45-50.

82. The unit dose form according to claim 81, wherein the host cell is at a dose of about 10^7 cells/m² to about 10^{11} cells/m².

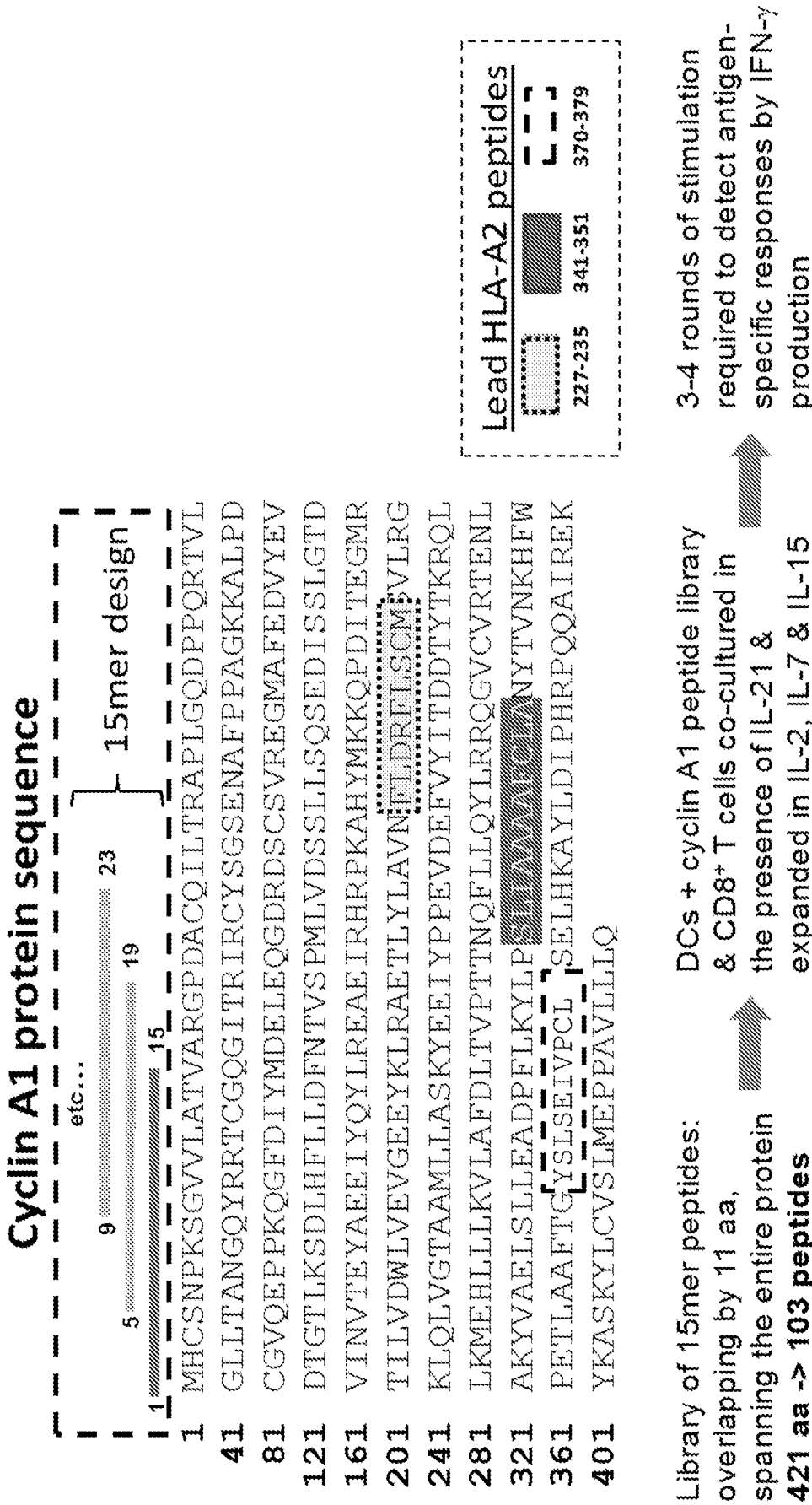


FIG. 1

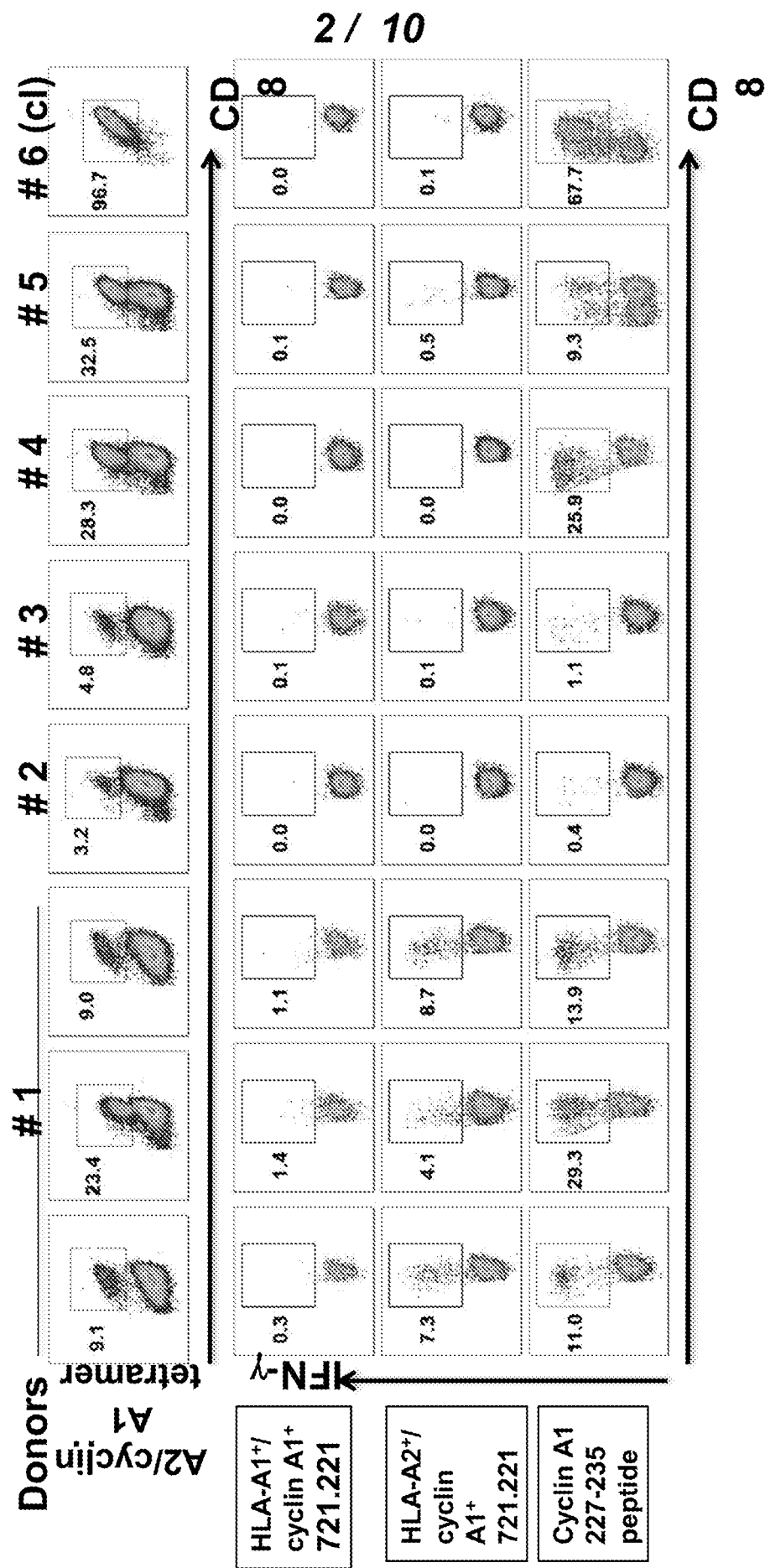


FIG. 2

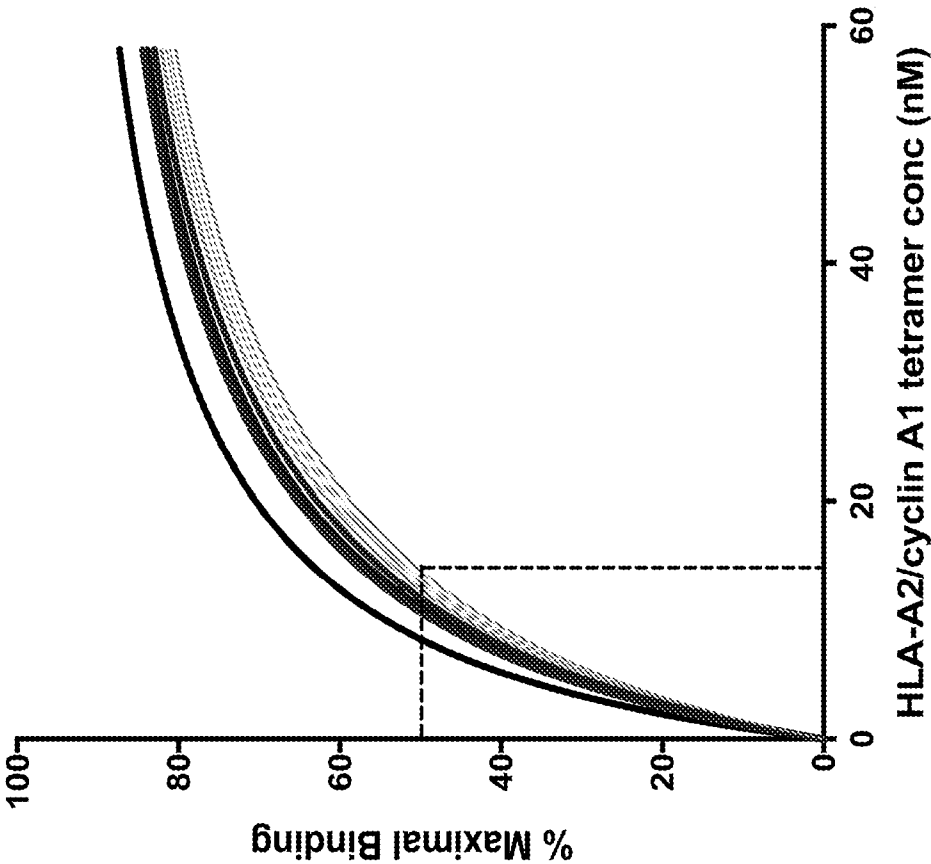


FIG. 3A

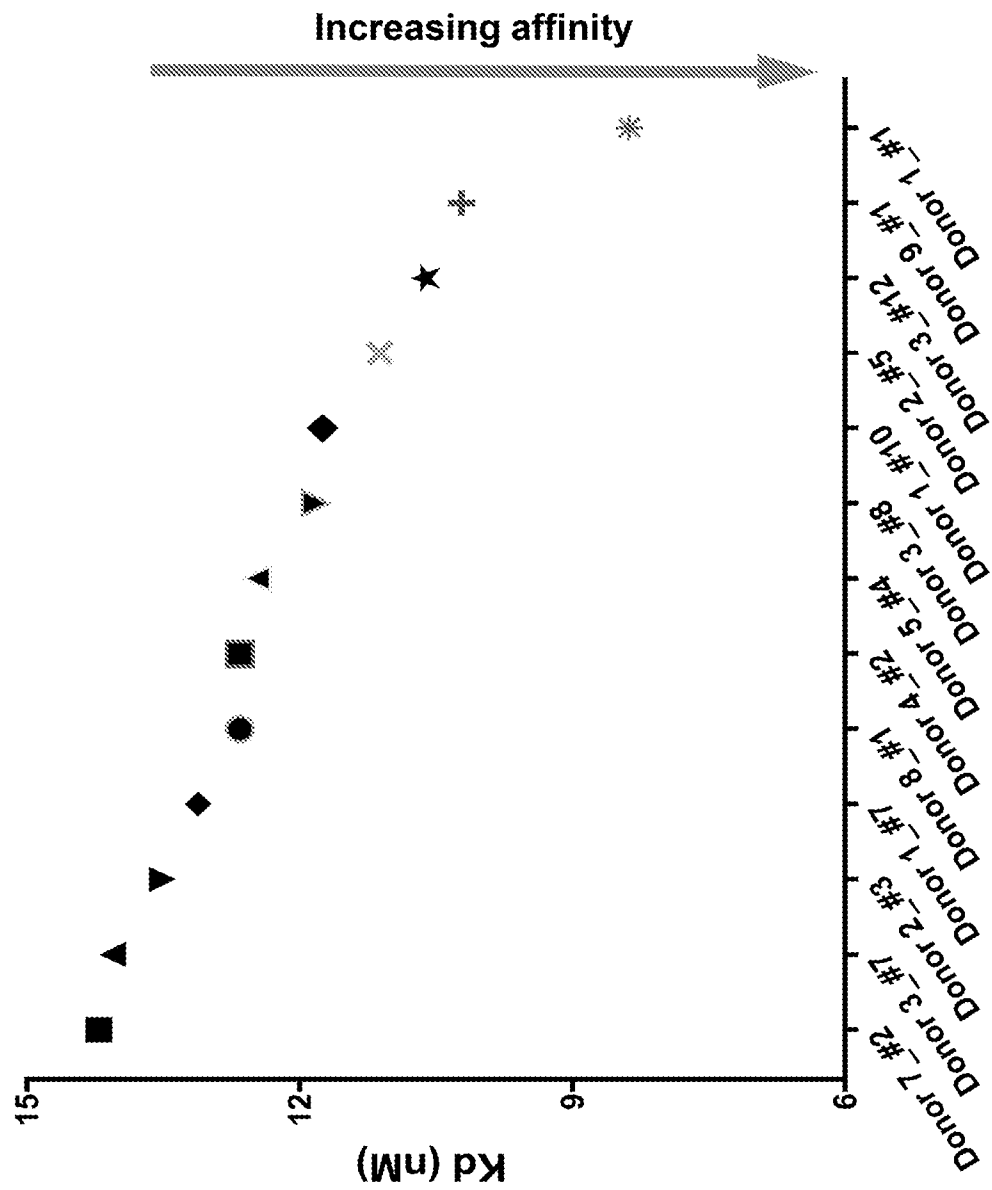


FIG. 3B

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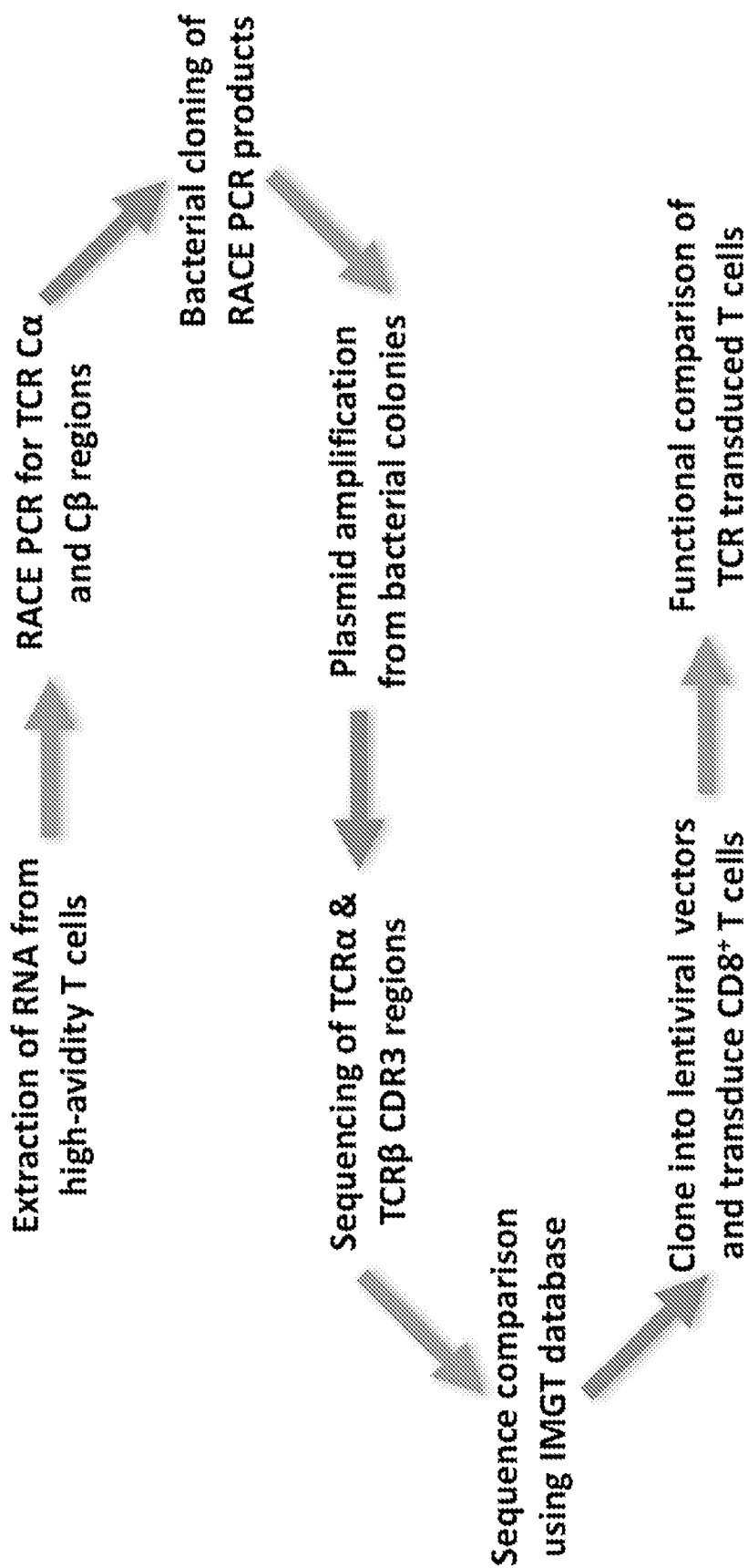


FIG. 4

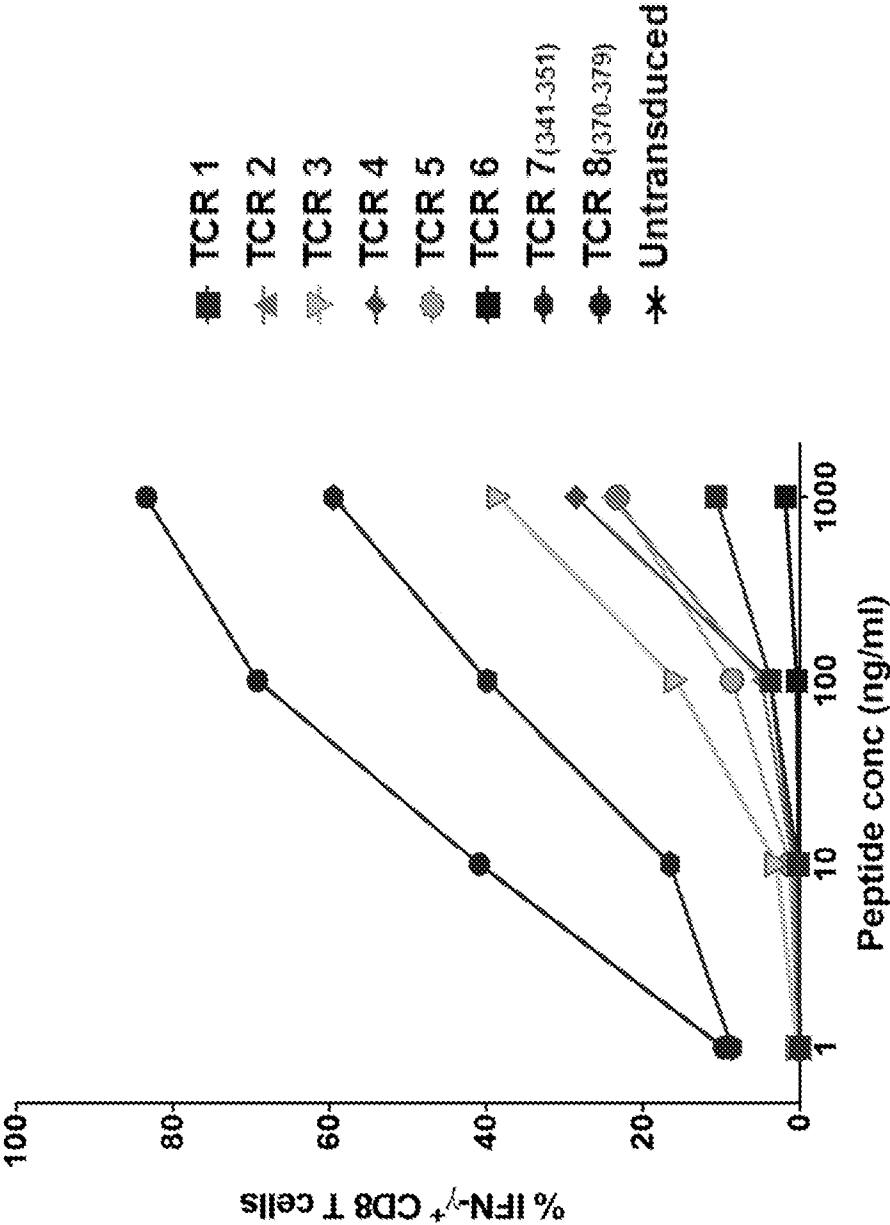


FIG. 5A

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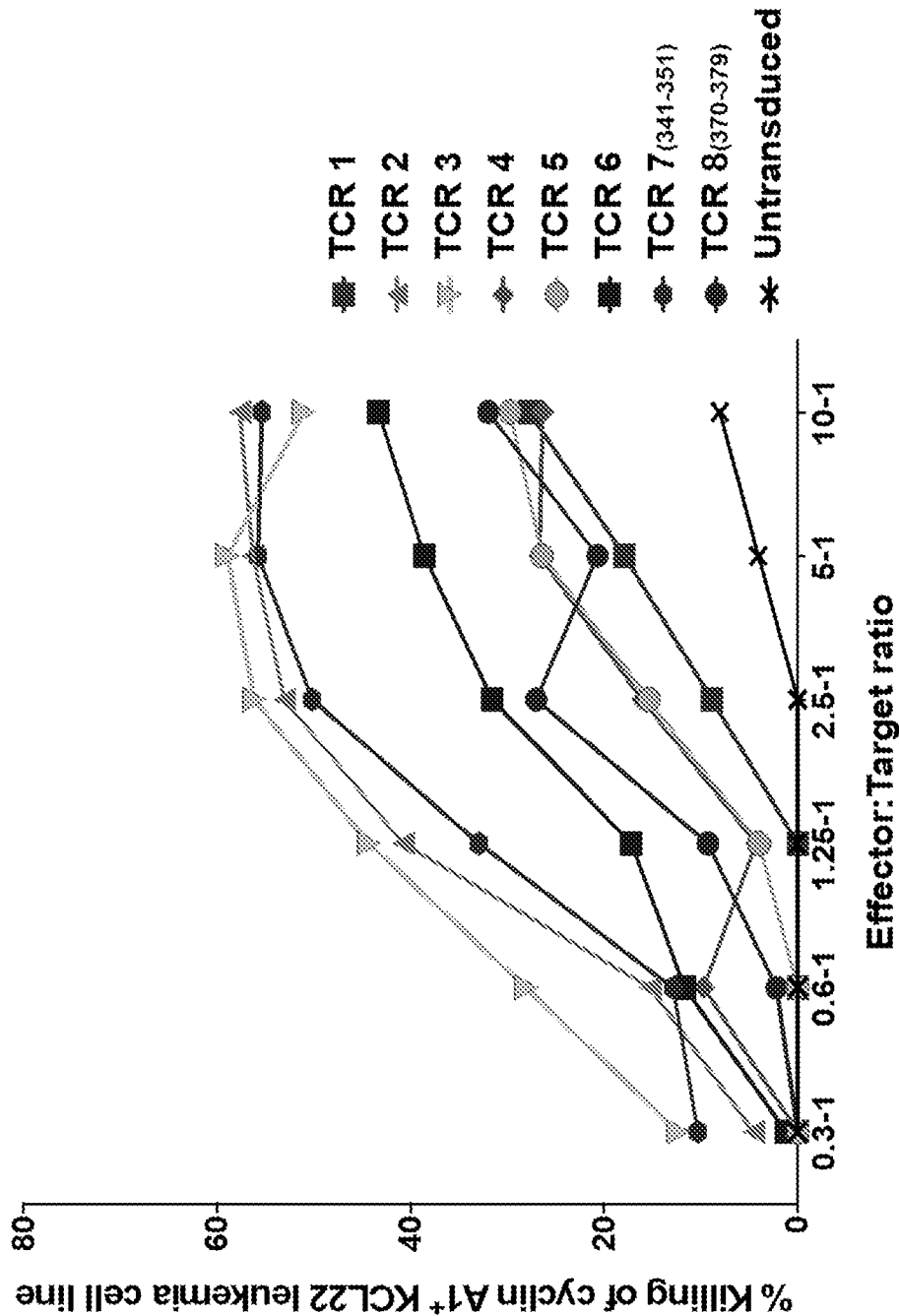


FIG. 5B

MHC binding & proteasome cleavage prediction

Algorithm	Peptide		
	227-235	341-351	370-379
SYFPEITHI: Binding score	20	24	29
NetMHCpan 4.0: IC ₅₀ (nM)	32.5	74.7	13.1
IEDB: ANN IC ₅₀ (nM)	27.03	113.39	12.05
BiMAS: Dissociation half-time	79.89	NA	5.459
MAPPP: Cleavage probability	0.9560	0	0

* IC₅₀ values <50 nM are considered high affinity, <500 nM intermediate affinity and <5000 nM low affinity.

FIG. 5C

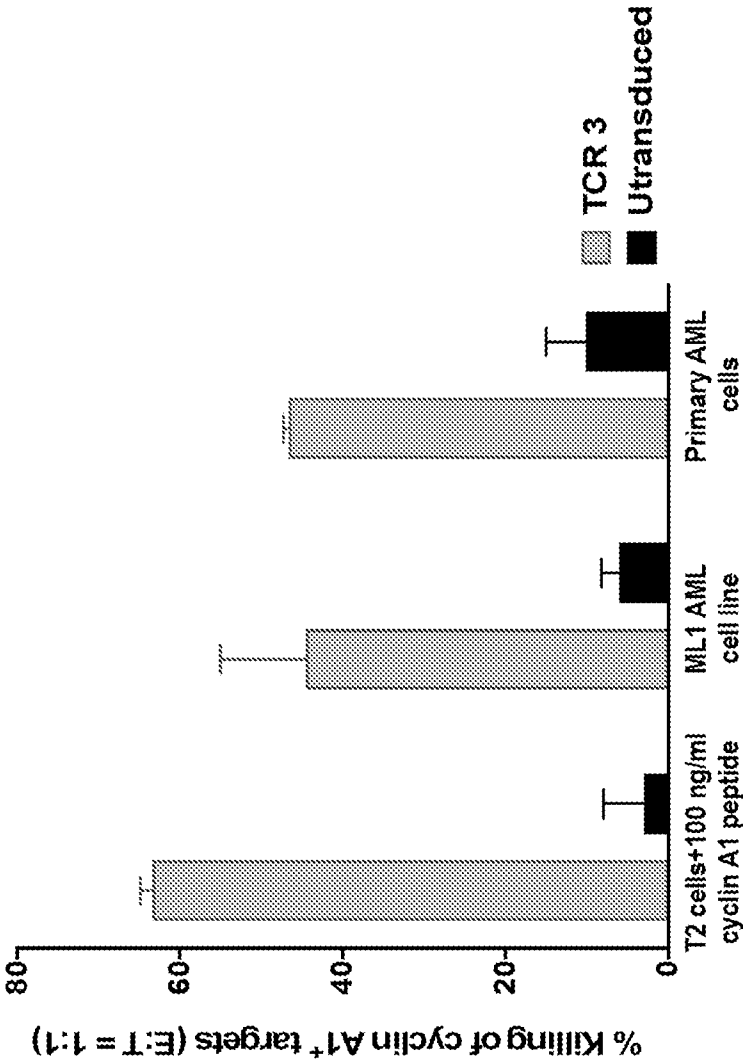


FIG. 5D

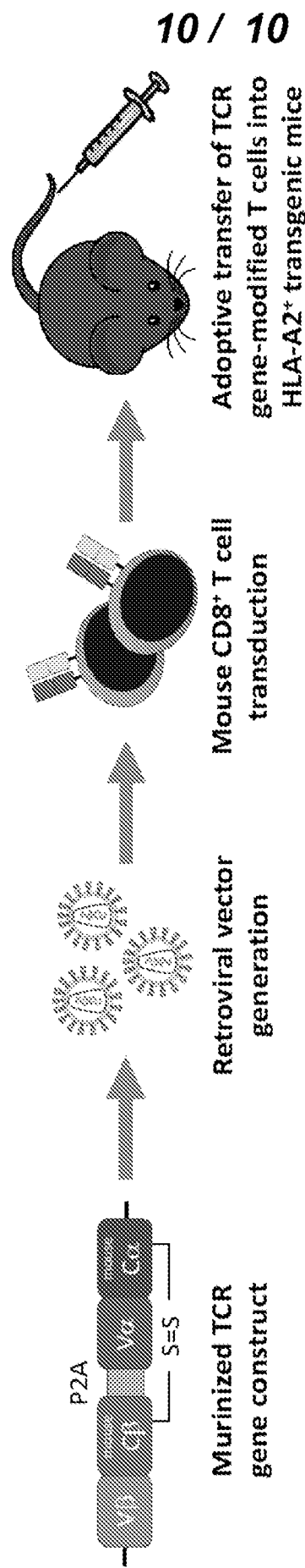


FIG. 6

SEQUENCE LISTING

<110> Fred Hutchinson Cancer Research Center
Perret, Rachel
Greenberg, Philip D.

<120> CYCLIN A1 SPECIFIC T CELL RECEPTORS AND USES THEREOF

<130> 360056.460W0

<140> PCT

<141> 2019-02-12

<150> US 62/667,207

<151> 2018-05-04

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			20					25					30			
Asp	Pro	Pro	Gln	Arg	Thr	Val	Leu	Gly	Leu	Leu	Thr	Ala	Asn	Gly	Gln	
		35					40					45				
Tyr	Arg	Arg	Thr	Cys	Gly	Gln	Gly	Ile	Thr	Arg	Ile	Arg	Cys	Tyr	Ser	
	50					55					60					
Gly	Ser	Glu	Asn	Ala	Phe	Pro	Pro	Ala	Gly	Lys	Lys	Ala	Leu	Pro	Asp	
65					70					75					80	
Cys	Gly	Val	Gln	Glu	Pro	Pro	Lys	Gln	Gly	Phe	Asp	Ile	Tyr	Met	Asp	
				85					90					95		
Glu	Leu	Glu	Gln	Gly	Asp	Arg	Asp	Ser	Cys	Ser	Val	Arg	Glu	Gly	Met	
			100					105					110			
Ala	Phe	Glu	Asp	Val	Tyr	Glu	Val	Asp	Thr	Gly	Thr	Leu	Lys	Ser	Asp	
		115					120					125				
Leu	His	Phe	Leu	Leu	Asp	Phe	Asn	Thr	Val	Ser	Pro	Met	Leu	Val	Asp	
	130					135					140					

Ser	Ser	Leu	Leu	Ser	Gln	Ser	Glu	Asp	Ile	Ser	Ser	Leu	Gly	Thr	Asp
145					150					155					160
Val	Ile	Asn	Val	Thr	Glu	Tyr	Ala	Glu	Glu	Ile	Tyr	Gln	Tyr	Leu	Arg
				165						170					175
Glu	Ala	Glu	Ile	Arg	His	Arg	Pro	Lys	Ala	His	Tyr	Met	Lys	Lys	Gln
			180					185					190		
Pro	Asp	Ile	Thr	Glu	Gly	Met	Arg	Thr	Ile	Leu	Val	Asp	Trp	Leu	Val
	195						200					205			
Glu	Val	Gly	Glu	Glu	Tyr	Lys	Leu	Arg	Ala	Glu	Thr	Leu	Tyr	Leu	Ala
	210					215					220				
Val	Asn	Phe	Leu	Asp	Arg	Phe	Leu	Ser	Cys	Met	Ser	Val	Leu	Arg	Gly
225					230					235					240
Lys	Leu	Gln	Leu	Val	Gly	Thr	Ala	Ala	Met	Leu	Leu	Ala	Ser	Lys	Tyr
				245					250						255
Glu	Glu	Ile	Tyr	Pro	Pro	Glu	Val	Asp	Glu	Phe	Val	Tyr	Ile	Thr	Asp
			260					265					270		
Asp	Thr	Tyr	Thr	Lys	Arg	Gln	Leu	Leu	Lys	Met	Glu	His	Leu	Leu	Leu
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Lys	Val	Leu	Ala	Phe	Asp	Leu	Thr	Val	Pro	Thr	Thr	Asn	Gln	Phe	Leu
	290					295					300				
Leu	Gln	Tyr	Leu	Arg	Arg	Gln	Gly	Val	Cys	Val	Arg	Thr	Glu	Asn	Leu
305					310					315					320
Ala	Lys	Tyr	Val	Ala	Glu	Leu	Ser	Leu	Leu	Glu	Ala	Asp	Pro	Phe	Leu
				325					330						335
Lys	Tyr	Leu	Pro	Ser	Leu	Ile	Ala	Ala	Ala	Ala	Phe	Cys	Leu	Ala	Asn
			340					345					350		
Tyr	Thr	Val	Asn	Lys	His	Phe	Trp	Pro	Glu	Thr	Leu	Ala	Ala	Phe	Thr
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Gly	Tyr	Ser	Leu	Ser	Glu	Ile	Val	Pro	Cys	Leu	Ser	Glu	Leu	His	Lys
	370					375					380				
Ala	Tyr	Leu	Asp	Ile	Pro	His	Arg	Pro	Gln	Gln	Ala	Ile	Arg	Glu	Lys
385					390					395					400
Tyr	Lys	Ala	Ser	Lys	Tyr	Leu	Cys	Val	Ser	Leu	Met	Glu	Pro	Pro	Ala
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				420											

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<400> 21

Cys	Ala	Tyr	Leu	Gly	Ala	Gly	Asn	Gln	Phe	Tyr	Phe
1				5					10		

<210> 22

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 7 Vbeta CDR3

<400> 22

Cys	Ala	Ser	Ser	Leu	Asn	Arg	Gly	Arg	Tyr	Gly	Tyr	Thr	Phe
1				5					10				

<210> 23

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 8 Valpha CDR3

<400> 23

Cys	Ala	Leu	Ser	Glu	Leu	Ala	Ser	Gly	Gly	Ser	Tyr	Ile	Pro	Thr	Phe
1				5					10					15	

<210> 24

<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR number 8 Vbeta CDR3

<400> 24
Cys Ala Ser Ser Phe Arg Leu Ala Gly Gly Pro Ser Thr Asp Thr Gln
1 5 10 15
Tyr Phe

<210> 25
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> P2A peptide encoding nucleic acid

<400> 25
ggttccggag ccacgaactt ctctctgtta aagcaagcag gagacgtgga agaaaacccc
60
g g t c c c
66

<210> 26
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> T2A peptide encoding nucleic acid

<400> 26
ggaagcggag agggcagagg aagtctgcta acatgcggtg acgtcgagga gaatcctgga
60
c c t
63

<210> 27
<211> 69
<212> DNA
<213> Artificial Sequence

<220>

<223> E2A peptide encoding nucleic acid

<400> 27

ggaagcggac agtgtactaa ttatgctctc ttgaaattgg ctggagatgt tgagagcaac
60

c c t g g a c c t
69

<210> 28

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> F2A peptide encoding nucleic acid

<400> 28

ggaagcggag tgaacagac tttgaatttt gaccttctca agttggcggg agacgtggag
60

t c c a a c c c t g g a c c t
75

<210> 29

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> P2A peptide

<400> 29

Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
1 5 10 15

Glu Glu Asn Pro Gly Pro
20

<210> 30

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> T2A peptide

<400> 30

Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu
1 5 10 15
Glu Asn Pro Gly Pro
20

<210> 31

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> E2A peptide

<400> 31

Gly Ser Gly Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly Asp
1 5 10 15
Val Glu Ser Asn Pro Gly Pro
20

<210> 32

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> F2A peptide

<400> 32

Gly Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala
1 5 10 15
Gly Asp Val Glu Ser Asn Pro Gly Pro
20 25

<210> 33

<211> 142

<212> PRT

<213> Artificial Sequence

<220>

<223> TCRalpha constant domain polypeptide

<400> 33

Pro Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser

1				5					10					15		
Lys	Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	
			20					25					30			
Thr	Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp	Lys	
		35					40					45				
Thr	Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	Ala	Val	
	50					55					60					
Ala	Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn	Asn	
65				70				75						80		
Ser	Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	Ser	Cys	
			85					90					95			
Asp	Val	Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn	Leu	Asn	
		100					105				110					
Phe	Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu	Lys	Val	
	115					120					125					
Ala	Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser			
	130					135					140					

<210> 34

<211> 177

<212> PRT

<213> Artificial Sequence

<220>

<223> TCRbeta1 constant domain polypeptide

<400> 34

Glu	Asp	Leu	Asn	Lys	Val	Phe	Pro	Pro	Glu	Val	Ala	Val	Phe	Glu	Pro	
1				5				10					15			
Ser	Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr	Leu	Val	Cys	Leu	
		20						25				30				
Ala	Thr	Gly	Phe	Phe	Pro	Asp	His	Val	Glu	Leu	Ser	Trp	Trp	Val	Asn	
	35					40					45					
Gly	Lys	Glu	Val	His	Ser	Gly	Val	Ser	Thr	Asp	Pro	Gln	Pro	Leu	Lys	
	50					55				60						
Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys	Leu	Ser	Ser	Arg	Leu	
65				70				75						80		
Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn	His	Phe	Arg	Cys	
			85					90				95				
Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu	Trp	Thr	Gln	Asp	
		100						105				110				
Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu	Ala	Trp	Gly	Arg	
	115					120					125					
Ala	Asp	Cys	Gly	Phe	Thr	Ser	Val	Ser	Tyr	Gln	Gln	Gly	Val	Leu	Ser	
	130					135					140					

Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu	Tyr	Ala
145					150					155					160
Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val	Lys	Arg	Lys	Asp
				165					170					175	

Phe

<210> 35
 <211> 1821
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TCR number 5 construct; beta chain-P2A-alpha chain

<400> 35
 atgggcttca ggctcctctg ctgtgtggcc ttttgtctcc tgggagcagg cccagtggat
 60
 tctggagtca cacaaacccc aaagcacctg atcacagcaa ctggacagcg agtgacgctg
 120
 agatgctccc ctaggtctgg agacctctct gtgtactggg accaacagag cctggaccag
 180
 ggctccagt tcctcattca gtattataat ggagaagaga gagcaaaagg aaacattctt
 240
 gaacgattct ccgcacaaca gttccctgac ttgcactctg aactaaacct gagctctctg
 300
 gagctggggg actcagcttt gtatttctgt gccagcagcg tagggcaggg gtcctcctac
 360
 gagcagtact tcggggccggg caccaggctc acggtcacag aggacctgaa aaacgtgttc
 420
 ccacccgagg tcgctgtgtt tgagccatca gaagcagaga tctcccacac ccaaaaggcc
 480
 acactgggtg gcctggccac aggcttctac cccgaccacg tggagctgag ctggtgggtg
 540
 aatgggaagg aggtgcacag tggggtcagc acagaccgc agcccctcaa ggagcagccc
 600
 gccctcaatg actccagata ctgcctgagc agccgcctga gggctctcggc caccttctgg
 660
 cagaaccccc gcaaccactt ccgctgtcaa gtccagttct acgggctctc ggagaatgac
 720
 gagtggaccc aggatagggc caaacctgtc acccagatcg tcagcgccga ggcctggggg
 780
 agagcagact gtggcttcac ctccgagtct taccagcaag gggtcctgtc tgccaccatc
 840
 ctctatgaga tcttgctagg gaaggccacc ttgtatgccg tgctggtcag tgccctcgtg
 900

ctgatggcca tgggtcaagag aaaggattcc agaggcggtt ccggagccac gaacttctct
 960
 ctgttaaagc aagcaggaga cgtggaagaa aaccccggtc ccatggagac tctcctgaaa
 1020
 gtgctttcag gcaccttggt gtggcagttg acctgggtga gaagccaaca accagtgcag
 1080
 agtcctcaag ccgtgatcct ccgagaaggg gaagatgctg tcatcaactg cagttcctcc
 1140
 aaggcctttat attctgtaca ctggtacagg cagaagcatg gtgaagcacc cgtcttcctg
 1200
 atgatattac tgaaggggtgg agaacagaag ggtcatgaaa aaatatctgc ttcatttaat
 1260
 gaaaaaaagc agcaaagctc cctgtacctt acggcctccc agctcagtta ctcaggaacc
 1320
 tactttctgcg gcacagagga agctaacgac tacaagctca gctttggagc cggaaccaca
 1380
 gtaactgtaa gagcaaatat ccagaaccct gaccctgccg tgtaccagct gagagactct
 1440
 aaatccagtg acaagtctgt ctgcctattc accgattttg attctcaaac aaatgtgtca
 1500
 caaagtaagg attctgatgt gtatatcaca gacaaaactg tgctagacat gaggtctatg
 1560
 gacttcaaga gcaacagtgc tgtggcctgg agcaacaaat ctgactttgc atgtgcaaac
 1620
 gccttcaaca acagcattat tccagaagac accttcttcc ccagcccaga aagttcctgt
 1680
 gatgtcaagc tgggtcgagaa aagctttgaa acagatacga acctaaactt tcaaaacctg
 1740
 tcagtgattg gggtccgaat cctcctcctg aaagtggccg gggtttaatct gctcatgacg
 1800
 c t g c g g c t g t g g t c c a g c t g a
 1821

<210> 36

<211> 606

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 5 construct; beta chain-P2A-alpha chain

<400> 36

Met	Gly	Phe	Arg	Leu	Leu	Cys	Cys	Val	Ala	Phe	Cys	Leu	Leu	Gly	Ala
1				5				10				15			
Gly	Pro	Val	Asp	Ser	Gly	Val	Thr	Gln	Thr	Pro	Lys	His	Leu	Ile	Thr

			20					25					30				
Ala	Thr	Gly	Gln	Arg	Val	Thr	Leu	Arg	Cys	Ser	Pro	Arg	Ser	Gly	Asp		
		35					40					45					
Leu	Ser	Val	Tyr	Trp	Tyr	Gln	Gln	Ser	Leu	Asp	Gln	Gly	Leu	Gln	Phe		
	50					55					60						
Leu	Ile	Gln	Tyr	Tyr	Asn	Gly	Glu	Glu	Arg	Ala	Lys	Gly	Asn	Ile	Leu		
65					70					75					80		
Glu	Arg	Phe	Ser	Ala	Gln	Gln	Phe	Pro	Asp	Leu	His	Ser	Glu	Leu	Asn		
				85					90					95			
Leu	Ser	Ser	Leu	Glu	Leu	Gly	Asp	Ser	Ala	Leu	Tyr	Phe	Cys	Ala	Ser		
			100					105					110				
Ser	Val	Gly	Gln	Gly	Ser	Ser	Tyr	Glu	Gln	Tyr	Phe	Gly	Pro	Gly	Thr		
		115					120					125					
Arg	Leu	Thr	Val	Thr	Glu	Asp	Leu	Lys	Asn	Val	Phe	Pro	Pro	Glu	Val		
	130					135					140						
Ala	Val	Phe	Glu	Pro	Ser	Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala		
145					150					155					160		
Thr	Leu	Val	Cys	Leu	Ala	Thr	Gly	Phe	Tyr	Pro	Asp	His	Val	Glu	Leu		
				165					170					175			
Ser	Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Ser	Thr	Asp		
			180					185					190				
Pro	Gln	Pro	Leu	Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys		
		195					200					205					
Leu	Ser	Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg		
	210					215					220						
Asn	His	Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp		
225					230					235					240		
Glu	Trp	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala		
				245					250					255			
Glu	Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Glu	Ser	Tyr	Gln		
			260					265					270				
Gln	Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys		
		275					280					285					
Ala	Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met		
	290					295					300						
Val	Lys	Arg	Lys	Asp	Ser	Arg	Gly	Gly	Ser	Gly	Ala	Thr	Asn	Phe	Ser		
305					310					315					320		
Leu	Leu	Lys	Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Glu		
				325					330					335			
Thr	Leu	Leu	Lys	Val	Leu	Ser	Gly	Thr	Leu	Leu	Trp	Gln	Leu	Thr	Trp		
			340					345					350				
Val	Arg	Ser	Gln	Gln	Pro	Val	Gln	Ser	Pro	Gln	Ala	Val	Ile	Leu	Arg		
		355					360					365					
Glu	Gly	Glu	Asp	Ala	Val	Ile	Asn	Cys	Ser	Ser	Ser	Lys	Ala	Leu	Tyr		
	370					375					380						

Ser	Val	His	Trp	Tyr	Arg	Gln	Lys	His	Gly	Glu	Ala	Pro	Val	Phe	Leu
385					390					395					400
Met	Ile	Leu	Leu	Lys	Gly	Gly	Glu	Gln	Lys	Gly	His	Glu	Lys	Ile	Ser
				405					410					415	
Ala	Ser	Phe	Asn	Glu	Lys	Lys	Gln	Gln	Ser	Ser	Leu	Tyr	Leu	Thr	Ala
			420					425					430		
Ser	Gln	Leu	Ser	Tyr	Ser	Gly	Thr	Tyr	Phe	Cys	Gly	Thr	Glu	Glu	Ala
		435					440					445			
Asn	Asp	Tyr	Lys	Leu	Ser	Phe	Gly	Ala	Gly	Thr	Thr	Val	Thr	Val	Arg
	450					455					460				
Ala	Asn	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser
465					470					475					480
Lys	Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln
			485						490					495	
Thr	Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp	Lys
		500						505					510		
Thr	Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	Ala	Val
	515						520					525			
Ala	Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn	Asn
	530					535					540				
Ser	Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	Ser	Cys
545					550					555					560
Asp	Val	Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn	Leu	Asn
			565						570					575	
Phe	Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu	Lys	Val
		580					585						590		
Ala	Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser		
	595						600					605			

<210> 37

<211> 1493

<212> DNA

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 5 construct; beta chain-P2A-alpha chain with cysteine substitutions in beta and alpha chain constant domains (partial sequence)

<400> 37

ctcaataaaa gagccacaaa cccctcactc ggcgcgccac catgggcttc agactgttgt
60
gttgcgtaggc cttttgcctt cttggagctg gacctgtgga ttctggagtt acacagaccc
120

ctaagcacct	gattacagcc	acaggacaga	gagtgaccct	gagatgtagc	cctagaagcg
180					
gagatctgag	cgtgtattgg	taccagcaga	gcctggatca	aggactccag	tttctgatcc
240					
agtactacaa	cggcgaggag	agagccaagg	gcaatattct	ggagagggtt	tctgcccagc
300					
agttccctga	tctgcactct	gaactgaacc	tgtctagcct	ggaactggga	gattctgccc
360					
tgtacttttg	tgcctctagc	gttggacagg	gcagctctta	tgagcagtac	tttggacctg
420					
gcaccagact	gacagtgaca	gaagacctga	agaacgtggt	ccccccagag	gtggccgtgt
480					
tcgagcctag	cgaggccgag	atcagccaca	cccagaaagc	caccctcgtg	tgcctggcca
540					
ccggctttta	ccccgaccac	gtggaactgt	cttggtgggt	caacggcaaa	gaggtgcaca
600					
gcggcgtctg	caccgacccc	cagcccctga	aagagcagcc	cgccctgaac	gacagccggt
660					
actgtctgag	cagcagactg	agagtgtccg	ccaccttctg	gcagaacccc	cggaaccact
720					
tcagatgcca	ggtgcagttc	tacggcctga	gcgagaacga	cgagtggacc	caggaccggg
780					
ccaagcccgt	gacccagatc	gtgtctgctg	aggcctgggg	cagagccgat	tgcggcttca
840					
ccagcgagag	ctaccagcag	ggcgtgctga	gcgccaccat	cctgtacgag	atcctgctgg
900					
gcaaggccac	cctgtacgcc	gtgctgggtgt	ccgccctggt	gctgatggcc	atggtcaagc
960					
ggaaggacag	ccggggcggt	tccggagcca	cgaacttctc	tctgttaaag	caagcaggag
1020					
acgtggaaga	aaaccccgggt	cccatggaaa	ccctgctgaa	agtgctgagc	ggaacactgt
1080					
tatggcagct	tacatgggtg	aggtctcagc	aacctgtgca	atctccacag	gccgttatcc
1140					
tgagagaagg	agaagatgcc	gtgatcaact	gctctagctc	taaagccctg	tacagcgtgc
1200					
actggtacag	acagaaacac	ggagaagctc	ccgtgttcct	gatgattctg	ctgaaaggag
1260					
gcgagcagaa	gggacacgag	aagattttctg	ccagcttcaa	cgagaagaag	cagcagtcta
1320					
gcctgtacct	gacagcttct	cagctgagct	atagcggcac	ctacttttgt	ggcacagagg
1380					
aagccaacga	ctacaaactg	agctttggag	ccggcacaac	agtgacagtt	agagccaata
1440					
tccagaaccc	cgatcctgct	gtgtaccagc	tgcgggacag	caagagcagc	gac
1493					

<210> 38
 <211> 495
 <212> PRT
 <213> Artificial Sequence

<220>

<223> codon optimized TCR number 5 construct; beta
 chain-P2A-alpha chain with cysteine substitutions
 in beta and alpha chain constant domains (partial
 sequence)

<400> 38

Lys	Ser	Pro	Gln	Pro	Leu	Thr	Arg	Arg	Ala	Thr	Met	Gly	Phe	Arg	Leu	1	5	10	15
Leu	Cys	Cys	Val	Ala	Phe	Cys	Leu	Leu	Gly	Ala	Gly	Pro	Val	Asp	Ser	20	25	30	
Gly	Val	Thr	Gln	Thr	Pro	Lys	His	Leu	Ile	Thr	Ala	Thr	Gly	Gln	Arg	35	40	45	
Val	Thr	Leu	Arg	Cys	Ser	Pro	Arg	Ser	Gly	Asp	Leu	Ser	Val	Tyr	Trp	50	55	60	
Tyr	Gln	Gln	Ser	Leu	Asp	Gln	Gly	Leu	Gln	Phe	Leu	Ile	Gln	Tyr	Tyr	65	70	75	80
Asn	Gly	Glu	Glu	Arg	Ala	Lys	Gly	Asn	Ile	Leu	Glu	Arg	Phe	Ser	Ala	85	90	95	
Gln	Gln	Phe	Pro	Asp	Leu	His	Ser	Glu	Leu	Asn	Leu	Ser	Ser	Leu	Glu	100	105	110	
Leu	Gly	Asp	Ser	Ala	Leu	Tyr	Phe	Cys	Ala	Ser	Ser	Val	Gly	Gln	Gly	115	120	125	
Ser	Ser	Tyr	Glu	Gln	Tyr	Phe	Gly	Pro	Gly	Thr	Arg	Leu	Thr	Val	Thr	130	135	140	
Glu	Asp	Leu	Lys	Asn	Val	Phe	Pro	Pro	Glu	Val	Ala	Val	Phe	Glu	Pro	145	150	155	160
Ser	Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr	Leu	Val	Cys	Leu	165	170	175	
Ala	Thr	Gly	Phe	Tyr	Pro	Asp	His	Val	Glu	Leu	Ser	Trp	Trp	Val	Asn	180	185	190	
Gly	Lys	Glu	Val	His	Ser	Gly	Val	Cys	Thr	Asp	Pro	Gln	Pro	Leu	Lys	195	200	205	
Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys	Leu	Ser	Ser	Arg	Leu	210	215	220	
Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn	His	Phe	Arg	Cys	225	230	235	240
Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu	Trp	Thr	Gln	Asp	245	250	255	

<210> 39
<211> 1813
<212> DNA
<213> Artificial Sequence

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<223> TCR number 11 construct; beta chain-P2A-alpha  
chain
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atgggcacca ggctcttctt ctatgtggcc ctttgtctgc tgtgggcagg acacagggat
60
gctggaatca cccagagccc aagatacaag atcacagaga caggaaggca ggtgaccttg
120

atgtgtcacc 180	agacttggag	ccacagctat	atgtttctggt	atcgacaaga	cctgggacat
gggctgaggc 240	tgatctatta	ctcagcagct	gctgatatta	cagataaagg	agaagtcccc
gatggctatg 300	ttgtctccag	atccaagaca	gagaatttcc	ccctcactct	ggagtcagct
acccgctccc 360	agacatctgt	gtattttctgc	gccagcagtg	acggggggcgg	gcagtacttc
gggccgggca 420	ccaggctcac	ggtcacagag	gacctgaaaa	acgtgttccc	acccgaggtc
gctgtgtttg 480	agccatcaga	agcagagatc	tcccacaccc	aaaaggccac	actgggtgtgc
ctggccacag 540	gcttctaccc	cgaccacgtg	gagctgagct	ggtgggtgaa	tgggaaggag
gtgcacagtg 600	gggtcagcac	agacccgcag	cccctcaagg	agcagcccgc	cctcaatgac
tccagatact 660	gcctgagcag	ccgcctgagg	gtctcggcca	ccttctggca	gaacccccgc
aaccacttcc 720	gctgtcaagt	ccagttctac	gggctctcgg	agaatgacga	gtggaccacg
gatagggcca 780	aacctgtcac	ccagatcgtc	agcgccgagg	cctggggtag	agcagactgt
ggcttcacct 840	ccgagtctta	ccagcaaggg	gtcctgtctg	ccaccatcct	ctatgagatc
ttgctaggga 900	aggccacctt	gtatgccgtg	ctggtcagtg	ccctcgtgct	gatggccatg
gtcaagagaa 960	aggattccag	aggcggttcc	ggagccacga	acttctctct	gttaaagcaa
gcaggagacg 1020	tggaagaaaa	ccccgggtccc	atgaaaaagc	atctgacgac	cttcttggtg
attttgtggc 1080	tttattttta	taggggggaat	ggcaaaaacc	aagtggagca	gagtcctcag
tccctgatca 1140	tcctggaggg	aaagaactgc	actcttcaat	gcaattatac	agtgagcccc
ttcagcaact 1200	taaggtggta	taagcaagat	actgggagag	gtcctgtttc	cctgacaatc
atgactttca 1260	gtgagaacac	aaagtcgaac	ggaagatata	cagcaactct	ggatgcagac
acaaagcaaa 1320	gctctctgca	catcacagcc	tcccagctca	gcgattcagc	ctcctacatc
tgtgtggtgt 1380	gggggggggga	caccgacaag	ctcatctttg	ggactgggac	cagattacaa
gtctttccaa 1440	atatccagaa	ccctgaccct	gccgtgtacc	agctgagaga	ctctaaatcc
agtgacaagt 1500	ctgtctgcct	attcaccgat	tttgattctc	aaacaaatgt	gtcacaaagt

aaggattctg atgtgtatat cacagacaaa actgctagac atgaggtcta tggacttcaa
1560
gagcaacagt gctgtggcct ggagcaacaa atctgacttt gcatgtgcaa acgccttcaa
1620
caacagcatt attccagaag acaccttctt ccccagccca gaaagttcct gtgatgtcaa
1680
gctggtcgag aaaagctttg aaacagatac gaacctaaac tttcaaaacc tgtcagtgat
1740
tgggttccga atcctcctcc tgaaagtggc cgggtttaat ctgctcatga cgctgcggct
1800
g t g g t c c a g c t g a
1813

<210> 40

<211> 531

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 11 construct; beta chain-P2A-alpha chain

<400> 40

Met	Gly	Thr	Arg	Leu	Phe	Phe	Tyr	Val	Ala	Leu	Cys	Leu	Leu	Trp	Ala	1	5	10	15
Gly	His	Arg	Asp	Ala	Gly	Ile	Thr	Gln	Ser	Pro	Arg	Tyr	Lys	Ile	Thr	20	25	30	
Glu	Thr	Gly	Arg	Gln	Val	Thr	Leu	Met	Cys	His	Gln	Thr	Trp	Ser	His	35	40	45	
Ser	Tyr	Met	Phe	Trp	Tyr	Arg	Gln	Asp	Leu	Gly	His	Gly	Leu	Arg	Leu	50	55	60	
Ile	Tyr	Tyr	Ser	Ala	Ala	Ala	Asp	Ile	Thr	Asp	Lys	Gly	Glu	Val	Pro	65	70	75	80
Asp	Gly	Tyr	Val	Val	Ser	Arg	Ser	Lys	Thr	Glu	Asn	Phe	Pro	Leu	Thr	85	90	95	
Leu	Glu	Ser	Ala	Thr	Arg	Ser	Gln	Thr	Ser	Val	Tyr	Phe	Cys	Ala	Ser	100	105	110	
Ser	Asp	Gly	Gly	Gly	Gln	Tyr	Phe	Gly	Pro	Gly	Thr	Arg	Leu	Thr	Val	115	120	125	
Thr	Glu	Asp	Leu	Lys	Asn	Val	Phe	Pro	Pro	Glu	Val	Ala	Val	Phe	Glu	130	135	140	
Pro	Ser	Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr	Leu	Val	Cys	145	150	155	160
Leu	Ala	Thr	Gly	Phe	Tyr	Pro	Asp	His	Val	Glu	Leu	Ser	Trp	Trp	Val	165	170	175	

Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Ser	Thr	Asp	Pro	Gln	Pro	Leu
			180					185					190		
Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys	Leu	Ser	Ser	Arg
		195					200					205			
Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn	His	Phe	Arg
	210					215					220				
Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu	Trp	Thr	Gln
225					230					235					240
Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu	Ala	Trp	Gly
			245						250					255	
Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Glu	Ser	Tyr	Gln	Gln	Gly	Val	Leu
			260					265					270		
Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu	Tyr
		275					280					285			
Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val	Lys	Arg	Lys
	290					295					300				
Asp	Ser	Arg	Gly	Gly	Ser	Gly	Ala	Thr	Asn	Phe	Ser	Leu	Leu	Lys	Gln
305					310					315					320
Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Lys	Lys	His	Leu	Thr
			325						330					335	
Thr	Phe	Leu	Val	Ile	Leu	Trp	Leu	Tyr	Phe	Tyr	Arg	Gly	Asn	Gly	Lys
			340					345					350		
Asn	Gln	Val	Glu	Gln	Ser	Pro	Gln	Ser	Leu	Ile	Ile	Leu	Glu	Gly	Lys
		355					360					365			
Asn	Cys	Thr	Leu	Gln	Cys	Asn	Tyr	Thr	Val	Ser	Pro	Phe	Ser	Asn	Leu
	370					375					380				
Arg	Trp	Tyr	Lys	Gln	Asp	Thr	Gly	Arg	Gly	Pro	Val	Ser	Leu	Thr	Ile
385					390					395					400
Met	Thr	Phe	Ser	Glu	Asn	Thr	Lys	Ser	Asn	Gly	Arg	Tyr	Thr	Ala	Thr
			405						410					415	
Leu	Asp	Ala	Asp	Thr	Lys	Gln	Ser	Ser	Leu	His	Ile	Thr	Ala	Ser	Gln
		420						425					430		
Leu	Ser	Asp	Ser	Ala	Ser	Tyr	Ile	Cys	Val	Val	Trp	Gly	Gly	Asp	Thr
		435					440					445			
Asp	Lys	Leu	Ile	Phe	Gly	Thr	Gly	Thr	Arg	Leu	Gln	Val	Phe	Pro	Asn
	450					455					460				
Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser	Lys	Ser
465					470					475					480
Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Thr	Asn
			485						490					495	
Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp	Lys	Thr	Ala
		500						505					510		
Arg	His	Glu	Val	Tyr	Gly	Leu	Gln	Glu	Gln	Gln	Cys	Cys	Gly	Leu	Glu
		515					520					525			
Gln	Gln	Ile	</												

<210> 41

<211> 1484

<212> DNA

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 11 construct; beta chain-P2A-alpha chain with cysteine substitutions in beta and alpha chain constant domains (partial sequence)

<400> 41

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60
tctacgttgc cttttgcctg ctgtgggctg gacatagaga tgctggaatc acacagagcc
120
ccaggtacaa gatcacagag acaggaagac aggtgaccct gatgtgtcac caaacatgga
180
gccacagcta catgtttctgg tacagacagg atctgggaca cggactgaga ctgatctact
240
attctgctgc cgccgacatc accgataaag gagaagttcc tgacggctac gtggtgtcta
300
gaagcaaaac cgagaacttc cccctgacac tggaatctgc cacaagatct cagaccagcg
360
tgtacttttg cgctctttct gatggaggag gccagtattt tccaggcaca agactgacag
420
tgaccgagga cctgaagaac gtgttcccc cagaggtggc cgtgttcgag cctagcgagg
480
ccgagatcag ccacacccag aaagccaccc tcgtgtgcct ggccaccggc ttttaccceg
540
accacgtgga actgtcttgg tgggtcaacg gcaaagaggt gcacagcggc gtctgcaccg
600
accccagcc cctgaaagag cagcccggcc tgaacgacag ccggtactgt ctgagcagca
660
gactgagagt gtccgccacc ttctggcaga acccccggaa ccacttcaga tgccaggtgc
720
agttctacgg cctgagcgag aacgacgagt ggaccagga ccgggccaag cccgtgaccc
780
agatcgtgtc tgctgaggcc tggggcagag ccgattgcgg cttcaccagc gagagctacc
840
agcagggcgt gctgagcgcc accatcctgt acgagatcct gctgggcaag gccaccctgt
900
acgccgtgct ggtgtccgcc ctggtgctga tggccatggt caagcggaag gacagccggg
960

```

gcggttccgg agccacgaac ttctctctgt taaagcaagc aggagacgtg gaagaaaacc
 1020
 ccggtcccat gaagaagcac ctgaccacgt tcctgggtgat tctttggctg tacttctacc
 1080
 ggggcaacgg caaaaatcag gtggaacaaa gccccagag cctgattatt ctggagggca
 1140
 agaactgcac cctccagtgt aattacaccg tgagcccttt cagcaacctg agatggtaca
 1200
 agcaggatac cggaagagga cctgtgtctc tgaccatcat gacctttagc gagaacacca
 1260
 agagcaacgg caggatataca gccacactgg atgccgatac caagcagtct tctctgcaca
 1320
 ttaccgcctc tcagctgtct gattctgcca gctacatctg tgtgggtgtgg ggaggagata
 1380
 ccgataagct gatctttggc acaggcacca gactgcaagt gttccctaac atccagaacc
 1440
 ctgatcctgc cgtgtaccag ctgcgggaca gcaagagcag cgac
 1484

<210> 42

<211> 492

<212> PRT

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 11 construct; beta
 chain-P2A-alpha chain with cysteine substitutions
 in beta and alpha chain constant domains (partial
 sequence)

<400> 42

Lys	Ser	Pro	Gln	Pro	Leu	Thr	Arg	Arg	Ala	Thr	Met	Gly	Thr	Arg	Leu
1				5					10					15	
Phe	Phe	Tyr	Val	Ala	Leu	Cys	Leu	Leu	Trp	Ala	Gly	His	Arg	Asp	Ala
			20					25					30		
Gly	Ile	Thr	Gln	Ser	Pro	Arg	Tyr	Lys	Ile	Thr	Glu	Thr	Gly	Arg	Gln
		35					40					45			
Val	Thr	Leu	Met	Cys	His	Gln	Thr	Trp	Ser	His	Ser	Tyr	Met	Phe	Trp
	50					55					60				
Tyr	Arg	Gln	Asp	Leu	Gly	His	Gly	Leu	Arg	Leu	Ile	Tyr	Tyr	Ser	Ala
65					70				75					80	
Ala	Ala	Asp	Ile	Thr	Asp	Lys	Gly	Glu	Val	Pro	Asp	Gly	Tyr	Val	Val
			85					90						95	
Ser	Arg	Ser	Lys	Thr	Glu	Asn	Phe	Pro	Leu	Thr	Leu	Glu	Ser	Ala	Thr
			100					105					110		

Arg	Ser	Gln	Thr	Ser	Val	Tyr	Phe	Cys	Ala	Ser	Ser	Asp	Gly	Gly	Gly	
		115					120					125				
Gln	Tyr	Phe	Pro	Gly	Thr	Arg	Leu	Thr	Val	Thr	Glu	Asp	Leu	Lys	Asn	
	130					135					140					
Val	Phe	Pro	Pro	Glu	Val	Ala	Val	Phe	Glu	Pro	Ser	Glu	Ala	Glu	Ile	
145					150					155					160	
Ser	His	Thr	Gln	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ala	Thr	Gly	Phe	Tyr	
				165					170					175		
Pro	Asp	His	Val	Glu	Leu	Ser	Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	
			180					185					190			
Ser	Gly	Val	Cys	Thr	Asp	Pro	Gln	Pro	Leu	Lys	Glu	Gln	Pro	Ala	Leu	
		195					200					205				
Asn	Asp	Ser	Arg	Tyr	Cys	Leu	Ser	Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	
	210					215					220					
Phe	Trp	Gln	Asn	Pro	Arg	Asn	His	Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	
225					230					235					240	
Gly	Leu	Ser	Glu	Asn	Asp	Glu	Trp	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	
				245					250					255		
Thr	Gln	Ile	Val	Ser	Ala	Glu	Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	
			260					265					270			
Thr	Ser	Glu	Ser	Tyr	Gln	Gln	Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	
		275					280						285			
Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	
	290					295					300					
Leu	Val	Leu	Met	Ala	Met	Val	Lys	Arg	Lys	Asp	Ser	Arg	Gly	Gly	Ser	
305					310					315					320	
Gly	Ala	Thr	Asn	Phe	Ser	Leu	Leu	Lys	Gln	Ala	Gly	Asp	Val	Glu	Glu	
				325					330					335		
Asn	Pro	Gly	Pro	Met	Lys	Lys	His	Leu	Thr	Thr	Phe	Leu	Val	Ile	Leu	
			340					345					350			
Trp	Leu	Tyr	Phe	Tyr	Arg	Gly	Asn	Gly	Lys	Asn	Gln	Val	Glu	Gln	Ser	
		355					360						365			
Pro	Gln	Ser	Leu	Ile	Ile	Leu	Glu	Gly	Lys	Asn	Cys	Thr	Leu	Gln	Cys	
		370				375					380					
Asn	Tyr	Thr	Val	Ser	Pro	Phe	Ser	Asn	Leu	Arg	Trp	Tyr	Lys	Gln	Asp	
385					390					395					400	
Thr	Gly	Arg	Gly	Pro	Val	Ser	Leu	Thr	Ile	Met	Thr	Phe	Ser	Glu	Asn	
				405					410					415		
Thr	Lys	Ser	Asn	Gly	Arg	Tyr	Thr	Ala	Thr	Leu	Asp	Ala	Asp	Thr	Lys	
			420					425					430			
Gln	Ser	Ser	Leu	His	Ile	Thr	Ala	Ser	Gln	Leu	Ser	Asp	Ser	Ala	Ser	
		435					440					445				
Tyr	Ile	Cys	Val	Val	Trp	Gly	Gly	Asp	Thr	Asp	Lys	Leu	Ile	Phe	Gly	
	450					455					460					
Thr	Gly	Thr	Arg	Leu	Gln	Val	Phe	Pro	Asn	Ile	Gln	Asn	Pro	Asp	Pro	

465		470		475		480					
Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser	Lys	Ser	Ser	Asp
				485				490			

<210> 43
 <211> 828
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TCR number 6 alpha chain

<400> 43
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 agcagcatac tgaacgtgga acaaagtcct cagtcactgc atgttcagga gggagacagc
 120
 accaatttca cctgcagctt cccttccagc aatttttatg ccttacactg gtacagatgg
 180
 gaaactgcaa aaagccccga ggccttggtt gtaatgactt taaatgggga tgaaaagaag
 240
 aaaggacgaa taagtgccac tcttaatacc aaggagggtt acagctatct gtacatcaaa
 300
 ggatcccagc ctgaagactc agccacatac ctctgtgcct tagggcctta taacgactac
 360
 aagctcagct ttggagccgg aaccacagta actgtaagag caaatatcca gaaccctgac
 420
 cctgccgtgt accagctgag agactctaaa tccagtgaca agtctgtctg cctattcacc
 480
 gattttgatt ctcaaacaaa tgtgtcacia agtaaggatt ctgatgtgta tatcacagac
 540
 aaaactgtgc tagacatgag gtctatggac ttcaagagca acagtgcctg ggcctggagc
 600
 aacaaatctg actttgcatg tgcaaacgcc ttcaacaaca gcattattcc agaagacacc
 660
 ttcttcccca gccagaaaag ttcctgtgat gtcaagctgg tcgagaaaag ctttgaaaca
 720
 gatacgaacc taaactttca aaacctgtca gtgattgggt tccgaatcct cctcctgaaa
 780
 gtggccgggt ttaatctgct catgacgctg cggctgtggt ccagctga
 828

<210> 44
 <211> 275
 <212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 6 alpha chain

<400> 44

Met	Glu	Lys	Asn	Pro	Leu	Ala	Ala	Pro	Leu	Leu	Ile	Leu	Trp	Phe	His	
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Leu	Asp	Cys	Val	Ser	Ser	Ile	Leu	Asn	Val	Glu	Gln	Ser	Pro	Gln	Ser	
			20					25					30			
Leu	His	Val	Gln	Glu	Gly	Asp	Ser	Thr	Asn	Phe	Thr	Cys	Ser	Phe	Pro	
		35				40						45				
Ser	Ser	Asn	Phe	Tyr	Ala	Leu	His	Trp	Tyr	Arg	Trp	Glu	Thr	Ala	Lys	
	50					55				60						
Ser	Pro	Glu	Ala	Leu	Phe	Val	Met	Thr	Leu	Asn	Gly	Asp	Glu	Lys	Lys	
65					70					75					80	
Lys	Gly	Arg	Ile	Ser	Ala	Thr	Leu	Asn	Thr	Lys	Glu	Gly	Tyr	Ser	Tyr	
			85					90						95		
Leu	Tyr	Ile	Lys	Gly	Ser	Gln	Pro	Glu	Asp	Ser	Ala	Thr	Tyr	Leu	Cys	
			100					105					110			
Ala	Leu	Gly	Pro	Tyr	Asn	Asp	Tyr	Lys	Leu	Ser	Phe	Gly	Ala	Gly	Thr	
		115					120					125				
Thr	Val	Thr	Val	Arg	Ala	Asn	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	
	130					135					140					
Gln	Leu	Arg	Asp	Ser	Lys	Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	
145					150					155					160	
Asp	Phe	Asp	Ser	Gln	Thr	Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	
			165					170						175		
Tyr	Ile	Thr	Asp	Lys	Thr	Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	
			180					185					190			
Ser	Asn	Ser	Ala	Val	Ala	Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	
		195					200					205				
Asn	Ala	Phe	Asn	Asn	Ser	Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	
	210					215					220					
Pro	Glu	Ser	Ser	Cys	Asp	Val	Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	
225					230					235					240	
Asp	Thr	Asn	Leu	Asn	Phe	Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	
			245					250						255		
Leu	Leu	Leu	Lys	Val	Ala	Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	
			260					265						270		
Trp	Ser	Ser														
		275														

<210> 45

<211> 936

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR number 6 beta chain

<400> 45

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120
cagtgtaccc aggatatgaa ccataactac atgtactggt atcgacaaga cccaggcatg
180
gggctgaagc tgatttatta ttcagttggt gctggtatca ctgataaagg agaagtcccg
240
aatggctaca acgtctccag atcaaccaca gaggatttcc cgctcaggct ggagttggct
300
gctccctccc agacatctgt gtacttctgt gccagcagtg acaggtctaa caccggggag
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420
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480
ctggtgtgcc tggccacagg cttctacccc gaccacgtgg agctgagctg gtgggtgaat
540
gggaaggagg tgcacagtgg ggtcagcaca gaccgcagc ccctcaagga gcagcccgcc
600
ctcaatgact ccagatactg cctgagcagc cgcctgaggg tctcggccac cttctggcag
660
aacccccgca accacttccg ctgtcaagtc cagttctacg ggctctcgga gaatgacgag
720
tggaaccagg atagggccaa acctgtcacc cagatcgtca gcgccgaggc ctggggtaga
780
gcagactgtg gcttcacctc cgagtcttac cagcaagggg tcctgtctgc caccatcctc
840
tatgagatct tgctagggaa ggccaccttg tatgccgtgc tggtcagtgc cctcgtgctg
900
a t g g c c a t g g          t c a a g a g a a a          g g a t t c c a g a          g g c t a g
936
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<210> 46

<211> 311

<212> PRT

<213> Artificial Sequence

<210> 47
<211> 1499
<212> DNA
<213> Artificial Sequence

<220>

<223> codon optimized TCR number 6 construct; beta chain-P2A-alpha chain with cysteine substitutions in beta and alpha chain constant domains (partial sequence)

<400> 47

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60					
gctgtgcagc	ctttcctctc	ctgtgggcag	gtccagtgaa	tgctggtgtc	actcagaccc
120					
caaaattccg	catcctgaag	ataggacaga	gcatgacact	gcagtgtacc	caggatatga
180					
accataacta	catgtactgg	tatcgacaag	accagggcat	ggggctgaag	ctgatttatt
240					
attcagttgg	tgctggtatc	actgataaag	gagaagtccc	gaatggctac	aacgtctcca
300					
gatcaaccac	agaggatttc	ccgctcaggc	tggagttggc	tgctccctcc	cagacatctg
360					
tgtacttctg	tgccagcagt	gacaggtcta	acaccgggga	gctgtttttt	ggagaaggct
420					
ctaggctgac	cgtactggag	gacctgaaaa	acgtgttccc	acccgaggtc	gctgtgtttg
480					
agccatcaga	agcagagatc	tcccacaccc	aaaaggccac	actggtgtgc	ctggccacag
540					
gcttctaccc	cgaccacgtg	gagctgagct	gggtgggtgaa	tgggaaggag	gtgcacagtg
600					
gggtcagcac	agaccgcag	cccctcaagg	agcagcccgc	cctcaatgac	tccagatact
660					
gcctgagcag	ccgcctgagg	gtctcggcca	ccttctggca	gaacccccgc	aaccacttcc
720					
gctgtcaagt	ccagttctac	gggctctcgg	agaatgacga	gtggacccag	gatagggcca
780					
aacctgtcac	ccagatcgtc	agcgccgagg	cctggggtag	agcagactgt	ggcttcacct
840					
ccgagtctta	ccagcaaggg	gtcctgtctg	ccaccatcct	ctatgagatc	ttgctagggg
900					
aggccacctt	gtatgccgtg	ctggtcagtg	ccctcgtgct	gatggccatg	gtcaagagaa
960					
aggattccag	aggcggttcc	ggagccacga	acttctctct	gttaaagcaa	gcaggagacg
1020					

tggaagaaaa	ccccggtccc	atggagaaga	atcctttggc	agccccatta	ctaatacctct
1080					
ggtttcatct	tgactgcgtg	agcagcatac	tgaacgtgga	acaaagtcct	cagtcactgc
1140					
atgttcagga	gggagacagc	accaatttca	cctgcagctt	cccttccagc	aatttttatg
1200					
ccttacactg	gtacagatgg	gaaactgcaa	aaagccccga	ggccttgttt	gtaatgactt
1260					
taaatgggga	tgaaaagaag	aaaggacgaa	taagtgccac	tcttaatacc	aaggagggtt
1320					
acagctattt	gtacatcaaa	ggatcccagc	ctgaagactc	agccacatac	ctctgtgcct
1380					
tagggcctta	taacgactac	aagctcagct	ttggagccgg	aaccacagta	actgtaagag
1440					
caaatatcca	gaaccctgac	cctgccgtgt	accagctgcg	ggacagcaag	agcagcgac
1499					

<210> 48

<211> 1815

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR number 1 construct; beta chain-P2A-alpha chain

<400> 48

atgggccccg	ggctcctctg	ctgggcactg	ctttgtctcc	tgggagcagg	cttagtggac
60					
gctggagtca	cccaaagtcc	cacacacctg	atcaaaacga	gaggacagca	agtgactctg
120					
agatgctctc	ctaagtctgg	gcatgacact	gtgtcctggg	accaacaggc	cctgggtcag
180					
gggccccagt	ttatctttca	gtattatgag	gaggaagaga	gacagagagg	caacttcctt
240					
gatcgattct	caggtcacca	gttccctaac	tatagctctg	agctgaatgt	gaacgccttg
300					
ttgctggggg	actcggccct	ctatctctgt	gccagcagct	tcttcagcca	agagaccag
360					
tacttcgggc	caggcacgcg	gctcctgggt	ctcgaggacc	tgaaaaacgt	gttcccaccc
420					
gaggctcgctg	tgtttgagcc	atcagaagca	gagatctccc	acacccaaaa	ggccacactg
480					
gtgtgcctgg	ccacaggctt	ctacccccgac	cacgtggagc	tgagctgggtg	ggatgaatggg
540					
aaggaggtgc	acagtggggg	cagcacagac	ccgcagcccc	tcaaggagca	gccccccctc
600					

aatgactcca	gatactgcct	gagcagccgc	ctgaggggtct	cggccacctt	ctggcagaac
660					
ccccgcaacc	acttccgctg	tcaagtccag	ttctacgggc	tctcggagaa	tgacgagtgg
720					
accagagata	gggccaaacc	tgtcaccag	atcgtcagcg	ccgaggcctg	gggtagagca
780					
gactgtggct	tcacctccga	gtcttaccag	caaggggtcc	tgtctgccac	catcctctat
840					
gagatcttgc	tagggaaggc	caccttgtat	gccgtgctgg	tcagtgccct	cgtgctgatg
900					
gccatgggtca	agagaaagga	ttccagaggc	ggttccggag	ccacgaactt	ctctctgtta
960					
aagcaagcag	gagacgtgga	agaaaacccc	gggtcccatgg	agaccctctt	gggcctgctt
1020					
atcctttggc	tgacgtgca	atgggtgagc	agcaaacagg	aggtgacaca	gattcctgca
1080					
gctctgagtg	tcccagaagg	agaaaacttg	gttctcaact	gcagtttcac	tgatagcgct
1140					
atttacaacc	tccagtgggt	taggcaggac	cctgggaaag	gtctcacatc	tctgttgctt
1200					
attcagtcaa	gtcagagaga	gcaaacaagt	ggaagactta	atgcctcgct	ggataaatca
1260					
tcaggacgta	gtactttata	cattgcagct	tctcagcctg	gtgactcagc	cacctacctc
1320					
tgtgccgtgg	agggggatag	cagctataaa	ttgatcttcg	ggagtgggac	cagactgctg
1380					
gtcaggcctg	atatccagaa	ccctgaccct	gccgtgtacc	agctgagaga	ctctaaatcc
1440					
agtgacaagt	ctgtctgcct	attcaccgat	tttgattctc	aaacaaatgt	gtcacaaagt
1500					
aaggattctg	atgtgtatat	cacagacaaa	actgtgctag	acatgagggtc	tatggacttc
1560					
aagagcaaca	gtgctgtggc	ctggagcaac	aaatctgact	ttgcatgtgc	aaacgccttc
1620					
aacaacagca	ttattccaga	agacaccttc	ttccccagcc	cagaaagttc	ctgtgatgtc
1680					
aagctgggtcg	agaaaagctt	tgaaacagat	acgaacctaa	actttcaaaa	cctgtcagtg
1740					
attggggttcc	gaatcctcct	cctgaaagtg	gccgggttta	atctgctcat	gacgctgcgg
1800					
c t g t g g t c c a					g c t g a
1815					

<210> 49

<211> 604

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 1 construct; beta chain-P2A-alpha chain

<400> 49

Met	Gly	Pro	Gly	Leu	Leu	Cys	Trp	Ala	Leu	Leu	Cys	Leu	Leu	Gly	Ala	
1				5					10					15		
Gly	Leu	Val	Asp	Ala	Gly	Val	Thr	Gln	Ser	Pro	Thr	His	Leu	Ile	Lys	
			20					25					30			
Thr	Arg	Gly	Gln	Gln	Val	Thr	Leu	Arg	Cys	Ser	Pro	Lys	Ser	Gly	His	
		35					40					45				
Asp	Thr	Val	Ser	Trp	Tyr	Gln	Gln	Ala	Leu	Gly	Gln	Gly	Pro	Gln	Phe	
	50					55					60					
Ile	Phe	Gln	Tyr	Tyr	Glu	Glu	Glu	Glu	Arg	Gln	Arg	Gly	Asn	Phe	Pro	
65					70					75					80	
Asp	Arg	Phe	Ser	Gly	His	Gln	Phe	Pro	Asn	Tyr	Ser	Ser	Glu	Leu	Asn	
				85					90					95		
Val	Asn	Ala	Leu	Leu	Leu	Gly	Asp	Ser	Ala	Leu	Tyr	Leu	Cys	Ala	Ser	
			100						105				110			
Ser	Phe	Phe	Ser	Gln	Glu	Thr	Gln	Tyr	Phe	Gly	Pro	Gly	Thr	Arg	Leu	
		115					120					125				
Leu	Val	Leu	Glu	Asp	Leu	Lys	Asn	Val	Phe	Pro	Pro	Glu	Val	Ala	Val	
	130					135					140					
Phe	Glu	Pro	Ser	Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr	Leu	
145					150					155					160	
Val	Cys	Leu	Ala	Thr	Gly	Phe	Tyr	Pro	Asp	His	Val	Glu	Leu	Ser	Trp	
				165					170					175		
Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Ser	Thr	Asp	Pro	Gln	
			180						185				190			
Pro	Leu	Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys	Leu	Ser	
	195						200					205				
Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn	His	
	210					215					220					
Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu	Trp	
225					230					235					240	
Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu	Ala	
				245					250					255		
Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Glu	Ser	Tyr	Gln	Gln	Gly	
			260					265					270			
Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	
	275						280					285				
Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val	Lys	
	290					295					300					

Arg	Lys	Asp	Ser	Arg	Gly	Gly	Ser	Gly	Ala	Thr	Asn	Phe	Ser	Leu	Leu
305					310					315					320
Lys	Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Glu	Thr	Leu
				325					330						335
Leu	Gly	Leu	Leu	Ile	Leu	Trp	Leu	Gln	Leu	Gln	Trp	Val	Ser	Ser	Lys
			340					345					350		
Gln	Glu	Val	Thr	Gln	Ile	Pro	Ala	Ala	Leu	Ser	Val	Pro	Glu	Gly	Glu
		355					360					365			
Asn	Leu	Val	Leu	Asn	Cys	Ser	Phe	Thr	Asp	Ser	Ala	Ile	Tyr	Asn	Leu
	370					375					380				
Gln	Trp	Phe	Arg	Gln	Asp	Pro	Gly	Lys	Gly	Leu	Thr	Ser	Leu	Leu	Leu
385					390					395					400
Ile	Gln	Ser	Ser	Gln	Arg	Glu	Gln	Thr	Ser	Gly	Arg	Leu	Asn	Ala	Ser
				405					410						415
Leu	Asp	Lys	Ser	Ser	Gly	Arg	Ser	Thr	Leu	Tyr	Ile	Ala	Ala	Ser	Gln
			420					425					430		
Pro	Gly	Asp	Ser	Ala	Thr	Tyr	Leu	Cys	Ala	Val	Glu	Gly	Asp	Ser	Ser
		435					440					445			
Tyr	Lys	Leu	Ile	Phe	Gly	Ser	Gly	Thr	Arg	Leu	Leu	Val	Arg	Pro	Asp
	450					455					460				
Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser	Lys	Ser
465					470					475					480
Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Thr	Asn
				485					490					495	
Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp	Lys	Thr	Val
			500					505					510		
Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	Ala	Val	Ala	Trp
		515					520					525			
Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn	Asn	Ser	Ile
	530					535					540				
Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	Ser	Cys	Asp	Val
545					550					555					560
Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn	Leu	Asn	Phe	Gln
				565					570					575	
Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu	Lys	Val	Ala	Gly
			580					585					590		
Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser				
		595					600								

<210> 50

<211> 1487

<212> DNA

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 1 construct; beta
chain-P2A-alpha chain with cysteine substitutions
in beta and alpha chain constant domains (partial
sequence)

<400> 50

ctcaataaaa	gagcccacaa	cccctcactc	ggcgcgccac	catgggacct	ggactgcttt
60					
gttgggctct	tctgtgtctg	cttggagctg	gactgggtga	tgctggagtt	acacagagcc
120					
ctacacacct	gatcaagaca	agaggacagc	aggtgaccct	gagatgtagc	cctaaatctg
180					
gccacgatac	cgtgagctgg	tatcaacagg	ctctgggaca	aggacctcag	ttcatcttcc
240					
agtactacga	ggaggaggag	agacagagag	gcaatttccc	tgacaggttt	agcggacacc
300					
agttcccaa	ttacagctct	gagctgaacg	tgaatgccct	tcttctggga	gattctgccc
360					
tgtatctgtg	tgccagcagc	ttcttttagcc	aggaaaccca	gtacttcggc	ccaggaacaa
420					
gactgctggg	tcttgaagac	ctgaagaacg	tggtccccc	agagggtggc	gtgttcgagc
480					
ctagcgaggc	cgagatcagc	cacacccaga	aagccaccct	cgtgtgcctg	gccaccggct
540					
tttaccgccg	ccacgtggaa	ctgtcttggg	gggtcaacgg	caaagagggtg	cacagcggcg
600					
tctgcaccga	ccccagccc	ctgaaagagc	agcccgccct	gaacgacagc	cgggtactgtc
660					
tgagcagcag	actgagagtg	tccgccacct	tctggcagaa	cccccggaac	cacttcagat
720					
gccaggtgca	gttctacggc	ctgagcgaga	acgacgagtg	gaccaggagc	cgggccaagc
780					
ccgtgaccga	gatcgtgtct	gctgaggcct	ggggcagagc	cgattgcggc	ttcaccagcg
840					
agagctacca	gcagggcggtg	ctgagcgcca	ccatcctgta	cgagatcctg	ctgggcaagg
900					
ccaccctgta	cgccgtgctg	gtgtccgccc	tggtgctgat	ggccatgggtc	aagcggaagg
960					
acagccgggg	cggttccgga	gccacgaact	tctctctgtt	aaagcaagca	ggagacgtgg
1020					
aagaaaaccc	cgggtcccatg	gaaaccctgt	taggcctgct	cattctgtgg	ttacagctcc
1080					
aatgggtgag	cagcaaacag	gaagtgaccc	agattcctgc	tgccttatct	gtgcctgaag
1140					
gcgaaaatct	ggtgctgaat	tgcagcttca	ccgattctgc	catctacaac	ctccagtggg
1200					

tcagacagga tccaggaaaa ggcctgacat ctcttctgct gatccagtct agccagagag
1260
agcagacaag cggaagactg aatgcctctc tggacaagag cagcgggaaga tctaccctgt
1320
atattgccgc ctctcagcct ggagattctg ccacatatct gtgtgccgtg gagggagata
1380
gcagctataa gctgatcttc ggcagcggca caagattact ggtgagacct gacatccaga
1440
accctgatcc tgctgtgtac cagctgcggg acagcaagag cagcgac
1487

<210> 51

<211> 493

<212> PRT

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 1 construct; beta
chain-P2A-alpha chain with cysteine substitutions
in beta and alpha chain constant domains (partial
sequence)

<400> 51

Lys	Ser	Pro	Gln	Pro	Leu	Thr	Arg	Arg	Ala	Thr	Met	Gly	Pro	Gly	Leu
1				5					10					15	
Leu	Cys	Trp	Ala	Leu	Leu	Cys	Leu	Leu	Gly	Ala	Gly	Leu	Val	Asp	Ala
			20					25					30		
Gly	Val	Thr	Gln	Ser	Pro	Thr	His	Leu	Ile	Lys	Thr	Arg	Gly	Gln	Gln
		35					40					45			
Val	Thr	Leu	Arg	Cys	Ser	Pro	Lys	Ser	Gly	His	Asp	Thr	Val	Ser	Trp
	50					55					60				
Tyr	Gln	Gln	Ala	Leu	Gly	Gln	Gly	Pro	Gln	Phe	Ile	Phe	Gln	Tyr	Tyr
65					70				75					80	
Glu	Glu	Glu	Glu	Arg	Gln	Arg	Gly	Asn	Phe	Pro	Asp	Arg	Phe	Ser	Gly
				85				90						95	
His	Gln	Phe	Pro	Asn	Tyr	Ser	Ser	Glu	Leu	Asn	Val	Asn	Ala	Leu	Leu
			100					105					110		
Leu	Gly	Asp	Ser	Ala	Leu	Tyr	Leu	Cys	Ala	Ser	Ser	Phe	Phe	Ser	Gln
		115					120					125			
Glu	Thr	Gln	Tyr	Phe	Gly	Pro	Gly	Thr	Arg	Leu	Leu	Val	Leu	Glu	Asp
	130				135						140				
Leu	Lys	Asn	Val	Phe	Pro	Pro	Glu	Val	Ala	Val	Phe	Glu	Pro	Ser	Glu
145					150				155					160	
Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ala	Thr
				165				170						175	

<210>	52
<211>	813
<212>	DNA
<213>	Artificial Sequence

<213> Artificial Sequence

<220>

<223> TCR number 2 alpha chain

<400> 52

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atggagaccc tcttgggcct gcttatcctt tggtgcagc tgcaatgggt gagcagcaaa
60
caggaggtga cgcagattcc tgcagctctg agtgtcccag aaggagaaaa cttgggttctc
120
aactgcagtt tcaactgatag cgctatttac aacctccagt ggtttaggca ggaccctggg
180
aaaggtctca catctctgtt gcttattcag tcaagtcaga gagagcaaac aagtggaaga
240
cttaatgcct cgctggataa atcatcagga cgtagtactt tatacattgc agctttctcag
300
cctgggtgact cagccaccta cctctgtgct gtgatcggcg aacagaattt tgtctttggt
360
cccggaacca gattgtccgt gctgccctat atccagaacc ctgaccctgc cgtgtaccag
420
ctgagagact ctaaattccag tgacaagtct gtctgcctat tcaccgattt tgatttctcaa
480
acaaatgtgt cacaaagtaa ggattctgat gtgtatatca cagacaaaac tgtgctagac
540
atgaggtcta tggacttcaa gagcaacagt gctgtggcct ggagcaacaa atctgacttt
600
gcatgtgcaa acgccttcaa caacagcatt attccagaag acaccttctt cccagccca
660
gaaagttcct gtgatgtcaa gctggtcgag aaaagctttg aaacagatac gaacctaaac
720
tttcaaaacc tgtcagtgat tgggttccga atcctcctcc tgaaagtggc cgggtttaat
780
c t g c t c a t g a          c g c t g c g g c t          g t g g t c c a g c          t g a
813
```

<210> 53

<211> 270

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 2 alpha chain

<400> 53

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Met Glu Thr Leu Leu Gly Leu Leu Ile Leu Trp Leu Gln Leu Gln Trp
  1                   5                   10                   15
```

Val	Ser	Ser	Lys	Gln	Glu	Val	Thr	Gln	Ile	Pro	Ala	Ala	Leu	Ser	Val
			20					25					30		
Pro	Glu	Gly	Glu	Asn	Leu	Val	Leu	Asn	Cys	Ser	Phe	Thr	Asp	Ser	Ala
		35					40					45			
Ile	Tyr	Asn	Leu	Gln	Trp	Phe	Arg	Gln	Asp	Pro	Gly	Lys	Gly	Leu	Thr
	50					55					60				
Ser	Leu	Leu	Leu	Ile	Gln	Ser	Ser	Gln	Arg	Glu	Gln	Thr	Ser	Gly	Arg
65					70					75				80	
Leu	Asn	Ala	Ser	Leu	Asp	Lys	Ser	Ser	Gly	Arg	Ser	Thr	Leu	Tyr	Ile
			85						90					95	
Ala	Ala	Ser	Gln	Pro	Gly	Asp	Ser	Ala	Thr	Tyr	Leu	Cys	Ala	Val	Ile
			100					105					110		
Gly	Glu	Gln	Asn	Phe	Val	Phe	Gly	Pro	Gly	Thr	Arg	Leu	Ser	Val	Leu
		115					120					125			
Pro	Tyr	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser
	130					135					140				
Lys	Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln
145					150					155					160
Thr	Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp	Lys
			165						170					175	
Thr	Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	Ala	Val
			180					185						190	
Ala	Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn	Asn
		195					200					205			
Ser	Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	Ser	Cys
	210					215					220				
Asp	Val	Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn	Leu	Asn
225					230					235					240
Phe	Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu	Lys	Val
			245						250					255	
Ala	Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser		
			260					265					270		

<210> 54

<211> 948

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR number 2 beta chain

<400> 54

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atgggcacca ggctcctctg ctgggcagcc ctgtgcctcc tgggggcaga tcacacaggt
60
gctggagtct cccagacccc cagtaacaag gtcacagaga agggaaaata tgtagagctc
120

```

```

aggtgtgatc caatttcagg tcatactgcc ctttactggg accgacaaag cctggggcag
180
ggcccagagt ttctaattta cttccaaggc acgggtgcgg cagatgactc agggctgccc
240
aacgatcggg tctttgcagt caggcctgag ggatccgtct ctactctgaa gatccagcgc
300
acagagcggg gggactcagc cgtgtatctc tgtgccagca gcttaagtgg gttaggctct
360
ggggccaacg tcctgacttt cggggccggc agcaggctga ccgtgctgga ggacctgaaa
420
aacgtgttcc cacccgaggt cgctgtgttt gagccatcag aagcagagat ctcccacacc
480
caaaaggcca cactgggtgtg cctggccaca ggcttctacc ccgaccacgt ggagctgagc
540
tggtgggtga atgggaagga ggtgcacagt ggggtcagca cagaccgcga gccctcaag
600
gagcagcccg ccctcaatga ctccagatac tgcctgagca gccgcctgag ggtctcggcc
660
accttctggc agaacccccg caaccacttc cgctgtcaag tccagttcta cgggctctcg
720
gagaatgacg agtggacca ggatagggcc aaacctgtca cccagatcgt cagcgccgag
780
gcctggggta gagcagactg tggcttcacc tccgagtctt accagcaagg ggtcctgtct
840
gccaccatcc tctatgagat cttgctaggg aaggccacct tgtatgccgt gctggtcagt
900
gccctcgtgc tgatggccat ggtcaagaga aaggattcca gaggctag
948

```

<210> 55

<211> 315

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 2 beta chain

<400> 55

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Met Gly Thr Arg Leu Leu Cys Trp Ala Ala Leu Cys Leu Leu Gly Ala
 1             5             10             15
Asp His Thr Gly Ala Gly Val Ser Gln Thr Pro Ser Asn Lys Val Thr
          20             25             30
Glu Lys Gly Lys Tyr Val Glu Leu Arg Cys Asp Pro Ile Ser Gly His
          35             40             45
Thr Ala Leu Tyr Trp Tyr Arg Gln Ser Leu Gly Gln Gly Pro Glu Phe

```

50						55					60				
Leu	Ile	Tyr	Phe	Gln	Gly	Thr	Gly	Ala	Ala	Asp	Asp	Ser	Gly	Leu	Pro
65					70					75					80
Asn	Asp	Arg	Phe	Phe	Ala	Val	Arg	Pro	Glu	Gly	Ser	Val	Ser	Thr	Leu
				85					90					95	
Lys	Ile	Gln	Arg	Thr	Glu	Arg	Gly	Asp	Ser	Ala	Val	Tyr	Leu	Cys	Ala
			100					105					110		
Ser	Ser	Leu	Ser	Gly	Leu	Gly	Ser	Gly	Ala	Asn	Val	Leu	Thr	Phe	Gly
		115					120					125			
Ala	Gly	Ser	Arg	Leu	Thr	Val	Leu	Glu	Asp	Leu	Lys	Asn	Val	Phe	Pro
	130					135					140				
Pro	Glu	Val	Ala	Val	Phe	Glu	Pro	Ser	Glu	Ala	Glu	Ile	Ser	His	Thr
145					150				155					160	
Gln	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ala	Thr	Gly	Phe	Tyr	Pro	Asp	His
			165					170						175	
Val	Glu	Leu	Ser	Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val
		180						185					190		
Ser	Thr	Asp	Pro	Gln	Pro	Leu	Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser
		195					200					205			
Arg	Tyr	Cys	Leu	Ser	Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln
	210					215					220				
Asn	Pro	Arg	Asn	His	Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser
225					230					235				240	
Glu	Asn	Asp	Glu	Trp	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile
			245					250					255		
Val	Ser	Ala	Glu	Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Glu
		260					265						270		
Ser	Tyr	Gln	Gln	Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu
		275					280					285			
Leu	Gly	Lys	Ala	Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu
	290					295					300				
Met	Ala	Met	Val	Lys	Arg	Lys	Asp	Ser	Arg	Gly					
305					310					315					

<210> 56

<211> 1496

<212> DNA

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 2 construct; beta chain-P2A-alpha chain with cysteine substitutions in beta and alpha chain constant domains (partial sequence)

<400> 56

ctcaataaaa	gagcccacaa	cccctcactc	ggcgcgccac	catgggcacc	agactgctgt
60					
gttgggctgc	tctgtgtctg	ctgggagccg	atcatacagg	tgccggtgtc	agccagacac
120					
ctagcaacaa	agtgaccgag	aagggcaaat	acgtggaact	gagatgcgac	cccatcagcg
180					
gacacacagc	cctgtactgg	tacagacagt	ctctcggcca	gggacctgag	ttcctgatct
240					
acttccaagg	caccggcgct	gccgatgata	gcggcctgcc	taacgataga	ttcttcgccg
300					
tcagaccgga	gggcagcgtg	tccacactga	agatccagag	aaccgagagg	ggcgacagcg
360					
ccgtgtatct	gtgtgcctct	tctctgtctg	gcctcggctc	tggcgctaac	gtgctgacat
420					
ttggcgccgg	aagcagactg	accgtgctgg	aagatctgaa	gaacgtgttc	ccacctgagg
480					
tggccgtgtt	cgagccttct	gaggccgaga	tcagccacac	acagaaagcc	acactcgtgt
540					
gtctggccac	cggcttctat	cccgaccatg	tggaactgtc	ttggtgggtc	aacggcaaag
600					
aggtgcacag	cggcgtctgt	acagatcccc	agcctctgaa	agaacagccc	gctctgaacg
660					
acagccggta	ctgtctgtcc	tccagactga	gagtgtccgc	caccttctgg	cagaacccca
720					
gaaaccactt	cagatgccag	gtgcagttct	acggcctgag	cgagaacgat	gagtggaccc
780					
aggatagagc	caagcctgtg	acacagatcg	tgtctgccga	agcctggggc	agagccgatt
840					
gtggctttac	cagcgagagc	taccagcagg	gcgtgctgtc	tgccacaatc	ctgtacgaga
900					
tcctgctggg	caaagccact	ctgtacgccg	tgctgggtgtc	tgccctgggtg	ctgatggcca
960					
tgggtcaagcg	gaaggacagc	agaggcggtt	ccggagccac	gaacttctct	ctgttaaagc
1020					
aagcaggaga	cgtggaagaa	aaccccggtc	ccatggaaac	actgctgggc	ctgctgatcc
1080					
tgtggctgca	actgcaatgg	gtgtccagca	agcaagaagt	gacacagatc	cctgccgctc
1140					
tgtctgtgcc	tgagggcgaa	aacctgggtg	tgaactgcag	cttcaccgac	agcgccatct
1200					
acaacctgca	gtggttcaga	caggaccccc	gcaagggact	gacaagcctg	ctgctgattc
1260					
agagcagcca	gagagagcag	accagcggca	gactgaatgc	cagcctggat	aagtcctccg
1320					

gcagaagcac cctgtatatc gccgcttctc agcctggcga tagcgccaca tatctgtgtg
1380
ccgtgatcgg cgagcagaac ttcgtgtttg gccctggcac aagactgagc gtgctgccct
1440
acattcagaa ccccgatcct gccgtgtacc agctgcggga cagcaagagc agcgac
1496

<210> 57

<211> 496

<212> PRT

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 2 construct; beta
chain-P2A-alpha chain with cysteine substitutions
in beta and alpha chain constant domains (partial
sequence)

<400> 57

Lys	Ser	Pro	Gln	Pro	Leu	Thr	Arg	Arg	Ala	Thr	Met	Gly	Thr	Arg	Leu
1				5					10					15	
Leu	Cys	Trp	Ala	Ala	Leu	Cys	Leu	Leu	Gly	Ala	Asp	His	Thr	Gly	Ala
			20					25					30		
Gly	Val	Ser	Gln	Thr	Pro	Ser	Asn	Lys	Val	Thr	Glu	Lys	Gly	Lys	Tyr
		35					40					45			
Val	Glu	Leu	Arg	Cys	Asp	Pro	Ile	Ser	Gly	His	Thr	Ala	Leu	Tyr	Trp
	50					55					60				
Tyr	Arg	Gln	Ser	Leu	Gly	Gln	Gly	Pro	Glu	Phe	Leu	Ile	Tyr	Phe	Gln
65					70				75					80	
Gly	Thr	Gly	Ala	Ala	Asp	Asp	Ser	Gly	Leu	Pro	Asn	Asp	Arg	Phe	Phe
				85					90					95	
Ala	Val	Arg	Pro	Glu	Gly	Ser	Val	Ser	Thr	Leu	Lys	Ile	Gln	Arg	Thr
			100					105					110		
Glu	Arg	Gly	Asp	Ser	Ala	Val	Tyr	Leu	Cys	Ala	Ser	Ser	Leu	Ser	Gly
		115					120					125			
Leu	Gly	Ser	Gly	Ala	Asn	Val	Leu	Thr	Phe	Gly	Ala	Gly	Ser	Arg	Leu
	130					135					140				
Thr	Val	Leu	Glu	Asp	Leu	Lys	Asn	Val	Phe	Pro	Pro	Glu	Val	Ala	Val
145					150				155					160	
Phe	Glu	Pro	Ser	Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr	Leu
				165					170					175	
Val	Cys	Leu	Ala	Thr	Gly	Phe	Tyr	Pro	Asp	His	Val	Glu	Leu	Ser	Trp
			180					185					190		
Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Cys	Thr	Asp	Pro	Gln
		195					200					205			

Pro	Leu	Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys	Leu	Ser	210	215	220
Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn	His	225	230	235
Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu	Trp	245	250	255
Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu	Ala	260	265	270
Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Glu	Ser	Tyr	Gln	Gln	Gly	275	280	285
Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	290	295	300
Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val	Lys	305	310	315
Arg	Lys	Asp	Ser	Arg	Gly	Gly	Ser	Gly	Ala	Thr	Asn	Phe	Ser	Leu	Leu	325	330	335
Lys	Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Glu	Thr	Leu	340	345	350
Leu	Gly	Leu	Leu	Ile	Leu	Trp	Leu	Gln	Leu	Gln	Trp	Val	Ser	Ser	Lys	355	360	365
Gln	Glu	Val	Thr	Gln	Ile	Pro	Ala	Ala	Leu	Ser	Val	Pro	Glu	Gly	Glu	370	375	380
Asn	Leu	Val	Leu	Asn	Cys	Ser	Phe	Thr	Asp	Ser	Ala	Ile	Tyr	Asn	Leu	385	390	395
Gln	Trp	Phe	Arg	Gln	Asp	Pro	Gly	Lys	Gly	Leu	Thr	Ser	Leu	Leu	Leu	405	410	415
Ile	Gln	Ser	Ser	Gln	Arg	Glu	Gln	Thr	Ser	Gly	Arg	Leu	Asn	Ala	Ser	420	425	430
Leu	Asp	Lys	Ser	Ser	Gly	Arg	Ser	Thr	Leu	Tyr	Ile	Ala	Ala	Ser	Gln	435	440	445
Pro	Gly	Asp	Ser	Ala	Thr	Tyr	Leu	Cys	Ala	Val	Ile	Gly	Glu	Gln	Asn	450	455	460
Phe	Val	Phe	Gly	Pro	Gly	Thr	Arg	Leu	Ser	Val	Leu	Pro	Tyr	Ile	Gln	465	470	475
Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser	Lys	Ser	Ser	Asp	485	490	495

<210> 58

<211> 825

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR number 3 alpha chain

<400> 58

```
atgatgaaat ccttgagagt tttactagtg atcctgtggc ttcagttgag ctgggtttgg
60
agccaacaga aggaggtgga gcagaattct ggaccctca gtgttccaga gggagccatt
120
gcctctctca actgcactta cagtgaccga ggttcccagt ccttcttctg gtacagacaa
180
tattctggga aaagccctga gttgataatg tccatatact ccaatgggtga caaagaagat
240
ggaaggttta cagcacagct caataaagcc agccagtatg tttctctgct catcagagac
300
tcccagccca gtgattcagc cacctacctc tgtgccgtcg attctggggg ttaccagaaa
360
gttacctttg gaactggaac aaagctccaa gtcaccccaa atatccagaa ccctgaccct
420
gccgtgtacc agctgagaga ctctaaatcc agtgacaagt ctgtctgcct attcaccgat
480
tttgattctc aaacaaatgt gtcacaaagt aaggattctg atgtgtatat cacagacaaa
540
actgtgctag acatgaggtc tatggacttc aagagcaaca gtgctgtggc ctggagcaac
600
aaatctgact ttgcatgtgc aaacgccttc aacaacagca ttattccaga agacaccttc
660
ttcccagcc cagaaagttc ctgtgatgtc aagctggtcg agaaaagctt tgaaacagat
720
acgaacctaa actttcaaaa cctgtcagtg attgggttcc gaatcctcct cctgaaagtg
780
gccgggttta atctgctcat gacgctgcgg ctgtggtcca gctga
825
```

<210> 59

<211> 274

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 3 alpha chain

<400> 59

```
Met Met Lys Ser Leu Arg Val Leu Leu Val Ile Leu Trp Leu Gln Leu
 1           5           10           15
Ser Trp Val Trp Ser Gln Gln Lys Glu Val Glu Gln Asn Ser Gly Pro
      20           25           30
Leu Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys Thr Tyr Ser
      35           40           45
```

Asp	Arg	Gly	Ser	Gln	Ser	Phe	Phe	Trp	Tyr	Arg	Gln	Tyr	Ser	Gly	Lys
50						55					60				
Ser	Pro	Glu	Leu	Ile	Met	Ser	Ile	Tyr	Ser	Asn	Gly	Asp	Lys	Glu	Asp
65					70					75					80
Gly	Arg	Phe	Thr	Ala	Gln	Leu	Asn	Lys	Ala	Ser	Gln	Tyr	Val	Ser	Leu
				85					90					95	
Leu	Ile	Arg	Asp	Ser	Gln	Pro	Ser	Asp	Ser	Ala	Thr	Tyr	Leu	Cys	Ala
			100					105					110		
Val	Asp	Ser	Gly	Gly	Tyr	Gln	Lys	Val	Thr	Phe	Gly	Thr	Gly	Thr	Lys
		115					120					125			
Leu	Gln	Val	Ile	Pro	Asn	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln
	130					135					140				
Leu	Arg	Asp	Ser	Lys	Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp
145				150						155					160
Phe	Asp	Ser	Gln	Thr	Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr
			165						170					175	
Ile	Thr	Asp	Lys	Thr	Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser
		180						185					190		
Asn	Ser	Ala	Val	Ala	Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn
	195						200					205			
Ala	Phe	Asn	Asn	Ser	Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro
	210					215						220			
Glu	Ser	Ser	Cys	Asp	Val	Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp
225				230						235					240
Thr	Asn	Leu	Asn	Phe	Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu
			245						250					255	
Leu	Leu	Lys	Val	Ala	Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp
		260						265					270		

Ser Ser

<210> 60

<211> 930

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR number 3 and TCR number 10 beta chain

<400> 60

atgggcacca ggctcctctg ctgggcagcc ctgtgcctcc tgggggcaga tcacacaggt
60

gctggagtct cccagacccc cagtaacaag gtcacagaga agggaaaata tgtagagctc
120

aggtgtgatc caatttcagg tcatactgcc ctttactggt accgacaaag cctggggcag
180

```

ggcccagagt ttctaattta cttccaaggc acgggtgcgg cagatgactc agggctgccc
240
aacgatcggg tctttgcagt caggcctgag ggatccgtct ctactctgaa gatccagcgc
300
acagagcggg gggactcagc cgtgtatctc tgtgccagca gcttaaatat gaacactgaa
360
gctttctttg gacaaggcac cagactcaca gttgtagagg acctgaacaa ggtgttccca
420
cccgaggtcg ctgtgtttga gccatcagaa gcagagatct cccacacca aaaggccaca
480
ctgggtgtgcc tggccacagg cttcttcccc gaccacgtgg agctgagctg gtgggtgaat
540
gggaaggagg tgcacagtgg ggtcagcacg gacccgcagc ccctcaagga gcagcccgcc
600
ctcaatgact ccagatactg cctgagcagc cgcctgaggg tctcggccac cttctggcag
660
aacccccgca accacttccg ctgtcaagtc cagttctacg ggctctcgga gaatgacgag
720
tggaaccagg atagggccaa acccgtcacc cagatcgtca gcgccgaggg ctggggtaga
780
gcagactgtg gctttacctc ggtgtcctac cagcaagggg tcctgtctgc caccatcctc
840
tatgagatcc tgctagggaa ggccaccctg tatgctgtgc tggtcagcgc ccttgtgttg
900
a t g g c c a t g g           t c a a g a g a a a           g g a t t t c t g a
930

```

<210> 61

<211> 309

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 3 and TCR number 10 beta chain

<400> 61

```

Met Gly Thr Arg Leu Leu Cys Trp Ala Ala Leu Cys Leu Leu Gly Ala
 1           5           10           15
Asp His Thr Gly Ala Gly Val Ser Gln Thr Pro Ser Asn Lys Val Thr
          20           25           30
Glu Lys Gly Lys Tyr Val Glu Leu Arg Cys Asp Pro Ile Ser Gly His
          35           40           45
Thr Ala Leu Tyr Trp Tyr Arg Gln Ser Leu Gly Gln Gly Pro Glu Phe
          50           55           60
Leu Ile Tyr Phe Gln Gly Thr Gly Ala Ala Asp Asp Ser Gly Leu Pro

```

65					70					75				80
Asn	Asp	Arg	Phe	Phe	Ala	Val	Arg	Pro	Glu	Gly	Ser	Val	Ser	Thr
				85					90				95	
Lys	Ile	Gln	Arg	Thr	Glu	Arg	Gly	Asp	Ser	Ala	Val	Tyr	Leu	Cys
			100					105					110	
Ser	Ser	Leu	Asn	Met	Asn	Thr	Glu	Ala	Phe	Phe	Gly	Gln	Gly	Thr
		115					120					125		
Leu	Thr	Val	Val	Glu	Asp	Leu	Asn	Lys	Val	Phe	Pro	Pro	Glu	Val
	130					135				140				
Val	Phe	Glu	Pro	Ser	Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala
145					150					155				160
Leu	Val	Cys	Leu	Ala	Thr	Gly	Phe	Phe	Pro	Asp	His	Val	Glu	Leu
			165					170					175	
Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Ser	Thr	Asp
		180						185					190	
Gln	Pro	Leu	Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys
	195					200						205		
Ser	Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg
	210					215					220			
His	Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp
225				230					235					240
Trp	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala
			245					250					255	
Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Val	Ser	Tyr	Gln
		260					265					270		
Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys
	275					280					285			
Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met
	290				295					300				
Lys	Arg	Lys	Asp	Phe										
305														

<210> 62

<211> 1490

<212> DNA

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 3 construct; beta chain-P2A-alpha chain with cysteine substitutions in beta and alpha chain constant domains (partial sequence)

<400> 62

ctcaataaaa gagcccacaa cccctcactc ggcgcgccac catgggcacc agactgctgt
60

gttggggccgc	tctgtgtctg	ctggggcgccg	atcatacagg	cgctggcggtg	tcccagaccc
120					
ccagcaacaa	agtgaccgag	aagggcaaata	acgtggaact	gagatgcgac	cccatcagcg
180					
gccacaccgc	cctgtactgg	tacagacagt	ctctggggcca	gggccccgag	ttcctgatata
240					
attttccagg	caccggcgct	gccgacgaca	gcggcctgcc	taacgataga	ttcttcgccg
300					
tgcggccccga	gggcagcggtg	tccacactga	agatccagag	aaccgagcgg	ggcgacagcg
360					
ccgtgtatct	gtgtgccagc	agcctgaata	tgaacaccga	ggcattcttt	gggcagggca
420					
cccggctgac	cgtggtggaa	gatctgaaca	aggtgttccc	cccagagggtg	gccgtgttcg
480					
agccttctga	ggccgagatc	agccacaccc	agaaagccac	cctcgtgtgc	ctggccaccg
540					
gctttttccc	cgaccatgtg	gaactgtctt	gggtgggtcaa	cggcaaagag	gtgcacagcg
600					
gagtgtccac	cgaccctcag	cccctgaaag	aacagcccgc	cctgaacgac	agccggtact
660					
gcctgagcag	cagactgaga	gtgtccgccca	ccttctggca	gaacccccgg	aaccacttca
720					
gatgccagggt	gcagttctac	ggcctgagcg	agaacgacga	gtggaccag	gacagagcca
780					
agcccgtgac	ccagatcgtg	tctgccgaag	cctggggcag	agccgattgc	ggctttacct
840					
ccgtgtccta	tcagcagggc	gtgctgagcg	ccaccatcct	gtacgagatc	ctgctgggca
900					
aggccaccct	gtacgccgtg	ctggtgtctg	ccctgggtgct	gatggccatg	gtcaagcgga
960					
aggacttcgg	ttccggagcc	acgaacttct	ctctgttaaa	gcaagcagga	gacgtggaag
1020					
aaaaccccgg	tcccatgatg	aagtccttgc	gggtgctgct	cgtgatcctg	tggctgcagc
1080					
tgtcttggggt	gtggtcccag	cagaaagagg	tggaacagaa	cagcggccct	ctgagcgtgc
1140					
cagagggcgc	cattgctagc	ctgaattgca	cctacagcga	ccggggcagc	cagagcttct
1200					
tctggtatcg	gcagtacagc	ggcaagagcc	ccgagctgat	catgagcatc	tacagcaacg
1260					
gcgacaaaga	ggacggccgg	ttcaccgccc	agctgaacaa	agccagccag	tacgtgtcac
1320					
tgctgatccg	ggacagccag	cccagcgata	gcgccacata	cctgtgcgcc	gtggatagcg
1380					
gcggctacca	gaaagtgacc	ttcggcaccg	gcaccaagct	gcaagtgatc	cccaacatcc
1440					

agaaccccgga ccccgctgtg taccagctgc gggacagcaa gagcagcgac
1490

<210> 63

<211> 494

<212> PRT

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 3 construct; beta
chain-P2A-alpha chain with cysteine substitutions
in beta and alpha chain constant domains (partial
sequence)

<400> 63

Lys	Ser	Pro	Gln	Pro	Leu	Thr	Arg	Arg	Ala	Thr	Met	Gly	Thr	Arg	Leu
1				5					10					15	
Leu	Cys	Trp	Ala	Ala	Leu	Cys	Leu	Leu	Gly	Ala	Asp	His	Thr	Gly	Ala
			20					25					30		
Gly	Val	Ser	Gln	Thr	Pro	Ser	Asn	Lys	Val	Thr	Glu	Lys	Gly	Lys	Tyr
		35					40					45			
Val	Glu	Leu	Arg	Cys	Asp	Pro	Ile	Ser	Gly	His	Thr	Ala	Leu	Tyr	Trp
	50				55						60				
Tyr	Arg	Gln	Ser	Leu	Gly	Gln	Gly	Pro	Glu	Phe	Leu	Ile	Tyr	Phe	Gln
65					70					75					80
Gly	Thr	Gly	Ala	Ala	Asp	Asp	Ser	Gly	Leu	Pro	Asn	Asp	Arg	Phe	Phe
				85				90						95	
Ala	Val	Arg	Pro	Glu	Gly	Ser	Val	Ser	Thr	Leu	Lys	Ile	Gln	Arg	Thr
			100					105					110		
Glu	Arg	Gly	Asp	Ser	Ala	Val	Tyr	Leu	Cys	Ala	Ser	Ser	Leu	Asn	Met
		115					120					125			
Asn	Thr	Glu	Ala	Phe	Phe	Gly	Gln	Gly	Thr	Arg	Leu	Thr	Val	Val	Glu
	130					135					140				
Asp	Leu	Asn	Lys	Val	Phe	Pro	Pro	Glu	Val	Ala	Val	Phe	Glu	Pro	Ser
145					150					155					160
Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ala
			165					170						175	
Thr	Gly	Phe	Phe	Pro	Asp	His	Val	Glu	Leu	Ser	Trp	Trp	Val	Asn	Gly
		180					185						190		
Lys	Glu	Val	His	Ser	Gly	Val	Ser	Thr	Asp	Pro	Gln	Pro	Leu	Lys	Glu
		195					200					205			
Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys	Leu	Ser	Ser	Arg	Leu	Arg
	210				215						220				
Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn	His	Phe	Arg	Cys	Gln
225					230					235					240

Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu	Trp	Thr	Gln	Asp	Arg	
				245					250					255		
Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu	Ala	Trp	Gly	Arg	Ala	
			260					265					270			
Asp	Cys	Gly	Phe	Thr	Ser	Val	Ser	Tyr	Gln	Gln	Gly	Val	Leu	Ser	Ala	
		275					280					285				
Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu	Tyr	Ala	Val	
	290					295					300					
Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val	Lys	Arg	Lys	Asp	Phe	
305					310					315					320	
Gly	Ser	Gly	Ala	Thr	Asn	Phe	Ser	Leu	Leu	Lys	Gln	Ala	Gly	Asp	Val	
			325					330						335		
Glu	Glu	Asn	Pro	Gly	Pro	Met	Met	Lys	Ser	Leu	Arg	Val	Leu	Leu	Val	
			340					345					350			
Ile	Leu	Trp	Leu	Gln	Leu	Ser	Trp	Val	Trp	Ser	Gln	Gln	Lys	Glu	Val	
	355						360					365				
Glu	Gln	Asn	Ser	Gly	Pro	Leu	Ser	Val	Pro	Glu	Gly	Ala	Ile	Ala	Ser	
	370					375					380					
Leu	Asn	Cys	Thr	Tyr	Ser	Asp	Arg	Gly	Ser	Gln	Ser	Phe	Phe	Trp	Tyr	
385					390					395					400	
Arg	Gln	Tyr	Ser	Gly	Lys	Ser	Pro	Glu	Leu	Ile	Met	Ser	Ile	Tyr	Ser	
			405					410						415		
Asn	Gly	Asp	Lys	Glu	Asp	Gly	Arg	Phe	Thr	Ala	Gln	Leu	Asn	Lys	Ala	
			420					425					430			
Ser	Gln	Tyr	Val	Ser	Leu	Leu	Ile	Arg	Asp	Ser	Gln	Pro	Ser	Asp	Ser	
	435					440						445				
Ala	Thr	Tyr	Leu	Cys	Ala	Val	Asp	Ser	Gly	Gly	Tyr	Gln	Lys	Val	Thr	
	450					455					460					
Phe	Gly	Thr	Gly	Thr	Lys	Leu	Gln	Val	Ile	Pro	Asn	Ile	Gln	Asn	Pro	
465					470					475					480	
Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser	Lys	Ser	Ser	Asp			
			485					490								

<210> 64

<211> 819

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR number 10 alpha chain

<400> 64

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atggaaactc tcctgggagt gtctttggtg attctatggc ttcaactggc taggggtgaac
60
agtcaacagg gagaagagga tcctcaggcc ttgagcatcc aggagggtga aaatgccacc
120

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atgaactgca gttacaaaac tagtataaac aatttacagt ggtatagaca aaattcaggt
 180
 agaggccttg tccacctaata ttttaatacgt tcaaatagaaa gagagaaaca cagtggaga
 240
 ttaagagtca cgcttgacac ttccaagaaa agcagttcct tgttgatcac ggcttcccgg
 300
 gcagcagaca ctgcttctta cttctgtgct acggacgaga gtagcaacta taaactgaca
 360
 tttggaaaag gaactctctt aaccgtgaat ccaaataatcc agaaccctga ccctgccgtg
 420
 taccagctga gagactctaa atccagtgac aagtctgtct gcctattcac cgattttgat
 480
 tctcaaacia atgtgtcaca aagtaaggat tctgatgtgt atatcacaga caaaactgtg
 540
 ctagacatga ggtctatgga cttcaagagc aacagtgctg tggcctggag caacaaatct
 600
 gactttgcat gtgcaaacgc cttcaacaac agcattattc cagaagacac cttcttcccc
 660
 agcccagaaa gttcctgtga tgtcaagctg gtcgagaaaa gctttgaaac agatacgaac
 720
 ctaaactttc aaaacctgtc agtgattggg ttccgaatcc tcctcctgaa agtggccggg
 780
 tttaatctgc tcatgacgct gcggtgtgg tccagctga
 819

<210> 65

<211> 272

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 10 alpha chain

<400> 65

Met	Glu	Thr	Leu	Leu	Gly	Val	Ser	Leu	Val	Ile	Leu	Trp	Leu	Gln	Leu
1				5					10					15	
Ala	Arg	Val	Asn	Ser	Gln	Gln	Gly	Glu	Glu	Asp	Pro	Gln	Ala	Leu	Ser
			20					25					30		
Ile	Gln	Glu	Gly	Glu	Asn	Ala	Thr	Met	Asn	Cys	Ser	Tyr	Lys	Thr	Ser
		35					40					45			
Ile	Asn	Asn	Leu	Gln	Trp	Tyr	Arg	Gln	Asn	Ser	Gly	Arg	Gly	Leu	Val
	50					55					60				
His	Leu	Ile	Leu	Ile	Arg	Ser	Asn	Glu	Arg	Glu	Lys	His	Ser	Gly	Arg
65					70				75					80	
Leu	Arg	Val	Thr	Leu	Asp	Thr	Ser	Lys	Lys	Ser	Ser	Ser	Leu	Leu	Ile

				85					90					95			
Thr	Ala	Ser	Arg	Ala	Ala	Asp	Thr	Ala	Ser	Tyr	Phe	Cys	Ala	Thr	Asp		
			100					105					110				
Glu	Ser	Ser	Asn	Tyr	Lys	Leu	Thr	Phe	Gly	Lys	Gly	Thr	Leu	Leu	Thr		
		115					120					125					
Val	Asn	Pro	Asn	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg		
	130					135					140						
Asp	Ser	Lys	Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp		
145					150				155					160			
Ser	Gln	Thr	Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr		
			165					170					175				
Asp	Lys	Thr	Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser		
		180					185					190					
Ala	Val	Ala	Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe		
	195					200					205						
Asn	Asn	Ser	Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser		
	210					215					220						
Ser	Cys	Asp	Val	Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn		
225					230				235					240			
Leu	Asn	Phe	Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu		
			245					250					255				
Lys	Val	Ala	Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser		
		260					265					270					

<210> 66

<211> 1484

<212> DNA

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 10 construct; beta chain-P2A-alpha chain with cysteine substitutions in beta and alpha chain constant domains (partial sequence)

<400> 66

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ctcaataaaa gagccacaaa cccctcactc ggcgcgccac catgggcacc agactgctgt
60
gttggggccgc tctgtgtctg ctggggcgccg atcatacagg cgctggcgctg tcccagaccc
120
ccagcaacaa agtgaccgag aagggcaaata acgtggaact gagatgcgac cccatcagcg
180
gccacaccgc cctgtactgg tacagacagt ctctgggcca gggccccgag ttcttgatat
240
attttcaggg caccggcgct gccgacgaca gcggcctgcc taacgataga ttcttcgccg
300

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tgcggcccga	gggcagcgtg	tccacactga	agatccagag	aaccgagcgg	ggcgacagcg
360					
ccgtgtatct	gtgtgccagc	agcctgaata	tgaacaccga	ggcattcttt	gggcagggca
420					
cccggctgac	cgtggtggaa	gatctgaaca	aggtgttccc	cccagaggtg	gccgtgttcg
480					
agccttctga	ggccgagatc	agccacaccc	agaaagccac	cctcgtgtgc	ctggccaccg
540					
gctttttccc	cgaccatgtg	gaactgtctt	gggtgggtcaa	cggcaaagag	gtgcacagcg
600					
gagtgtccac	cgaccctcag	cccctgaaag	aacagcccgc	cctgaacgac	agccggtact
660					
gcctgagcag	cagactgaga	gtgtccgcc	ccttctggca	gaacccccgg	aaccacttca
720					
gatgccaggt	gcagttctac	ggcctgagcg	agaacgacga	gtggaccag	gacagagcca
780					
agcccgtgac	ccagatcgtg	tctgccgaag	cctggggcag	agccgattgc	ggctttacct
840					
ccgtgtccta	tcagcagggc	gtgctgagcg	ccaccatcct	gtacgagatc	ctgctgggca
900					
aggccaccct	gtacgccgtg	ctggtgtctg	ccctgggtgct	gatggccatg	gtcaagcgga
960					
aggacttcgg	ttccggagcc	acgaacttct	ctctgttaaa	gcaagcagga	gacgtggaag
1020					
aaaacccccg	tcccatggaa	accctgctgg	gagtgtccct	cgtgatcctg	tggctgcagc
1080					
tggccagagt	gaacagccag	cagggggaag	aggatcccca	ggccctgagc	attcaggaag
1140					
gcgagaacgc	caccatgaac	tgcagctaca	agaccagcat	caacaacctg	cagtgggtaca
1200					
ggcagaacag	cggcagaggc	ctggtgcacc	tgatcctgat	cagaagcaac	gagagagaga
1260					
agcactccgg	acggctgaga	gtgaccctgg	acacctccaa	gaagtcctcc	agcctgctga
1320					
tcaccgccag	cagagccgcc	gataccgcc	gctacttctg	cgccacagac	gagagcagca
1380					
actacaagct	gaccttcggc	aagggcacac	tgctgacagt	gaaccccaac	atccagaacc
1440					
ccgacccccg	tgtgtaccag	ctgcgggaca	gcaagagcag	cgac	
1484					

<210> 67

<211> 492

<212> PRT

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 10 construct
polypeptide; beta chain-P2A-alpha chain with
cysteine substitutions in beta and alpha chain
constant domains (partial sequence)

<400> 67

Lys	Ser	Pro	Gln	Pro	Leu	Thr	Arg	Arg	Ala	Thr	Met	Gly	Thr	Arg	Leu
1				5					10					15	
Leu	Cys	Trp	Ala	Ala	Leu	Cys	Leu	Leu	Gly	Ala	Asp	His	Thr	Gly	Ala
			20					25					30		
Gly	Val	Ser	Gln	Thr	Pro	Ser	Asn	Lys	Val	Thr	Glu	Lys	Gly	Lys	Tyr
		35					40					45			
Val	Glu	Leu	Arg	Cys	Asp	Pro	Ile	Ser	Gly	His	Thr	Ala	Leu	Tyr	Trp
	50					55					60				
Tyr	Arg	Gln	Ser	Leu	Gly	Gln	Gly	Pro	Glu	Phe	Leu	Ile	Tyr	Phe	Gln
65					70					75					80
Gly	Thr	Gly	Ala	Ala	Asp	Asp	Ser	Gly	Leu	Pro	Asn	Asp	Arg	Phe	Phe
				85					90					95	
Ala	Val	Arg	Pro	Glu	Gly	Ser	Val	Ser	Thr	Leu	Lys	Ile	Gln	Arg	Thr
			100					105					110		
Glu	Arg	Gly	Asp	Ser	Ala	Val	Tyr	Leu	Cys	Ala	Ser	Ser	Leu	Asn	Met
		115					120					125			
Asn	Thr	Glu	Ala	Phe	Phe	Gly	Gln	Gly	Thr	Arg	Leu	Thr	Val	Val	Glu
	130					135						140			
Asp	Leu	Asn	Lys	Val	Phe	Pro	Pro	Glu	Val	Ala	Val	Phe	Glu	Pro	Ser
145					150					155					160
Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ala
				165					170				175		
Thr	Gly	Phe	Phe	Pro	Asp	His	Val	Glu	Leu	Ser	Trp	Trp	Val	Asn	Gly
			180					185					190		
Lys	Glu	Val	His	Ser	Gly	Val	Ser	Thr	Asp	Pro	Gln	Pro	Leu	Lys	Glu
		195					200					205			
Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys	Leu	Ser	Ser	Arg	Leu	Arg
	210					215						220			
Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn	His	Phe	Arg	Cys	Gln
225					230					235					240
Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu	Trp	Thr	Gln	Asp	Arg
				245					250					255	
Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu	Ala	Trp	Gly	Arg	Ala
			260					265					270		
Asp	Cys	Gly	Phe	Thr	Ser	Val	Ser	Tyr	Gln	Gln	Gly	Val	Leu	Ser	Ala
		275					280					285			
Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu	Tyr	Ala	Val

290	295	300
Leu Val Ser Ala Leu Val	Leu Met Ala Met Val	Lys Arg Lys Asp Phe
305	310	315
Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val		320
	325	330
Glu Glu Asn Pro Gly Pro Met Glu Thr Leu Leu Gly Val Ser Leu Val		335
	340	345
Ile Leu Trp Leu Gln Leu Ala Arg Val Asn Ser Gln Gln Gly Glu Glu		350
	355	360
Asp Pro Gln Ala Leu Ser Ile Gln Glu Gly Glu Asn Ala Thr Met Asn		365
	370	375
Cys Ser Tyr Lys Thr Ser Ile Asn Asn Leu Gln Trp Tyr Arg Gln Asn		380
385	390	395
Ser Gly Arg Gly Leu Val His Leu Ile Leu Ile Arg Ser Asn Glu Arg		400
	405	410
Glu Lys His Ser Gly Arg Leu Arg Val Thr Leu Asp Thr Ser Lys Lys		415
	420	425
Ser Ser Ser Leu Leu Ile Thr Ala Ser Arg Ala Ala Asp Thr Ala Ser		430
	435	440
Tyr Phe Cys Ala Thr Asp Glu Ser Ser Asn Tyr Lys Leu Thr Phe Gly		445
	450	455
Lys Gly Thr Leu Leu Thr Val Asn Pro Asn Ile Gln Asn Pro Asp Pro		460
465	470	475
Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp		480
	485	490

<210> 68

<211> 825

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR number 7 alpha chain

<400> 68

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atggagaaga atcctttggc agccccatta ctaatcctct ggtttcatct tgactgcgtg
60
agcagcatac tgaacgtgga acaaagtcct cagtcactgc atgttcagga gggagacagc
120
accaatttca cctgcagctt cccttccagc aatttttatg ccttacactg gtacagatgg
180
gaaactgcaa aaagccccga ggccttgttt gtaatgactt taaatgggga tgaaaagaag
240
aaaggacgaa taagtgccac tcttaatacc aaggagggtt acagctatgt gtacatcaaa
300

```

ggatcccagc ctgaagactc agccacatac ctctgtgcct atttaggggc cggttaaccag
 360
 ttctattttg ggacagggac aagtttgacg gtcattccaa atatccagaa ccctgaccct
 420
 gccgtgtacc agctgagaga ctctaaatcc agtgacaagt ctgtctgcct attcaccgat
 480
 tttgattctc aaacaaatgt gtcacaaagt aaggattctg atgtgtatat cacagacaaa
 540
 actgtgctag acatgaggtc tatggacttc aagagcaaca gtgctgtggc ctggagcaac
 600
 aaatctgact ttgcatgtgc aaacgccttc aacaacagca ttattccaga agacaccttc
 660
 ttccccagcc cagaaagttc ctgtgatgtc aagctggtcg agaaaagctt tgaaacagat
 720
 acgaacctaa actttcaaaa cctgtcagtg attgggttcc gaatcctcct cctgaaagtg
 780
 gccggggttta atctgctcat gacgctgcgg ctgtgggtcca gctga
 825

<210> 69

<211> 274

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 7 alpha chain

<400> 69

Met	Glu	Lys	Asn	Pro	Leu	Ala	Ala	Pro	Leu	Leu	Ile	Leu	Trp	Phe	His
1				5				10						15	
Leu	Asp	Cys	Val	Ser	Ser	Ile	Leu	Asn	Val	Glu	Gln	Ser	Pro	Gln	Ser
			20					25					30		
Leu	His	Val	Gln	Glu	Gly	Asp	Ser	Thr	Asn	Phe	Thr	Cys	Ser	Phe	Pro
		35				40						45			
Ser	Ser	Asn	Phe	Tyr	Ala	Leu	His	Trp	Tyr	Arg	Trp	Glu	Thr	Ala	Lys
	50					55				60					
Ser	Pro	Glu	Ala	Leu	Phe	Val	Met	Thr	Leu	Asn	Gly	Asp	Glu	Lys	Lys
65				70						75				80	
Lys	Gly	Arg	Ile	Ser	Ala	Thr	Leu	Asn	Thr	Lys	Glu	Gly	Tyr	Ser	Tyr
			85					90					95		
Leu	Tyr	Ile	Lys	Gly	Ser	Gln	Pro	Glu	Asp	Ser	Ala	Thr	Tyr	Leu	Cys
			100					105					110		
Ala	Tyr	Leu	Gly	Ala	Gly	Asn	Gln	Phe	Tyr	Phe	Gly	Thr	Gly	Thr	Ser
		115				120						125			
Leu	Thr	Val	Ile	Pro	Asn	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln

130		135		140
Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp				
145		150		155
Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr				
	165		170	
Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser				
	180		185	
Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn				
	195		200	
Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro				
	210		215	
Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp				
225		230		235
Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu				
	245		250	
Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp				
	260		265	
Ser Ser				

<210> 70

<211> 930

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR number 7 beta chain

<400> 70

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atgagcaacc aggtgctctg ctgtgtggtc ctttgtttcc tgggagcaaa caccgtggat
60
ggtggaatca ctcagtcccc aaagtacctg ttcagaaagg aaggacagaa tgtgaccctg
120
agttgtgaac agaatttgaa ccacgatgcc atgtactggg accgacagga cccagggcaa
180
gggctgagat tgatctacta ctcacagata gtaaattgact ttcagaaagg agatatagct
240
gaaggggtaca gcgtctctcg ggagaagaag gaatcctttc ctctcactgt gacatcggcc
300
caaaagaacc cgacagcttt ctatctctgt gccagtagcc tcaacagggg ccgctatggc
360
tacaccttcg gttcggggac cagggttaacc gttgtagagg acctgaacaa ggtgttccca
420
cccgaggtcg ctgtgtttga gccatcagaa gcagagatct cccacacca aaaggccaca
480

```

ctggtgtgcc tggccacagg cttcttcccc gaccacgtgg agctgagctg gtgggtgaat
 540
 gggaaggagg tgcacagtgg ggtcagcacg gacccgcagc ccctcaagga gcagcccgcc
 600
 ctcaatgact ccagatactg cctgagcagc cgcctgaggg tctcggccac cttctggcag
 660
 aacccccgca accacttccg ctgtcaagtc cagttctacg ggctctcgga gaatgacgag
 720
 tggacccagg atagggccaa acccgtcacc cagatcgtca gcgccgaggg ctggggtaga
 780
 gcagactgtg gctttacctc ggtgtcctac cagcaagggg tcctgtctgc caccatcctc
 840
 tatgagatcc tgctagggaa ggccaccctg tatgctgtgc tggtcagcgc ccttgtgttg
 900
 a t g g c c a t g g t c a a g a g a a a g g a t t t c t g a
 930

<210> 71

<211> 309

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 7 beta chain

<400> 71

Met	Ser	Asn	Gln	Val	Leu	Cys	Cys	Val	Val	Leu	Cys	Phe	Leu	Gly	Ala
1				5				10						15	
Asn	Thr	Val	Asp	Gly	Gly	Ile	Thr	Gln	Ser	Pro	Lys	Tyr	Leu	Phe	Arg
			20					25					30		
Lys	Glu	Gly	Gln	Asn	Val	Thr	Leu	Ser	Cys	Glu	Gln	Asn	Leu	Asn	His
		35					40					45			
Asp	Ala	Met	Tyr	Trp	Tyr	Arg	Gln	Asp	Pro	Gly	Gln	Gly	Leu	Arg	Leu
	50					55				60					
Ile	Tyr	Tyr	Ser	Gln	Ile	Val	Asn	Asp	Phe	Gln	Lys	Gly	Asp	Ile	Ala
65				70						75				80	
Glu	Gly	Tyr	Ser	Val	Ser	Arg	Glu	Lys	Lys	Glu	Ser	Phe	Pro	Leu	Thr
			85					90					95		
Val	Thr	Ser	Ala	Gln	Lys	Asn	Pro	Thr	Ala	Phe	Tyr	Leu	Cys	Ala	Ser
			100					105					110		
Ser	Leu	Asn	Arg	Gly	Arg	Tyr	Gly	Tyr	Thr	Phe	Gly	Ser	Gly	Thr	Arg
		115					120					125			
Leu	Thr	Val	Val	Glu	Asp	Leu	Asn	Lys	Val	Phe	Pro	Pro	Glu	Val	Ala
	130					135					140				
Val	Phe	Glu	Pro	Ser	Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr

145					150					155				160	
Leu	Val	Cys	Leu	Ala	Thr	Gly	Phe	Phe	Pro	Asp	His	Val	Glu	Leu	Ser
				165					170					175	
Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Ser	Thr	Asp	Pro
			180					185					190		
Gln	Pro	Leu	Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys	Leu
		195					200					205			
Ser	Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn
	210					215					220				
His	Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu
225					230					235					240
Trp	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu
			245						250					255	
Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Val	Ser	Tyr	Gln	Gln
			260					265					270		
Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala
		275					280					285			
Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val
	290					295					300				
Lys	Arg	Lys	Asp	Phe											
305															

<210> 72

<211> 1490

<212> DNA

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 7 construct; beta chain-P2A-alpha chain with cysteine substitutions in beta and alpha chain constant domains (partial sequence)

<400> 72

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ctcaataaaa gagccacaa cccctcactc ggcgcgccac catgagcaac caggtcttgt
60
gctgtgtggt gctgtgcttt cttggcgcca atacagtgga tggcggcatt acacagagcc
120
ctaagtacct gttccggaag gaaggccaga acgtgacact gtcttgcgag caaaacctga
180
accacgatgc catgtactgg tacagacagg atcctggaca gggacttagg ctgatctact
240
atagccagat cgtgaacgac ttccagaagg gcgatattgc cgagggctat tctgtgtctc
300

```

```

gggagaaaaa ggagagcttc cctctgacag tgacatctgc ccagaagaat cctaccgcct
360
tctacctttg tgccagctct ctgaatcggg gcagatacgg atacaccttt ggatctggca
420
ccagactgac agtgggtggaa gatctgaaca aggtgttccc cccagagggtg gccgtgttcg
480
agccttctga ggccgagatc tcccacaccc agaaagccac cctcgtgtgc ctggccaccg
540
gctttttccc cgaccacgtg gaactgtctt ggtgggtcaa cggcaaagag gtgcaactccg
600
gcgtgtgcac cgatccccag cctctgaaag aacagcccgc cctgaacgac agccggtact
660
gcctgagcag cagactgaga gtgtccgcca ccttctggca gaacccccgg aaccacttca
720
gatgccaggt gcagttctac ggcctgagcg agaacgacga gtggaccag gacagagcca
780
agcccgtgac acagatcgtg tctgccgaag cctggggcag agccgattgc ggctttacct
840
ccgtgtccta tcagcagggc gtgctgagcg ccacaatcct gtacgagatc ctgctgggca
900
aggccaccct gtacgccgtg ctggtgtctg ccctggtgct gatggccatg gtcaagcgga
960
aggacttcgg ttccggagcc acgaacttct ctctgttaaa gcaagcagga gacgtggaag
1020
aaaaccccgg tcccatggag aagaaccccc ttgcagcacc tctgcttatt ctgtggttcc
1080
acctggattg cgtgagctct atcctgaatg tggagcagtc tcctcagtct ctgcatgttc
1140
aggaaggcga tagcaccaac ttcacctgta gctttcccag cagcaacttc tatgccctgc
1200
actggtacag atgggaaaca gccaaaagcc ctgaagccct gttcgtgatg acccttaatg
1260
gcgatgagaa gaagaagggc cggatttctg ccaccctgaa tacaaaagag ggctacagct
1320
acctgtacat caagggatct cagcctgagg atagcgccac atatctgtgt gcctatctgg
1380
gagccggcaa tcagttctat ttcggaacag gcaccagcct gaccgtgatt cctaatatcc
1440
agaaccccga tcctgccgtg taccagctgc gggacagcaa gagcagcgac
1490

```

<210> 73

<211> 494

<212> PRT

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 7 construct; beta chain-P2A-alpha chain with cysteine substitutions in beta and alpha chain constant domains (partial sequence)

<400> 73

Lys	Ser	Pro	Gln	Pro	Leu	Thr	Arg	Arg	Ala	Thr	Met	Ser	Asn	Gln	Val
1				5					10					15	
Leu	Cys	Cys	Val	Val	Leu	Cys	Phe	Leu	Gly	Ala	Asn	Thr	Val	Asp	Gly
			20					25					30		
Gly	Ile	Thr	Gln	Ser	Pro	Lys	Tyr	Leu	Phe	Arg	Lys	Glu	Gly	Gln	Asn
		35					40					45			
Val	Thr	Leu	Ser	Cys	Glu	Gln	Asn	Leu	Asn	His	Asp	Ala	Met	Tyr	Trp
	50					55					60				
Tyr	Arg	Gln	Asp	Pro	Gly	Gln	Gly	Leu	Arg	Leu	Ile	Tyr	Tyr	Ser	Gln
65					70				75					80	
Ile	Val	Asn	Asp	Phe	Gln	Lys	Gly	Asp	Ile	Ala	Glu	Gly	Tyr	Ser	Val
				85				90						95	
Ser	Arg	Glu	Lys	Lys	Glu	Ser	Phe	Pro	Leu	Thr	Val	Thr	Ser	Ala	Gln
			100					105					110		
Lys	Asn	Pro	Thr	Ala	Phe	Tyr	Leu	Cys	Ala	Ser	Ser	Leu	Asn	Arg	Gly
		115					120					125			
Arg	Tyr	Gly	Tyr	Thr	Phe	Gly	Ser	Gly	Thr	Arg	Leu	Thr	Val	Val	Glu
	130					135					140				
Asp	Leu	Asn	Lys	Val	Phe	Pro	Pro	Glu	Val	Ala	Val	Phe	Glu	Pro	Ser
145					150					155				160	
Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ala
				165				170					175		
Thr	Gly	Phe	Phe	Pro	Asp	His	Val	Glu	Leu	Ser	Trp	Trp	Val	Asn	Gly
			180					185					190		
Lys	Glu	Val	His	Ser	Gly	Val	Cys	Thr	Asp	Pro	Gln	Pro	Leu	Lys	Glu
		195				200					205				
Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys	Leu	Ser	Ser	Arg	Leu	Arg
	210					215					220				
Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn	His	Phe	Arg	Cys	Gln
225					230					235				240	
Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu	Trp	Thr	Gln	Asp	Arg
				245				250					255		
Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu	Ala	Trp	Gly	Arg	Ala
			260					265					270		
Asp	Cys	Gly	Phe	Thr	Ser	Val	Ser	Tyr	Gln	Gln	Gly	Val	Leu	Ser	Ala
		275					280					285			
Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu	Tyr	Ala	Val

290	295	300
Leu Val Ser Ala Leu Val	Leu Met Ala Met Val	Lys Arg Lys Asp Phe
305	310	315
Gly Ser Gly Ala Thr Asn	Phe Ser Leu Leu Lys	Gln Ala Gly Asp Val
325	330	335
Glu Glu Asn Pro Gly Pro	Met Glu Lys Asn Pro	Leu Ala Ala Pro Leu
340	345	350
Leu Ile Leu Trp Phe His	Leu Asp Cys Val Ser	Ser Ile Leu Asn Val
355	360	365
Glu Gln Ser Pro Gln Ser	Leu His Val Gln Glu	Gly Asp Ser Thr Asn
370	375	380
Phe Thr Cys Ser Phe Pro	Ser Ser Asn Phe Tyr	Ala Leu His Trp Tyr
385	390	395
Arg Trp Glu Thr Ala Lys	Ser Pro Glu Ala Leu	Phe Val Met Thr Leu
405	410	415
Asn Gly Asp Glu Lys Lys	Lys Gly Arg Ile Ser	Ala Thr Leu Asn Thr
420	425	430
Lys Glu Gly Tyr Ser Tyr	Leu Tyr Ile Lys Gly	Ser Gln Pro Glu Asp
435	440	445
Ser Ala Thr Tyr Leu Cys	Ala Tyr Leu Gly Ala	Gly Asn Gln Phe Tyr
450	455	460
Phe Gly Thr Gly Thr Ser	Leu Thr Val Ile Pro	Asn Ile Gln Asn Pro
465	470	475
Asp Pro Ala Val Tyr Gln	Leu Arg Asp Ser Lys	Ser Ser Asp
485	490	

<210> 74

<211> 837

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR number 8 alpha chain

<400> 74

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atgctgactg ccagcctggt gagggcagtc atagcctcca tctgtgttgt atccagcatg
60
gctcagaagg taactcaagc gcagactgaa atttctgtgg tggagaagga ggatgtgacc
120
ttggactgtg tgtatgaaac ccgtgatact acttattact tattctggta caagcaacca
180
ccaagtggag aattgggtttt ccttattcgt cggaactctt ttgatgagca aatgaaata
240
agtggtcggt attcttggaa cttccagaaa tccaccagtt ccttcaactt caccatcaca
300

```

gcctcacaag tcgtggactc agcagtatac ttctgtgctc tgagtgagct agcatcagga
 360
 ggaagctaca tacctacatt tggaagagga accagcctta ttgttcatcc gtatatccag
 420
 aaccctgacc ctgccgtgta ccagctgaga gactctaaat ccagtgacaa gtctgtctgc
 480
 ctattcaccg attttgattc tcaaacaaat gtgtcacaaa gtaaggattc tgatgtgtat
 540
 atcacagaca aaactgtgct agacatgagg tctatggact tcaagagcaa cagtgtgtg
 600
 gcctggagca acaaactctga ctttgcatgt gcaaacgcct tcaacaacag cattattcca
 660
 gaagacacct tcttccccag cccagaaagt tcctgtgatg tcaagctggg cgagaaaagc
 720
 ttgaaacag atacgaacct aaactttcaa aacctgtcag tgattggggt ccgaatcctc
 780
 ctctgaaag tggccgggtt taatctgctc atgacgctgc ggctgtggtc cagctga
 837

<210> 75

<211> 278

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 8 alpha chain

<400> 75

Met	Leu	Thr	Ala	Ser	Leu	Leu	Arg	Ala	Val	Ile	Ala	Ser	Ile	Cys	Val
1				5					10					15	
Val	Ser	Ser	Met	Ala	Gln	Lys	Val	Thr	Gln	Ala	Gln	Thr	Glu	Ile	Ser
			20					25					30		
Val	Val	Glu	Lys	Glu	Asp	Val	Thr	Leu	Asp	Cys	Val	Tyr	Glu	Thr	Arg
		35					40					45			
Asp	Thr	Thr	Tyr	Tyr	Leu	Phe	Trp	Tyr	Lys	Gln	Pro	Pro	Ser	Gly	Glu
		50				55				60					
Leu	Val	Phe	Leu	Ile	Arg	Arg	Asn	Ser	Phe	Asp	Glu	Gln	Asn	Glu	Ile
65					70					75				80	
Ser	Gly	Arg	Tyr	Ser	Trp	Asn	Phe	Gln	Lys	Ser	Thr	Ser	Ser	Phe	Asn
				85				90						95	
Phe	Thr	Ile	Thr	Ala	Ser	Gln	Val	Val	Asp	Ser	Ala	Val	Tyr	Phe	Cys
			100					105					110		
Ala	Leu	Ser	Glu	Leu	Ala	Ser	Gly	Gly	Ser	Tyr	Ile	Pro	Thr	Phe	Gly
		115					120					125			
Arg	Gly	Thr	Ser	Leu	Ile	Val	His	Pro	Tyr	Ile	Gln	Asn	Pro	Asp	Pro

130	135	140
Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys		
145	150	155
Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp		160
	165	170
Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met		175
	180	185
Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe		190
	195	200
Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe		205
	210	215
Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser		220
225	230	235
Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly		240
	245	250
Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr		255
	260	265
Leu Arg Leu Trp Ser Ser		270
275		

<210> 76

<211> 948

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR number 8 beta chain

<400> 76

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atggggccccg ggctcctctg ctgggcactg ctttgtctcc tgggagcagg cttagtggac
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gctggagtca cccaaagtcc cacacacctg atcaaaacga gaggacagca agtgactctg
120
agatgctctc ctaagtctgg gcatgacact gtgtcctggg accaacaggc cctggggtcag
180
gggccccagt ttatctttca gtattatgag gaggaagaga gacagagagg caacttcct
240
gatcgattct caggtcacca gttccctaac tatagctctg agctgaatgt gaacgccttg
300
ttgctggggg actcggccct ctatctctgt gccagcagct ttaggctagc gggggggcct
360
agcacagata cgcagtatth tggcccaggc acccggctga cagtgtctga ggacctgaaa
420
aacgtgttcc cacccgaggt cgctgtgttt gagccatcag aagcagagat ctccacacc
480

```

caaaaggcca cactgggtgtg cctggccaca ggcttctacc ccgaccacgt ggagctgagc
 540
 tgggtgggtga atgggaagga ggtgcacagt ggggtcagca cagacccgca gcccctcaag
 600
 gagcagcccg ccctcaatga ctccagatac tgcctgagca gccgcctgag ggtctcggcc
 660
 accttctggc agaacccccg caaccacttc cgctgtcaag tccagttcta cgggctctcg
 720
 gagaatgacg agtggaccca ggatagggcc aaacctgtca cccagatcgt cagcgccgag
 780
 gcctggggta gagcagactg tggcttcacc tccgagtctt accagcaagg ggtcctgtct
 840
 gccaccatcc tctatgagat cttgctaggg aaggccacct tgtatgccgt gctggtcagt
 900
 gccctcgtgc tgatggccat ggtcaagaga aaggattcca gaggctag
 948

<210> 77

<211> 315

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 8 beta chain

<400> 77

Met	Gly	Pro	Gly	Leu	Leu	Cys	Trp	Ala	Leu	Leu	Cys	Leu	Leu	Gly	Ala
1				5					10					15	
Gly	Leu	Val	Asp	Ala	Gly	Val	Thr	Gln	Ser	Pro	Thr	His	Leu	Ile	Lys
			20					25					30		
Thr	Arg	Gly	Gln	Gln	Val	Thr	Leu	Arg	Cys	Ser	Pro	Lys	Ser	Gly	His
		35					40					45			
Asp	Thr	Val	Ser	Trp	Tyr	Gln	Gln	Ala	Leu	Gly	Gln	Gly	Pro	Gln	Phe
	50					55					60				
Ile	Phe	Gln	Tyr	Tyr	Glu	Glu	Glu	Glu	Arg	Gln	Arg	Gly	Asn	Phe	Pro
65					70				75					80	
Asp	Arg	Phe	Ser	Gly	His	Gln	Phe	Pro	Asn	Tyr	Ser	Ser	Glu	Leu	Asn
			85					90					95		
Val	Asn	Ala	Leu	Leu	Leu	Gly	Asp	Ser	Ala	Leu	Tyr	Leu	Cys	Ala	Ser
		100						105					110		
Ser	Phe	Arg	Leu	Ala	Gly	Gly	Pro	Ser	Thr	Asp	Thr	Gln	Tyr	Phe	Gly
		115					120					125			
Pro	Gly	Thr	Arg	Leu	Thr	Val	Leu	Glu	Asp	Leu	Lys	Asn	Val	Phe	Pro
	130					135					140				
Pro	Glu	Val	Ala	Val	Phe	Glu	Pro	Ser	Glu	Ala	Glu	Ile	Ser	His	Thr

145					150					155				160	
Gln	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ala	Thr	Gly	Phe	Tyr	Pro	Asp	His
				165					170					175	
Val	Glu	Leu	Ser	Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val
			180					185					190		
Ser	Thr	Asp	Pro	Gln	Pro	Leu	Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser
		195					200					205			
Arg	Tyr	Cys	Leu	Ser	Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln
	210					215					220				
Asn	Pro	Arg	Asn	His	Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser
225					230					235				240	
Glu	Asn	Asp	Glu	Trp	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile
			245					250					255		
Val	Ser	Ala	Glu	Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Glu
		260				265						270			
Ser	Tyr	Gln	Gln	Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu
	275					280					285				
Leu	Gly	Lys	Ala	Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu
	290				295					300					
Met	Ala	Met	Val	Lys	Arg	Lys	Asp	Ser	Arg	Gly					
305					310					315					

<210> 78

<211> 1520

<212> DNA

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 8 construct; beta chain-P2A-alpha chain with cysteine substitutions in beta and alpha chain constant domains (partial sequence)

<400> 78

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ctcaataaaa gagccacaa cccctcactc ggcgcgccac catgggacct ggactgcttt
60
gttgggctct tctgtgtctg cttggagctg gactggttga tgctggagtt acacagagcc
120
ctacacacct gatcaagaca agaggacagc aggtgaccct gagatgtagc cctaaatctg
180
gccacgatac cgtgagctgg tatcaacagg ctctgggaca aggacctcag ttcattcttc
240
agtactacga ggaggaggag agacagagag gcaatttccc tgacaggttt agcggacacc
300
agttcccaaa ttacagctct gagctgaacg tgaatgccct tcttctggga gattctgccc
360

```

tgtatctgtg	tgccagcagc	tttagactgg	ctggaggacc	tagcaccgat	acacagtatt
420					
ttggacctgg	caccaggctg	acagtgttag	aagacctgaa	gaacgtgttc	ccccagagg
480					
tggccgtgtt	cgagcctagc	gaggccgaga	tcagccacac	ccagaaagcc	accctcgtgt
540					
gcctggccac	cggctttttac	cccgaccacg	tggaactgtc	ttggtgggtc	aacggcaaag
600					
aggtgcacag	cggcgtctgc	accgaccccc	agccccctgaa	agagcagccc	gccctgaacg
660					
acagccggta	ctgtctgagc	agcagactga	gagtgtccgc	caccttctgg	cagaaccccc
720					
ggaaccactt	cagatgccag	gtgcagttct	acggcctgag	cgagaacgac	gagtggaccc
780					
aggaccgggc	caagcccgtg	accagatcg	tgtctgctga	ggcctggggc	agagccgatt
840					
gcggcttcac	cagcgagagc	taccagcagg	gcgtgctgag	cgccaccatc	ctgtacgaga
900					
tcctgctggg	caaggccacc	ctgtacgccg	tgctgggtgtc	cgccctgggtg	ctgatggcca
960					
tggtcaagcg	gaaggacagc	cggggcggtt	ccggagccac	gaacttctct	ctgttaaagc
1020					
aagcaggaga	cgtggaagaa	aaccccggtc	ccatgttgac	cgcttctctc	ttacgtgccg
1080					
tgattgccag	catctgtgtg	gttagctcta	tggcccagaa	ggtgacacaa	gctcagacag
1140					
agatcagcgt	ggtggagaaa	gaggatgtga	ccctggattg	cgtgtacgag	accagagata
1200					
ccacctacta	cctgtttctgg	tacaagcagc	ctccttctgg	agaactgggtg	ttcctgatca
1260					
gacggaacag	cttcgatgag	cagaacgaga	ttagcggcag	gtatagctgg	aacttccaga
1320					
agagcaccag	cagcttcaac	ttcaccatca	cagcctctca	ggtgggtggat	tctgccgtgt
1380					
acttttgtgc	cctgtctgaa	ctggcctctg	gaggaagcta	tatccctaca	ttcggcagag
1440					
gcacaagcct	gattgtgcac	ccttacatcc	agaaccctga	tcctgctgtg	taccagctgc
1500					
g g g a c a g c a a				g a g c a g c g a c	
1520					

<210> 79

<211> 504

<212> PRT

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 8 construct
polypeptide; beta chain-P2A-alpha chain with
cysteine substitutions in beta and alpha chain
constant domains (partial sequence)

<400> 79

Lys	Ser	Pro	Gln	Pro	Leu	Thr	Arg	Arg	Ala	Thr	Met	Gly	Pro	Gly	Leu
1				5					10					15	
Leu	Cys	Trp	Ala	Leu	Leu	Cys	Leu	Leu	Gly	Ala	Gly	Leu	Val	Asp	Ala
			20					25					30		
Gly	Val	Thr	Gln	Ser	Pro	Thr	His	Leu	Ile	Lys	Thr	Arg	Gly	Gln	Gln
		35					40					45			
Val	Thr	Leu	Arg	Cys	Ser	Pro	Lys	Ser	Gly	His	Asp	Thr	Val	Ser	Trp
	50					55					60				
Tyr	Gln	Gln	Ala	Leu	Gly	Gln	Gly	Pro	Gln	Phe	Ile	Phe	Gln	Tyr	Tyr
65					70					75					80
Glu	Glu	Glu	Glu	Arg	Gln	Arg	Gly	Asn	Phe	Pro	Asp	Arg	Phe	Ser	Gly
				85					90					95	
His	Gln	Phe	Pro	Asn	Tyr	Ser	Ser	Glu	Leu	Asn	Val	Asn	Ala	Leu	Leu
			100					105					110		
Leu	Gly	Asp	Ser	Ala	Leu	Tyr	Leu	Cys	Ala	Ser	Ser	Phe	Arg	Leu	Ala
		115					120					125			
Gly	Gly	Pro	Ser	Thr	Asp	Thr	Gln	Tyr	Phe	Gly	Pro	Gly	Thr	Arg	Leu
	130					135					140				
Thr	Val	Leu	Glu	Asp	Leu	Lys	Asn	Val	Phe	Pro	Pro	Glu	Val	Ala	Val
145					150					155					160
Phe	Glu	Pro	Ser	Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr	Leu
				165					170					175	
Val	Cys	Leu	Ala	Thr	Gly	Phe	Tyr	Pro	Asp	His	Val	Glu	Leu	Ser	Trp
			180					185					190		
Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Cys	Thr	Asp	Pro	Gln
		195					200					205			
Pro	Leu	Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys	Leu	Ser
	210					215					220				
Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn	His
225					230					235					240
Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu	Trp
			245						250					255	
Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu	Ala
		260						265					270		
Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Glu	Ser	Tyr	Gln	Gln	Gly
		275					280					285			
Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr

290	295	300
Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys		
305	310	315
Arg Lys Asp Ser Arg Gly Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu		320
	325	330
Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Leu Thr Ala		335
	340	345
Ser Leu Leu Arg Ala Val Ile Ala Ser Ile Cys Val Val Ser Ser Met		350
	355	360
Ala Gln Lys Val Thr Gln Ala Gln Thr Glu Ile Ser Val Val Glu Lys		365
	370	375
Glu Asp Val Thr Leu Asp Cys Val Tyr Glu Thr Arg Asp Thr Thr Tyr		380
385	390	395
Tyr Leu Phe Trp Tyr Lys Gln Pro Pro Ser Gly Glu Leu Val Phe Leu		400
	405	410
Ile Arg Arg Asn Ser Phe Asp Glu Gln Asn Glu Ile Ser Gly Arg Tyr		415
	420	425
Ser Trp Asn Phe Gln Lys Ser Thr Ser Ser Phe Asn Phe Thr Ile Thr		430
	435	440
Ala Ser Gln Val Val Asp Ser Ala Val Tyr Phe Cys Ala Leu Ser Glu		445
	450	455
Leu Ala Ser Gly Gly Ser Tyr Ile Pro Thr Phe Gly Arg Gly Thr Ser		460
465	470	475
Leu Ile Val His Pro Tyr Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln		480
	485	490
Leu Arg Asp Ser Lys Ser Ser Asp		495
	500	

<210> 80

<211> 1836

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR number 4 construct; beta chain-P2A-alpha chain

<400> 80

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60
ggagctggag tctcccagtc cccagtaac aaggtcacag agaagggaaa ggatgtagag
120
ctcaggtgtg atccaatttc aggtcatact gccctttact ggtaccgaca gagcctgggg
180
cagggcctgg agtttttaat ttacttccaa ggcaacagtg caccagacaa atcagggctg
240

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cccagtgatc	gcttctctgc	agagaggact	gggggatccg	tctccactct	gacgatccag
300					
cgcacacagc	aggaggactc	ggccgtgtat	ctctgtgcca	gcagcttagt	ggtcgggctcc
360					
tacgagcagt	acttcggggc	gggcaccagg	ctcacgggtca	cagaggacct	gaaaaacgtg
420					
ttcccacccg	aggtcgctgt	gtttgagcca	tcagaagcag	agatctccca	cacccaaaag
480					
gccacactgg	tgtgcctggc	cacaggcttc	taccccgacc	acgtggagct	gagctggtgg
540					
gtgaatggga	aggagggtgca	cagtggggtc	agcacagacc	cgcagcccct	caaggagcag
600					
cccgccctca	atgactccag	atactgcctg	agcagccgcc	tgaggggtctc	ggccaccttc
660					
tggcagaacc	cccgcaacca	cttccgctgt	caagtccagt	tctacgggct	ctcggagaat
720					
gacgagtgga	cccaggatag	ggccaaacct	gtcacccaga	tcgtcagcgc	cgaggcctgg
780					
ggtagagcag	actgtggctt	cacctccgag	tcttaccagc	aaggggtcct	gtctgccacc
840					
atcctctatg	agatcttgct	agggaaggcc	accttgatatg	ccgtgctggg	cagtgccctc
900					
gtgctgatgg	ccatgggtcaa	gagaaaggat	tccagaggcg	gttccggagc	cacgaacttc
960					
tctctgttaa	agcaagcagg	agacgtggaa	gaaaaccccg	gtcccatgga	aactctcctg
1020					
ggagtgtctt	tggtgattct	atggcttcaa	ctggctaggg	tgaacagtca	acagggagaa
1080					
gaggatcctc	aggccttgag	catccaggag	ggtgaaaatg	ccaccatgaa	ctgcagttac
1140					
aaaactagta	taaacaattt	acagtgggtat	agacaaaatt	caggtagagg	ccttgtccac
1200					
ctaattttaa	tacgttcaaa	tgaaagagag	aaacacagtg	gaagattaag	agtcacgctt
1260					
gacacttcca	agaaaagcag	ttccttgttg	atcacggctt	cccgggcagc	agacactgct
1320					
tcttacttct	gtgctacgga	cgcgtgggaa	tctaactttg	gaaatgagaa	attaaccttt
1380					
gggactggaa	caagactcac	catcataccc	aatatccaga	accctgaccc	tgccgtgtac
1440					
cagctgagag	actctaaatc	cagtgacaag	tctgtctgcc	tattcaccga	ttttgattct
1500					
caaacaaatg	tgtcacaaag	taaggattct	gatgtgtata	tcacagacaa	aactgtgcta
1560					
gacatgaggt	ctatggactt	caagagcaac	agtgctgtgg	cctggagcaa	caaatctgac
1620					

Thr 1	Met	Gly	Thr	Arg 5	Leu	Leu	Phe	Trp	Val 10	Ala	Phe	Cys	Leu	Leu 15	Gly
Ala	Asp	His	Thr 20	Gly	Ala	Gly	Val 25	Ser	Gln	Ser	Pro	Ser 30	Asn	Lys	Val
Thr	Glu	Lys 35	Gly	Lys	Asp	Val 40	Glu	Leu	Arg	Cys	Asp 45	Pro	Ile	Ser	Gly
His	Thr 50	Ala	Leu	Tyr	Trp	Tyr 55	Arg	Gln	Ser	Leu	Gly 60	Gln	Gly	Leu	Glu
Phe 65	Leu	Ile	Tyr	Phe	Gln 70	Gly	Asn	Ser	Ala	Pro 75	Asp	Lys	Ser	Gly	Leu 80
Pro	Ser	Asp	Arg 85	Phe	Ser	Ala	Glu	Arg 90	Thr	Gly	Gly	Ser	Val 95	Ser	Thr
Leu	Thr	Ile	Gln 100	Arg	Thr	Gln	Gln	Glu 105	Asp	Ser	Ala	Val	Tyr 110	Leu	Cys
Ala	Ser	Ser 115	Leu	Val	Val	Gly	Ser 120	Tyr	Glu	Gln	Tyr	Phe 125	Gly	Pro	Gly
Thr	Arg 130	Leu	Thr	Val	Thr	Glu 135	Asp	Leu	Lys	Asn	Val 140	Phe	Pro	Pro	Glu
Val 145	Ala	Val	Phe	Glu	Pro 150	Ser	Glu	Ala	Glu	Ile 155	Ser	His	Thr	Gln	Lys 160
Ala	Thr	Leu	Val	Cys 165	Leu	Ala	Thr	Gly	Phe 170	Tyr	Pro	Asp	His 175	Val	Glu
Leu	Ser	Trp	Trp 180	Val	Asn	Gly	Lys	Glu 185	Val	His	Ser	Gly	Val 190	Ser	Thr
Asp	Pro	Gln 195	Pro	Leu	Lys	Glu	Gln 200	Pro	Ala	Leu	Asn	Asp 205	Ser	Arg	Tyr
Cys	Leu	Ser	Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro

	210					215					220				
Arg	Asn	His	Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn
225					230					235					240
Asp	Glu	Trp	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser
				245					250					255	
Ala	Glu	Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Glu	Ser	Tyr
			260				265						270		
Gln	Gln	Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly
		275					280					285			
Lys	Ala	Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala
	290					295					300				
Met	Val	Lys	Arg	Lys	Asp	Ser	Arg	Gly	Gly	Ser	Gly	Ala	Thr	Asn	Phe
305					310					315				320	
Ser	Leu	Leu	Lys	Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met
				325					330				335		
Glu	Thr	Leu	Leu	Gly	Val	Ser	Leu	Val	Ile	Leu	Trp	Leu	Gln	Leu	Ala
			340					345					350		
Arg	Val	Asn	Ser	Gln	Gln	Gly	Glu	Glu	Asp	Pro	Gln	Ala	Leu	Ser	Ile
		355					360					365			
Gln	Glu	Gly	Glu	Asn	Ala	Thr	Met	Asn	Cys	Ser	Tyr	Lys	Thr	Ser	Ile
	370					375					380				
Asn	Asn	Leu	Gln	Trp	Tyr	Arg	Gln	Asn	Ser	Gly	Arg	Gly	Leu	Val	His
385					390					395				400	
Leu	Ile	Leu	Ile	Arg	Ser	Asn	Glu	Arg	Glu	Lys	His	Ser	Gly	Arg	Leu
				405					410				415		
Arg	Val	Thr	Leu	Asp	Thr	Ser	Lys	Lys	Ser	Ser	Ser	Leu	Leu	Ile	Thr
			420					425					430		
Ala	Ser	Arg	Ala	Ala	Asp	Thr	Ala	Ser	Tyr	Phe	Cys	Ala	Thr	Asp	Ala
		435					440					445			
Trp	Glu	Ser	Asn	Phe	Gly	Asn	Glu	Lys	Leu	Thr	Phe	Gly	Thr	Gly	Thr
	450					455					460				
Arg	Leu	Thr	Ile	Ile	Pro	Asn	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr
465					470					475				480	
Gln	Leu	Arg	Asp	Ser	Lys	Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr
				485					490				495		
Asp	Phe	Asp	Ser	Gln	Thr	Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val
			500					505					510		
Tyr	Ile	Thr	Asp	Lys	Thr	Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys
		515					520					525			
Ser	Asn	Ser	Ala	Val	Ala	Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala
	530					535					540				
Asn	Ala	Phe	Asn	Asn	Ser	Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser
545					550					555				560	
Pro	Glu	Ser	Ser	Cys	Asp	Val	Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr
				565					570					575	

Asp	Thr	Asn	Leu	Asn	Phe	Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile
			580					585					590		
Leu	Leu	Leu	Lys	Val	Ala	Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu
		595					600					605			
Trp	Ser	Ser													
	610														

<210> 82

<211> 1837

<212> DNA

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 4 construct; beta chain-P2A-alpha chain with cysteine substitutions in beta and alpha chain constant domains

<400> 82

caccatgggc	accagactgc	tgttctgggt	ggccttctgt	ctgctgggcg	ccgatcatatc
60					
aggcgctggc	gtgtcccaga	gccccagcaa	caaagtgacc	gagaagggca	aggacgtgga
120					
actgagatgc	gaccccatca	gcggccacac	cgccctgtac	tggtacagac	agtctctggg
180					
ccagggcctg	gaattcctga	tatattttca	gggcaacagc	gccctgaca	agagcggcct
240					
gccctccgat	agattcagcg	ccgagagaac	aggcggcagc	gtgtccaccc	tgaccatcca
300					
gagaacccag	caggaagata	gcgccgtgta	cctgtgcgcc	agcagcctgg	tcgtgggcag
360					
ctacgagcag	tactttggcc	caggcacccg	gctgaccgtg	accgaggatc	tgaagaacgt
420					
gttcccccca	gaggtggccg	tgttcgagcc	ttctgaggcc	gagatcagcc	acaccagaa
480					
agccaccctc	gtgtgtcttg	ccaccggctt	ctaccccgac	catgtggaac	tgtcttggtg
540					
ggtcaacggc	aaagaggtgc	actccggcgt	gtgcaccgat	ccccagcctc	tgaaagaaca
600					
gcccggccctg	aacgacagcc	ggtactgcct	gagcagcaga	ctgagagtgt	ccgccacctt
660					
ctggcagaac	ccccggaacc	acttcagatg	ccagggtgcag	ttctacggcc	tgagcgagaa
720					
cgacgagtgg	accaggaca	gagccaagcc	cgtgaccag	atcgtgtctg	ccgaagcctg
780					
gggcagagcc	gattgcggct	ttaccagcga	gagctaccag	cagggcgtgc	tgagcgccac
840					

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catcctgtac gagattctgc tgggaaaggc cacactgtac gccgtgctgg tgtctgccct
900
ggtgctgatg gccatgggtca agcggaagga cagcagaggc ggttccggag ccacgaactt
960
ctctctgtta aagcaagcag gagacgtgga agaaaacccc ggtcccatgg aaaccctgct
1020
gggagtgtcc ctcgtgatcc tgtggctgca gctggccaga gtgaacagcc agcaggggga
1080
agaggatcca caggccctga gcattcagga aggcgagAAC gccaccatga actgcagcta
1140
caagaccagc atcaacaacc tgcagtggta caggcagaac tccggcagag gcctggtgca
1200
cctgatcctg atcagaagca acgagagaga gaagcacagc ggacggctga gagtgaccct
1260
ggacacctcc aagaagtcca gctccctgct gatcaccgcc agcagagccg ccgataccgc
1320
cagctacttc tgtgccacag acgcctggga gagcaacttc ggcaacgaga agctgacctt
1380
cggcaccggc acaagactga ccatcatccc caacatccag aaccccgacc ccgccgtgta
1440
tcagctgaga gacagcaaga gcagcgacaa gtccgtgtgc ctgttcaccg acttcgacag
1500
ccagaccaat gtgtcccagt ccaaggacag cgacgtgtac atcaccgata agtgcgctgct
1560
ggacatgcgc agcatggact tcaagagcaa ctccgccgtg gcctggtcca acaagagcga
1620
tttcgcctgc gccaacgcct tcaacaacag cattatcccc gaggacacat tcttccaag
1680
ccccgagagc agctgcgacg tgaagctgggt ggaaaagagc ttcgagacag acaccaacct
1740
gaacttccag aacctgagcg tgatcggcct ccggatcctg ctgctgaagg tggccggcctt
1800
c a a c c t g c t g           a t g a c c c t g a           g a c t g t g g t c           c a g c t g a
1837

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<210> 83

<211> 611

<212> PRT

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 4 construct; beta
chain-P2A-alpha chain with cysteine substitutions
in beta and alpha chain constant domains

<400> 83

Thr	Met	Gly	Thr	Arg	Leu	Leu	Phe	Trp	Val	Ala	Phe	Cys	Leu	Leu	Gly
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Ala	Asp	His	Thr	Gly	Ala	Gly	Val	Ser	Gln	Ser	Pro	Ser	Asn	Lys	Val
			20					25					30		
Thr	Glu	Lys	Gly	Lys	Asp	Val	Glu	Leu	Arg	Cys	Asp	Pro	Ile	Ser	Gly
		35					40				45				
His	Thr	Ala	Leu	Tyr	Trp	Tyr	Arg	Gln	Ser	Leu	Gly	Gln	Gly	Leu	Glu
	50					55					60				
Phe	Leu	Ile	Tyr	Phe	Gln	Gly	Asn	Ser	Ala	Pro	Asp	Lys	Ser	Gly	Leu
65					70					75					80
Pro	Ser	Asp	Arg	Phe	Ser	Ala	Glu	Arg	Thr	Gly	Gly	Ser	Val	Ser	Thr
				85					90					95	
Leu	Thr	Ile	Gln	Arg	Thr	Gln	Gln	Glu	Asp	Ser	Ala	Val	Tyr	Leu	Cys
			100					105					110		
Ala	Ser	Ser	Leu	Val	Val	Gly	Ser	Tyr	Glu	Gln	Tyr	Phe	Gly	Pro	Gly
		115					120					125			
Thr	Arg	Leu	Thr	Val	Thr	Glu	Asp	Leu	Lys	Asn	Val	Phe	Pro	Pro	Glu
	130					135					140				
Val	Ala	Val	Phe	Glu	Pro	Ser	Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys
145					150					155					160
Ala	Thr	Leu	Val	Cys	Leu	Ala	Thr	Gly	Phe	Tyr	Pro	Asp	His	Val	Glu
				165					170					175	
Leu	Ser	Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Cys	Thr
			180					185					190		
Asp	Pro	Gln	Pro	Leu	Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr
		195					200					205			
Cys	Leu	Ser	Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro
	210					215					220				
Arg	Asn	His	Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn
225					230					235					240
Asp	Glu	Trp	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser
				245					250					255	
Ala	Glu	Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Glu	Ser	Tyr
			260					265					270		
Gln	Gln	Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly
		275					280					285			
Lys	Ala	Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala
	290					295					300				
Met	Val	Lys	Arg	Lys	Asp	Ser	Arg	Gly	Gly	Ser	Gly	Ala	Thr	Asn	Phe
305					310					315					320
Ser	Leu	Leu	Lys	Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met
				325					330					335	
Glu	Thr	Leu	Leu	Gly	Val	Ser	Leu	Val	Ile	Leu	Trp	Leu	Gln	Leu	Ala
			340					345					350		

Arg	Val	Asn	Ser	Gln	Gln	Gly	Glu	Glu	Asp	Pro	Gln	Ala	Leu	Ser	Ile	
		355					360				365					
Gln	Glu	Gly	Glu	Asn	Ala	Thr	Met	Asn	Cys	Ser	Tyr	Lys	Thr	Ser	Ile	
		370				375					380					
Asn	Asn	Leu	Gln	Trp	Tyr	Arg	Gln	Asn	Ser	Gly	Arg	Gly	Leu	Val	His	
385					390					395					400	
Leu	Ile	Leu	Ile	Arg	Ser	Asn	Glu	Arg	Glu	Lys	His	Ser	Gly	Arg	Leu	
				405					410					415		
Arg	Val	Thr	Leu	Asp	Thr	Ser	Lys	Lys	Ser	Ser	Ser	Leu	Leu	Ile	Thr	
			420					425					430			
Ala	Ser	Arg	Ala	Ala	Asp	Thr	Ala	Ser	Tyr	Phe	Cys	Ala	Thr	Asp	Ala	
		435					440					445				
Trp	Glu	Ser	Asn	Phe	Gly	Asn	Glu	Lys	Leu	Thr	Phe	Gly	Thr	Gly	Thr	
	450					455					460					
Arg	Leu	Thr	Ile	Ile	Pro	Asn	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	
465					470					475					480	
Gln	Leu	Arg	Asp	Ser	Lys	Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	
				485					490					495		
Asp	Phe	Asp	Ser	Gln	Thr	Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	
			500					505					510			
Tyr	Ile	Thr	Asp	Lys	Cys	Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	
		515					520					525				
Ser	Asn	Ser	Ala	Val	Ala	Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	
	530					535					540					
Asn	Ala	Phe	Asn	Asn	Ser	Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	
545					550					555					560	
Pro	Glu	Ser	Ser	Cys	Asp	Val	Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	
				565				570						575		
Asp	Thr	Asn	Leu	Asn	Phe	Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	
			580					585					590			
Leu	Leu	Leu	Lys	Val	Ala	Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	
		595					600					605				
Trp	Ser	Ser														
		610														

<210> 84

<211> 178

<212> PRT

<213> Artificial Sequence

<220>

<223> TCRbeta2 constant domain

<400> 84

Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro Ser

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			20					25					30			
Thr	Gly	Phe	Tyr	Pro	Asp	His	Val	Glu	Leu	Ser	Trp	Trp	Val	Asn	Gly	
		35					40					45				
Lys	Glu	Val	His	Ser	Gly	Val	Ser	Thr	Asp	Pro	Gln	Pro	Leu	Lys	Glu	
	50					55					60					
Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys	Leu	Ser	Ser	Arg	Leu	Arg	
65					70				75						80	
Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn	His	Phe	Arg	Cys	Gln	
				85				90					95			
Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu	Trp	Thr	Gln	Asp	Arg	
		100					105					110				
Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu	Ala	Trp	Gly	Arg	Ala	
		115					120					125				
Asp	Cys	Gly	Phe	Thr	Ser	Glu	Ser	Tyr	Gln	Gln	Gly	Val	Leu	Ser	Ala	
	130					135					140					
Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu	Tyr	Ala	Val	
145					150				155						160	
Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val	Lys	Arg	Lys	Asp	Ser	
				165				170						175		

Arg Gly

<210> 85

<211> 335

<212> PRT

<213> Artificial Sequence

<220>

<223> truncated EGFR polypeptide lacking signal peptide

<400> 85

Arg	Lys	Val	Cys	Asn	Gly	Ile	Gly	Ile	Gly	Glu	Phe	Lys	Asp	Ser	Leu	
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Ser	Ile	Asn	Ala	Thr	Asn	Ile	Lys	His	Phe	Lys	Asn	Cys	Thr	Ser	Ile	
		20					25					30				
Ser	Gly	Asp	Leu	His	Ile	Leu	Pro	Val	Ala	Phe	Arg	Gly	Asp	Ser	Phe	
	35					40					45					
Thr	His	Thr	Pro	Pro	Leu	Asp	Pro	Gln	Glu	Leu	Asp	Ile	Leu	Lys	Thr	
	50				55				60							
Val	Lys	Glu	Ile	Thr	Gly	Phe	Leu	Leu	Ile	Gln	Ala	Trp	Pro	Glu	Asn	
65					70				75						80	
Arg	Thr	Asp	Leu	His	Ala	Phe	Glu	Asn	Leu	Glu	Ile	Ile	Arg	Gly	Arg	
				85				90					95			

Thr	Lys	Gln	His	Gly	Gln	Phe	Ser	Leu	Ala	Val	Val	Ser	Leu	Asn	Ile		
			100					105					110				
Thr	Ser	Leu	Gly	Leu	Arg	Ser	Leu	Lys	Glu	Ile	Ser	Asp	Gly	Asp	Val		
		115					120					125					
Ile	Ile	Ser	Gly	Asn	Lys	Asn	Leu	Cys	Tyr	Ala	Asn	Thr	Ile	Asn	Trp		
	130					135					140						
Lys	Lys	Leu	Phe	Gly	Thr	Ser	Gly	Gln	Lys	Thr	Lys	Ile	Ile	Ser	Asn		
145					150					155					160		
Arg	Gly	Glu	Asn	Ser	Cys	Lys	Ala	Thr	Gly	Gln	Val	Cys	His	Ala	Leu		
			165					170						175			
Cys	Ser	Pro	Glu	Gly	Cys	Trp	Gly	Pro	Glu	Pro	Arg	Asp	Cys	Val	Ser		
		180					185						190				
Cys	Arg	Asn	Val	Ser	Arg	Gly	Arg	Glu	Cys	Val	Asp	Lys	Cys	Asn	Leu		
	195					200					205						
Leu	Glu	Gly	Glu	Pro	Arg	Glu	Phe	Val	Glu	Asn	Ser	Glu	Cys	Ile	Gln		
	210					215					220						
Cys	His	Pro	Glu	Cys	Leu	Pro	Gln	Ala	Met	Asn	Ile	Thr	Cys	Thr	Gly		
225					230				235						240		
Arg	Gly	Pro	Asp	Asn	Cys	Ile	Gln	Cys	Ala	His	Tyr	Ile	Asp	Gly	Pro		
			245				250							255			
His	Cys	Val	Lys	Thr	Cys	Pro	Ala	Gly	Val	Met	Gly	Glu	Asn	Asn	Thr		
		260					265						270				
Leu	Val	Trp	Lys	Tyr	Ala	Asp	Ala	Gly	His	Val	Cys	His	Leu	Cys	His		
	275					280					285						
Pro	Asn	Cys	Thr	Tyr	Gly	Cys	Thr	Gly	Pro	Gly	Leu	Glu	Gly	Cys	Pro		
	290					295					300						
Thr	Asn	Gly	Pro	Lys	Ile	Pro	Ser	Ile	Ala	Thr	Gly	Met	Val	Gly	Ala		
305					310				315						320		
Leu	Leu	Leu	Leu	Leu	Val	Val	Ala	Leu	Gly	Ile	Gly	Leu	Phe	Met			
			325					330						335			

<210> 86

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 6 construct; beta chain-P2A-alpha chain with cysteine substitutions in beta and alpha chain constant domains (partial sequence)

<400> 86

Lys	Ser	Pro	Gln	Pro	Leu	Thr	Arg	Arg	Ala	Thr	Met	Ser	Ile	Ser	Leu		
1				5					10					15			

Leu	Cys	Cys	Ala	Ala	Phe	Pro	Leu	Leu	Trp	Ala	Gly	Pro	Val	Asn	Ala	
			20				25						30			
Gly	Val	Thr	Gln	Thr	Pro	Lys	Phe	Arg	Ile	Leu	Lys	Ile	Gly	Gln	Ser	
		35					40					45				
Met	Thr	Leu	Gln	Cys	Thr	Gln	Asp	Met	Asn	His	Asn	Tyr	Met	Tyr	Trp	
	50					55					60					
Tyr	Arg	Gln	Asp	Pro	Gly	Met	Gly	Leu	Lys	Leu	Ile	Tyr	Tyr	Ser	Val	
65					70					75					80	
Gly	Ala	Gly	Ile	Thr	Asp	Lys	Gly	Glu	Val	Pro	Asn	Gly	Tyr	Asn	Val	
			85					90						95		
Ser	Arg	Ser	Thr	Thr	Glu	Asp	Phe	Pro	Leu	Arg	Leu	Glu	Leu	Ala	Ala	
			100					105					110			
Pro	Ser	Gln	Thr	Ser	Val	Tyr	Phe	Cys	Ala	Ser	Ser	Asp	Arg	Ser	Asn	
		115					120					125				
Thr	Gly	Glu	Leu	Phe	Phe	Gly	Glu	Gly	Ser	Arg	Leu	Thr	Val	Leu	Glu	
	130					135					140					
Asp	Leu	Lys	Asn	Val	Phe	Pro	Pro	Glu	Val	Ala	Val	Phe	Glu	Pro	Ser	
145					150					155					160	
Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ala	
			165					170						175		
Thr	Gly	Phe	Tyr	Pro	Asp	His	Val	Glu	Leu	Ser	Trp	Trp	Val	Asn	Gly	
		180						185					190			
Lys	Glu	Val	His	Ser	Gly	Val	Ser	Thr	Asp	Pro	Gln	Pro	Leu	Lys	Glu	
		195					200				205					
Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys	Leu	Ser	Ser	Arg	Leu	Arg	
	210					215					220					
Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn	His	Phe	Arg	Cys	Gln	
225					230					235					240	
Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu	Trp	Thr	Gln	Asp	Arg	
			245						250					255		
Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu	Ala	Trp	Gly	Arg	Ala	
			260					265					270			
Asp	Cys	Gly	Phe	Thr	Ser	Glu	Ser	Tyr	Gln	Gln	Gly	Val	Leu	Ser	Ala	
		275					280					285				
Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu	Tyr	Ala	Val	
	290					295					300					
Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val	Lys	Arg	Lys	Asp	Ser	
305					310					315					320	
Arg	Gly	Gly	Ser	Gly	Ala	Thr	Asn	Phe	Ser	Leu	Leu	Lys	Gln	Ala	Gly	
			325					330						335		
Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Glu	Lys	Asn	Pro	Leu	Ala	Ala	
			340					345					350			
Pro	Leu	Leu	Ile	Leu	Trp	Phe	His	Leu	Asp	Cys	Val	Ser	Ser	Ile	Leu	
		355					360					365				
Asn	Val	Glu	Gln	Ser	Pro	Gln	Ser	Leu	His	Val	Gln	Glu	Gly	Asp	Ser	

370	375	380													
Thr	Asn	Phe	Thr	Cys	Ser	Phe	Pro	Ser	Ser	Asn	Phe	Tyr	Ala	Leu	His
385					390					395					400
Trp	Tyr	Arg	Trp	Glu	Thr	Ala	Lys	Ser	Pro	Glu	Ala	Leu	Phe	Val	Met
				405						410					415
Thr	Leu	Asn	Gly	Asp	Glu	Lys	Lys	Lys	Gly	Arg	Ile	Ser	Ala	Thr	Leu
			420						425					430	
Asn	Thr	Lys	Glu	Gly	Tyr	Ser	Tyr	Leu	Tyr	Ile	Lys	Gly	Ser	Gln	Pro
		435					440					445			
Glu	Asp	Ser	Ala	Thr	Tyr	Leu	Cys	Ala	Leu	Gly	Pro	Tyr	Asn	Asp	Tyr
	450					455					460				
Lys	Leu	Ser	Phe	Gly	Ala	Gly	Thr	Thr	Val	Thr	Val	Arg	Ala	Asn	Ile
465					470					475					480
Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser	Lys	Ser	Ser
				485					490					495	

Asp

<210> 87
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR number 5 Valpha CDR1

<400> 87
 Lys Ala Leu Tyr Ser
 1 5

<210> 88
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR number 5 Valpha CDR2

<400> 88
 Leu Leu Lys Gly Gly Glu Gln
 1 5

<210> 89
 <211> 11
 <212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 5 Valpha CDR3

<400> 89

Gly	Thr	Glu	Glu	Ala	Asn	Asp	Tyr	Lys	Leu	Ser
1				5					10	

<210> 90

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 5 Valpha variable region

<400> 90

Gln	Gln	Pro	Val	Gln	Ser	Pro	Gln	Ala	Val	Ile	Leu	Arg	Glu	Gly	Glu
1				5					10					15	
Asp	Ala	Val	Ile	Asn	Cys	Ser	Ser	Ser	Lys	Ala	Leu	Tyr	Ser	Val	His
			20					25					30		
Trp	Tyr	Arg	Gln	Lys	His	Gly	Glu	Ala	Pro	Val	Phe	Leu	Met	Ile	Leu
		35					40					45			
Leu	Lys	Gly	Gly	Glu	Gln	Lys	Gly	His	Glu	Lys	Ile	Ser	Ala	Ser	Phe
	50					55					60				
Asn	Glu	Lys	Lys	Gln	Gln	Ser	Ser	Leu	Tyr	Leu	Thr	Ala	Ser	Gln	Leu
65					70				75						80
Ser	Tyr	Ser	Gly	Thr	Tyr	Phe	Cys	Gly	Thr	Glu	Glu	Ala	Asn	Asp	Tyr
				85					90					95	
Lys	Leu	Ser	Phe	Gly	Ala	Gly	Thr	Thr	Val	Thr	Val	Arg			
			100					105							

<210> 91

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 5 Vbeta CDR1

<400> 91

Ser	Gly	Asp	Leu	Ser
1				5

<210> 92
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR number 5 Vbeta CDR2

<400> 92
Tyr Tyr Asn Gly Glu Glu
1 5

<210> 93
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR number 5 Vbeta CDR3

<400> 93
Ala Ser Ser Val Gly Gln Gly Ser Ser Tyr
1 5 10

<210> 94
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR number 5 Vbeta variable region

<400> 94
Asp Ser Gly Val Thr Gln Thr Pro Lys His Leu Ile Thr Ala Thr Gly
1 5 10 15
Gln Arg Val Thr Leu Arg Cys Ser Pro Arg Ser Gly Asp Leu Ser Val
20 25 30
Tyr Trp Tyr Gln Gln Ser Leu Asp Gln Gly Leu Gln Phe Leu Ile Gln
35 40 45
Tyr Tyr Asn Gly Glu Glu Arg Ala Lys Gly Asn Ile Leu Glu Arg Phe
50 55 60
Ser Ala Gln Gln Phe Pro Asp Leu His Ser Glu Leu Asn Leu Ser Ser
65 70 75 80
Leu Glu Leu Gly Asp Ser Ala Leu Tyr Phe Cys Ala Ser Ser Val Gly
85 90 95

Gln Gly Ser Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg Leu Thr
100 105 110
Val Thr

<210> 95
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR number 9 and TCR number 11 Valpha CDR1

<400> 95
Val Ser Pro Phe Ser Asn
1 5

<210> 96
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR number 9 and TCR number 11 Valpha CDR2

<400> 96
Thr Phe Ser Glu Asn Thr
1 5

<210> 97
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR number 9 and TCR number 11 Valpha CDR3

<400> 97
Val Val Trp Gly Gly Asp Thr Asp Lys Leu Ile
1 5 10

<210> 98
<211> 111
<212> PRT
<213> Artificial Sequence

<220>

<223> TCR number 9 and TCR number 11 Valpha variable region

<400> 98

Lys	Asn	Gln	Val	Glu	Gln	Ser	Pro	Gln	Ser	Leu	Ile	Ile	Leu	Glu	Gly
1				5					10					15	
Lys	Asn	Cys	Thr	Leu	Gln	Cys	Asn	Tyr	Thr	Val	Ser	Pro	Phe	Ser	Asn
			20					25					30		
Leu	Arg	Trp	Tyr	Lys	Gln	Asp	Thr	Gly	Arg	Gly	Pro	Val	Ser	Leu	Thr
		35					40					45			
Ile	Met	Thr	Phe	Ser	Glu	Asn	Thr	Lys	Ser	Asn	Gly	Arg	Tyr	Thr	Ala
	50					55					60				
Thr	Leu	Asp	Ala	Asp	Thr	Lys	Gln	Ser	Ser	Leu	His	Ile	Thr	Ala	Ser
65					70					75					80
Gln	Leu	Ser	Asp	Ser	Ala	Ser	Tyr	Ile	Cys	Val	Val	Trp	Gly	Gly	Asp
			85						90				95		
Thr	Asp	Lys	Leu	Ile	Phe	Gly	Thr	Gly	Thr	Arg	Leu	Gln	Val	Phe	
			100					105					110		

<210> 99

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 11 Vbeta CDR1

<400> 99

Trp	Ser	His	Ser	Tyr
1			5	

<210> 100

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 11 Vbeta CDR2

<400> 100

Ser	Ala	Ala	Ala	Asp	Ile
1				5	

<210> 101
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR number 11 Vbeta CDR3

<400> 101
Ala Ser Ser Asp Gly Gly Gly Gln Tyr
1 5

<210> 102
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR number 11 Vbeta variable region

<400> 102
Asp Ala Gly Ile Thr Gln Ser Pro Arg Tyr Lys Ile Thr Glu Thr Gly
1 5 10 15
Arg Gln Val Thr Leu Met Cys His Gln Thr Trp Ser His Ser Tyr Met
20 25 30
Phe Trp Tyr Arg Gln Asp Leu Gly His Gly Leu Arg Leu Ile Tyr Tyr
35 40 45
Ser Ala Ala Ala Asp Ile Thr Asp Lys Gly Glu Val Pro Asp Gly Tyr
50 55 60
Val Val Ser Arg Ser Lys Thr Glu Asn Phe Pro Leu Thr Leu Glu Ser
65 70 75 80
Ala Thr Arg Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Ser Asp Gly
85 90 95
Gly Gly Gln Tyr Phe Pro Gly Thr Arg Leu Thr Val Thr
100 105

<210> 103
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR number 6 and TCR number 7 Valpha CDR1

<400> 103

Ser Ser Asn Phe Tyr Ala
1 5

<210> 104

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 6 Valpha CDR2

<400> 104

Met Thr Leu Asn Gly Asp Glu
1 5

<210> 105

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 6 Valpha CDR3

<400> 105

Cys Ala Leu Gly Pro Tyr Asn Asp Tyr Lys Leu Ser Phe
1 5 10

<210> 106

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 6 Valpha variant region

<400> 106

Ile	Leu	Asn	Val	Glu	Gln	Ser	Pro	Gln	Ser	Leu	His	Val	Gln	Glu	Gly
1				5					10					15	
Asp	Ser	Thr	Asn	Phe	Thr	Cys	Ser	Phe	Pro	Ser	Ser	Asn	Phe	Tyr	Ala
			20					25					30		
Leu	His	Trp	Tyr	Arg	Trp	Glu	Thr	Ala	Lys	Ser	Pro	Glu	Ala	Leu	Phe
		35					40					45			
Val	Met	Thr	Leu	Asn	Gly	Asp	Glu	Lys	Lys	Lys	Gly	Arg	Ile	Ser	Ala
	50					55					60				
Thr	Leu	Asn	Thr	Lys	Glu	Gly	Tyr	Ser	Tyr	Leu	Tyr	Ile	Lys	Gly	Ser

65					70					75					80
Gln	Pro	Glu	Asp	Ser	Ala	Thr	Tyr	Leu	Cys	Ala	Leu	Gly	Pro	Tyr	Asn
				85					90					95	
Asp	Tyr	Lys	Leu	Ser	Phe	Gly	Ala	Gly	Thr	Thr	Val	Thr	Val	Arg	Ala
			100					105					110		

<210> 107
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR number 6 Vbeta CDR1

<400> 107
 Met Asn His Asn Tyr
 1 5

<210> 108
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR number 6 Vbeta CDR2

<400> 108
 Ser Val Gly Ala Gly Ile
 1 5

<210> 109
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR number 6 Vbeta CDR3

<400> 109
 Ala Ser Ser Asp Arg Ser Asn Thr Gly Glu Leu Phe
 1 5 10

<210> 110
 <211> 113
 <212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 6 Vbeta variable region

<400> 110

Asn	Ala	Gly	Val	Thr	Gln	Thr	Pro	Lys	Phe	Arg	Ile	Leu	Lys	Ile	Gly
1				5				10						15	
Gln	Ser	Met	Thr	Leu	Gln	Cys	Thr	Gln	Asp	Met	Asn	His	Asn	Tyr	Met
			20					25					30		
Tyr	Trp	Tyr	Arg	Gln	Asp	Pro	Gly	Met	Gly	Leu	Lys	Leu	Ile	Tyr	Tyr
		35					40					45			
Ser	Val	Gly	Ala	Gly	Ile	Thr	Asp	Lys	Gly	Glu	Val	Pro	Asn	Gly	Tyr
	50					55				60					
Asn	Val	Ser	Arg	Ser	Thr	Thr	Glu	Asp	Phe	Pro	Leu	Arg	Leu	Glu	Leu
65					70				75					80	
Ala	Ala	Pro	Ser	Gln	Thr	Ser	Val	Tyr	Phe	Cys	Ala	Ser	Ser	Asp	Arg
			85						90					95	
Ser	Asn	Thr	Gly	Glu	Leu	Phe	Phe	Gly	Glu	Gly	Ser	Arg	Leu	Thr	Val
			100					105					110		

Leu

<210> 111

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 1 and TCR number 2 Valpha CDR1

<400> 111

Asp	Ser	Ala	Ile	Tyr	Asn
1				5	

<210> 112

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 1 and TCR number 2 Valpha CDR2

<400> 112

Ile Gln Ser Ser Gln Arg Glu

1

5

<210> 113
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR number 1 Valpha CDR3

<400> 113
Ala Val Glu Gly Asp Ser Ser Tyr Lys Leu Ile
1 5 10

<210> 114
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR number 1 Valpha variable region

<400> 114
Lys Gln Glu Val Thr Gln Ile Pro Ala Ala Leu Ser Val Pro Glu Gly
1 5 10 15
Glu Asn Leu Val Leu Asn Cys Ser Phe Thr Asp Ser Ala Ile Tyr Asn
20 25 30
Leu Gln Trp Phe Arg Gln Asp Pro Gly Lys Gly Leu Thr Ser Leu Leu
35 40 45
Leu Ile Gln Ser Ser Gln Arg Glu Gln Thr Ser Gly Arg Leu Asn Ala
50 55 60
Ser Leu Asp Lys Ser Ser Gly Arg Ser Thr Leu Tyr Ile Ala Ala Ser
65 70 75 80
Gln Pro Gly Asp Ser Ala Thr Tyr Leu Cys Ala Val Glu Gly Asp Ser
85 90 95
Ser Tyr Lys Leu Ile Phe Gly Ser Gly Thr Arg Leu Leu Val Arg Pro
100 105 110

<210> 115
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR number 1 and TCR number 8 Vbeta CDR1

<400> 115
Ser Gly His Asp Thr
1 5

<210> 116
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR number 1 and TCR number 8 Vbeta CDR2

<400> 116
Tyr Tyr Glu Glu Glu Glu
1 5

<210> 117
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR number 1 Vbeta CDR3

<400> 117
Ala Ser Ser Phe Phe Ser Gln Glu Thr Gln Tyr
1 5 10

<210> 118
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR number 1 Vbeta variable region

<400> 118
Asp Ala Gly Val Thr Gln Ser Pro Thr His Leu Ile Lys Thr Arg Gly
1 5 10 15
Gln Gln Val Thr Leu Arg Cys Ser Pro Lys Ser Gly His Asp Thr Val
20 25 30
Ser Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Gln Phe Ile Phe Gln
35 40 45
Tyr Tyr Glu Glu Glu Glu Arg Gln Arg Gly Asn Phe Pro Asp Arg Phe

50						55						60				
Ser	Gly	His	Gln	Phe	Pro	Asn	Tyr	Ser	Ser	Glu	Leu	Asn	Val	Asn	Ala	
65					70					75					80	
Leu	Leu	Leu	Gly	Asp	Ser	Ala	Leu	Tyr	Leu	Cys	Ala	Ser	Ser	Phe	Phe	
			85						90					95		
Ser	Gln	Glu	Thr	Gln	Tyr	Phe	Gly	Pro	Gly	Thr	Arg	Leu	Leu	Val	Leu	
			100					105					110			

<210> 119

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 2 Valpha CDR3

<400> 119

Ala	Val	Ile	Gly	Glu	Gln	Asn	Phe	Val
1					5			

<210> 120

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 2 Valpha variable region

<400> 120

Lys	Gln	Glu	Val	Thr	Gln	Ile	Pro	Ala	Ala	Leu	Ser	Val	Pro	Glu	Gly
1				5					10					15	
Glu	Asn	Leu	Val	Leu	Asn	Cys	Ser	Phe	Thr	Asp	Ser	Ala	Ile	Tyr	Asn
		20						25					30		
Leu	Gln	Trp	Phe	Arg	Gln	Asp	Pro	Gly	Lys	Gly	Leu	Thr	Ser	Leu	Leu
		35					40					45			
Leu	Ile	Gln	Ser	Ser	Gln	Arg	Glu	Gln	Thr	Ser	Gly	Arg	Leu	Asn	Ala
	50					55					60				
Ser	Leu	Asp	Lys	Ser	Ser	Gly	Arg	Ser	Thr	Leu	Tyr	Ile	Ala	Ala	Ser
65					70					75					80
Gln	Pro	Gly	Asp	Ser	Ala	Thr	Tyr	Leu	Cys	Ala	Val	Ile	Gly	Glu	Gln
			85						90					95	
Asn	Phe	Val	Phe	Gly	Pro	Gly	Thr	Arg	Leu	Ser	Val	Leu	Pro		
			100					105					110		

<210> 121

<211> 5
<212> PRT
<213> Artificial Sequence

<220>

<223> TCR number 2, TCR number 3, and TCR number 10
Vbeta CDR1

<400> 121
Ser Gly His Thr Ala
1 5

<210> 122
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> TCR number 2, TCR number 3, and TCR number 10
Vbeta CDR2

<400> 122
Phe Gln Gly Thr Gly Ala
1 5

<210> 123
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> TCR number 2 Vbeta CDR3

<400> 123
Ala Ser Ser Leu Ser Gly Leu Gly Ser Gly Ala Asn Val Leu Thr
1 5 10 15

<210> 124
<211> 117
<212> PRT
<213> Artificial Sequence

<220>

<223> TCR number 2 Vbeta variable region

<400> 124

Gly	Ala	Gly	Val	Ser	Gln	Thr	Pro	Ser	Asn	Lys	Val	Thr	Glu	Lys	Gly
1				5					10					15	
Lys	Tyr	Val	Glu	Leu	Arg	Cys	Asp	Pro	Ile	Ser	Gly	His	Thr	Ala	Leu
		20						25					30		
Tyr	Trp	Tyr	Arg	Gln	Ser	Leu	Gly	Gln	Gly	Pro	Glu	Phe	Leu	Ile	Tyr
		35					40					45			
Phe	Gln	Gly	Thr	Gly	Ala	Ala	Asp	Asp	Ser	Gly	Leu	Pro	Asn	Asp	Arg
	50					55					60				
Phe	Phe	Ala	Val	Arg	Pro	Glu	Gly	Ser	Val	Ser	Thr	Leu	Lys	Ile	Gln
65					70					75					80
Arg	Thr	Glu	Arg	Gly	Asp	Ser	Ala	Val	Tyr	Leu	Cys	Ala	Ser	Ser	Leu
			85						90					95	
Ser	Gly	Leu	Gly	Ser	Gly	Ala	Asn	Val	Leu	Thr	Phe	Gly	Ala	Gly	Ser
			100					105					110		
Arg	Leu	Thr	Val	Leu											
			115												

<210> 125

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 3 Valpha CDR1

<400> 125

Asp	Arg	Gly	Ser	Gln	Ser
1				5	

<210> 126

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 3 Valpha CDR2

<400> 126

Ile	Tyr	Ser	Asn	Gly	Asp
1				5	

<210> 127

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 3 Valpha CDR3

<400> 127

Ala	Val	Asp	Ser	Gly	Gly	Tyr	Gln	Lys	Val	Thr
1				5					10	

<210> 128

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 3 Valpha variable region

<400> 128

Gln	Lys	Glu	Val	Glu	Gln	Asn	Ser	Gly	Pro	Leu	Ser	Val	Pro	Glu	Gly
1				5				10						15	
Ala	Ile	Ala	Ser	Leu	Asn	Cys	Thr	Tyr	Ser	Asp	Arg	Gly	Ser	Gln	Ser
			20					25					30		
Phe	Phe	Trp	Tyr	Arg	Gln	Tyr	Ser	Gly	Lys	Ser	Pro	Glu	Leu	Ile	Met
		35					40					45			
Ser	Ile	Tyr	Ser	Asn	Gly	Asp	Lys	Glu	Asp	Gly	Arg	Phe	Thr	Ala	Gln
	50				55					60					
Leu	Asn	Lys	Ala	Ser	Gln	Tyr	Val	Ser	Leu	Leu	Ile	Arg	Asp	Ser	Gln
65					70				75						80
Pro	Ser	Asp	Ser	Ala	Thr	Tyr	Leu	Cys	Ala	Val	Asp	Ser	Gly	Gly	Tyr
				85					90					95	
Gln	Lys	Val	Thr	Phe	Gly	Thr	Gly	Thr	Lys	Leu	Gln	Val	Ile		
			100					105					110		

<210> 129

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 3 Vbeta CDR3

<400> 129

Ala	Ser	Ser	Leu	Asn	Met	Asn	Thr	Glu	Ala	Phe
1				5					10	

<210> 130
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR number 3 Vbeta variable region

<400> 130
Gly Ala Gly Val Ser Gln Thr Pro Ser Asn Lys Val Thr Glu Lys Gly
1 5 10 15
Lys Tyr Val Glu Leu Arg Cys Asp Pro Ile Ser Gly His Thr Ala Leu
20 25 30
Tyr Trp Tyr Arg Gln Ser Leu Gly Gln Gly Pro Glu Phe Leu Ile Tyr
35 40 45
Phe Gln Gly Thr Gly Ala Ala Asp Asp Ser Gly Leu Pro Asn Asp Arg
50 55 60
Phe Phe Ala Val Arg Pro Glu Gly Ser Val Ser Thr Leu Lys Ile Gln
65 70 75 80
Arg Thr Glu Arg Gly Asp Ser Ala Val Tyr Leu Cys Ala Ser Ser Leu
85 90 95
Asn Met Asn Thr Glu Ala Phe Phe Gly Gln Gly Thr Arg Leu Thr Val
100 105 110
Val

<210> 131
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR number 10 and TCR number 4 Valpha CDR1

<400> 131
Thr Ser Ile Asn Asn
1 5

<210> 132
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR number 10 and TCR number 4 Valpha CDR2

<400> 132

Ile Arg Ser Asn Glu Arg Glu
1 5

<210> 133

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 10 Valpha CDR3

<400> 133

Ala Thr Asp Glu Ser Ser Asn Tyr Lys Leu Thr
1 5 10

<210> 134

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 10 Valpha variable region

<400> 134

Ser	Gln	Gln	Gly	Glu	Glu	Asp	Pro	Gln	Ala	Leu	Ser	Ile	Gln	Glu	Gly
1				5					10					15	
Glu	Asn	Ala	Thr	Met	Asn	Cys	Ser	Tyr	Lys	Thr	Ser	Ile	Asn	Asn	Leu
			20					25					30		
Gln	Trp	Tyr	Arg	Gln	Asn	Ser	Gly	Arg	Gly	Leu	Val	His	Leu	Ile	Leu
		35					40					45			
Ile	Arg	Ser	Asn	Glu	Arg	Glu	Lys	His	Ser	Gly	Arg	Leu	Arg	Val	Thr
	50					55				60					
Leu	Asp	Thr	Ser	Lys	Lys	Ser	Ser	Ser	Leu	Leu	Ile	Thr	Ala	Ser	Arg
65					70					75					80
Ala	Ala	Asp	Thr	Ala	Ser	Tyr	Phe	Cys	Ala	Thr	Asp	Glu	Ser	Ser	Asn
				85					90					95	
Tyr	Lys	Leu	Thr	Phe	Gly	Lys	Gly	Thr	Leu	Leu	Thr	Val	Asn		
			100					105					110		

<210> 135

<211> 178

<212> PRT

<213> Artificial Sequence

<220>

<223> TCRbeta2 constant domain, cysteine modified

<400> 135

Asp	Leu	Lys	Asn	Val	Phe	Pro	Pro	Glu	Val	Ala	Val	Phe	Glu	Pro	Ser	
1				5					10					15		
Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ala	
			20					25					30			
Thr	Gly	Phe	Tyr	Pro	Asp	His	Val	Glu	Leu	Ser	Trp	Trp	Val	Asn	Gly	
		35					40					45				
Lys	Glu	Val	His	Ser	Gly	Val	Cys	Thr	Asp	Pro	Gln	Pro	Leu	Lys	Glu	
	50					55					60					
Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys	Leu	Ser	Ser	Arg	Leu	Arg	
65					70					75					80	
Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn	His	Phe	Arg	Cys	Gln	
				85					90					95		
Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu	Trp	Thr	Gln	Asp	Arg	
		100						105					110			
Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu	Ala	Trp	Gly	Arg	Ala	
		115					120						125			
Asp	Cys	Gly	Phe	Thr	Ser	Glu	Ser	Tyr	Gln	Gln	Gly	Val	Leu	Ser	Ala	
	130					135					140					
Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu	Tyr	Ala	Val	
145					150					155					160	
Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val	Lys	Arg	Lys	Asp	Ser	
				165					170					175		

Arg Gly

<210> 136

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 10 Vbeta variable region

<400> 136

Gly	Ala	Gly	Val	Ser	Gln	Thr	Pro	Ser	Asn	Lys	Val	Thr	Glu	Lys	Gly	
1				5					10					15		
Lys	Tyr	Val	Glu	Leu	Arg	Cys	Asp	Pro	Ile	Ser	Gly	His	Thr	Ala	Leu	
			20					25					30			
Tyr	Trp	Tyr	Arg	Gln	Ser	Leu	Gly	Gln	Gly	Pro	Glu	Phe	Leu	Ile	Tyr	
		35					40					45				

Phe	Gln	Gly	Thr	Gly	Ala	Ala	Asp	Asp	Ser	Gly	Leu	Pro	Asn	Asp	Arg
50						55					60				
Phe	Phe	Ala	Val	Arg	Pro	Glu	Gly	Ser	Val	Ser	Thr	Leu	Lys	Ile	Gln
65					70					75					80
Arg	Thr	Glu	Arg	Gly	Asp	Ser	Ala	Val	Tyr	Leu	Cys	Ala	Ser	Ser	Leu
				85					90					95	
Asn	Met	Asn	Thr	Glu	Ala	Phe	Phe	Gly	Gln	Gly	Thr	Arg	Leu	Thr	Val
			100					105					110		
Val															

<210> 137
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR number 4 Valpha CDR3

Ala	Thr	Asp	Ala	Trp	Glu	Ser	Asn	Phe	Gly	Asn	Glu	Lys	Leu	Thr
1				5					10					15

<210> 138
 <211> 114
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR number 4 Valpha variable region

Ser	Gln	Gln	Gly	Glu	Glu	Asp	Pro	Gln	Ala	Leu	Ser	Ile	Gln	Glu	Gly
1				5					10					15	
Glu	Asn	Ala	Thr	Met	Asn	Cys	Ser	Tyr	Lys	Thr	Ser	Ile	Asn	Asn	Leu
			20					25					30		
Gln	Trp	Tyr	Arg	Gln	Asn	Ser	Gly	Arg	Gly	Leu	Val	His	Leu	Ile	Leu
		35					40					45			
Ile	Arg	Ser	Asn	Glu	Arg	Glu	Lys	His	Ser	Gly	Arg	Leu	Arg	Val	Thr
	50					55				60					
Leu	Asp	Thr	Ser	Lys	Lys	Ser	Ser	Ser	Leu	Leu	Ile	Thr	Ala	Ser	Arg
65					70					75					80
Ala	Ala	Asp	Thr	Ala	Ser	Tyr	Phe	Cys	Ala	Thr	Asp	Ala	Trp	Glu	Ser
				85				90						95	
Asn	Phe	Gly	Asn	Glu	Lys	Leu	Thr	Phe	Gly	Thr	Gly	Thr	Arg	Leu	Thr

	100	105	110
Ile Ile			
<210> 139			
<211> 6			
<212> PRT			
<213> Artificial Sequence			
<220>			
<223> TCR number 4 Vbeta CDR2			
<400> 139			
Phe Gln Gly Asn Ser Ala			
1 5			
<210> 140			
<211> 12			
<212> PRT			
<213> Artificial Sequence			
<220>			
<223> TCR number 4 Vbeta CDR3			
<400> 140			
Ala Ser Ser Leu Val Val Gly Ser Tyr Glu Gln Tyr			
1 5 10			
<210> 141			
<211> 114			
<212> PRT			
<213> Artificial Sequence			
<220>			
<223> TCR number 4 Vbeta variable region			
<400> 141			
Gly Ala Gly Val Ser Gln Ser Pro Ser Asn Lys Val Thr Glu Lys Gly			
1 5 10 15			
Lys Asp Val Glu Leu Arg Cys Asp Pro Ile Ser Gly His Thr Ala Leu			
20 25 30			
Tyr Trp Tyr Arg Gln Ser Leu Gly Gln Gly Leu Glu Phe Leu Ile Tyr			
35 40 45			
Phe Gln Gly Asn Ser Ala Pro Asp Lys Ser Gly Leu Pro Ser Asp Arg			
50 55 60			

Phe	Ser	Ala	Glu	Arg	Thr	Gly	Gly	Ser	Val	Ser	Thr	Leu	Thr	Ile	Gln
65					70					75					80
Arg	Thr	Gln	Gln	Glu	Asp	Ser	Ala	Val	Tyr	Leu	Cys	Ala	Ser	Ser	Leu
				85					90					95	
Val	Val	Gly	Ser	Tyr	Glu	Gln	Tyr	Phe	Gly	Pro	Gly	Thr	Arg	Leu	Thr
			100					105					110		
Val	Thr														

<210> 142

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 7 Valpha CDR2

<400> 142

Met	Thr	Leu	Asn	Gly	Asp	Glu
1				5		

<210> 143

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 7 Valpha CDR3

<400> 143

Ala	Tyr	Leu	Gly	Ala	Gly	Asn	Gln	Phe	Tyr
1				5				10	

<210> 144

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 7 Valpha variable region

<400> 144

Ile	Leu	Asn	Val	Glu	Gln	Ser	Pro	Gln	Ser	Leu	His	Val	Gln	Glu	Gly
1				5				10					15		
Asp	Ser	Thr	Asn	Phe	Thr	Cys	Ser	Phe	Pro	Ser	Ser	Asn	Phe	Tyr	Ala

			20					25					30				
Leu	His	Trp	Tyr	Arg	Trp	Glu	Thr	Ala	Lys	Ser	Pro	Glu	Ala	Leu	Phe		
		35					40					45					
Val	Met	Thr	Leu	Asn	Gly	Asp	Glu	Lys	Lys	Lys	Gly	Arg	Ile	Ser	Ala		
	50				55						60						
Thr	Leu	Asn	Thr	Lys	Glu	Gly	Tyr	Ser	Tyr	Leu	Tyr	Ile	Lys	Gly	Ser		
65					70					75					80		
Gln	Pro	Glu	Asp	Ser	Ala	Thr	Tyr	Leu	Cys	Ala	Tyr	Leu	Gly	Ala	Gly		
			85					90						95			
Asn	Gln	Phe	Tyr	Phe	Gly	Thr	Gly	Thr	Ser	Leu	Thr	Val	Ile				
			100					105					110				

<210> 145

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 7 Vbeta CDR1

<400> 145

Leu	Asn	His	Asp	Ala
1			5	

<210> 146

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 7 Vbeta CDR2

<400> 146

Ser	Gln	Ile	Val	Asn	Asp
1				5	

<210> 147

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 7 Vbeta CDR3

<400> 147

Ala Ser Ser Leu Asn Arg Gly Arg Tyr Gly Tyr Thr
1 5 10

<210> 148

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 7 Vbeta variable region

<400> 148

Asp Gly Gly Ile Thr Gln Ser Pro Lys Tyr Leu Phe Arg Lys Glu Gly
1 5 10 15
Gln Asn Val Thr Leu Ser Cys Glu Gln Asn Leu Asn His Asp Ala Met
20 25 30
Tyr Trp Tyr Arg Gln Asp Pro Gly Gln Gly Leu Arg Leu Ile Tyr Tyr
35 40 45
Ser Gln Ile Val Asn Asp Phe Gln Lys Gly Asp Ile Ala Glu Gly Tyr
50 55 60
Ser Val Ser Arg Glu Lys Lys Glu Ser Phe Pro Leu Thr Val Thr Ser
65 70 75 80
Ala Gln Lys Asn Pro Thr Ala Phe Tyr Leu Cys Ala Ser Ser Leu Asn
85 90 95
Arg Gly Arg Tyr Gly Tyr Thr Phe Gly Ser Gly Thr Arg Leu Thr Val
100 105 110
Val

<210> 149

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 8 Valpha CDR1

<400> 149

Thr Arg Asp Thr Thr Tyr Tyr
1 5

<210> 150

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 8 Valpha CDR2

<400> 150

Arg Asn Ser Phe Asp Glu Gln Asn
1 5

<210> 151

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 8 Valpha CDR3

<400> 151

Ala Leu Ser Glu Leu Ala Ser Gly Gly Ser Tyr Ile Pro Thr
1 5 10

<210> 152

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 8 Valpha variable region

<400> 152

Ala Gln Lys Val Thr Gln Ala Gln Thr Glu Ile Ser Val Val Glu Lys
1 5 10 15
Glu Asp Val Thr Leu Asp Cys Val Tyr Glu Thr Arg Asp Thr Thr Tyr
20 25 30
Tyr Leu Phe Trp Tyr Lys Gln Pro Pro Ser Gly Glu Leu Val Phe Leu
35 40 45
Ile Arg Arg Asn Ser Phe Asp Glu Gln Asn Glu Ile Ser Gly Arg Tyr
50 55 60
Ser Trp Asn Phe Gln Lys Ser Thr Ser Ser Phe Asn Phe Thr Ile Thr
65 70 75 80
Ala Ser Gln Val Val Asp Ser Ala Val Tyr Phe Cys Ala Leu Ser Glu
85 90 95
Leu Ala Ser Gly Gly Ser Tyr Ile Pro Thr Phe Gly Arg Gly Thr Ser
100 105 110
Leu Ile Val His Pro
115

<210> 153
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR number 8 Vbeta CDR1

<400> 153
Ala Ser Ser Phe Arg Leu Ala Gly Gly Pro Ser Thr Asp Thr Gln Tyr
1 5 10 15

<210> 154
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR number 8 Vbeta variable region

<400> 154
Asp Ala Gly Val Thr Gln Ser Pro Thr His Leu Ile Lys Thr Arg Gly
1 5 10 15
Gln Gln Val Thr Leu Arg Cys Ser Pro Lys Ser Gly His Asp Thr Val
20 25 30
Ser Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Gln Phe Ile Phe Gln
35 40 45
Tyr Tyr Glu Glu Glu Glu Arg Gln Arg Gly Asn Phe Pro Asp Arg Phe
50 55 60
Ser Gly His Gln Phe Pro Asn Tyr Ser Ser Glu Leu Asn Val Asn Ala
65 70 75 80
Leu Leu Leu Gly Asp Ser Ala Leu Tyr Leu Cys Ala Ser Ser Phe Arg
85 90 95
Leu Ala Gly Gly Pro Ser Thr Asp Thr Gln Tyr Phe Gly Pro Gly Thr
100 105 110
Arg Leu Thr Val Leu
115

<210> 155
<211> 177
<212> PRT
<213> Artificial Sequence

<220>

<223> TCRbeta1 constant domain, cysteine modified

<400> 155

Glu	Asp	Leu	Asn	Lys	Val	Phe	Pro	Pro	Glu	Val	Ala	Val	Phe	Glu	Pro
1				5					10					15	
Ser	Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr	Leu	Val	Cys	Leu
			20					25						30	
Ala	Thr	Gly	Phe	Phe	Pro	Asp	His	Val	Glu	Leu	Ser	Trp	Trp	Val	Asn
		35					40					45			
Gly	Lys	Glu	Val	His	Ser	Gly	Val	Cys	Thr	Asp	Pro	Gln	Pro	Leu	Lys
	50					55					60				
Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys	Leu	Ser	Ser	Arg	Leu
65					70					75					80
Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn	His	Phe	Arg	Cys
				85				90						95	
Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu	Trp	Thr	Gln	Asp
			100					105						110	
Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu	Ala	Trp	Gly	Arg
		115					120					125			
Ala	Asp	Cys	Gly	Phe	Thr	Ser	Val	Ser	Tyr	Gln	Gln	Gly	Val	Leu	Ser
	130					135					140				
Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu	Tyr	Ala
145					150					155					160
Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val	Lys	Arg	Lys	Asp
				165					170					175	

Phe

<210> 156

<211> 141

<212> PRT

<213> Artificial Sequence

<220>

<223> TCRalpha constant domain

<400> 156

Asn	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser	Lys
1				5					10					15	
Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Thr
			20					25						30	
Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp	Lys	Thr
		35					40					45			
Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	Ala	Val	Ala
	50					55						60			

Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn	Asn	Ser
65					70					75					80
Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	Ser	Cys	Asp
				85					90					95	
Val	Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn	Leu	Asn	Phe
			100					105					110		
Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu	Lys	Val	Ala
		115					120					125			
Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser			
	130					135					140				

<210> 157

<211> 140

<212> PRT

<213> Artificial Sequence

<220>

<223> TCRalpha constant domain

<400> 157

Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser	Lys	Ser
1				5					10					15	
Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Thr	Asn
			20					25					30		
Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp	Lys	Thr	Val
		35					40					45			
Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	Ala	Val	Ala	Trp
	50					55					60				
Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn	Asn	Ser	Ile
65				70					75					80	
Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	Ser	Cys	Asp	Val
			85						90					95	
Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn	Leu	Asn	Phe	Gln
			100					105					110		
Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu	Lys	Val	Ala	Gly
		115					120					125			
Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser				
	130					135					140				

<210> 158

<211> 142

<212> PRT

<213> Artificial Sequence

<220>

<223> TCRalpha constant domain, cysteine modified

<400> 158

Pro	Asn	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser	
1				5					10					15		
Lys	Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	
			20					25					30			
Thr	Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp	Lys	
		35					40					45				
Cys	Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	Ala	Val	
	50					55					60					
Ala	Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn	Asn	
65					70				75					80		
Ser	Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	Ser	Cys	
				85				90						95		
Asp	Val	Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn	Leu	Asn	
			100					105					110			
Phe	Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu	Lys	Val	
		115					120					125				
Ala	Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser			
	130					135					140					

<210> 159

<211> 141

<212> PRT

<213> Artificial Sequence

<220>

<223> TCRalpha constant domain, cysteine modified

<400> 159

Asn	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser	Lys	
1				5					10					15		
Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Thr	
			20					25					30			
Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp	Lys	Cys	
		35					40					45				
Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	Ala	Val	Ala	
	50					55					60					
Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn	Asn	Ser	
65					70				75					80		
Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	Ser	Cys	Asp	
				85				90						95		
Val	Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn	Leu	Asn	Phe	
			100					105					110			

Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu	Lys	Val	Ala
		115					120					125			
Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser			
		130					135					140			

<210> 160
 <211> 140
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCRalpha constant domain, cysteine modified

Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser	Lys	Ser
1				5					10					15	
Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Thr	Asn
		20						25					30		
Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp	Lys	Cys	Val
		35					40					45			
Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	Ala	Val	Ala	Trp
	50					55					60				
Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn	Asn	Ser	Ile
65					70				75					80	
Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	Ser	Cys	Asp	Val
				85					90					95	
Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn	Leu	Asn	Phe	Gln
			100					105					110		
Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu	Lys	Val	Ala	Gly
		115					120					125			
Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser				
		130					135				140				

<210> 161
 <211> 1821
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> codon optimized TCR number 5 construct; beta chain-P2A-alpha chain with cysteine substitutions in beta and alpha chain constant domains

<400> 161
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120					
agatgtagcc	ctagaagcgg	agatctgagc	gtgtattggg	accagcagag	cctggatcaa
180					
ggactccagt	ttctgatcca	gtactacaac	ggcgaggaga	gagccaaggg	caatattctg
240					
gagaggtttt	ctgcccagca	gttccttgat	ctgcactctg	aactgaacct	gtctagcctg
300					
gaactgggag	attctgccct	gtacttttgt	gcctctagcg	ttggacaggg	cagctcttat
360					
gagcagtact	ttggacctgg	caccagactg	acagtgacag	aagacctgaa	gaacgtgttc
420					
ccccagagg	tggccgtggt	cgagcctagc	gaggccgaga	tcagccacac	ccagaaagcc
480					
accctcgtgt	gcctggccac	cggtctttac	cccgaccacg	tggaactgtc	ttggtgggtc
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600					
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660					
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720					
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780					
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900					
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960					
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1020					
gtgctgagcg	gaacactggt	atggcagctt	acatgggtga	ggctctcagca	acctgtgcaa
1080					
tctccacagg	ccgttatcct	gagagaagga	gaagatgccg	tgatcaactg	ctctagctct
1140					
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1200					
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1260					
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1320					
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1380					
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1440					

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agcgtgatcg gcttccggat cctgctgctg aaggtggccg gcttcaacct gctgatgacc
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1821

<210> 162

<211> 606

<212> PRT

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 5 construct; beta
chain-P2A-alpha chain with cysteine substitutions
in beta and alpha chain constant domains

<400> 162

Met	Gly	Phe	Arg	Leu	Leu	Cys	Cys	Val	Ala	Phe	Cys	Leu	Leu	Gly	Ala
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			20					25					30		
Ala	Thr	Gly	Gln	Arg	Val	Thr	Leu	Arg	Cys	Ser	Pro	Arg	Ser	Gly	Asp
		35					40					45			
Leu	Ser	Val	Tyr	Trp	Tyr	Gln	Gln	Ser	Leu	Asp	Gln	Gly	Leu	Gln	Phe
	50					55				60					
Leu	Ile	Gln	Tyr	Tyr	Asn	Gly	Glu	Glu	Arg	Ala	Lys	Gly	Asn	Ile	Leu
65					70				75					80	
Glu	Arg	Phe	Ser	Ala	Gln	Gln	Phe	Pro	Asp	Leu	His	Ser	Glu	Leu	Asn
			85					90					95		
Leu	Ser	Ser	Leu	Glu	Leu	Gly	Asp	Ser	Ala	Leu	Tyr	Phe	Cys	Ala	Ser
		100					105						110		
Ser	Val	Gly	Gln	Gly	Ser	Ser	Tyr	Glu	Gln	Tyr	Phe	Gly	Pro	Gly	Thr
	115						120					125			
Arg	Leu	Thr	Val	Thr	Glu	Asp	Leu	Lys	Asn	Val	Phe	Pro	Pro	Glu	Val
	130				135				140						
Ala	Val	Phe	Glu	Pro	Ser	Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala

145					150					155					160
Thr	Leu	Val	Cys	Leu	Ala	Thr	Gly	Phe	Tyr	Pro	Asp	His	Val	Glu	Leu
				165					170					175	
Ser	Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Cys	Thr	Asp
			180					185					190		
Pro	Gln	Pro	Leu	Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys
		195					200					205			
Leu	Ser	Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg
	210					215					220				
Asn	His	Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp
225					230					235					240
Glu	Trp	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala
				245				250						255	
Glu	Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Glu	Ser	Tyr	Gln
			260					265					270		
Gln	Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys
		275					280						285		
Ala	Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met
	290					295					300				
Val	Lys	Arg	Lys	Asp	Ser	Arg	Gly	Gly	Ser	Gly	Ala	Thr	Asn	Phe	Ser
305					310					315					320
Leu	Leu	Lys	Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Glu
				325				330						335	
Thr	Leu	Leu	Lys	Val	Leu	Ser	Gly	Thr	Leu	Leu	Trp	Gln	Leu	Thr	Trp
			340					345					350		
Val	Arg	Ser	Gln	Gln	Pro	Val	Gln	Ser	Pro	Gln	Ala	Val	Ile	Leu	Arg
		355					360					365			
Glu	Gly	Glu	Asp	Ala	Val	Ile	Asn	Cys	Ser	Ser	Ser	Lys	Ala	Leu	Tyr
	370					375					380				
Ser	Val	His	Trp	Tyr	Arg	Gln	Lys	His	Gly	Glu	Ala	Pro	Val	Phe	Leu
385					390					395					400
Met	Ile	Leu	Leu	Lys	Gly	Gly	Glu	Gln	Lys	Gly	His	Glu	Lys	Ile	Ser
				405				410						415	
Ala	Ser	Phe	Asn	Glu	Lys	Lys	Gln	Gln	Ser	Ser	Leu	Tyr	Leu	Thr	Ala
			420					425					430		
Ser	Gln	Leu	Ser	Tyr	Ser	Gly	Thr	Tyr	Phe	Cys	Gly	Thr	Glu	Glu	Ala
		435					440					445			
Asn	Asp	Tyr	Lys	Leu	Ser	Phe	Gly	Ala	Gly	Thr	Thr	Val	Thr	Val	Arg
	450					455					460				
Ala	Asn	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser
465					470					475					480
Lys	Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln
				485				490						495	
Thr	Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp	Lys
			500					505					510		

Cys	Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	Ala	Val
		515					520					525			
Ala	Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn	Asn
	530					535					540				
Ser	Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	Ser	Cys
545					550					555					560
Asp	Val	Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn	Leu	Asn
			565						570					575	
Phe	Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu	Lys	Val
		580						585					590		
Ala	Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser		
	595						600					605			

<210> 163

<211> 1818

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR number 9 construct; beta chain-P2A-alpha chain

<400> 163

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120
cgctgtgtcc ccatctctaa tcacttatac ttctattggg acagacaaat cttgggggcag
180
aaagtcgagt ttctgggtttc cttttataat aatgaaatct cagagaagtc tgaaatatct
240
gatgatcaat tctcagttga aaggcctgat ggatcaaatt tcactctgaa gatccggtcc
300
acaaagctgg aggactcagc catgtacttc tgtgccatcc tggatggaga aggttcaccc
360
ctccactttg ggaatgggac caggctcact gtgacagagg acctgaacaa ggtgttccca
420
cccgaggtcg ctgtgtttga gccatcagaa gcagagatct cccacacca aaaggccaca
480
ctgggtgtgcc tggccacagg cttcttccct gaccacgtgg agctgagctg gtgggtgaat
540
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600
ctcaatgact ccagatactg cctgagcagc cgcctgaggg tctcggccac cttctggcag
660
aacccccgca accacttccg ctgtcaagtc cagttctacg ggctctcgga gaatgacgag
720

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840					
tatgagatcc	tgctagggaa	ggccaccctg	tatgctgtgc	tggtcagcgc	ccttgtgttg
900					
atggccatgg	tcaagagaaa	ggatttcggt	tccggagcca	cgaacttctc	tctgttaaag
960					
caagcaggag	acgtggaaga	aaaccccggg	cccatgaaaa	agcatctgac	gaccttcttg
1020					
gtgattttgt	ggctttatct	ttataggggg	aatggcaaaa	accaagtgga	gcagagtcct
1080					
cagtccctga	tcatacctgga	gggaaagaac	tgcactcttc	aatgcaatta	tacagtgagc
1140					
cccttcagca	acttaagggt	gtataagcaa	gatactggga	gaggtcctgt	ttccctgaca
1200					
atcatgactt	tcagtgagaa	cacaaagtcg	aacggaagat	atacagcaac	tctggatgca
1260					
gacacaaagc	aaagctctct	gcacatcaca	gcctcccagc	tcagcgattc	agcctcctac
1320					
atctgtgtgg	tgtggggggg	ggacaccgac	aagctcatct	ttgggactgg	gaccagatta
1380					
caagtctttc	caaatatcca	gaaccctgac	cctgccgtgt	accagctgag	agactctaaa
1440					
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1500					
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1560					
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1620					
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1680					
gtcaagctgg	tcgagaaaag	ctttgaaaca	gatacgaacc	taaactttca	aaacctgtca
1740					
gtgattgggt	tccgaatcct	cctcctgaaa	gtggccgggt	ttaatctgct	catgacgctg
1800					
c g g c t g t g g t				c c a g c t g a	
1818					

<210> 164

<400> 164
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<210> 165

<211> 605

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 9 construct; beta chain-P2A-alpha chain

<400> 165

Met	Asp	Thr	Trp	Leu	Val	Cys	Trp	Ala	Ile	Phe	Ser	Leu	Leu	Lys	Ala
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Gly	Leu	Thr	Glu	Pro	Glu	Val	Thr	Gln	Thr	Pro	Ser	His	Gln	Val	Thr
			20					25					30		
Gln	Met	Gly	Gln	Glu	Val	Ile	Leu	Arg	Cys	Val	Pro	Ile	Ser	Asn	His
		35					40					45			
Leu	Tyr	Phe	Tyr	Trp	Tyr	Arg	Gln	Ile	Leu	Gly	Gln	Lys	Val	Glu	Phe
	50					55					60				
Leu	Val	Ser	Phe	Tyr	Asn	Asn	Glu	Ile	Ser	Glu	Lys	Ser	Glu	Ile	Phe
65					70					75					80
Asp	Asp	Gln	Phe	Ser	Val	Glu	Arg	Pro	Asp	Gly	Ser	Asn	Phe	Thr	Leu
				85					90					95	
Lys	Ile	Arg	Ser	Thr	Lys	Leu	Glu	Asp	Ser	Ala	Met	Tyr	Phe	Cys	Ala
			100					105						110	
Ile	Leu	Asp	Gly	Glu	Gly	Ser	Pro	Leu	His	Phe	Gly	Asn	Gly	Thr	Arg
		115					120					125			
Leu	Thr	Val	Thr	Glu	Asp	Leu	Asn	Lys	Val	Phe	Pro	Pro	Glu	Val	Ala
	130					135					140				
Val	Phe	Glu	Pro	Ser	Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr
145					150					155					160
Leu	Val	Cys	Leu	Ala	Thr	Gly	Phe	Phe	Pro	Asp	His	Val	Glu	Leu	Ser
				165					170					175	
Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Ser	Thr	Asp	Pro
			180					185						190	
Gln	Pro	Leu	Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys	Leu
		195					200					205			
Ser	Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn
	210					215					220				
His	Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu
225				230						235					240
Trp	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu
				245					250					255	
Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Val	Ser	Tyr	Gln	Gln
		260					265						270		
Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala
		275					280					285			
Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val

290						295					300				
Lys	Arg	Lys	Asp	Phe	Gly	Ser	Gly	Ala	Thr	Asn	Phe	Ser	Leu	Leu	Lys
305					310					315					320
Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Lys	Lys	His	Leu
				325					330					335	
Thr	Thr	Phe	Leu	Val	Ile	Leu	Trp	Leu	Tyr	Phe	Tyr	Arg	Gly	Asn	Gly
			340					345					350		
Lys	Asn	Gln	Val	Glu	Gln	Ser	Pro	Gln	Ser	Leu	Ile	Ile	Leu	Glu	Gly
		355					360					365			
Lys	Asn	Cys	Thr	Leu	Gln	Cys	Asn	Tyr	Thr	Val	Ser	Pro	Phe	Ser	Asn
	370					375					380				
Leu	Arg	Trp	Tyr	Lys	Gln	Asp	Thr	Gly	Arg	Gly	Pro	Val	Ser	Leu	Thr
385					390					395					400
Ile	Met	Thr	Phe	Ser	Glu	Asn	Thr	Lys	Ser	Asn	Gly	Arg	Tyr	Thr	Ala
				405					410					415	
Thr	Leu	Asp	Ala	Asp	Thr	Lys	Gln	Ser	Ser	Leu	His	Ile	Thr	Ala	Ser
			420					425					430		
Gln	Leu	Ser	Asp	Ser	Ala	Ser	Tyr	Ile	Cys	Val	Val	Trp	Gly	Gly	Asp
		435					440					445			
Thr	Asp	Lys	Leu	Ile	Phe	Gly	Thr	Gly	Thr	Arg	Leu	Gln	Val	Phe	Pro
	450					455					460				
Asn	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser	Lys
465					470					475					480
Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Thr
				485					490					495	
Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp	Lys	Thr
			500					505					510		
Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	Ala	Val	Ala
		515					520					525			
Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn	Asn	Ser
	530					535					540				
Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	Ser	Cys	Asp
545					550					555					560
Val	Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn	Leu	Asn	Phe
				565					570					575	
Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu	Lys	Val	Ala
			580					585					590		
Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser			
		595					600					605			

<210> 166

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 9 Vbeta variable region

<400> 166

Glu	Pro	Glu	Val	Thr	Gln	Thr	Pro	Ser	His	Gln	Val	Thr	Gln	Met	Gly	
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Gln	Glu	Val	Ile	Leu	Arg	Cys	Val	Pro	Ile	Ser	Asn	His	Leu	Tyr	Phe	
		20					25				30					
Tyr	Trp	Tyr	Arg	Gln	Ile	Leu	Gly	Gln	Lys	Val	Glu	Phe	Leu	Val	Ser	
	35					40				45						
Phe	Tyr	Asn	Asn	Glu	Ile	Ser	Glu	Lys	Ser	Glu	Ile	Phe	Asp	Asp	Gln	
50					55					60						
Phe	Ser	Val	Glu	Arg	Pro	Asp	Gly	Ser	Asn	Phe	Thr	Leu	Lys	Ile	Arg	
65				70					75					80		
Ser	Thr	Lys	Leu	Glu	Asp	Ser	Ala	Met	Tyr	Phe	Cys	Ala	Ile	Leu	Asp	
			85					90					95			
Gly	Glu	Gly	Ser	Pro	Leu	His	Phe	Gly	Asn	Gly	Thr	Arg	Leu	Thr	Val	
			100					105					110			
Thr																

<210> 167

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 9 Vbeta CDR1

<400> 167

Ser	Asn	His	Leu	Tyr	Phe	
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<210> 168

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 9 Vbeta CDR2

<400> 168

Phe	Tyr	Asn	Asn	Glu	Ile	
1			5			

<210> 169
<211> 1818
<212> DNA
<213> Artificial Sequence

<220>

<223> codon optimized TCR number 9 construct; beta
chain-P2A-alpha chain with cysteine substitutions
in beta and alpha chain constant domains

<400> 169

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120
agatgtgtgc ctatcagcaa ccacctgtac ttctactggg accggcagat tctgggccag
180
aaagtggagt ttctggtgag cttctacaac aacgagatca gcgagaagag cgagatcttc
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gatgaccagt tcagcgtgga gagaccagat ggaagcaact ttaccctgaa gatccggagc
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accaagctgg aagattctgc catgtacttc tgcgccatcc tggatggaga gggatctcct
360
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420
ccagaggtgg ccgtgttcga gccttctgag gccgagatct cccacaccca gaaagccacc
480
ctcgtgtgcc tggccaccgg ctttttcccc gaccacgtgg aactgtcttg gtgggtcaac
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780
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900
atggccatgg tcaagcgga ggacttcggt tccggagcca cgaacttctc tctgttaaag
960
caagcaggag acgtggaaga aaacccccgt cccatgaaga agcacctgac cacgttcctg
1020
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gtgattcttt ggctgtactt ctaccggggc aacggcaaaa atcagggtgga acaaagcccc
1080
cagagcctga ttattctgga gggcaagaac tgcaccctcc agtgtaatta caccgtgagc
1140
cctttcagca acctgagatg gtacaagcag gataccggaa gaggacctgt gtctctgacc
1200
atcatgacct ttagcgagaa caccaagagc aacggcaggt atacagccac actggatgcc
1260
gataccaagc agtcttctct gcacattacc gcctctcagc tgtctgattc tgccagctac
1320
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1380
caagtgttcc ctaacatcca gaaccctgat cctgccgtgt accagctgcg ggacagcaag
1440
agcagcgaca agagcgtgtg cctgttcacc gacttcgaca gccagaccaa cgtgtcccag
1500
agcaaggaca gcgacgtgta catcaccgat aagtgcgtgc tggacatgcg gagcatggac
1560
ttcaagagca acagcgccgt ggcctgggtc aacaagagcg acttcgcctg cgccaacgcc
1620
ttcaacaaca gcattatccc cgaggacaca ttcttcccaa gccccgagag cagctgcgac
1680
gtgaagctgg tggaaaagag cttcgagaca gacaccaacc tgaacttcca gaacctcagc
1740
gtgatcggct tccggatcct gctgctgaag gtggccggct tcaacctgct gatgacctg
1800
c g g c t g t g g t c c a g c t g a
1818

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<210> 170

<211> 605

<212> PRT

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 9 construct; beta
chain-P2A-alpha chain with cysteine substitutions
in beta and alpha chain constant domains

<400> 170

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Gly Leu Thr Glu Pro Glu Val Thr Gln Thr Pro Ser His Gln Val Thr
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Gln Met Gly Gln Glu Val Ile Leu Arg Cys Val Pro Ile Ser Asn His

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Leu	Tyr	Phe	Tyr	Trp	Tyr	Arg	Gln	Ile	Leu	Gly	Gln	Lys	Val	Glu	Phe
50						55					60				
Leu	Val	Ser	Phe	Tyr	Asn	Asn	Glu	Ile	Ser	Glu	Lys	Ser	Glu	Ile	Phe
65					70					75					80
Asp	Asp	Gln	Phe	Ser	Val	Glu	Arg	Pro	Asp	Gly	Ser	Asn	Phe	Thr	Leu
				85					90					95	
Lys	Ile	Arg	Ser	Thr	Lys	Leu	Glu	Asp	Ser	Ala	Met	Tyr	Phe	Cys	Ala
			100					105					110		
Ile	Leu	Asp	Gly	Glu	Gly	Ser	Pro	Leu	His	Phe	Gly	Asn	Gly	Thr	Arg
		115					120					125			
Leu	Thr	Val	Thr	Glu	Asp	Leu	Asn	Lys	Val	Phe	Pro	Pro	Glu	Val	Ala
130						135					140				
Val	Phe	Glu	Pro	Ser	Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr
145					150					155					160
Leu	Val	Cys	Leu	Ala	Thr	Gly	Phe	Phe	Pro	Asp	His	Val	Glu	Leu	Ser
				165					170					175	
Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Cys	Thr	Asp	Pro
			180					185					190		
Gln	Pro	Leu	Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys	Leu
		195					200					205			
Ser	Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn
		210				215					220				
His	Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu
225				230						235					240
Trp	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu
				245					250					255	
Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Val	Ser	Tyr	Gln	Gln
			260					265					270		
Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala
		275					280					285			
Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val
		290			295						300				
Lys	Arg	Lys	Asp	Phe	Gly	Ser	Gly	Ala	Thr	Asn	Phe	Ser	Leu	Leu	Lys
305					310					315					320
Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Lys	Lys	His	Leu
				325					330					335	
Thr	Thr	Phe	Leu	Val	Ile	Leu	Trp	Leu	Tyr	Phe	Tyr	Arg	Gly	Asn	Gly
			340					345					350		
Lys	Asn	Gln	Val	Glu	Gln	Ser	Pro	Gln	Ser	Leu	Ile	Ile	Leu	Glu	Gly
		355					360					365			
Lys	Asn	Cys	Thr	Leu	Gln	Cys	Asn	Tyr	Thr	Val	Ser	Pro	Phe	Ser	Asn
		370				375					380				
Leu	Arg	Trp	Tyr	Lys	Gln	Asp	Thr	Gly	Arg	Gly	Pro	Val	Ser	Leu	Thr
385					390					395					400

Ile	Met	Thr	Phe	Ser	Glu	Asn	Thr	Lys	Ser	Asn	Gly	Arg	Tyr	Thr	Ala	
				405					410						415	
Thr	Leu	Asp	Ala	Asp	Thr	Lys	Gln	Ser	Ser	Leu	His	Ile	Thr	Ala	Ser	
			420					425					430			
Gln	Leu	Ser	Asp	Ser	Ala	Ser	Tyr	Ile	Cys	Val	Val	Trp	Gly	Gly	Asp	
		435					440					445				
Thr	Asp	Lys	Leu	Ile	Phe	Gly	Thr	Gly	Thr	Arg	Leu	Gln	Val	Phe	Pro	
	450					455					460					
Asn	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser	Lys	
465					470					475					480	
Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Thr	
			485						490					495		
Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp	Lys	Cys	
			500					505					510			
Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	Ala	Val	Ala	
		515					520					525				
Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn	Asn	Ser	
	530					535					540					
Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	Ser	Cys	Asp	
545					550					555					560	
Val	Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn	Leu	Asn	Phe	
			565						570					575		
Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu	Lys	Val	Ala	
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Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser				
		595					600					605				

<210> 171

<211> 1827

<212> DNA

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 6 construct; beta
chain-P2A-alpha chain with cysteine substitutions
in beta and alpha chain constant domains

<400> 171

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120
cagtgtaccc aggatatgaa ccataactac atgtactggt atcgacaaga cccaggcatg
180
gggctgaagc tgatttatta ttcagttggt gctggtatca ctgataaagg agaagtcccg
240

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aatggctaca	acgtctccag	atcaaccaca	gaggatttcc	cgctcaggct	ggagttggct
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gctccctccc	agacatctgt	gtacttctgt	gccagcagtg	acaggtctaa	caccggggag
360					
ctgttttttg	gagaaggctc	taggctgacc	gtactggagg	acctgaaaaa	cgtgttccca
420					
cccgaggtcg	ctgtgtttga	gccatcagaa	gcagagatct	cccacacca	aaaggccaca
480					
ctgggtgtgcc	tggccacagg	cttctacccc	gaccacgtgg	agctgagctg	gtgggtgaat
540					
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600					
ctcaatgact	ccagatactg	cctgagcagc	cgcttgaggg	tctcggccac	cttctggcag
660					
aacccccgca	accacttccg	ctgtcaagtc	cagttctacg	ggctctcgga	gaatgacgag
720					
tggacccagg	atagggccaa	acctgtcacc	cagatcgtca	gcgccgaggc	ctggggtaga
780					
gcagactgtg	gcttcacctc	cgagtcttac	cagcaagggg	tcctgtctgc	caccatcctc
840					
tatgagatct	tgctagggaa	ggccaccttg	tatgccgtgc	tggtcagtgc	cctcgtgctg
900					
atggccatgg	tcaagagaaa	ggattccaga	ggcggttccg	gagccacgaa	cttctctctg
960					
ttaaagcaag	caggagacgt	ggaagaaaac	cccgggtccca	tggagaagaa	tcctttggca
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1080					
caaagtcctc	agtcactgca	tggttcaggag	ggagacagca	ccaatttcac	ctgcagcttc
1140					
ccttccagca	atTTTTatgc	cttacactgg	tacagatggg	aaactgcaaa	aagccccgag
1200					
gccttgtttg	taatgacttt	aaatggggat	gaaaagaaga	aaggacgaat	aagtgccact
1260					
cttaatacca	aggaggggta	cagctatttg	tacatcaaag	gatcccagcc	tgaagactca
1320					
gccacatacc	tctgtgcctt	agggccttat	aacgactaca	agctcagctt	tggagccgga
1380					
accacagtaa	ctgtaagagc	aaatatccag	aaccctgacc	ctgccgtgta	ccagctgcgg
1440					
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1500					
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1560					
agcatggact	tcaagagcaa	cagcgccgtg	gcctgggtcca	acaagagcga	cttcgcctgc
1620					

gccaacgcct tcaacaacag cattatcccc gaggacacat tcttcccaag ccccgagagc
 1680
 agctgcgacg tgaagctggg ggaaaagagc ttcgagacag acaccaacct gaacttccag
 1740
 aacctcagcg tgatcggcct ccggatcctg ctgctgaagg tggccggcct caacctgctg
 1800
 a t g a c c c t g c g g c t g t g g t c c a g c t g a
 1827

<210> 172

<211> 608

<212> PRT

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 6 construct; beta
 chain-P2A-alpha chain with cysteine substitutions
 in beta and alpha chain constant domains

<400> 172

Met	Ser	Ile	Ser	Leu	Leu	Cys	Cys	Ala	Ala	Phe	Pro	Leu	Leu	Trp	Ala
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			20					25					30		
Lys	Ile	Gly	Gln	Ser	Met	Thr	Leu	Gln	Cys	Thr	Gln	Asp	Met	Asn	His
		35					40					45			
Asn	Tyr	Met	Tyr	Trp	Tyr	Arg	Gln	Asp	Pro	Gly	Met	Gly	Leu	Lys	Leu
	50					55				60					
Ile	Tyr	Tyr	Ser	Val	Gly	Ala	Gly	Ile	Thr	Asp	Lys	Gly	Glu	Val	Pro
65				70						75				80	
Asn	Gly	Tyr	Asn	Val	Ser	Arg	Ser	Thr	Thr	Glu	Asp	Phe	Pro	Leu	Arg
			85						90					95	
Leu	Glu	Leu	Ala	Ala	Pro	Ser	Gln	Thr	Ser	Val	Tyr	Phe	Cys	Ala	Ser
			100					105					110		
Ser	Asp	Arg	Ser	Asn	Thr	Gly	Glu	Leu	Phe	Phe	Gly	Glu	Gly	Ser	Arg
		115					120					125			
Leu	Thr	Val	Leu	Glu	Asp	Leu	Lys	Asn	Val	Phe	Pro	Pro	Glu	Val	Ala
	130					135					140				
Val	Phe	Glu	Pro	Ser	Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr
145					150					155					160
Leu	Val	Cys	Leu	Ala	Thr	Gly	Phe	Tyr	Pro	Asp	His	Val	Glu	Leu	Ser
			165						170					175	
Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Cys	Thr	Asp	Pro
		180						185					190		
Gln	Pro	Leu	Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys	Leu

		195					200					205				
Ser	Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn	
	210					215					220					
His	Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu	
225					230					235					240	
Trp	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu	
				245					250					255		
Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Glu	Ser	Tyr	Gln	Gln	
			260					265					270			
Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	
		275					280					285				
Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val	
	290					295					300					
Lys	Arg	Lys	Asp	Ser	Arg	Gly	Gly	Ser	Gly	Ala	Thr	Asn	Phe	Ser	Leu	
305					310					315					320	
Leu	Lys	Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Glu	Lys	
				325					330					335		
Asn	Pro	Leu	Ala	Ala	Pro	Leu	Leu	Ile	Leu	Trp	Phe	His	Leu	Asp	Cys	
			340					345					350			
Val	Ser	Ser	Ile	Leu	Asn	Val	Glu	Gln	Ser	Pro	Gln	Ser	Leu	His	Val	
		355					360					365				
Gln	Glu	Gly	Asp	Ser	Thr	Asn	Phe	Thr	Cys	Ser	Phe	Pro	Ser	Ser	Asn	
	370					375					380					
Phe	Tyr	Ala	Leu	His	Trp	Tyr	Arg	Trp	Glu	Thr	Ala	Lys	Ser	Pro	Glu	
385					390					395					400	
Ala	Leu	Phe	Val	Met	Thr	Leu	Asn	Gly	Asp	Glu	Lys	Lys	Lys	Gly	Arg	
				405					410					415		
Ile	Ser	Ala	Thr	Leu	Asn	Thr	Lys	Glu	Gly	Tyr	Ser	Tyr	Leu	Tyr	Ile	
			420					425					430			
Lys	Gly	Ser	Gln	Pro	Glu	Asp	Ser	Ala	Thr	Tyr	Leu	Cys	Ala	Leu	Gly	
		435					440					445				
Pro	Tyr	Asn	Asp	Tyr	Lys	Leu	Ser	Phe	Gly	Ala	Gly	Thr	Thr	Val	Thr	
	450					455					460					
Val	Arg	Ala	Asn	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	
465					470					475					480	
Asp	Ser	Lys	Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	
				485					490					495		
Ser	Gln	Thr	Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	
			500					505					510			
Asp	Lys	Cys	Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	
		515					520					525				
Ala	Val	Ala	Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	
	530					535					540					
Asn	Asn	Ser	Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	
545					550					555					560	

Ser	Cys	Asp	Val	Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn
				565				570						575	
Leu	Asn	Phe	Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu
			580					585					590		
Lys	Val	Ala	Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser
		595					600					605			

<210> 173

<211> 1815

<212> DNA

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 1 construct; beta chain-P2A-alpha chain with cysteine substitutions in beta and alpha chain constant domains

<400> 173

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120
agatgtagcc ctaaattctgg ccacgatacc gtgagctggg atcaacaggc tctgggacaa
180
ggacctcagt tcattcttcca gtactacgag gaggaggaga gacagagagg caatttcctt
240
gacaggttta gcggacacca gttccccaat tacagctctg agctgaacgt gaatgccctt
300
cttctgggag attctgccct gtatctgtgt gccagcagct tctttagcca ggaaaccag
360
tacttcggcc caggaacaag actgctgggt cttgaagacc tgaagaacgt gttcccccca
420
gaggtggccg tgttcgagcc tagcgaggcc gagatcagcc acaccagaa agccaccctc
480
gtgtgcctgg ccaccggcct ttaccccgac cacgtggaac tgtcttggtg ggtcaacggc
540
aaagaggtgc acagcggcgt ctgcaccgac cccagcccc tgaaagagca gcccgcctg
600
aacgacagcc ggtactgtct gagcagcaga ctgagagtgt ccgccacctt ctggcagaac
660
ccccggaacc acttcagatg ccaggtgcag ttctacggcc tgagcgagaa cgacgagtgg
720
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780
gattgcggct tcaccagcga gagctaccag cagggcgtgc tgagcgccac catcctgtac
840

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gagatcctgc tgggcaaggc caccctgtac gccgtgctgg tgtccgccct ggtgctgatg
900
gccatgggtca agcggaagga cagccggggc ggttccggag ccacgaactt ctctctgtta
960
aagcaagcag gagacgtgga agaaaacccc ggtcccatgg aaaccctggt aggctgctc
1020
attctgtggt tacagctcca atgggtgagc agcaaacagg aagtgacca gattcctgct
1080
gccttatctg tgcctgaagg cgaaaatctg gtgctgaatt gcagcttcac cgattctgcc
1140
atctacaacc tccagtgggt cagacaggat ccaggaaaag gcctgacatc tcttctgctg
1200
atccagtcta gccagagaga gcagacaagc ggaagactga atgcctctct ggacaagagc
1260
agcggaagat ctaccctgta tattgccgcc tctcagcctg gagattctgc cacatatctg
1320
tgtgccgtgg agggagatag cagctataag ctgatcttcg gcagcggcac aagattactg
1380
gtgagacctg acatccagaa ccctgatcct gctgtgtacc agctgcggga cagcaagagc
1440
agcgacaaga gcgtgtgcct gttcaccgac ttcgacagcc agaccaacgt gtcccagagc
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1560
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1620
aacaacagca ttatccccga ggacacattc ttcccaagcc ccgagagcag ctgcgacgtg
1680
aagctgggtg aaaagagctt cgagacagac accaacctga acttccagaa cctcagcgtg
1740
atcggcttcc ggatcctgct gctgaagggt gccggcttca acctgctgat gaccctgcgg
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c t g t g g t c c a g c t g a
1815

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<210> 174

<211> 604

<212> PRT

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 1 construct; beta chain-P2A-alpha chain with cysteine substitutions in beta and alpha chain constant domains

<400> 174

Met	Gly	Pro	Gly	Leu	Leu	Cys	Trp	Ala	Leu	Leu	Cys	Leu	Leu	Gly	Ala
1				5					10					15	
Gly	Leu	Val	Asp	Ala	Gly	Val	Thr	Gln	Ser	Pro	Thr	His	Leu	Ile	Lys
			20					25					30		
Thr	Arg	Gly	Gln	Gln	Val	Thr	Leu	Arg	Cys	Ser	Pro	Lys	Ser	Gly	His
		35					40					45			
Asp	Thr	Val	Ser	Trp	Tyr	Gln	Gln	Ala	Leu	Gly	Gln	Gly	Pro	Gln	Phe
	50					55					60				
Ile	Phe	Gln	Tyr	Tyr	Glu	Glu	Glu	Glu	Arg	Gln	Arg	Gly	Asn	Phe	Pro
65					70					75					80
Asp	Arg	Phe	Ser	Gly	His	Gln	Phe	Pro	Asn	Tyr	Ser	Ser	Glu	Leu	Asn
				85					90					95	
Val	Asn	Ala	Leu	Leu	Leu	Gly	Asp	Ser	Ala	Leu	Tyr	Leu	Cys	Ala	Ser
			100					105					110		
Ser	Phe	Phe	Ser	Gln	Glu	Thr	Gln	Tyr	Phe	Gly	Pro	Gly	Thr	Arg	Leu
		115					120					125			
Leu	Val	Leu	Glu	Asp	Leu	Lys	Asn	Val	Phe	Pro	Pro	Glu	Val	Ala	Val
	130					135					140				
Phe	Glu	Pro	Ser	Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr	Leu
145					150					155					160
Val	Cys	Leu	Ala	Thr	Gly	Phe	Tyr	Pro	Asp	His	Val	Glu	Leu	Ser	Trp
				165					170					175	
Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Cys	Thr	Asp	Pro	Gln
			180					185					190		
Pro	Leu	Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys	Leu	Ser
		195					200					205			
Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn	His
	210					215					220				
Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu	Trp
225					230					235					240
Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu	Ala
				245					250					255	
Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Glu	Ser	Tyr	Gln	Gln	Gly
			260					265					270		
Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr
		275					280					285			
Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val	Lys
	290					295					300				
Arg	Lys	Asp	Ser	Arg	Gly	Gly	Ser	Gly	Ala	Thr	Asn	Phe	Ser	Leu	Leu
305					310					315					320
Lys	Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Glu	Thr	Leu
				325					330					335	
Leu	Gly	Leu	Leu	Ile	Leu	Trp	Leu	Gln	Leu	Gln	Trp	Val	Ser	Ser	Lys
			340					345					350		

Gln	Glu	Val	Thr	Gln	Ile	Pro	Ala	Ala	Leu	Ser	Val	Pro	Glu	Gly	Glu
		355					360					365			
Asn	Leu	Val	Leu	Asn	Cys	Ser	Phe	Thr	Asp	Ser	Ala	Ile	Tyr	Asn	Leu
	370					375					380				
Gln	Trp	Phe	Arg	Gln	Asp	Pro	Gly	Lys	Gly	Leu	Thr	Ser	Leu	Leu	Leu
385					390					395					400
Ile	Gln	Ser	Ser	Gln	Arg	Glu	Gln	Thr	Ser	Gly	Arg	Leu	Asn	Ala	Ser
				405					410					415	
Leu	Asp	Lys	Ser	Ser	Gly	Arg	Ser	Thr	Leu	Tyr	Ile	Ala	Ala	Ser	Gln
			420					425					430		
Pro	Gly	Asp	Ser	Ala	Thr	Tyr	Leu	Cys	Ala	Val	Glu	Gly	Asp	Ser	Ser
		435					440					445			
Tyr	Lys	Leu	Ile	Phe	Gly	Ser	Gly	Thr	Arg	Leu	Leu	Val	Arg	Pro	Asp
	450					455					460				
Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser	Lys	Ser
465					470					475					480
Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Thr	Asn
				485					490					495	
Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp	Lys	Cys	Val
			500					505					510		
Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	Ala	Val	Ala	Trp
		515					520					525			
Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn	Asn	Ser	Ile
	530					535					540				
Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	Ser	Cys	Asp	Val
545					550					555					560
Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn	Leu	Asn	Phe	Gln
				565					570					575	
Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu	Lys	Val	Ala	Gly
			580				585						590		
Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser				
		595					600								

<210> 175

<211> 1824

<212> DNA

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 2 construct; beta chain-P2A-alpha chain with cysteine substitutions in beta and alpha chain constant domains

<400> 175

atgggcacca gactgctgtg ttgggctgct ctgtgtctgc tgggagccga tcatacaggt
60

gccggtgtca	gccagacacc	tagcaacaaa	gtgaccgaga	agggcaaata	cgtggaactg
120					
agatgcgacc	ccatcagcgg	acacacagcc	ctgtactggg	acagacagtc	tctcggccag
180					
ggacctgagt	tcctgatcta	cttccaaggc	accggcgctg	ccgatgatag	cggcctgcct
240					
aacgatagat	tcttcgccgt	cagacccgag	ggcagcgtgt	ccacactgaa	gatccagaga
300					
accgagaggg	gcgacagcgc	cgtgtatctg	tgtgcctctt	ctctgtctgg	cctcggctct
360					
ggcgctaacg	tgctgacatt	tggcgccgga	agcagactga	ccgtgctgga	agatctgaag
420					
aacgtgttcc	cacctgaggt	ggccgtgttc	gagccttctg	aggccgagat	cagccacaca
480					
cagaaagcca	cactcgtgtg	tctggccacc	ggcttctatc	ccgaccatgt	ggaactgtct
540					
tggtgggtca	acggcaaaga	ggtgcacagc	ggcgtctgta	cagatcccca	gcctctgaaa
600					
gaacagcccg	ctctgaacga	cagccggtac	tgtctgtcct	ccagactgag	agtgtccgcc
660					
accttctggc	agaaccccag	aaaccacttc	agatgccagg	tgcagttcta	cggcctgagc
720					
gagaacgatg	agtggacca	ggatagagcc	aagcctgtga	cacagatcgt	gtctgccgaa
780					
gcctggggca	gagccgattg	tggctttacc	agcgagagct	accagcaggg	cgtgctgtct
840					
gccacaatcc	tgtacgagat	cctgctgggc	aaagccactc	tgtacgccgt	gctgggtgtct
900					
gccctgggtgc	tgatggccat	ggtcaagcgg	aaggacagca	gaggcggttc	cggagccacg
960					
aacttctctc	tgttaaagca	agcaggagac	gtggaagaaa	accccggtcc	catggaaaca
1020					
ctgctggggc	tgctgatact	gtggctgcaa	ctgcaatggg	tgtccagcaa	gcaagaagtg
1080					
acacagatcc	ctgccgctct	gtctgtgcct	gagggcgaaa	acctggtgct	gaactgcagc
1140					
ttcaccgaca	gcgccatcta	caacctgcag	tggttcagac	aggaccccg	caagggactg
1200					
acaagcctgc	tgctgattca	gagcagccag	agagagcaga	ccagcggcag	actgaatgcc
1260					
agcctggata	agtcctccgg	cagaagcacc	ctgtatatcg	ccgcttctca	gcctggcgat
1320					
agcgccacat	atctgtgtgc	cgtgatcggc	gagcagaact	tcgtgtttgg	ccctggcaca
1380					
agactgagcg	tgctgcccta	cattcagaac	cccgatcctg	ccgtgtacca	gctgcgggac
1440					

agcaagagca gcgacaagag cgtgtgcctg ttcaccgact tcgacagcca gaccaacgtg
 1500
 tcccagagca aggacagcga cgtgtacatc accgataagt gcgtgctgga catgcggagc
 1560
 atggacttca agagcaacag cgccgtggcc tgggtccaaca agagcgactt cgcctgcgcc
 1620
 aacgccttca acaacagcat tatccccgag gacacattct tcccaagccc cgagagcagc
 1680
 tgcgacgtga agctgggtgga aaagagcttc gagacagaca ccaacctgaa cttccagaac
 1740
 ctcagcgtga tcggcttccg gatcctgctg ctgaagggtgg ccgggcttcaa cctgctgatg
 1800
 a c c c t g c g g c t g t g g t c c a g c t g a
 1824

<210> 176

<211> 607

<212> PRT

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 2 construct
 polypeptide; beta chain-P2A-alpha chain with
 cysteine substitutions in beta and alpha chain
 constant domains

<400> 176

Met	Gly	Thr	Arg	Leu	Leu	Cys	Trp	Ala	Ala	Leu	Cys	Leu	Leu	Gly	Ala
1				5				10						15	
Asp	His	Thr	Gly	Ala	Gly	Val	Ser	Gln	Thr	Pro	Ser	Asn	Lys	Val	Thr
			20					25					30		
Glu	Lys	Gly	Lys	Tyr	Val	Glu	Leu	Arg	Cys	Asp	Pro	Ile	Ser	Gly	His
		35				40						45			
Thr	Ala	Leu	Tyr	Trp	Tyr	Arg	Gln	Ser	Leu	Gly	Gln	Gly	Pro	Glu	Phe
	50				55					60					
Leu	Ile	Tyr	Phe	Gln	Gly	Thr	Gly	Ala	Ala	Asp	Asp	Ser	Gly	Leu	Pro
65				70						75				80	
Asn	Asp	Arg	Phe	Phe	Ala	Val	Arg	Pro	Glu	Gly	Ser	Val	Ser	Thr	Leu
			85					90					95		
Lys	Ile	Gln	Arg	Thr	Glu	Arg	Gly	Asp	Ser	Ala	Val	Tyr	Leu	Cys	Ala
		100					105						110		
Ser	Ser	Leu	Ser	Gly	Leu	Gly	Ser	Gly	Ala	Asn	Val	Leu	Thr	Phe	Gly
		115				120						125			
Ala	Gly	Ser	Arg	Leu	Thr	Val	Leu	Glu	Asp	Leu	Lys	Asn	Val	Phe	Pro
	130					135						140			

Pro	Glu	Val	Ala	Val	Phe	Glu	Pro	Ser	Glu	Ala	Glu	Ile	Ser	His	Thr
145					150					155					160
Gln	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ala	Thr	Gly	Phe	Tyr	Pro	Asp	His
				165					170					175	
Val	Glu	Leu	Ser	Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val
			180					185					190		
Cys	Thr	Asp	Pro	Gln	Pro	Leu	Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser
		195				200					205				
Arg	Tyr	Cys	Leu	Ser	Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln
	210					215					220				
Asn	Pro	Arg	Asn	His	Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser
225					230					235					240
Glu	Asn	Asp	Glu	Trp	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile
				245					250					255	
Val	Ser	Ala	Glu	Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Glu
			260					265					270		
Ser	Tyr	Gln	Gln	Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu
		275				280						285			
Leu	Gly	Lys	Ala	Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu
	290					295					300				
Met	Ala	Met	Val	Lys	Arg	Lys	Asp	Ser	Arg	Gly	Gly	Ser	Gly	Ala	Thr
305					310					315					320
Asn	Phe	Ser	Leu	Leu	Lys	Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly
				325					330					335	
Pro	Met	Glu	Thr	Leu	Leu	Gly	Leu	Leu	Ile	Leu	Trp	Leu	Gln	Leu	Gln
			340						345				350		
Trp	Val	Ser	Ser	Lys	Gln	Glu	Val	Thr	Gln	Ile	Pro	Ala	Ala	Leu	Ser
		355					360					365			
Val	Pro	Glu	Gly	Glu	Asn	Leu	Val	Leu	Asn	Cys	Ser	Phe	Thr	Asp	Ser
	370					375					380				
Ala	Ile	Tyr	Asn	Leu	Gln	Trp	Phe	Arg	Gln	Asp	Pro	Gly	Lys	Gly	Leu
385					390					395					400
Thr	Ser	Leu	Leu	Leu	Ile	Gln	Ser	Ser	Gln	Arg	Glu	Gln	Thr	Ser	Gly
				405					410					415	
Arg	Leu	Asn	Ala	Ser	Leu	Asp	Lys	Ser	Ser	Gly	Arg	Ser	Thr	Leu	Tyr
			420					425					430		
Ile	Ala	Ala	Ser	Gln	Pro	Gly	Asp	Ser	Ala	Thr	Tyr	Leu	Cys	Ala	Val
		435					440					445			
Ile	Gly	Glu	Gln	Asn	Phe	Val	Phe	Gly	Pro	Gly	Thr	Arg	Leu	Ser	Val
	450					455					460				
Leu	Pro	Tyr	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp
465					470					475					480
Ser	Lys	Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser
				485					490					495	
Gln	Thr	Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp

			500					505					510				
Lys	Cys	Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	Ala		
		515					520					525					
Val	Ala	Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn		
	530					535					540						
Asn	Ser	Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	Ser		
545					550					555					560		
Cys	Asp	Val	Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn	Leu		
			565						570					575			
Asn	Phe	Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu	Lys		
		580						585				590					
Val	Ala	Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser			
	595						600					605					

<210> 177

<211> 1818

<212> DNA

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 3 construct; beta
chain-P2A-alpha chain with cysteine substitutions
in beta and alpha chain constant domains

<400> 177

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gctggcgtgt cccagacccc cagcaacaaa gtgaccgaga agggcaaata cgtggaactg
120
agatgcgacc ccatcagcgg ccacaccgcc ctgtactggt acagacagtc tctggggccag
180
ggccccgagt tcctgatata ttttcagggc accggcgctg ccgacgacag cggcctgcct
240
aacgatagat tcttcgccgt gcggccccgag ggcagcgtgt ccacactgaa gatccagaga
300
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480
ctcgtgtgcc tggccaccgg ctttttcccc gaccatgtgg aactgtcttg gtgggtcaac
540
ggcaaagagg tgcacagcgg agtgtgcacc gaccctcagc ccctgaaaga acagcccgcc
600

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ctgaacgaca	gccggtactg	cctgagcagc	agactgagag	tgtccgccac	cttctggcag
660					
aacccccgga	accacttcag	atgccagggtg	cagttctacg	gcctgagcga	gaacgacgag
720					
tggacccagg	acagagccaa	gcccgtgacc	cagatcgtgt	ctgccgaagc	ctggggcaga
780					
gccgattgcg	gctttacctc	cgtgtcctat	cagcagggcg	tgctgagcgc	caccatcctg
840					
tacgagatcc	tgctgggcaa	ggccaccctg	tacgccgtgc	tggtgtctgc	cctgggtgctg
900					
atggccatgg	tcaagcggaa	ggacttcggt	tccggagcca	cgaacttctc	tctgttaaag
960					
caagcaggag	acgtggaaga	aaaccccgggt	cccatgatga	agtccctgcg	ggtgctgctc
1020					
gtgatcctgt	ggctgcagct	gtcttgggtg	tggtcccagc	agaaagaggt	ggaacagaac
1080					
agcggccctc	tgagcgtgcc	agagggcgcc	attgctagcc	tgaattgcac	ctacagcgac
1140					
cggggcagcc	agagcttctt	ctggtatcgg	cagtacagcg	gcaagagccc	cgagctgatk
1200					
atgagcatct	acagcaacgg	cgacaaagag	gacggccggt	tcaccgccc	gctgaacaaa
1260					
gccagccagt	acgtgtcact	gctgatccgg	gacagccagc	ccagcgatag	cgccacatac
1320					
ctgtgcgccg	tgatagcgg	cggctaccag	aaagtgacct	tcggcaccgg	caccaagctg
1380					
caagtgatcc	ccaacatcca	gaaccccagc	cccgtgtgtg	accagctgcg	ggacagcaag
1440					
agcagcgaca	agagcgtgtg	cctgttcacc	gacttcgaca	gccagaccaa	cgtgtcccag
1500					
agcaaggaca	gcgacgtgta	catcaccgat	aagtgcgtgc	tgacatgcg	gagcatggac
1560					
ttcaagagca	acagcgccgt	ggcctgggtcc	aacaagagcg	acttcgcctg	cgccaacgcc
1620					
ttcaacaaca	gcattatccc	cgaggacaca	ttcttcccaa	gccccgagag	cagctgcgac
1680					
gtgaagctgg	tggaagagag	cttcgagaca	gacaccaacc	tgaacttcca	gaacctcagc
1740					
gtgatcggct	tccggatcct	gctgctgaag	gtggccggct	tcaacctgct	gatgaccctg
1800					
c g g c t g t g g t				c c a g c t g a	
1818					

<210> 178

<211> 605

<212> PRT

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 3 construct; beta
chain-P2A-alpha chain with cysteine substitutions
in beta and alpha chain constant domains

<400> 178

Met	Gly	Thr	Arg	Leu	Leu	Cys	Trp	Ala	Ala	Leu	Cys	Leu	Leu	Gly	Ala	
1				5				10						15		
Asp	His	Thr	Gly	Ala	Gly	Val	Ser	Gln	Thr	Pro	Ser	Asn	Lys	Val	Thr	
			20					25					30			
Glu	Lys	Gly	Lys	Tyr	Val	Glu	Leu	Arg	Cys	Asp	Pro	Ile	Ser	Gly	His	
		35					40					45				
Thr	Ala	Leu	Tyr	Trp	Tyr	Arg	Gln	Ser	Leu	Gly	Gln	Gly	Pro	Glu	Phe	
	50					55					60					
Leu	Ile	Tyr	Phe	Gln	Gly	Thr	Gly	Ala	Ala	Asp	Asp	Ser	Gly	Leu	Pro	
65				70						75					80	
Asn	Asp	Arg	Phe	Phe	Ala	Val	Arg	Pro	Glu	Gly	Ser	Val	Ser	Thr	Leu	
			85						90					95		
Lys	Ile	Gln	Arg	Thr	Glu	Arg	Gly	Asp	Ser	Ala	Val	Tyr	Leu	Cys	Ala	
		100						105					110			
Ser	Ser	Leu	Asn	Met	Asn	Thr	Glu	Ala	Phe	Phe	Gly	Gln	Gly	Thr	Arg	
		115					120					125				
Leu	Thr	Val	Val	Glu	Asp	Leu	Asn	Lys	Val	Phe	Pro	Pro	Glu	Val	Ala	
	130					135					140					
Val	Phe	Glu	Pro	Ser	Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr	
145					150					155					160	
Leu	Val	Cys	Leu	Ala	Thr	Gly	Phe	Phe	Pro	Asp	His	Val	Glu	Leu	Ser	
			165						170					175		
Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Cys	Thr	Asp	Pro	
		180						185					190			
Gln	Pro	Leu	Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys	Leu	
		195					200					205				
Ser	Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn	
	210					215					220					
His	Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu	
225				230						235					240	
Trp	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu	
			245						250					255		
Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Val	Ser	Tyr	Gln	Gln	
		260					265						270			
Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	
		275					280					285				

Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val
290							295				300				
Lys	Arg	Lys	Asp	Phe	Gly	Ser	Gly	Ala	Thr	Asn	Phe	Ser	Leu	Leu	Lys
305					310					315					320
Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Met	Lys	Ser	Leu
				325					330					335	
Arg	Val	Leu	Leu	Val	Ile	Leu	Trp	Leu	Gln	Leu	Ser	Trp	Val	Trp	Ser
				340				345					350		
Gln	Gln	Lys	Glu	Val	Glu	Gln	Asn	Ser	Gly	Pro	Leu	Ser	Val	Pro	Glu
		355					360					365			
Gly	Ala	Ile	Ala	Ser	Leu	Asn	Cys	Thr	Tyr	Ser	Asp	Arg	Gly	Ser	Gln
	370					375					380				
Ser	Phe	Phe	Trp	Tyr	Arg	Gln	Tyr	Ser	Gly	Lys	Ser	Pro	Glu	Leu	Ile
385					390					395					400
Met	Ser	Ile	Tyr	Ser	Asn	Gly	Asp	Lys	Glu	Asp	Gly	Arg	Phe	Thr	Ala
				405					410					415	
Gln	Leu	Asn	Lys	Ala	Ser	Gln	Tyr	Val	Ser	Leu	Leu	Ile	Arg	Asp	Ser
			420					425					430		
Gln	Pro	Ser	Asp	Ser	Ala	Thr	Tyr	Leu	Cys	Ala	Val	Asp	Ser	Gly	Gly
		435					440					445			
Tyr	Gln	Lys	Val	Thr	Phe	Gly	Thr	Gly	Thr	Lys	Leu	Gln	Val	Ile	Pro
	450					455					460				
Asn	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser	Lys
465					470					475					480
Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Thr
				485					490					495	
Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp	Lys	Cys
			500					505					510		
Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	Ala	Val	Ala
		515					520					525			
Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn	Asn	Ser
	530					535					540				
Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	Ser	Cys	Asp
545					550					555					560
Val	Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn	Leu	Asn	Phe
				565					570					575	
Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu	Lys	Val	Ala
			580					585					590		
Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser			
		595					600					605			

<210> 179

<211> 1812

<212> DNA

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 10 construct; beta
chain-P2A-alpha chain with cysteine substitutions
in beta and alpha chain constant domains

<400> 179

atgggacacca	gactgctgtg	ttggggccgct	ctgtgtctgc	tgggcgccga	tcatacaggc
60					
gctggcgtgt	cccagacccc	cagcaacaaa	gtgaccgaga	agggcaaata	cgtggaactg
120					
agatgcgacc	ccatcagcgg	ccacaccgcc	ctgtactggt	acagacagtc	tctgggccag
180					
ggccccgagt	tcctgatata	ttttcagggc	accggcgctg	ccgacgacag	cggcctgcct
240					
aacgatagat	tcttcgccgt	gcggccccgag	ggcagcgtgt	ccacactgaa	gatccagaga
300					
accgagcggg	gcgacagcgc	cgtgtatctg	tgtgccagca	gcctgaatat	gaacaccgag
360					
gcattctttg	ggcagggcac	ccggctgacc	gtggtggaag	atctgaacaa	ggtgttcccc
420					
ccagaggtgg	ccgtgttcga	gccttctgag	gccgagatca	gccacacca	gaaagccacc
480					
ctcgtgtgcc	tggccaccgg	ctttttcccc	gaccatgtgg	aactgtcttg	gtgggtcaac
540					
ggcaaagagg	tgcacagcgg	agtgtgcacc	gaccctcagc	ccctgaaaga	acagcccggc
600					
ctgaacgaca	gccggtactg	cctgagcagc	agactgagag	tgtccgccac	cttctggcag
660					
aacccccgga	accacttcag	atgccagggt	cagttctacg	gcctgagcga	gaacgacgag
720					
tggaccaggg	acagagccaa	gcccgtgacc	cagatcgtgt	ctgccgaagc	ctggggcaga
780					
gccgattgcg	gctttacctc	cgtgtcctat	cagcagggcg	tgctgagcgc	caccatcctg
840					
tacgagatcc	tgctgggcaa	ggccaccctg	tacgccgtgc	tgggtgtctgc	cctgggtgctg
900					
atggccatgg	tcaagcggaa	ggacttcggt	tccggagcca	cgaacttctc	tctgttaaag
960					
caagcaggag	acgtggaaga	aaacccccggt	cccatggaaa	ccctgctggg	agtgtccctc
1020					
gtgatcctgt	ggctgcagct	ggccagagtg	aacagccagc	agggggaaga	ggatccccag
1080					
gccctgagca	ttcaggaagg	cgagaacgcc	accatgaact	gcagctacaa	gaccagcatc
1140					

```

aacaacctgc agtggtacag gcagaacagc ggcagaggcc tgggtgcacct gatcctgata
1200
agaagcaacg agagagagaa gcactccgga cggctgagag tgaccctgga cacctccaag
1260
aagtcctcca gcctgctgat caccgccagc agagccgccg ataccgccag ctacttctgc
1320
gccacagacg agagcagcaa ctacaagctg accttcggca agggcacact gctgacagtg
1380
aaccccaaca tccagaaccc cgaccccgct gtgtaccagc tgcgggacag caagagcagc
1440
gacaagagcg tgtgcctggt caccgacttc gacagccaga ccaacgtgtc ccagagcaag
1500
gacagcgacg tgtacatcac cgataagtgc gtgctggaca tgcggagcat ggacttcaag
1560
agcaacagcg ccgtggcctg gtccaacaag agcgacttcg cctgcgccaa cgccttcaac
1620
aacagcatta tccccgagga cacattcttc ccaagccccg agagcagctg cgacgtgaag
1680
ctggttgaaa agagcttcga gacagacacc aacctgaact tccagaacct cagcgtgata
1740
ggcttccgga tcctgctgct gaagggtggcc ggcttcaacc tgctgatgac cctgcggctg
1800
t g g t c c a g c t g a
1812

```

<210> 180

<211> 603

<212> PRT

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 10 construct; beta
chain-P2A-alpha chain with cysteine substitutions
in beta and alpha chain constant domains

<400> 180

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Met Gly Thr Arg Leu Leu Cys Trp Ala Ala Leu Cys Leu Leu Gly Ala
 1           5           10           15
Asp His Thr Gly Ala Gly Val Ser Gln Thr Pro Ser Asn Lys Val Thr
          20           25           30
Glu Lys Gly Lys Tyr Val Glu Leu Arg Cys Asp Pro Ile Ser Gly His
          35           40           45
Thr Ala Leu Tyr Trp Tyr Arg Gln Ser Leu Gly Gln Gly Pro Glu Phe
          50           55           60
Leu Ile Tyr Phe Gln Gly Thr Gly Ala Ala Asp Asp Ser Gly Leu Pro

```

65					70					75					80
Asn	Asp	Arg	Phe	Phe	Ala	Val	Arg	Pro	Glu	Gly	Ser	Val	Ser	Thr	Leu
				85					90					95	
Lys	Ile	Gln	Arg	Thr	Glu	Arg	Gly	Asp	Ser	Ala	Val	Tyr	Leu	Cys	Ala
			100					105					110		
Ser	Ser	Leu	Asn	Met	Asn	Thr	Glu	Ala	Phe	Phe	Gly	Gln	Gly	Thr	Arg
		115					120					125			
Leu	Thr	Val	Val	Glu	Asp	Leu	Asn	Lys	Val	Phe	Pro	Pro	Glu	Val	Ala
	130					135					140				
Val	Phe	Glu	Pro	Ser	Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr
145					150					155					160
Leu	Val	Cys	Leu	Ala	Thr	Gly	Phe	Phe	Pro	Asp	His	Val	Glu	Leu	Ser
				165					170					175	
Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Cys	Thr	Asp	Pro
			180					185					190		
Gln	Pro	Leu	Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys	Leu
		195					200					205			
Ser	Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn
	210					215					220				
His	Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu
225					230					235					240
Trp	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu
			245						250					255	
Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Val	Ser	Tyr	Gln	Gln
			260					265					270		
Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala
		275					280					285			
Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val
	290					295					300				
Lys	Arg	Lys	Asp	Phe	Gly	Ser	Gly	Ala	Thr	Asn	Phe	Ser	Leu	Leu	Lys
305					310					315					320
Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Glu	Thr	Leu	Leu
				325					330					335	
Gly	Val	Ser	Leu	Val	Ile	Leu	Trp	Leu	Gln	Leu	Ala	Arg	Val	Asn	Ser
			340					345					350		
Gln	Gln	Gly	Glu	Glu	Asp	Pro	Gln	Ala	Leu	Ser	Ile	Gln	Glu	Gly	Glu
		355					360					365			
Asn	Ala	Thr	Met	Asn	Cys	Ser	Tyr	Lys	Thr	Ser	Ile	Asn	Asn	Leu	Gln
	370					375					380				
Trp	Tyr	Arg	Gln	Asn	Ser	Gly	Arg	Gly	Leu	Val	His	Leu	Ile	Leu	Ile
385					390					395					400
Arg	Ser	Asn	Glu	Arg	Glu	Lys	His	Ser	Gly	Arg	Leu	Arg	Val	Thr	Leu
				405					410					415	
Asp	Thr	Ser	Lys	Lys	Ser	Ser	Ser	Leu	Leu	Ile	Thr	Ala	Ser	Arg	Ala
			420					425					430		

Ala	Asp	Thr	Ala	Ser	Tyr	Phe	Cys	Ala	Thr	Asp	Glu	Ser	Ser	Asn	Tyr
		435					440					445			
Lys	Leu	Thr	Phe	Gly	Lys	Gly	Thr	Leu	Leu	Thr	Val	Asn	Pro	Asn	Ile
	450					455					460				
Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser	Lys	Ser	Ser
465					470					475					480
Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Thr	Asn	Val
			485						490					495	
Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp	Lys	Cys	Val	Leu
		500					505						510		
Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	Ala	Val	Ala	Trp	Ser
	515						520					525			
Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn	Asn	Ser	Ile	Ile
	530					535					540				
Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	Ser	Cys	Asp	Val	Lys
545					550					555					560
Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn	Leu	Asn	Phe	Gln	Asn
			565					570						575	
Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu	Lys	Val	Ala	Gly	Phe
		580					585						590		
Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser					
	595						600								

<210> 181

<211> 1818

<212> DNA

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 7 construct; beta chain-P2A-alpha chain with cysteine substitutions in beta and alpha chain constant domains

<400> 181

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atgagcaacc aggtcttgtg ctgtgtggtg ctgtgctttc ttggcgccaa tacagtggat
60
ggcggcatta cacagagccc taagtacctg ttccggaaag aaggccagaa cgtgacactg
120
tcttgcgagc aaaacctgaa ccacgatgcc atgtactggt acagacagga tcctggacag
180
ggacttaggc tgatctacta tagccagatc gtgaacgact tccagaaggg cgatattgcc
240
gagggctatt ctgtgtctcg ggagaaaaag gagagcttcc ctctgacagt gacatctgcc
300
cagaagaatc ctaccgcctt ctacctttgt gccagctctc tgaatcgggg cagatacgga
360

```

tacacctttg	gatctggcac	cagactgaca	gtggtggaag	atctgaacaa	ggtgttcccc
420					
ccagaggtgg	ccgtgttcga	gccttctgag	gccgagatct	cccacaccca	gaaagccacc
480					
ctcgtgtgcc	tggccaccgg	ctttttcccc	gaccacgtgg	aactgtcttg	gtgggtcaac
540					
ggcaaagagg	tgcactccgg	cgtgtgcacc	gatccccagc	ctctgaaaga	acagcccgcc
600					
ctgaacgaca	gccggtactg	cctgagcagc	agactgagag	tgtccgccac	cttctggcag
660					
aacccccgga	accacttcag	atgccaggtg	cagttctacg	gcctgagcga	gaacgacgag
720					
tggacccagg	acagagccaa	gcccgtgaca	cagatcgtgt	ctgccgaagc	ctggggcaga
780					
gccgattgcg	gctttacctc	cgtgtcctat	cagcagggcg	tgctgagcgc	cacaatcctg
840					
tacgagatcc	tgctgggcaa	ggccaccctg	tacgccgtgc	tgggtgtctgc	cctggtgctg
900					
atggccatgg	tcaagcggaa	ggacttcggt	tccggagcca	cgaacttctc	tctgttaaag
960					
caagcaggag	acgtggaaga	aaaccccggg	cccatggaga	agaaccccct	tgcagcacct
1020					
ctgcttattc	tgtggttcca	cctggattgc	gtgagctcta	tcctgaatgt	ggagcagtct
1080					
cctcagtctc	tgcatgttca	ggaaggcgat	agcaccaact	tcacctgtag	ctttcccagc
1140					
agcaacttct	atgccctgca	ctggtacaga	tgggaaacag	ccaaaagccc	tgaagccctg
1200					
ttcgtgatga	cccttaatgg	cgatgagaag	aagaagggcc	ggattttctgc	caccctgaat
1260					
acaaaagagg	gctacagcta	cctgtacatc	aagggatctc	agcctgagga	tagcgccaca
1320					
tatctgtgtg	cctatctggg	agccggcaat	cagttctatt	tcggaacagg	caccagcctg
1380					
accgtgattc	ctaatatcca	gaaccccgat	cctgccgtgt	accagctgcg	ggacagcaag
1440					
agcagcgaca	agagcgtgtg	cctgttcacc	gacttcgaca	gccagaccaa	cgtgtcccag
1500					
agcaaggaca	gcgacgtgta	catcaccgat	aagtgcgtgc	tggacatgcg	gagcatggac
1560					
ttcaagagca	acagcgccgt	ggcctgggtcc	aacaagagcg	acttcgcctg	cgccaacgcc
1620					
ttcaacaaca	gcattatccc	cgaggacaca	ttcttcccaa	gccccgagag	cagctgcgac
1680					
gtgaagctgg	tggaaaagag	cttcgagaca	gacaccaacc	tgaacttcca	gaacctcagc
1740					

gtgatcggct tccggatcct gctgctgaag gtggccggct tcaacctgct gatgaccctg
1800
c g g c t g t g g t c c a g c t g a
1818

<210> 182
<211> 605
<212> PRT
<213> Artificial Sequence

<220>
<223> codon optimized TCR number 7 construct; beta
chain-P2A-alpha chain with cysteine substitutions
in beta and alpha chain constant domains

<400> 182
Met Ser Asn Gln Val Leu Cys Cys Val Val Leu Cys Phe Leu Gly Ala
1 5 10 15
Asn Thr Val Asp Gly Gly Ile Thr Gln Ser Pro Lys Tyr Leu Phe Arg
20 25 30
Lys Glu Gly Gln Asn Val Thr Leu Ser Cys Glu Gln Asn Leu Asn His
35 40 45
Asp Ala Met Tyr Trp Tyr Arg Gln Asp Pro Gly Gln Gly Leu Arg Leu
50 55 60
Ile Tyr Tyr Ser Gln Ile Val Asn Asp Phe Gln Lys Gly Asp Ile Ala
65 70 75 80
Glu Gly Tyr Ser Val Ser Arg Glu Lys Lys Glu Ser Phe Pro Leu Thr
85 90 95
Val Thr Ser Ala Gln Lys Asn Pro Thr Ala Phe Tyr Leu Cys Ala Ser
100 105 110
Ser Leu Asn Arg Gly Arg Tyr Gly Tyr Thr Phe Gly Ser Gly Thr Arg
115 120 125
Leu Thr Val Val Glu Asp Leu Asn Lys Val Phe Pro Pro Glu Val Ala
130 135 140
Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
145 150 155 160
Leu Val Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val Glu Leu Ser
165 170 175
Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro
180 185 190
Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu
195 200 205
Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn
210 215 220
His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu

225					230					235				240	
Trp	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu
				245					250					255	
Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Val	Ser	Tyr	Gln	Gln
			260					265					270		
Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala
		275					280					285			
Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val
	290					295				300					
Lys	Arg	Lys	Asp	Phe	Gly	Ser	Gly	Ala	Thr	Asn	Phe	Ser	Leu	Leu	Lys
305					310					315					320
Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Glu	Lys	Asn	Pro
			325						330					335	
Leu	Ala	Ala	Pro	Leu	Leu	Ile	Leu	Trp	Phe	His	Leu	Asp	Cys	Val	Ser
			340					345					350		
Ser	Ile	Leu	Asn	Val	Glu	Gln	Ser	Pro	Gln	Ser	Leu	His	Val	Gln	Glu
		355					360					365			
Gly	Asp	Ser	Thr	Asn	Phe	Thr	Cys	Ser	Phe	Pro	Ser	Ser	Asn	Phe	Tyr
	370					375					380				
Ala	Leu	His	Trp	Tyr	Arg	Trp	Glu	Thr	Ala	Lys	Ser	Pro	Glu	Ala	Leu
385					390					395					400
Phe	Val	Met	Thr	Leu	Asn	Gly	Asp	Glu	Lys	Lys	Lys	Gly	Arg	Ile	Ser
			405					410						415	
Ala	Thr	Leu	Asn	Thr	Lys	Glu	Gly	Tyr	Ser	Tyr	Leu	Tyr	Ile	Lys	Gly
			420					425					430		
Ser	Gln	Pro	Glu	Asp	Ser	Ala	Thr	Tyr	Leu	Cys	Ala	Tyr	Leu	Gly	Ala
		435					440					445			
Gly	Asn	Gln	Phe	Tyr	Phe	Gly	Thr	Gly	Thr	Ser	Leu	Thr	Val	Ile	Pro
	450					455					460				
Asn	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser	Lys
465					470					475					480
Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Thr
			485						490					495	
Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp	Lys	Cys
			500					505					510		
Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	Ala	Val	Ala
		515					520					525			
Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn	Asn	Ser
	530					535					540				
Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	Ser	Cys	Asp
545					550					555					560
Val	Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn	Leu	Asn	Phe
			565						570					575	
Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu	Lys	Val	Ala
			580					585					590		

Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser
		595					600					605

<210> 183

<211> 1848

<212> DNA

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 8 construct; beta chain-P2A-alpha chain with cysteine substitutions in beta and alpha chain constant domains

<400> 183

atgggacctg	gactgctttg	ttgggctctt	ctgtgtctgc	ttggagctgg	actggttgat
60					
gctggagtta	cacagagccc	tacacacctg	atcaagacaa	gaggacagca	ggtgaccctg
120					
agatgtagcc	ctaaatctgg	ccacgatacc	gtgagctggg	atcaacaggc	tctgggacaa
180					
ggacctcagt	tcattcttcca	gtactacgag	gaggaggaga	gacagagagg	caatttcctt
240					
gacaggttta	gcggacacca	gttccccaat	tacagctctg	agctgaacgt	gaatgccctt
300					
cttctgggag	attctgccct	gtatctgtgt	gccagcagct	ttagactggc	tggaggacct
360					
agcaccgata	cacagtattt	tggacctggc	accaggctga	cagtgttaga	agacctgaag
420					
aacgtgttcc	ccccagaggt	ggccgtgttc	gagcctagcg	aggccgagat	cagccacacc
480					
cagaaagcca	ccctcgtgtg	cctggccacc	ggctttttacc	ccgaccacgt	ggaactgtct
540					
tggtgggtca	acggcaaaga	ggtgcacagc	ggcgtctgca	ccgaccccca	gcccctgaaa
600					
gagcagcccg	ccctgaacga	cagccggtac	tgtctgagca	gcagactgag	agtgtccgcc
660					
accttctggc	agaacccccg	gaaccacttc	agatgccagg	tgcagttcta	cggcctgagc
720					
gagaacgacg	agtggaccca	ggaccggggc	aagcccgtga	cccagatcgt	gtctgctgag
780					
gcctggggca	gagccgattg	cggcttcacc	agcgagagct	accagcaggg	cgtgctgagc
840					
gccaccatcc	tgtacgagat	cctgctgggc	aaggccaccc	tgtacgccgt	gctgggtgtcc
900					
gccctgggtgc	tgatggccat	ggtcaagcgg	aaggacagcc	ggggcggttc	cggagccacg
960					

```

aacttctctc  tgttaaagca  agcaggagac  gtggaagaaa  accccggtcc  catgttgacc
1020
gcttctctct  tacgtgccgt  gattgccagc  atctgtgtgg  ttagctctat  ggcccagaag
1080
gtgacacaag  ctcagacaga  gatcagcgtg  gtggagaaag  aggatgtgac  cctggattgc
1140
gtgtacgaga  ccagagatac  cacctactac  ctgttctggt  acaagcagcc  tccttctgga
1200
gaactggtgt  tcctgatcag  acggaacagc  ttcgatgagc  agaacgagat  tagcggcagg
1260
tatagctgga  acttccagaa  gagcaccagc  agcttcaact  tcaccatcac  agcctctcag
1320
gtgggtggatt  ctgccgtgta  cttttgtgcc  ctgtctgaac  tggcctctgg  aggaagctat
1380
atccctacat  tcggcagagg  cacaagcctg  attgtgcacc  cttacatcca  gaaccctgat
1440
cctgctgtgt  accagctgcg  ggacagcaag  agcagcgaca  agagcgtgtg  cctgttcacc
1500
gacttcgaca  gccagaccaa  cgtgtcccag  agcaaggaca  gcgacgtgta  catcaccgat
1560
aagtgcgtgc  tggacatgcg  gagcatggac  ttcaagagca  acagcgccgt  ggcctgggtcc
1620
aacaagagcg  acttcgcctg  cgccaacgcc  ttcaacaaca  gcattatccc  cgaggacaca
1680
ttcttcccaa  gccccgagag  cagctgcgac  gtgaagctgg  tggaaaagag  cttcgagaca
1740
gacaccaacc  tgaacttcca  gaacctcagc  gtgatcggct  tccggatcct  gctgctgaag
1800
gtggccggct  tcaacctgct  gatgaccctg  cggctgtggt  ccagctga
1848

```

<210> 184

<211> 615

<212> PRT

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 8 construct; beta
chain-P2A-alpha chain with cysteine substitutions
in beta and alpha chain constant domains

<400> 184

```

Met Gly Pro Gly Leu Leu Cys Trp Ala Leu Leu Cys Leu Leu Gly Ala
 1           5           10          15
Gly Leu Val Asp Ala Gly Val Thr Gln Ser Pro Thr His Leu Ile Lys

```

			20					25					30				
Thr	Arg	Gly	Gln	Gln	Val	Thr	Leu	Arg	Cys	Ser	Pro	Lys	Ser	Gly	His		
		35					40					45					
Asp	Thr	Val	Ser	Trp	Tyr	Gln	Gln	Ala	Leu	Gly	Gln	Gly	Pro	Gln	Phe		
	50					55					60						
Ile	Phe	Gln	Tyr	Tyr	Glu	Glu	Glu	Glu	Arg	Gln	Arg	Gly	Asn	Phe	Pro		
65					70					75					80		
Asp	Arg	Phe	Ser	Gly	His	Gln	Phe	Pro	Asn	Tyr	Ser	Ser	Glu	Leu	Asn		
				85					90					95			
Val	Asn	Ala	Leu	Leu	Leu	Gly	Asp	Ser	Ala	Leu	Tyr	Leu	Cys	Ala	Ser		
			100					105					110				
Ser	Phe	Arg	Leu	Ala	Gly	Gly	Pro	Ser	Thr	Asp	Thr	Gln	Tyr	Phe	Gly		
		115					120					125					
Pro	Gly	Thr	Arg	Leu	Thr	Val	Leu	Glu	Asp	Leu	Lys	Asn	Val	Phe	Pro		
	130					135					140						
Pro	Glu	Val	Ala	Val	Phe	Glu	Pro	Ser	Glu	Ala	Glu	Ile	Ser	His	Thr		
145					150					155					160		
Gln	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ala	Thr	Gly	Phe	Tyr	Pro	Asp	His		
				165					170					175			
Val	Glu	Leu	Ser	Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val		
			180					185					190				
Cys	Thr	Asp	Pro	Gln	Pro	Leu	Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser		
		195					200					205					
Arg	Tyr	Cys	Leu	Ser	Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln		
	210					215					220						
Asn	Pro	Arg	Asn	His	Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser		
225					230					235					240		
Glu	Asn	Asp	Glu	Trp	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile		
				245					250					255			
Val	Ser	Ala	Glu	Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Glu		
			260					265					270				
Ser	Tyr	Gln	Gln	Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu		
		275				280						285					
Leu	Gly	Lys	Ala	Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu		
	290					295					300						
Met	Ala	Met	Val	Lys	Arg	Lys	Asp	Ser	Arg	Gly	Gly	Ser	Gly	Ala	Thr		
305					310					315					320		
Asn	Phe	Ser	Leu	Leu	Lys	Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly		
				325					330					335			
Pro	Met	Leu	Thr	Ala	Ser	Leu	Leu	Arg	Ala	Val	Ile	Ala	Ser	Ile	Cys		
			340					345					350				
Val	Val	Ser	Ser	Met	Ala	Gln	Lys	Val	Thr	Gln	Ala	Gln	Thr	Glu	Ile		
		355				360						365					
Ser	Val	Val	Glu	Lys	Glu	Asp	Val	Thr	Leu	Asp	Cys	Val	Tyr	Glu	Thr		
	370					375					380						

Arg	Asp	Thr	Thr	Tyr	Tyr	Leu	Phe	Trp	Tyr	Lys	Gln	Pro	Pro	Ser	Gly	385	390	395	400
Glu	Leu	Val	Phe	Leu	Ile	Arg	Arg	Asn	Ser	Phe	Asp	Glu	Gln	Asn	Glu	405	410	415	
Ile	Ser	Gly	Arg	Tyr	Ser	Trp	Asn	Phe	Gln	Lys	Ser	Thr	Ser	Ser	Phe	420	425	430	
Asn	Phe	Thr	Ile	Thr	Ala	Ser	Gln	Val	Val	Asp	Ser	Ala	Val	Tyr	Phe	435	440	445	
Cys	Ala	Leu	Ser	Glu	Leu	Ala	Ser	Gly	Gly	Ser	Tyr	Ile	Pro	Thr	Phe	450	455	460	
Gly	Arg	Gly	Thr	Ser	Leu	Ile	Val	His	Pro	Tyr	Ile	Gln	Asn	Pro	Asp	465	470	475	480
Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser	Lys	Ser	Ser	Asp	Lys	Ser	Val	485	490	495	
Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Thr	Asn	Val	Ser	Gln	Ser	Lys	500	505	510	
Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp	Lys	Cys	Val	Leu	Asp	Met	Arg	Ser	515	520	525	
Met	Asp	Phe	Lys	Ser	Asn	Ser	Ala	Val	Ala	Trp	Ser	Asn	Lys	Ser	Asp	530	535	540	
Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn	Asn	Ser	Ile	Ile	Pro	Glu	Asp	Thr	545	550	555	560
Phe	Phe	Pro	Ser	Pro	Glu	Ser	Ser	Cys	Asp	Val	Lys	Leu	Val	Glu	Lys	565	570	575	
Ser	Phe	Glu	Thr	Asp	Thr	Asn	Leu	Asn	Phe	Gln	Asn	Leu	Ser	Val	Ile	580	585	590	
Gly	Phe	Arg	Ile	Leu	Leu	Leu	Lys	Val	Ala	Gly	Phe	Asn	Leu	Leu	Met	595	600	605	
Thr	Leu	Arg	Leu	Trp	Ser	Ser										610	615		

<210> 185

<211> 1815

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR number 11 construct; beta chain-P2A-alpha chain

<400> 185

atgggcacca ggctcttctt ctatgtggcc ctttgtctgc tgtgggcagg acacagggat
60
gctggaatca cccagagccc aagatacaag atcacagaga caggaaggca ggtgaccttg
120

atgtgtcacc 180	agacttggag	ccacagctat	atgtttctggt	atcgacaaga	cctgggacat
gggctgaggc 240	tgatctatta	ctcagcagct	gctgatatta	cagataaagg	agaagtcccc
gatggctatg 300	ttgtctccag	atccaagaca	gagaatttcc	ccctcactct	ggagtcagct
acccgctccc 360	agacatctgt	gtattttctgc	gccagcagtg	acggggggcgg	gcagtacttc
gggccgggca 420	ccaggctcac	ggtcacagag	gacctgaaaa	acgtgttccc	acccgaggtc
gctgtgtttg 480	agccatcaga	agcagagatc	tcccacaccc	aaaaggccac	actgggtgtgc
ctggccacag 540	gcttctaccc	cgaccacgtg	gagctgagct	ggtgggtgaa	tgggaaggag
gtgcacagtg 600	gggtcagcac	agaccgcag	cccctcaagg	agcagcccgc	cctcaatgac
tccagatact 660	gcctgagcag	ccgcctgagg	gtctcggcca	ccttctggca	gaacccccgc
aaccacttcc 720	gctgtcaagt	ccagttctac	gggctctcgg	agaatgacga	gtggaccacg
gatagggcca 780	aacctgtcac	ccagatcgtc	agcgccgagg	cctggggtag	agcagactgt
ggcttcacct 840	ccgagtctta	ccagcaaggg	gtcctgtctg	ccaccatcct	ctatgagatc
ttgctaggga 900	aggccacctt	gtatgccgtg	ctggtcagtg	ccctcgtgct	gatggccatg
gtcaagagaa 960	aggattccag	aggcggttcc	ggagccacga	acttctctct	gttaaagcaa
gcaggagacg 1020	tggaagaaaa	ccccgggtccc	atgaaaaagc	atctgacgac	cttcttggtg
attttgtggc 1080	tttattttta	taggggggaat	ggcaaaaacc	aagtggagca	gagtcctcag
tccctgatca 1140	tcctggaggg	aaagaactgc	actcttcaat	gcaattatac	agtgagcccc
ttcagcaact 1200	taaggtggta	taagcaagat	actgggagag	gtcctgtttc	cctgacaatc
atgactttca 1260	gtgagaacac	aaagtcgaac	ggaagatata	cagcaactct	ggatgcagac
acaaagcaaa 1320	gctctctgca	catcacagcc	tcccagctca	gcgattcagc	ctcctacatc
tgtgtggtgt 1380	gggggggggga	caccgacaag	ctcatctttg	ggactgggac	cagattacaa
gtctttccaa 1440	atatccagaa	ccctgaccct	gccgtgtacc	agctgagaga	ctctaaatcc
agtgacaagt 1500	ctgtctgcct	attcaccgat	tttgattctc	aaacaaatgt	gtcacaaagt

aaggattctg atgtgtatat cacagacaaa acttggctag acatgaggtc tatggacttc
1560
aagagcaaca gtgctgtggc ctggagcaac aaatctgact ttgcatgtgc aaacgccttc
1620
aacaacagca ttattccaga agacaccttc ttccccagcc cagaaagttc ctgtgatgtc
1680
aagctggtcg agaaaagctt tgaaacagat acgaacctaa actttcaaaa cctgtcagtg
1740
attgggttcc gaatcctcct cctgaaagtg gccgggttta atctgctcat gacgctgcgg
1800
c t g t g g t c c a g c t g a
1815

<210> 186

<211> 604

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 11 construct; beta chain-P2A-alpha chain

<400> 186

Met	Gly	Thr	Arg	Leu	Phe	Phe	Tyr	Val	Ala	Leu	Cys	Leu	Leu	Trp	Ala
1				5					10					15	
Gly	His	Arg	Asp	Ala	Gly	Ile	Thr	Gln	Ser	Pro	Arg	Tyr	Lys	Ile	Thr
			20					25					30		
Glu	Thr	Gly	Arg	Gln	Val	Thr	Leu	Met	Cys	His	Gln	Thr	Trp	Ser	His
		35					40					45			
Ser	Tyr	Met	Phe	Trp	Tyr	Arg	Gln	Asp	Leu	Gly	His	Gly	Leu	Arg	Leu
	50					55					60				
Ile	Tyr	Tyr	Ser	Ala	Ala	Ala	Asp	Ile	Thr	Asp	Lys	Gly	Glu	Val	Pro
65				70						75				80	
Asp	Gly	Tyr	Val	Val	Ser	Arg	Ser	Lys	Thr	Glu	Asn	Phe	Pro	Leu	Thr
			85					90					95		
Leu	Glu	Ser	Ala	Thr	Arg	Ser	Gln	Thr	Ser	Val	Tyr	Phe	Cys	Ala	Ser
			100				105						110		
Ser	Asp	Gly	Gly	Gly	Gln	Tyr	Phe	Gly	Pro	Gly	Thr	Arg	Leu	Thr	Val
		115				120					125				
Thr	Glu	Asp	Leu	Lys	Asn	Val	Phe	Pro	Pro	Glu	Val	Ala	Val	Phe	Glu
	130				135						140				
Pro	Ser	Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr	Leu	Val	Cys
145				150					155					160	
Leu	Ala	Thr	Gly	Phe	Tyr	Pro	Asp	His	Val	Glu	Leu	Ser	Trp	Trp	Val
			165				170						175		

Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Ser	Thr	Asp	Pro	Gln	Pro	Leu	
			180					185					190			
Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys	Leu	Ser	Ser	Arg	
		195					200					205				
Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn	His	Phe	Arg	
	210					215					220					
Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu	Trp	Thr	Gln	
225					230					235					240	
Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu	Ala	Trp	Gly	
			245						250					255		
Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Glu	Ser	Tyr	Gln	Gln	Gly	Val	Leu	
		260						265					270			
Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu	Tyr	
		275					280					285				
Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val	Lys	Arg	Lys	
	290					295					300					
Asp	Ser	Arg	Gly	Gly	Ser	Gly	Ala	Thr	Asn	Phe	Ser	Leu	Leu	Lys	Gln	
305					310					315					320	
Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Lys	Lys	His	Leu	Thr	
			325					330						335		
Thr	Phe	Leu	Val	Ile	Leu	Trp	Leu	Tyr	Phe	Tyr	Arg	Gly	Asn	Gly	Lys	
		340						345					350			
Asn	Gln	Val	Glu	Gln	Ser	Pro	Gln	Ser	Leu	Ile	Ile	Leu	Glu	Gly	Lys	
		355					360					365				
Asn	Cys	Thr	Leu	Gln	Cys	Asn	Tyr	Thr	Val	Ser	Pro	Phe	Ser	Asn	Leu	
	370					375					380					
Arg	Trp	Tyr	Lys	Gln	Asp	Thr	Gly	Arg	Gly	Pro	Val	Ser	Leu	Thr	Ile	
385					390					395					400	
Met	Thr	Phe	Ser	Glu	Asn	Thr	Lys	Ser	Asn	Gly	Arg	Tyr	Thr	Ala	Thr	
			405						410					415		
Leu	Asp	Ala	Asp	Thr	Lys	Gln	Ser	Ser	Leu	His	Ile	Thr	Ala	Ser	Gln	
		420						425					430			
Leu	Ser	Asp	Ser	Ala	Ser	Tyr	Ile	Cys	Val	Val	Trp	Gly	Gly	Asp	Thr	
		435					440					445				
Asp	Lys	Leu	Ile	Phe	Gly	Thr	Gly	Thr	Arg	Leu	Gln	Val	Phe	Pro	Asn	
	450					455					460					
Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser	Lys	Ser	
465					470					475					480	
Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Thr	Asn	
			485						490					495		
Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp	Lys	Thr	Trp	
		500						505					510			
Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	Ala	Val	Ala	Trp	
	515						520					525				
Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn	Asn	Ser	Ile	

530		535		540											
Ile	Pro	Glu	Asp	Thr	Phe	Pro	Ser	Pro	Glu	Ser	Ser	Cys	Asp	Val	
545		550		555		560									
Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn	Leu	Asn	Phe	Gln
		565		570		575									
Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu	Lys	Val	Ala	Gly
		580		585		590									
Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser				
	595			600											

<210> 187

<211> 1812

<212> DNA

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 11 construct; beta chain-P2A-alpha chain with cysteine substitutions in beta and alpha chain constant domains

<400> 187

atgggcacac	ggctttttctt	ctacgttgcc	ctttgcctgc	tgtgggctgg	acatagagat
60					
gctggaatca	cacagagccc	caggtacaag	atcacagaga	caggaagaca	ggtgaccctg
120					
atgtgtcacc	aaacatggag	ccacagctac	atgttctggt	acagacagga	tctgggacac
180					
ggactgagac	tgatctacta	ttctgctgcc	gccgacatca	ccgataaagg	agaagttcct
240					
gacggctacg	tggtgtctag	aagcaaaacc	gagaacttcc	ccctgacact	ggaatctgcc
300					
acaagatctc	agaccagcgt	gtacttttgc	gcctcttctg	atggaggagg	ccagtatttt
360					
ccaggcacia	gactgacagt	gaccgaggac	ctgaagaacg	tgttcccccc	agaggtggcc
420					
gtgttcgagc	ctagcgaggc	cgagatcagc	cacacccaga	aagccaccct	cgtgtgcctg
480					
gccaccggct	tttaccgccg	ccacgtggaa	ctgtcttggg	gggtcaacgg	caaagagggt
540					
cacagcggcg	tctgcaccga	ccccagccc	ctgaaagagc	agcccgccct	gaacgacagc
600					
cggtactgtc	tgagcagcag	actgagagtg	tccgccacct	tctggcagaa	cccccggaac
660					
cacttcagat	gccaggtgca	gttctacggc	ctgagcgaga	acgacgagtg	gacccaggac
720					

cgggccaagc	ccgtgaccca	gatcgtgtct	gctgaggcct	ggggcagagc	cgattgcggc
780					
ttcaccagcg	agagctacca	gcagggcgctg	ctgagcgcca	ccatcctgta	cgagatcctg
840					
ctgggcaagg	ccaccctgta	cgccgtgctg	gtgtccgccc	tggtgctgat	ggccatggtc
900					
aagcgggaagg	acagccgggg	cggttccgga	gccacgaact	tctctctgtt	aaagcaagca
960					
ggagacgtgg	aagaaaaccc	cggtcccatg	aagaagcacc	tgaccacgtt	cctgggtgatt
1020					
ctttggctgt	acttctaccg	gggcaacggc	aaaaatcagg	tggaacaaag	ccccagagc
1080					
ctgattattc	tggagggcaa	gaactgcacc	ctccagtgtg	attacaccgt	gagccctttc
1140					
agcaacctga	gatggtacaa	gcaggatacc	ggaagaggac	ctgtgtctct	gaccatcatg
1200					
accttttagcg	agaacaccaa	gagcaacggc	aggtatacag	ccacactgga	tgccgatacc
1260					
aagcagtctt	ctctgcacat	taccgcctct	cagctgtctg	attctgccag	ctacatctgt
1320					
gtggtgtggg	gaggagatac	cgataagctg	atctttggca	caggcaccag	actgcaagtg
1380					
ttccctaaca	tccagaaccc	tgatcctgcc	gtgtaccagc	tgcgggacag	caagagcagc
1440					
gacaagagcg	tgtgcctggt	caccgacttc	gacagccaga	ccaacgtgtc	ccagagcaag
1500					
gacagcgacg	tgtacatcac	cgataagtgc	gtgctggaca	tgcggagcat	ggacttcaag
1560					
agcaacagcg	ccgtggcctg	gtccaacaag	agcgacttcg	cctgcgccaa	cgccttcaac
1620					
aacagcatta	tccccgagga	cacattcttc	ccaagccccg	agagcagctg	cgacgtgaag
1680					
ctggtggaaa	agagcttcga	gacagacacc	aacctgaact	tccagaacct	cagcgtgatc
1740					
ggcttccgga	tcctgctgct	gaaggtggcc	ggcttcaacc	tgctgatgac	cctgcggctg
1800					
t g g t c c a g c t					g a
1812					

<210> 188

<211> 603

<212> PRT

<213> Artificial Sequence

<220>

<223> codon optimized TCR number 11 construct; beta chain-P2A-alpha chain with cysteine substitutions in beta and alpha chain constant domains

<400> 188

Met 1	Gly	Thr	Arg	Leu 5	Phe	Phe	Tyr	Val	Ala 10	Leu	Cys	Leu	Leu	Trp 15	Ala
Gly	His	Arg	Asp 20	Ala	Gly	Ile	Thr	Gln 25	Ser	Pro	Arg	Tyr	Lys 30	Ile	Thr
Glu	Thr	Gly 35	Arg	Gln	Val	Thr	Leu 40	Met	Cys	His	Gln	Thr	Trp 45	Ser	His
Ser	Tyr 50	Met	Phe	Trp	Tyr	Arg 55	Gln	Asp	Leu	Gly	His 60	Gly	Leu	Arg	Leu
Ile 65	Tyr	Tyr	Ser	Ala	Ala 70	Ala	Asp	Ile	Thr	Asp 75	Lys	Gly	Glu	Val	Pro 80
Asp	Gly	Tyr	Val 85	Val	Ser	Arg	Ser	Lys	Thr 90	Glu	Asn	Phe	Pro	Leu 95	Thr
Leu	Glu	Ser	Ala 100	Thr	Arg	Ser	Gln	Thr 105	Ser	Val	Tyr	Phe	Cys 110	Ala	Ser
Ser	Asp	Gly 115	Gly	Gly	Gln	Tyr	Phe 120	Pro	Gly	Thr	Arg	Leu	Thr 125	Val	Thr
Glu	Asp 130	Leu	Lys	Asn	Val	Phe 135	Pro	Pro	Glu	Val	Ala 140	Val	Phe	Glu	Pro
Ser 145	Glu	Ala	Glu	Ile	Ser 150	His	Thr	Gln	Lys	Ala 155	Thr	Leu	Val	Cys	Leu 160
Ala	Thr	Gly	Phe 165	Tyr	Pro	Asp	His	Val	Glu 170	Leu	Ser	Trp	Trp	Val 175	Asn
Gly	Lys	Glu	Val 180	His	Ser	Gly	Val	Cys 185	Thr	Asp	Pro	Gln	Pro	Leu 190	Lys
Glu	Gln	Pro 195	Ala	Leu	Asn	Asp	Ser 200	Arg	Tyr	Cys	Leu	Ser 205	Ser	Arg	Leu
Arg	Val 210	Ser	Ala	Thr	Phe 215	Trp	Gln	Asn	Pro	Arg	Asn 220	His	Phe	Arg	Cys
Gln 225	Val	Gln	Phe	Tyr	Gly 230	Leu	Ser	Glu	Asn	Asp 235	Glu	Trp	Thr	Gln	Asp 240
Arg	Ala	Lys	Pro 245	Val	Thr	Gln	Ile	Val	Ser 250	Ala	Glu	Ala	Trp	Gly 255	Arg
Ala	Asp	Cys	Gly 260	Phe	Thr	Ser	Glu	Ser 265	Tyr	Gln	Gln	Gly	Val 270	Leu	Ser
Ala	Thr 275	Ile	Leu	Tyr	Glu	Ile	Leu 280	Leu	Gly	Lys	Ala	Thr 285	Leu	Tyr	Ala
Val 290	Leu	Val	Ser	Ala	Leu	Val 295	Leu	Met	Ala	Met	Val 300	Lys	Arg	Lys	Asp
Ser 305	Arg	Gly	Gly	Ser	Gly 310	Ala	Thr	Asn	Phe	Ser 315	Leu	Leu	Lys	Gln	Ala 320

Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Lys	Lys	His	Leu	Thr	Thr	
				325					330					335		
Phe	Leu	Val	Ile	Leu	Trp	Leu	Tyr	Phe	Tyr	Arg	Gly	Asn	Gly	Lys	Asn	
			340					345					350			
Gln	Val	Glu	Gln	Ser	Pro	Gln	Ser	Leu	Ile	Ile	Leu	Glu	Gly	Lys	Asn	
		355					360					365				
Cys	Thr	Leu	Gln	Cys	Asn	Tyr	Thr	Val	Ser	Pro	Phe	Ser	Asn	Leu	Arg	
	370					375					380					
Trp	Tyr	Lys	Gln	Asp	Thr	Gly	Arg	Gly	Pro	Val	Ser	Leu	Thr	Ile	Met	
385					390					395					400	
Thr	Phe	Ser	Glu	Asn	Thr	Lys	Ser	Asn	Gly	Arg	Tyr	Thr	Ala	Thr	Leu	
				405					410					415		
Asp	Ala	Asp	Thr	Lys	Gln	Ser	Ser	Leu	His	Ile	Thr	Ala	Ser	Gln	Leu	
			420					425					430			
Ser	Asp	Ser	Ala	Ser	Tyr	Ile	Cys	Val	Val	Trp	Gly	Gly	Asp	Thr	Asp	
	435						440					445				
Lys	Leu	Ile	Phe	Gly	Thr	Gly	Thr	Arg	Leu	Gln	Val	Phe	Pro	Asn	Ile	
	450					455					460					
Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser	Lys	Ser	Ser	
465					470					475					480	
Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Thr	Asn	Val	
				485					490					495		
Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp	Lys	Cys	Val	Leu	
			500					505					510			
Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	Ala	Val	Ala	Trp	Ser	
	515						520					525				
Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn	Asn	Ser	Ile	Ile	
	530					535					540					
Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	Ser	Cys	Asp	Val	Lys	
545					550					555					560	
Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn	Leu	Asn	Phe	Gln	Asn	
				565					570					575		
Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu	Lys	Val	Ala	Gly	Phe	
			580					585					590			
Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser						
		595					600									

<210> 189

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 11 Vbeta CDR3

<400> 189

Cys	Ala	Ser	Ser	Asp	Gly	Gly	Gly	Gln	Tyr	Phe
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<210> 190

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR number 9 Vbeta CDR3

<400> 190

Ala	Ile	Leu	Asp	Gly	Glu	Gly	Ser	Pro	Leu	His
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