COMPOSITIONS AND METHODS FOR IMMUNOTHERAPY

PRIORITY

This Application claims the benefit of, and priority to, U.S. Provisional Application No. 61/838,547, filed June 24, 2013, and U.S. Provisional Application No. 61/948,916, filed March 6, 2014, which are hereby incorporated by reference in their entireties.

FIELD OF THE INVENTION

The present invention relates to compositions, including pharmaceutical compositions, and methods that are useful for immunotherapy.

BACKGROUND

An antigen-presenting cell (APC) is a cell that processes and displays antigenic peptides in complexes with major histocompatibility complex (MHC) proteins on their surfaces. Effector cells, such as T-cells, may recognize these peptide-MHC (pMHC) complexes using receptors, such as T-cell receptors (TCRs).

Dendritic cells (DCs) are an example of an antigen presenting cell that can be stimulated to effectively present antigen and support expansion of immune effect cells, thereby activating a cytotoxic response towards an antigen. In some immunotherapies, DCs are harvested from a patient and either pulsed with an antigen or transfected with a viral vector. Upon transfusion back into the patient these activated cells present tumor antigen to effector lymphocytes (*e.g.* $CD4^+$ T cells, $CD8^+$ T cells, and B cells). If properly executed this therapy can initiate a cytotoxic response against cells expressing antigens (including tumor antigens).

However, DC immunotherapy, like many immunotherapies faces significant limitations. For example, there is a discrepancy between strong and antigen-specific T cell responses in vaccinated cancer patients detectable *ex vivo* and only weak clinical

responses. Janikashvili N et al., Personalized dendritic cell-based tumor immunotherapy. *Immunotherapy* 2010 Jan. 1; 2(1):57.

There remains a need for compositions (including shelf-stable pharmaceutical compositions) and methods that are effective for immunotherapy, including antigen-specific immunotherapy.

BRIEF DESCRIPTION OF THE INVENTION

The present invention provides compositions and methods for immunotherapy, which include shelf-stable pharmaceutical compositions for inducing antigen-specific T cells in a patient. Such compositions are useful for the treatment of, for example, cancer and infectious disease. The composition in some aspects is an artificial antigen presenting cell (aAPC), which comprises a pharmaceutically acceptable bead or particle having antigen presenting complexes and optionally T cell co-stimulatory signals on its surface, to provide a patient with molecular complexes that present one or more antigens (e.g., tumor antigen(s)) in the proper context for activation of antigen-specific T cells. The bead or particles are designed to provide pharmacodynamic advantages, including circulating properties, biodistribution, and degradation kinetics, as well as activity. Such parameters include size, surface charge, polymer composition, ligand conjugation chemistry, ligand density, among others.

In some embodiments, the T-cell co-stimulatory signal is an anti-CD28 antibody or portion thereof, which may comprise human heavy chain amino acid sequences, including sequences selected from IgG, IgD, IgA, or IgM isotypes. In some embodiments, the immunoglobulin sequences include human IgG constant and variable sequences. The framework (FW) sequences may be modified to contain important or desired murine framework residues to maintain the integrity of the antigen-binding site(s). The complementarity determining regions (CDRs) may be based on a murine antibody amino acid sequence (e.g., 9.3 mAb), or other CD28 binding sequence of which many are known. In some embodiments, the antibody heavy chain is a variant of a human IGHV4 (e.g., IGHV4-59) germline FW. In some embodiments, the antibody comprises a light chain and the light chain is a variant of a human IGKV4-01 FW. The

antibody may comprise a constant region and the constant region may be human IgG4 or variant thereof.

The co-stimulatory molecule may be conjugated to a solid support with antigen-presenting molecular complexes, to induce antigen-specific T cells. The antigen-presenting molecular complex may include MHC Class I and/or Class II complexes, or portions thereof comprising an antigen-binding cleft. In some embodiments, the molecular complex comprises one or more HLA amino acid sequences (e.g., comprises the extracellular domain of HLA or antigen-presenting portion thereof), which may contain additional sequences, such as immunoglobulin sequences, or other dimerizing or stabilizing sequence. HLA-Ig dimerizing fusions in some embodiments provide advantages in stability and/or binding affinity.

Thus, in some embodiments, the invention provides a bead- or particle-conjugated molecular complex for presentation of antigen to T cells, where the complex comprises an amino acid sequence forming a Class I or Class II antigen binding cleft, or portion thereof. The amino acid sequences of the antigen presenting complex may include fusions to heterologous sequences, to provide stability, affinity, and steric advantages, for example. In some embodiments, the heterologous sequences include immunoglobulin sequences. In some embodiments, the molecular complex includes HLA (e.g., HLA-A2) amino acid sequences fused to heterologous sequences, such as immunoglobulin sequences. In some embodiments, the immunoglobulin comprises a human heavy chain immunoglobulin sequence (e.g., IGVH4), which can include immunoglobulin constant sequences to provide dimeric HLA, and may optionally comprise variable region sequences. The variable sequences if present can be optionally modified to reduce or eliminate potential antigen binding, and optionally with no murine FW residues. The HLA amino acid sequence may be HLA-A*02:01 (IMGT Accession No. HLA00005) or a derivative thereof.

The T cell co-stimulatory ligand and/or antigen presenting complexes (as well as other ligands disclosed herein, including targeting ligands) may be conjugated to a solid support for *ex vivo* or *in vivo* antigen presentation and antigen-specific T cell activation.

In some embodiments, the solid support is a bead or particle (e.g., PLGA or PLGA-PEG particle) with surface functional groups for coupling ligands. The particles are designed to provide pharmacodynamic advantages, including circulating properties, biodistribution, and degradation kinetics, as well as activity. Such parameters include size, surface charge, polymer composition, ligand conjugation chemistry, ligand density, among others.

The pharmaceutical composition in the various embodiments may further comprise an antigenic peptide for presentation to T cells, and which may be co-formulated with the ligand-conjugated bead or particle. In various embodiments, the pharmaceutical composition is shelf stable, and may be provided in lyophilized form for reconstitution prior to administration, or alternatively provided in another convenient format for administration to patients (e.g., by parenteral administration).

The pharmaceutical compositions described herein are useful for immunotherapy, for example, in methods for inducing the formation of antigen-specific cytotoxic T cells, by administering an effective amount of the composition to a patient in need. In particular, antigen presenting platforms can be useful for treating patients with infectious diseases, cancer, or autoimmune diseases, or to provide prophylactic protection to immunosuppressed patients.

The invention further provides polynucleotides encoding the amino acid sequences described herein, as well as host cells expressing the same.

This invention is further illustrated by the following non-limiting examples.

The details of the invention are set forth in the accompanying description and claims below. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, illustrative methods and materials are now described. Other features, objects, and advantages of the invention will be apparent from the description and from the claims. In the specification and the appended claims, the singular forms also include the plural unless the context clearly dictates otherwise. Unless defined otherwise, all technical and

scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs.

BRIEF DESCRIPTION OF THE DRAWINGS

FIGS. 1-3 show three humanized variable heavy sequences for anti-CD28; SEQ ID NOs: 1, 2, 3, 4, 5 and 6.

FIGS. 4-6 show three humanized variable light sequences for anti-CD28; SEQ ID NOs: 7, 8, 9, 10, 11 and 12.

FIG. 7 shows a modified constant heavy sequence; SEQ ID NOs: 13 and 14.

FIG. 8 shows a constant κ Light sequence; SEQ ID NOs: 15 and 16.

FIG. 9 shows a humanized non-CD28-binding variable region for constructing an HLA fusion; SEQ ID NOs: 17 and 18.

FIG. 10 shows the amino acid sequence for humanized HLA-IgG4HC; SEQ ID NO: 19.

FIG. 11 shows the amino acid sequence for Light Chain 3 (LC3, or Vκ3); SEQ ID NO: 20.

FIG. 12 shows the amino acid sequence for Heavy Chain 1 (HC1); SEQ ID NO: 21.

FIG. 13 shows the amino acid sequence for Heavy Chain 2 (HC2) ; SEQ ID NO: 22.

FIGS. 14-16 show expression constructs for expression in STABLEFAST-NS0 Cell Line.

FIG. 17 shows that the humanized anti-CD28 mAb is not a super-agonist.

FIG. 18 shows that the humanized anti-CD28 clones specifically stain CD28 on a human T-cell line. FIG 18(A): staining with murine anti-human CD8 mAb (clone 9.3, Isotype IgG2a); FIG18(B): staining with humanized anti-CD28 (isotype IgG4).

DETAILED DESCRIPTION OF THE INVENTION

The following abbreviations are used throughout: BLAST -Basic Local Alignment Search Tool, CDR- Complementarity determining region, Cκ-Kappa light chain constant region, Fc-Antibody fragment crystallisable region, Fw-Framework region (of variable regions), HLA-Human leukocyte antigen, MHC -Major histocompatibility complex, VH -Variable heavy, Vκ -Variable kappa light, and V region -Variable region of an antibody, either VH or Vκ.

The present invention provides compositions and methods for immunotherapy, which include shelf-stable pharmaceutical compositions for inducing antigen-specific T cells in a patient. In some embodiments, the compositions comprise dimeric HLA antigen presenting complexes. In some embodiments, the compositions comprise humanized immunoglobulin sequences or portions thereof, which may be employed as components of the ligands on artificial antigen presenting cells (aAPCs), to provide a patient with dimeric molecular complexes for presentation of one or more antigens (e.g., tumor antigen(s)) and optionally one or more co-stimulatory signals. Antigen presenting platforms, as described in more detail below, can be based on artificial solid supports, such as pharmaceutically acceptable supports including latex or polymeric beads or particles.

In some embodiments, the T-cell co-stimulatory signal is an anti-CD28 antibody or portion thereof. In some embodiments, the anti-CD28 antibody comprises sequences of at least one human immunoglobulin isotype selected from IgG1, IgG2, IgG3, IgG4, IgD, IgA, or IgM. For example, the anti-CD28 antibody may be an IgG isotype, and may contain sequences of one or more IgG germline framework sequences. For example, the anti-CD28 may contain a human IGHV4 heavy chain amino acid sequence, which may be modified with from one to fifteen amino acid modifications. The modifications may comprise murine framework residues to support the integrity of the antigen binding site(s).

The complementarity determining region (CDR) in some embodiments is based on a murine antibody amino acid sequence, which may optionally have from one to ten,

such as from one to five, amino acid modifications. In some embodiments, one, two, three, or more CDRs are based on mouse 9.3 mAb (Tan *et al.*. J. Exp. Med. 1993 177:165), which is publicly available. Exemplary CDRs are shown in **FIGURES 1-6**. In some embodiments, the antibody has the full set of heavy chain and/or full set of light chain CDRs of 9.3 mAb. For example, in some embodiments the heavy chain variable region contains one, two or three of the following CDRs, which optionally may each be modified by one, two, or three amino acid substitutions, deletions, or additions: CDR1 (DYGVH; SEQ ID NO: 23), CDR2 (VIWAGGGTNYNSALMS; SEQ ID NO: 24), and CDR3 (DKGYSYYYSMDY; SEQ ID NO: 25). In some embodiments, the light chain variable region contains one, two, or three of the following CDRs, which each may be modified by one, two, or three amino acid substitutions, deletions, or additions: CDR1 (RASESVEYYVTSLMQ; SEQ ID NO: 26), CDR2 (AASNVES; SEQ ID NO: 27), and CDR3 (QQSRKVPYT; SEQ ID NO: 28).

Alternative CDR sequences, variable regions, or CD28-binding ligands may be employed in various embodiments. Alternative ligands and antibodies are described in US Patent 7,612,170, US Patent 6,987,171, and US Patent 6,887,466, for example, and these disclosures are hereby incorporated by reference in their entireties.

In some embodiments, the antibody heavy chain comprises a variant of a human IGHV4-59 germline framework (FW), which is modified to include from 5 to 15 murine FW residues. In some embodiments, the antibody comprises light chain amino acid sequences, and the light chain sequences may be a variant of human IGKV4-01 FW sequences, and which may be modified to include from 3 to 15 murine FW residues.

The anti-CD28 human heavy chain sequence may be modified, for example, to comprise one or more (e.g., 2 or more, 3 or more, 4 or more, 5 or more, or all) murine Fw residues at positions 1, 3, 6, 37, 48, 67, 71, 73, 76, 78, 82, 82a, and 82c (based on Kabat numbering). The murine Fw residues at these positions can be as in 9.3 mAb. The light chain may be modified to comprise one or more (e.g., 2 or more, 3 or more, 4 or more, 5 or more, or all) murine Fw residues at positions 3, 4, 49, 70, 85, 87, and 80. Selected murine Fw residues may support the integrity of the antigen-binding sites. The

humanized anti-CD28 antibody maintains the affinity for CD28 and T cell co-stimulatory activity of 9.3 mAb, and is at least 40%, 50%, 75%, 80%, 90%, and in some embodiments 100% or more effective for CD28 binding than 9.3 mAb. In various embodiments, the anti-CD28 mAb is not a super agonist.

The antibody may comprise a constant region and the constant region may be any isotype. In some embodiments, the antibody constant region is human IgG4 or variant thereof. In some embodiments, the constant region comprises one or more hinge stabilizing mutations, which may be introduced in the CH chain (e.g., S241, which may be substituted with P). In some embodiments, the antibody comprises a constant region and the constant region comprises one or more mutations suitable for chemically coupling the antibody to a solid support. The one or more mutations suitable for coupling may create an amino acid side chain functional group (e.g., thiol, amine, or hydroxyl), such as an unpaired cysteine (e.g., at S473). Other changes to the constant region include those modifications to reduce Fc gamma receptor binding. For example, the CH chain may be modified at L248, e.g., L248E.

In some embodiments, the antibody is an antibody fragment, such as $F(ab')_2$ or Fab, or is a single chain antibody, or other antigen-binding antibody fragment. For example, the antibody fragment can be a single chain variable fragment of the humanized mAb described herein or other anti-CD28.

In some embodiments, the co-stimulatory molecule is a single chain variable fragment (scFv) comprising or consisting essentially of the antigen binding loops formed by the VH and VL chains of an antiCD28 mAb, such as an antibody described herein. scFv antibody constructs may comprise one or several (2, 3, 4, or 5) VH and VL hypervariable region chains (the portion of each chain that together form the 3-D antigenic epitope binding pockets) linked together in head-head or head-tail configurations by short peptide linkers. Such constructs can be conveniently produced via a completely synthetic route due to their smaller size. Further, scFv can exhibit lower potential for immunogenicity.

In other embodiments, the co-stimulatory ligand is a bi-specific construct comprising one or more HLA molecules joined to a scFv of a co-stimulatory molecule ligand or inhibitory ligand. The antigen presenting complex and co-stimulatory or inhibitory ligand may be conjugated through a peptide tether that allows the bi-specific construct to be covalently linked to a nanoparticle surface. In some embodiments, such constructs produce the same activity as nanoparticles containing larger constructs of HLA and co-stimulatory or inhibitory ligands each linked to the NP surface independently, thereby providing manufacturing advantages.

The co-stimulatory molecule may be conjugated to a solid support with antigen-presenting molecular complexes, to induce antigen-specific T cells. The antigen-presenting molecular complex may include MHC Class I and/or Class II complexes, or portions thereof comprising an antigen-binding cleft. In some embodiments, the molecular complex comprises one or two HLA amino acid sequences, which may contain additional heterologous sequences, such as immunoglobulin sequences. Alternative heterologous sequences include dimerizing amino acid sequences such as c-fos and c-jun. HLA-fusions in some embodiments provide additional advantages in stability and/or binding affinity.

In various embodiments, the antigen presenting complex is either an MHC class I molecular complex or an MHC class II molecular complex, or alternatively CD1d. The MHC class I molecular complex may comprise at least two fusion proteins. A first fusion protein comprises a first MHC class I α chain and a first immunoglobulin heavy chain and a second fusion protein comprises a second MHC class I α chain and a second immunoglobulin heavy chain. The first and second immunoglobulin heavy chains associate to form the MHC class I molecular complex. The MHC class I molecular complex comprises a first MHC class I peptide binding cleft and a second MHC class I peptide binding cleft. The MHC class II molecular complex can comprise at least four fusion proteins. Two first fusion proteins comprise (i) an immunoglobulin heavy chain and (ii) an extracellular domain of an MHC class IIβ chain. Two second fusion proteins comprise (i) an immunoglobulin light chain and (ii) an extracellular domain of an MHC class IIα chain. The two first and the two second fusion proteins associate to form the

MHC class II molecular complex. The extracellular domain of the MHC class IIβ chain of each first fusion protein and the extracellular domain of the MHC class IIα chain of each second fusion protein form an MHC class II peptide binding cleft. Antigenic peptides are bound to the peptide binding clefts. In various embodiments, the immunoglobulin sequence is a partial heavy chain sequence comprising the hinge region to support dimerization.

In some embodiments, the antigen presenting complex is a synthetic or recombinant HLA monomer engineered to contain an unpaired cysteine, or using a naturally occurring unpaired cysteine, for conjugation to nanoparticles. Further, the co-stimulatory signal (or other antibody-based ligand) may be a Fab or scFv. In such embodiments, the two signals may be combined in a single multi-functional construct comprising an HLA molecule tethered to an antigen binding antibody fragment (e.g., scFv) that binds to a desired receptor.

In other aspects and embodiments, the invention provides a bead- or particle-conjugated molecular complex for presentation of antigen to T cells, where the complex comprises a humanized immunoglobulin sequence or portion thereof fused to an antigen presenting sequence, e.g., an HLA amino acid sequence. In some embodiments, the immunoglobulin sequence is a human heavy chain sequence (e.g., IGHV4 framework). The variable region does not comprise an antigen binding activity to CD28, or other human protein. The HLA amino acid sequence may be HLA-A*02:01 (IMGT Accession No. HLA00005) or a derivative or fragment thereof, such as a derivative having from 1 to 10, or from 1 to 5, amino acid substitutions, deletions, or insertions. The humanized immunoglobulin sequence may further comprise a linker amino acid sequence between the HLA and immunoglobulin sequences. Preferably, the linker lacks immunogenicity. The molecular complex may further comprise β2 microglobulin peptide.

In various embodiments, the immunoglobulin fusion sequences is of IgG, IgD, IgA, or IgM isotype, and may be derived from any human germline framework. The germline framework includes IGHV4 (e.g., IGHV4-59), which may or may not contain

one or more of the murine framework residues described with respect to anti-CD28. In some embodiments, the heavy chain of the anti-CD28 antibody described above (with or without murine framework residues) is fused to HLA in accordance with this aspect, and in such embodiments, the variable region is modified to reduce or eliminate CD28 binding.

In some embodiments, the HLA fusion construct contains no variable chain sequences. For example, the HLA or antigen presenting complex can be fused to an Ig constant region sequence above the hinge region to provide a dimeric HLA. For example, an HLA or antigen presenting portion thereof may be conjugated to a CH1 portion of each IgG heavy chain. All IgG molecules consist of two identical heavy chains (constant and variable regions) joined together by disulfide bonds in the hinge region (upper and lower). For example, in some embodiments, an HLA molecule or antigen presenting complex is fused to the CH1 (N-terminal end of the IgH chain above the hinge region), thereby creating a dimeric fusion protein that is smaller due to lack of any VH and VL light chain sequences. Such a construct may provide manufacturing advantages, as well as exhibit less potential for immunogenicity.

In still other embodiments, the antigen presenting complexes (e.g., HLA sequences) do not contain Ig fusion partners, and are monomeric. For example, in some embodiments, the C-terminal end of the antigen presenting complex or HLA molecule (e.g. HLA-A2, etc.) contains a peptide tether sequence suitable for site-directed binding to a functional group (e.g. a maleimide moiety) on a solid/semi-solid substrate such as a synthetic nanoparticle (e.g. PLGA-PEG-maleimide block polymers, or other particles described herein). The tether sequence may contain any suitable sequence, which may be predominately composed of hydrophilic residues such as Gly, Ser, Ala, and Thr, such as two, three, four, or five repeats of GGGSG; SEQ ID NO: 29 or AAAGG; SEQ ID NO: 30, with cysteine residue incorporated somewhere within the about 5 to about 15 (or about 5 to about 10 amino acid) tether. The cysteine residue should be incorporated at a site predicted not to form intramolecular disulfide bonds.

In some embodiments, the HLA-Ig fusion or other HLA construct further comprises an antigenic peptide bound to the HLA for presentation to T cells. The antigenic peptide can comprise an antigenic portion of one or more of tyrosinase, hTERT, MAGE-1, MAGE-3, gp-100, NY-ESO-1, Melan A/Mart-1, HPV 16-E7, gp75/brown, BAGE, and S-100 and/or any of the antigenic peptides as described in WO 2004/006951 for presentation by Class I or Class II complexes, the contents of which are hereby incorporated by reference in their entirety. The HLA complexes may be attached to a solid support, such as a bead or particle as described, for presentation of antigen to T-cells optionally with co-stimulatory signal.

Other signals that can be provided with the antigen presenting complex include: CD80 (B7-1), CD86 (B7-2), B7-H3, 4-1BBL, CD27, CD30, CD134 (OX-40L), B7h (B7RP-1), CD40, LIGHT, (or Ig fusions, optionally humanized as described herein, of the such molecules or active portions thereof), antibodies that specifically bind to HVEM, antibodies that specifically bind to CD40L, antibodies that specifically bind to OX40, antibodies that specifically bind Fas, antibodies that specifically bind PD1, antibodies that specifically bind to GITR, and antibodies that specifically bind to 4-1BB.

Adhesion molecules useful for antigen presenting platforms of the invention may mediate the adhesion of the platform to a T cell or to a T cell precursor. Adhesion molecules useful in the present invention include, for example, ICAM-1 and LFA-3.

T cell growth factors affect proliferation and/or differentiation of T cells. Examples of T cell growth factors include cytokines (e.g., interleukins, interferons) and superantigens. Particularly useful cytokines include IL-2, IL-4, IL-7, IL-10, IL-12, IL-15, and gamma interferon. T cell growth factors may be encapsulated in the beads or particles or chemically conjugated or adsorbed to the surface. Thus, in some embodiments, the nanoparticles further comprise a therapeutic compound or protein/peptide entrapped in the hydrophobic core of the particle (e.g. a chemotherapy agent, cytokine or interleukin such as IL-2, a chemokine like CCL9 that attracts T cells, and/or a checkpoint inhibitor molecule like anti-PD1 antibody or anti-PD1 peptide).

Such an aAPC in some embodiments is constructed to target specific cells for stimulation or inhibition as well as reprogramming. In some embodiments, entrapped compounds are released by degradation of the particle matrix. Such an aAPC could make combination therapies more tolerable and efficacious by limiting unwanted activity due to off-target interactions.

Antigens presented in accordance with aspects of the invention include tumor associated antigens. Tumor-associated antigens include unique tumor antigens expressed exclusively by the tumor from which they are derived, shared tumor antigens expressed in many tumors but not in normal adult tissues (oncofetal antigens, cancer/testis antigens), and tissue-specific antigens expressed also by the normal tissue from which the tumor arose. Tumor-associated antigens can be, for example, embryonic antigens, antigens with abnormal post-translational modifications, differentiation antigens, products of mutated oncogenes or tumor suppressors, fusion proteins, or oncoviral proteins. A variety of tumor-associated antigens are known in the art, and many of these are commercially available. Oncofetal and embryonic antigens include carcinoembryonic antigen and alpha-fetoprotein (usually only highly expressed in developing embryos but frequently highly expressed by tumors of the liver and colon, respectively), placental alkaline phosphatase sialyl-Lewis X (expressed in adenocarcinoma), CA-125 and CA-19 (expressed in gastrointestinal, hepatic, and gynecological tumors), TAG-72 (expressed in colorectal rumors), epithelial glycoprotein 2 (expressed in many carcinomas), pancreatic oncofetal antigen, 5T4 (expressed in gastric carcinoma), alpha fetoprotein receptor (expressed in multiple tumor types, particularly mammary tumors), and M2A (expressed in germ cell neoplasia).

In some embodiments, at least one antigen is a Cancer/Testis (CT) antigen, which may include NY-ESO-1, MAGE-A, B, and C, CTAG-1, CTAG-45, GAGE, and SSX, which are normally expressed by germ cells of the testis and not in normal adult somatic tissues. However, numerous types of cancer cells have been shown to express CT antigens including melanoma, breast, liver, lung, ovary, and Hodgkin Lymphoma.

Tumor-associated differentiation antigens include tyrosinase (expressed in melanoma) and particular surface immunoglobulins (expressed in lymphomas).

Mutated oncogene or tumor-suppressor gene products include Ras and p53, both of which are expressed in many tumor types, Her-2/neu (expressed in breast - and gynecological cancers), EGF-R, estrogen receptor, progesterone receptor, retinoblastoma gene product, myc (associated with lung cancer), ras, p53 nonmutant associated with breast tumors, MAGE-1, and MAGE-3 (associated with melanoma, lung, and other cancers).

Other tumor antigens include fusion proteins such as BCR-ABL, which is expressed in chromic myeloid leukemia, and oncoviral proteins such as HPV type 16, E6, and E7, which are found in cervical carcinoma. Tissue-specific tumor antigens include melanotransferrin and MUCl (expressed in pancreatic and breast cancers); CD 10 (previously known as common acute lymphoblastic leukemia antigen, or CALLA) or surface immunoglobulin (expressed in B cell leukemias and lymphomas); the α chain of the IL-2 receptor, T cell receptor, CD45R, CD4+/CD8+ (expressed in T cell leukemias and lymphomas); prostate-specific antigen and prostatic acid-phosphatase (expressed in prostate carcinoma); gp100, MelanA/Mart-1, tyrosinase, gp75/brown, BAGE, and S-100 (expressed in melanoma); cytokeratins (expressed in various carcinomas); and CD19, CD20, and CD37 (expressed in lymphoma).

In some embodiments, the antigenic peptides include MART-1, gp100, NY-ESO-1, and MAGE-A3 which are presented by the HLA antigen presenting complexes described herein, such as the HLA-Ig fusion complex described herein.

In still other embodiments, the composition comprises a cocktail of a plurality of antigens of the tumor type, such as at least 2, 3, 4, 5, 6, 7, 8, 9, or 10 antigens (e.g., from 2 to 10 or from 3-8 antigens).

In some embodiments, the antigen is an autoantigen, which is an organism's own "self antigen" to which the organism produces an immune response. Autoantigens are involved in autoimmune diseases such as Goodpasture's syndrome, multiple sclerosis,

Graves' disease, myasthenia gravis, systemic lupus erythematosus, insulin-dependent diabetes mellitis, rheumatoid arthritis, pemphigus vulgaris, Addison's disease, dermatitis herpetiformis, celiac disease, and Hashimoto's thyroiditis. For example, diabetes-related autoantigens include insulin, glutamic acid decarboxylase (GAD) and other islet cell autoantigens, e.g., ICA 512/IA-2 protein tyrosine phosphatase, ICA12, ICA69, preproinsulin or an immunologically active fragment thereof (e.g., insulin B- chain, A chain, C peptide or an immunologically active fragment thereof), IGRP, HSP60, carboxypeptidase H, peripherin, gangliosides (e.g., GM1-2, GM3) or immunologically active fragments thereof.

In some embodiments, the antigen(s) are of infectious agents, such as components of protozoa, bacteria, fungi (both unicellular and multicellular), viruses, prions, intracellular parasites, helminths, and other infectious agents that can induce an immune response. Bacterial antigens include antigens of gram-positive cocci, gram positive bacilli, gram- negative bacteria, anaerobic bacteria, such as organisms of the families Actinomycetaceae, Bacillaceae, Bartonellaceae, Bordetellae, Captophagaceae, Corynebacteriaceae, Enterobacteriaceae, Legionellaceae, Micrococcaceae, Mycobacteriaceae, Nocardiaceae, Pasteurellaceae, Pseudomonadaceae, Spirochaetaceae, Vibrionaceae and organisms of the genera Acinetobacter, Brucella, Campylobacter, Erysipelothrix, Ewingella, Francisella, Gardnereïla, Helicobacter, Levinea, Listeria, Streptobacillus and Tropheryma. Antigens of protozoan infectious agents include antigens of malarial plasmodia, Leishmania species, Trypanosoma species and Schistosoma species. Fungal antigens include antigens of Aspergillus, Blastomyces, Candida, Coccidioides, Cryptococcus, Histoplasma, Paracoccicioides, Sporothrix, organisms of the order Mucorales, organisms inducing choromycosis and mycetoma and organisms of the genera Trichophyton, Microsporum, Epidermophyton, and Malassezia. Antigens of prions include the sialoglycoprotein PrP 27-30 of the prions that cause scrapie, bovine spongiform encephalopathies (BSE), feline spongiform encephalopathies, kuru, Creutzfeldt-Jakob Disease (CJD), Gerstmann-Strassler-Scheinker Disease (GSS), and fatal familial insomnia (FFI). Intracellular parasites from which antigenic peptides can be obtained include, but are not limited to, Chlamydiaceae, Mycoplasmataceae, Acholeplasmataceae, Rickettsiae, and organisms of

the genera Coxiella and Ehrlichia. Viral peptide antigens include, but are not limited to, those of adenovirus, herpes simplex virus, papilloma virus, respiratory syncytial virus, poxviruses, HIV, influenza viruses, and CMV. Particularly useful viral peptide antigens include HIV proteins such as HIV gag proteins (including, but not limited to, membrane anchoring (MA) protein, core capsid (CA) protein and nucleocapsid (NC) protein), HJV polymerase, influenza virus matrix (M) protein and influenza virus nucleocapsid (NP) protein, hepatitis B surface antigen (HBsAg), hepatitis B core protein (HBcAg), hepatitis e protein (HBeAg), hepatitis B DNA polymerase, hepatitis C antigens, and the like.

Antigens, including antigenic peptides, can be bound to an antigen binding cleft of an antigen presenting complex either actively or passively, as described in U.S. Patent 6,268,411 which is hereby incorporated by reference in its entirety. Optionally, an antigenic peptide can be covalently bound to a peptide binding cleft.

If desired, a peptide tether can be used to link an antigenic peptide to a peptide binding cleft. For example, crystallographic analyses of multiple class I MHC molecules indicate that the amino terminus of β2M is very close, approximately 20.5 Angstroms away, from the carboxyl terminus of an antigenic peptide resident in the MHC peptide binding cleft. Thus, using a relatively short linker sequence, approximately 13 amino acids in length, one can tether a peptide to the amino terminus of β2M. If the sequence is appropriate, that peptide will bind to the MHC binding groove (see U.S. Patent 6,268,411).

The antibody or fragment and/or antigen presenting complexes may be conjugated to a solid support for ex vivo or in vivo antigen presentation. Various solid supports are described in WO 2004/006951, the contents of which are hereby incorporated by reference in their entirety. In some embodiments, the solid support is a bead or particle with functional groups for coupling ligands. The material may be a biodegradable organic material, such as cellulose or dextran. In some embodiments, block co-polymers are selected to traffic to specific anatomical sites and biodegrade

over specific intervals, that is, have a longer or shorter plasma half-life, or a longer or short tissue residency time.

In some embodiments, the bead or particle comprises a polymer, such as one or more of cyclodextrin-containing polymers, cationic cyclodextrin-containing polymers, poly(D,L-lactic acid-co-glycolic acid) (PLGA), poly(caprolactone) (PCL), ethylene vinyl acetate polymer (EVA), poly(lactic acid) (PLA), poly(L-lactic acid) (PLLA), poly(glycolic acid) (PGA), poly(L-lactic acid-co-glycolic acid) (PLLGA), poly(D,L-lactide) (PDLA), poly(L- lactide) (PLLA), PLGA-b-poly(ethylene glycol)-PLGA (PLGA-bPEG-PLGA), PLLA-bPEG-PLLA, PLGA-PEG-maleimide (PLGA-PEG-mal), poly(D,L-lactide-co-caprolactone), poly(D,L-lactide-co-caprolactone-co- glycolide), poly(D,L-lactide-co-PEO-co-D,L-lactide), poly(D,L-lactide-co-PPO-co-D,L-lactide), polyalkyl cyanoacralate, polyurethane, poly-L-lysine (PLL), hydroxypropyl methacrylate (HPMA), polyethyleneglycol, poly-L-glutamic acid, poly(hydroxy acids), polyanhydrides, polyorthoesters, poly(ester amides), polyamides, poly(ester ethers), polycarbonates, polyalkylenes such as polyethylene and polypropylene, polyalkylene glycols such as poly(ethylene glycol) (PEG), polyalkylene oxides (PEO), polyalkylene terephthalates such as poly(ethylene terephthalate), polyvinyl alcohols (PVA), polyvinyl ethers, polyvinyl esters such as poly(vinyl acetate), polyvinyl halides such as poly(vinyl chloride) (PVC), polyvinylpyrrolidone, polysiloxanes, polystyrene (PS), polyurethanes, derivatized celluloses such as alkyl celluloses, hydroxyalkyl celluloses, cellulose ethers, cellulose esters, nitro celluloses, hydroxypropylcellulose, carboxymethylcellulose, polymers of acrylic acids, such as poly(methyl(meth)acrylate) (PMMA), poly(ethyl(meth)acrylate), poly(butyl(meth)acrylate), poly(isobutyl(meth)acrylate), poly(hexyl(meth)acrylate), poly(isodecyl(meth)acrylate), poly(lauryl(meth)acrylate), poly(phenyl(meth)acrylate), poly(methyl acrylate), poly(isopropyl acrylate), poly(isobutyl acrylate), poly(octadecyl acrylate) (polyacrylic acids), and copolymers and mixtures thereof, polydioxanone and its copolymers, polyhydroxyalkanoates, polypropylene fumarate), polyoxymethylene, poloxamers, poly(ortho)esters, poly(butyric acid), poly(valeric acid), poly(lactide-co-caprolactone), trimethylene carbonate, polyvinylpyrrolidone, polyorthoesters, polyphosphazenes, and polyphosphoesters, and blends and/or block copolymers of two or more such polymers.

Other pharmaceutically acceptable materials, such as latex, may also be used as the solid particle support.

In some embodiments, the antigen-presenting complex and co-stimulatory signal are conjugated to PLGA or PLGA-PEG particles having surface functional groups on the terminal end of the polymer (e.g., the end that faces outward towards the surface of the particle), such as PLGA-PEG-maleimide particles, which provide functional groups for chemical coupling on the hydrophilic exterior surface. In some embodiments, the aAPCs persist in peripheral blood circulation sufficiently long to allow distribution to target tissues, including trafficking to lymph nodes via blood/lymph exchange. The composition of the shell may also impact biodistribution. Thus, in various embodiments the particles have a hydrophilic shell, which can be accomplished by the PEG of the PLGA-PEG co-polymer. In various embodiments, the charge of the particles is slightly negative, for example, due to the combination of the COOH groups on the PLGA as well as by charge contributed by the targeting ligands attached to the surface of the particle. In some embodiments, the particles (either with or without conjugated ligand) have a surface charge of from about 0 to about -20 mV, or in some embodiments -5 to -15 mV, or about -10 mV.

Nanoparticles comprising PLGA-PEG copolymers are described in US Patent 8,420,123, for example, which is hereby incorporated by reference.

The particles can vary from being irregular in shape to being spherical and/or from having an uneven or irregular surface to having a smooth surface. Spherical particles have less surface area relative to particles of irregular size. If spherical particles are used, less reagent is necessary due to the reduced surface area. On the other hand, an irregularly shaped particle has a significantly greater surface area than a spherical particle, which provides an advantage for conjugated protein content per surface area and surface area contact for cells. For example, asymmetrical nanoparticles may have at least one surface having a radius of curvature along at least one axis which is in one of the following ranges: (a) about 1 nm to about 10 nm; (b) about 11 nm to about 100 nm; (c) about 101 nm to about 400 nm; (d) about 401 nm to

about 1 μm; (e) about 10 μm to about 20 μm; (f) about 20 μm to about 100 μm; and (g) about 101 μm to about 1 mm. In some embodiments, the asymmetric nanoparticle may has an asymmetrical shape defined by a dimension (a) along an x-axis, a dimension (b) along a y-axis, and a dimension (c) along a z-axis, wherein at least one of (a), (b), or (c) is not equal to at least one other dimension (a), (b), or (c). In some embodiments, the asymmetrical shape is an ellipsoid, which can be described by one of the following equations: a > b = c (prolate ellipsoid); a > b > c (tri-axial ellipsoid); and a = b > c (oblate ellipsoid). Asymmetrical nanoparticles that may be used in accordance with the invention are described in WO 2013/086500, which is hereby incorporated by reference in its entirety.

The size of particles can vary. The particle size (nominal diameter) in various embodiments is in the range from 0.05-50 μm, or in some embodiments 0.05-35 μm, or in some embodiments 0.05 to 10 μm, and in some embodiments is from about 0.05 to about 3.0, about 4.0, or about 5.0 μm. For example, in some embodiments, the particles are 50 to 500 nm in diameter or average diameter. In some embodiments, the particles have an average size of less than about 400 nm, about 300 nm, about 200 nm, or about 100 nm, to allow for better peripheral blood circulation. In some embodiments, the nanoparticles have an average size (e.g., diameter or largest axis) of about 100 nm, about 150 nm, or about 200 nm. The term "about", when connected to a numerical feature, means ±10%. In some embodiments, at least 90% of the particles are in the range of about 50 to about 250 nm, such as about 100 to about 150 nm. The particles can be uniform in size or can vary in size, with the average particle size preferably being as described above. In some embodiments, the particles are sufficiently small to take advantage of the "EPR effect" (enhanced permeability and retention effect).

Ligands and molecular complexes described herein can be chemically conjugated to the beads using any available process. Functional groups for ligand binding include PEG-COOH, PEG-NH2, PEG-SH or other functional group attached to a different polymer such as polycyanoacrylate or polycaprolactone.

For example, a solid support can be coated before proteins are bound to its surface. Once a coating chemistry has been chosen, the surface of a solid support can be activated to allow the specific attachment of particular protein molecules. Thus, coatings can be selected with a view to optimal reactivity and biocompatibility with various cell populations. Preferably, whatever coating chemistry is used provides a suitable matrix for further activation chemistry. Numerous such coatings are well known in the art. For example, solid supports can be coated with human serum albumin, tris (3-mercaptopropyl)-N-glycylamino) methane (U.S. Patent 6,074,884), gelatin-aminodextrans (U.S. Patent 5,466,609), or amino acid homopolymers or random copolymers. In one embodiment, a random amino acid copolymer comprising poly(glutamate, lysine, tyrosine) [6:3:1] is used; this copolymer is available from Sigma Chemical Co. as Product No. P8854. It is a linear random polymer of the amino acids glutamic acid, lysine, and tyrosine in a ratio of 6 parts glutamic acid, 3 parts lysine, and 1 part tyrosine. In another embodiment, an amino acid copolymer is used that includes lysine and tyrosine in a ratio of 4 parts lysine to 1 part tyrosine. In yet another embodiment, an amino acid copolymer is used that includes lysine and alanine in a ratio of 1 part lysine to 1 part alanine. In another embodiment, a solid support is coated with a synthetic polymer, then the synthetic polymer is activated before it is linked to a protein molecules.

In some embodiments, molecules are directly attached to solid supports by adsorption or by direct chemical bonding, including covalent bonding. See, e.g., Hermanson, BIOCONJUGATE TECHNIQUES, Academic Press, New York, 1996. A molecule itself can be directly activated with a variety of chemical functionalities, including nucleophilic groups, leaving groups, or electrophilic groups. Activating functional groups include alkyl and acyl halides, amines, sulfhydryls, aldehydes, unsaturated bonds, hydrazides, isocyanates, isothiocyanates, ketones, and other groups known to activate for chemical bonding. Alternatively, a molecule can be bound to a solid support through the use of a small molecule-coupling reagent. Non-limiting examples of coupling reagents include carbodiimides, maleimides, N-hydroxysuccinimide esters, bischloroethylamines, bifunctional aldehydes such as glutaraldehyde, anhydrides and the like. In other embodiments, a molecule can be

coupled to a solid support through affinity binding such as a biotin-streptavidin linkage or coupling, as is well known in the art. For example, streptavidin can be bound to a solid support by covalent or non-covalent attachment, and a biotinylated molecule can be synthesized using methods that are well known in the art.

In some embodiments, the particle or bead is a polymer, such as PLGA-PEG, PLGA-PEG-maleimide, or an ester-endcapped PLGA, in which functional groups for conjugation of surface ligands are created during polymerization. The maleimide group provides the formed particles with a hydrophilic "stealth" coating (PEG) on the outer surface of the particle as well as functional groups attached to this shell that can be used for covalent attachment of ligands that have at least one free sulfhydryl (-SH) group available. For example, HLA-Ig ligands and/or anti-CD28 can be constructed on a human IgG4 framework (as described herein) that contains a S473C substitution in the Fc. This unpaired cysteine residue at 473 of either HLA-Ig or anti-CD28 can be conjugated to the maleimide group attached to the PEG under mild reducing conditions. Mild reducing conditions are unlikely to irreversibly denature the proteins, especially the HLA-beta-2-microglobulin portion of the HLA-Ig molecule.

In an exemplary embodiment, the nanoparticles are in the range of from about 50 nm to as large as about 5 μm (e.g., the average diameter or largest axis), have a core (PLGA) that can be tuned for a specific biodegradation rate in vivo (by adjusting the LA:GA ratio and/or mw of the PLGA polymer), a hydrophilic outer shell that protects from opsonization by serum proteins and removal from circulation (acting like "PEG brushes"), surface functionalized with consistent control of ligand density (stochastic relationship of 1 molecule/maleimide group) and orientation of ligand away from the core. In some embodiments, the LA:GA ratio is from 60%/40% to 40%/60%, and in some embodiments is about 50%/50%. In some embodiments, the PLGA has a molecular weight of about 25K to about 35K (e.g., about 30K), and the PEG has a molecular weight of about 3K to about 10K, such as about 5K. In some embodiments, the core particle has a diameter of about 150 nm, or about 200 nm.

In an alternative embodiment, the support can be coated with a polymer that contains one or more chemical moieties or functional groups that are available for covalent attachment to a suitable reactant, typically through a linker.

Activation chemistries allow for specific, stable attachment of molecules to the surface of solid supports. There are numerous methods that can be used to attach proteins to functional groups. For example, the common cross-linker glutaraldehyde can be used to attach protein amine groups to an aminated solid support surface in a two-step process. The resultant linkage is hydrolytically stable. Other methods include use of cross-linkers containing n-hydro-succinimido (NHS) esters which react with amines on proteins, cross-linkers containing active halogens that react with amine-, sulfhydryl-, or histidine-containing proteins, cross-linkers containing epoxides that react with amines or sulfhydryl groups, conjugation between maleimide groups and sulfhydryl groups, and the formation of protein aldehyde groups by periodate oxidation of pendant sugar moieties followed by reductive amination.

The attachment of specific proteins to a solid support surface can be accomplished by direct coupling of the protein or by using indirect methods. Certain proteins will lend themselves to direct attachment or conjugation while other proteins or antibodies retain better functional activity when coupled to a linker or spacer protein such as anti-mouse IgG or streptavidin. If desired, linkers or attachment proteins can be used. Ligands, such as the antigen-presenting complexes and co-stimulatory molecules, may be modified with amino acid substitutions to allow chemical conjugation.

The ratio of particular proteins on the same solid support can be varied to increase the effectiveness of the solid support in antigen or antibody presentation. For example, ratios of antigen presenting complex to anti-CD28 can be at least about 30:1, or at least about 10:1, about 3:1, about 1:1, about 0.3:1; about 0.1 :1, and at least about 0.03:1. In some embodiments, the ratio is about 5:1, about 4:1, about 3:1, about 2:1, or about 1:1, about 1:2, about 1:3, about 1:4, or about 1:5. The total amount of protein coupled to the supports can be at least 10 mg/ml, at least 25 mg/ml, at least 50 mg/ml, at least 100 mg/ml, at least 150 mg/ml, or greater than 200 mg/ml. In some embodiments,

such as those employing PLGA or PLGA-PEG particles having surface functional groups (e.g., maleimide or ester), the total amount of protein coupled to the particles can be from 1 to 10 μg per mg of PLGA, or in some embodiments, from 2 to 6 μg per mg PLGA. In some embodiments, the ligand density of the particles is from about 10^3 to about 10^5 ligands / μm^2, or about 10^4 ligands / μm^2 in some embodiments. For example, for nanoparticles in the range of 100 to 200 nm in size, the nanoparticles on average have about 100 to about 1500 ligands, such as about 200 to about 1200 ligands, or about 400 to about 1000 ligands, or about 500 to about 800 ligands.

In various embodiments, the invention provides a pharmaceutical composition comprising a polymeric bead or particle, an anti-CD28 antibody as described herein, and/or a antigen-presenting complex, such as humanized Ig HLA fusion complex as described herein. The pharmaceutical composition may further comprise an antigenic peptide for presentation to T cells as described, and which may be co-formulated with the conjugated bead or particle. In various embodiments, the pharmaceutical composition is shelf stable, and in some embodiments, is provided in lyophilized form for reconstitution prior to administration, or provided in another "off-the-shelf" pharmaceutical preparation.

In some embodiments, the invention provides a pharmaceutical composition comprising PLGA or PLGA-PEG based nanoparticles, of from 50 to 500 nm in diameter or average diameter, and comprising surface-conjugated anti-CD28 antibodies and antigen-presenting complexes. The anti-CD28 antibody can be a humanized antibody, e.g., as described herein, and may be an antibody fragment such as a single chain variable fragment. The antigen presenting complex in some embodiments comprises at least one HLA antigen-binding cleft. The anti-CD28 and HLA complex can be coupled to the particles separately or together in the same reaction. The pharmaceutical composition can include at least one peptide antigen, such as a tumor antigen (e.g., MART-1), and which may be co-formulated with the particles without any active loading process.

The pharmaceutical compositions described herein are useful for immunotherapy, for example, in methods for inducing the formation of antigen-specific cytotoxic T cells, by administering an effective amount of the composition to a patient in need. In some embodiments, the patient is a cancer patient.

The particle-based antigen presenting platforms described herein can be administered to patients by any appropriate routes, including intravenous administration, intra-arterial administration, subcutaneous administration, intradermal administration, intralymphatic administration, and intra-tumoral administration. Patients include both human and veterinary patients.

Some exemplary embodiments the invention are described below.

In some embodiments the invention provides a pharmaceutical composition that comprises polymeric PLGA-PEG particles having a size in the range of about 100 to 200 nm, a surface charge of about -0 to -20 mV (and -5 to -15 mV in some embodiments), and from about 100 to 1500 protein ligands per particle. The protein ligands in some embodiments are each coupled to the particle through a sulfhydryl-maleimide chemistry. The ligands comprise a population of anti-CD28 antibody ligands, and a population of HLA ligands and one or more antigenic peptides for presentation to T cells. The composition comprises a pharmaceutically acceptable carrier for intravenous, intra-arterial, subcutaneous, intradermal, intralymphatic, or intra-tumoral administration.

In some embodiments, the particles are substantially spherical or about spherical.

In some embodiments, the PLGA is a polymer of about 50% lactic acid (LA) and 50% glycolic acid (GA).

In some embodiments, the PLGA polymer has a molecular weight of about 30K, and the PEG has a molecular weight of about 3K to about 10K, such as about 5K.

In some embodiments, the composition has from 400 to 1000 ligands per particle.

In some embodiments, the anti-CD28 antibody ligands comprise a human IGHV4-59 germline framework optionally having from 5 to 15 murine framework residues, and a IGKV4-01 germline framework optionally having from 3 to 15 murine framework residues.

In some embodiments, the anti-CD28 is a ScFv.

In some embodiments, the HLA is HLA-A*02:01, which may comprise a fusion to immunoglobulin sequences above the hinge region sufficient to provide a dimeric HLA construct.

In some embodiments, the composition is lyophilized.

In particular, antigen presenting platforms can be useful for treating patients with infectious diseases, cancer, or autoimmune diseases, or to provide prophylactic protection to immunosuppressed patients.

Infectious diseases that can be treated include those caused by bacteria, viruses, prions, fungi, parasites, helminths, etc. Such diseases include AIDS, hepatitis, CMV infection, and post-transplant lymphoproliferative disorder (PTLD). CMV, for example, is the most common viral pathogen found in organ transplant patients and is a major cause of morbidity and mortality in patients undergoing bone marrow or peripheral blood stem cell transplants (Zaia, Hematol. Oncol. Clin. North Am. 4, 603-23, 1990). This is due to the immunocompromised status of these patients, which permits reactivation of latent virus in seropositive patients or opportunistic infection in seronegative individuals. Current treatment focuses on the use of antiviral compounds such as gancyclovir, which have drawbacks, the most significant being the development of drug-resistant CMV. A useful alternative to these treatments is a prophylactic immunotherapeutic regimen involving the generation of virus-specific CTL derived from the patient or from an appropriate donor before initiation of the transplant procedure.

PTLD occurs in a significant fraction of transplant patients and results from Epstein-Barr virus (EBV) infection. EBV infection is believed to be present in approximately 90% of the adult population in the United States (Anagnostopoulos & Hummel, Histopathology 29, 291-2) 15, 1996). Active viral replication and infection is kept in check by the immune system, but, as in cases of CMV, individuals immunocompromised by transplantation therapies lose the controlling T cell populations, which permits viral reactivation. This represents a serious impediment to transplant protocols. EBV may also be involved in tumor promotion in a variety of hematological and non-hematological cancers. There is also a strong association between EBV and nasopharyngeal carcinomas. Thus a prophylactic treatment with EBV-specific T cells offers an excellent alternative to current therapies.

Cancers that can be treated according to the invention include melanoma, carcinomas, e.g., colon, head and neck cancer, duodenal, prostate, breast, lung, ovarian, ductal, colon, hepatic, pancreatic, renal, endometrial, stomach, dysplastic oral mucosa, polyposis, invasive oral cancer, non-small cell lung carcinoma, transitional and squamous cell urinary carcinoma etc.; neurological malignancies, e.g., neuroblastoma, gliomas, etc.; hematological malignancies, e.g., chronic myelogenous leukemia, childhood acute leukemia, non-Hodgkin's lymphomas, chronic lymphocytic leukemia, malignant cutaneous T-cells, mycosis fungoides, non-MF cutaneous T-cell lymphoma, lymphomatoid papulosis, T-cell rich cutaneous lymphoid hyperplasia, bullous pemphigoid, discoid lupus erythematosus, lichen planus, etc.; and the like.. See, e.g., Mackensen et al, Int. J. Cancer 86, 385-92, 2000; Jonuleit et al., Int. J. Cancer 93, 243-51, 2001; Lan et al., J. Immunotherapy 24, 66-78, 2001; Meidenbauer et al, J. Immunol. 170(4), 2161-69, 2003.

In some embodiments, the invention provides a method for treating cancer, including those cancers identified above, through administration of the pharmaceutical composition described herein to activate T-cells having anti-tumor activity. In some embodiments, the therapy is provided together with one or more immune checkpoint inhibitors, such as Nivolumab, Pembrolizumab, and Ipilimumab. In some embodiments, the additional therapy is anti-CTLA4 or anti-PD1, or anti-PD-L1. The

additional therapy or checkpoint inhibitor may be administered separately through its conventional regimen, or may be administered as an additional ligand to the nanoparticles described herein, or attached to a separate population of nanoparticles. In some embodiments, the one or more immune checkpoint inhibitors are provided as initial therapy, and therapy with the nanoparticles described herein initiated subsequently, for example, after from about 1 to about 8 weeks of checkpoint inhibitor therapy, or after about 2 to about 4 weeks of checkpoint inhibitor therapy. In some embodiments, the one or more checkpoint inhibitors are provided concomitantly with the nanoparticle therapy, for example at initiation of therapy and about every two weeks, or at initiation of therapy and about every two weeks for the one or more checkpoint inhibitors and about every four weeks for the nanoparticle therapy. In some embodiments, the patient is resistant or shows only a partial or transient response to checkpoint inhibitor therapy, and the aAPCs described herein enhance tumor regression in these patient. In still other embodiments, for cancers that are typically resistant to checkpoint inhibitor therapy, the compositions described herein expand the successful use of checkpoint inhibitors to such cancers.

In some embodiments, the peptide antigen is selected in a personalized basis for the patient, based on an analysis of the patient's tumor. For example, a process described by Ionov Y., A high throughput method for identifying personalized tumor-associated antigens, *Oncotarget* 1(2):148-155 (2010) (which is hereby incorporated by reference) may be used, or other process. In these embodiments, the nanoparticles can be provided (on an "off-the shelf" basis), and tumor antigens selected and loaded in a personalized basis.

Autoimmune diseases that can be treated include asthma, systemic lupus erythematosus, rheumatoid arthritis, type I diabetes, multiple sclerosis, Crohn's disease, ulcerative colitis, psoriasis, myasthenia gravis, Goodpasture's syndrome, Graves' disease, pemphigus vulgaris, Addison's disease, dermatitis herpetiformis, celiac disease, and Hashimoto's thyroiditis.

Antigen-specific helper T cells can be used to activate macrophages or to activate B cells to produce specific antibodies that can be used, for example, to treat infectious diseases and cancer. Antibody-producing B cells themselves also can be used for this purpose.

The invention further provides polynucleotides encoding the amino acid sequences described herein, as well as host cells expressing the same.

This invention is further illustrated by the following non-limiting examples.

EXAMPLES

Example 1: Design of Germline Humanized Variable Regions and Human Constant Region Sequences

This Example demonstrates, inter alia, a design of sequences for germline humanized (CDR grafted) antibodies from a mouse anti-CD28 antibody template; a design of human constant region sequences including human IgG4 containing the S241P (Kabat numbering) hinge stabilizing mutation, the L248E (Kabat numbering) mutation to remove residual Fc gamma receptor binding and a Cys residue (S473C, Kabat numbering) suitable for coupling the antibody; a design of a variant germline humanized antibody V domain with potential non-binding to CD28; a design of a linker sequence for the fusion of HLA-A*02:01 to the N-terminus of the germline humanized antibodies that does not contain potential T cell epitopes.

The starting anti-CD28 antibody was the murine 9.3 monoclonal antibody (Tan *et al.*. J. Exp. Med. 1993 177:165). Structural models of the 9.3 antibody V regions were produced using Swiss PDB and analyzed in order to identify amino acids in the V regions that were likely to be essential for the binding properties of the antibody. All residues contained within the CDRs (using both Kabat and Chothia definitions) together with a number of framework residues were considered to be of potential importance for binding. Both the VH and Vκ sequences of anti-CD28 contain typical framework (Fw) residues and the CDR 1, 2 and 3 motifs are comparable to many murine antibodies.

For humanization, the human IGHV4-59 germline Fw was selected as a template for the heavy chain (in preference to the IGHV3/OR16-10 selected by Tan *et al.* J. Immunol 2002 **169**:1119-1125). The IGKV4-01 germline Fw was selected as a template for the light chain. These Fws both have 62% homology to their respective murine VH and Vκ sequences. The murine CDRs were grafted into these Fws and varying numbers of murine Fw residues were also included to create three humanized VH variants and three humanized Vκ variants (**FIGURES 1-6**).

For the heavy chain Fw, Fw1 residues 1 and 3 were thought to be important for antigen binding since they are adjacent to the binding pocket, while residue 6 was considered to affect the conformation of both the beta strand supporting residues 1 and 3 and the conformation of CDR3. Therefore these murine Fw residues were retained in all variants.

In Fw2, residue 37 was considered to be important for maintaining the interface between the VH and Vκ, while residue 48 was considered to support the conformation of CDR2; therefore both of these residues were retained in all variants.

In Fw3, residues 73, 76 and 78 directly contact CDR1, while residue 71 contacts both CDR1 and CDR2; therefore these residues are likely to be required for antigen binding (depending upon the contribution of CDR1 and CDR2) and were therefore retained in all variants. Residue 71 can sometimes indirectly affect the conformation of CDR1 by influencing the conformation of residues 71 to 78, while residues 82a and 82c may also indirectly influence the conformation of CDR2. These residues were therefore retained in VH1 only. Residues 67 and 82 are adjacent in the three dimensional structure and interact to fill space which can affect the conformation of CDR2 and potentially influence the beta strands supporting CDRs 1 and 3. Therefore these residues were retained in variants VH1 and VH2.

For the light chain Fw, Fw1 residue 3 is adjacent to the binding pocket and can be directly involved in antigen binding, while residue 4 directly supports the conformation of CDR3. Therefore these murine Fw residues were retained in all variants.

In Fw2, residue 49 supports the conformation of CDR2 and is also critical for the interface between the heavy and light chains where it directly supports the conformation of heavy chain CDR3, thus was retained in all variants.

In Fw3, residues 85 and 87 were considered important for the interface of the heavy and light chains and also to support the conformation of CDR3 and were therefore retained in all variants. Residue 80 was considered to potentially have indirect effects on the conformation of CDRs 2 and 3 and was retained in Vκ1 only. Residue 70 commonly salt bridges with light chain residue R24 and therefore has important conformational effects upon the Vκ domain. In anti-CD28, this salt bridge is absent (since residue 70 is N rather than D) and introducing this interaction could be disadvantageous; however in the murine antibody N70 is glycosylated (NFS) and it would be beneficial to remove this during humanization; therefore the murine N was retained in Vκ1 and Vκ2, but changed to D in Vκ3.

Constant region sequences based upon human IgG4/κ were designed to incorporate a hinge stabilizing mutation (S241P) and a mutation in the lower hinge that removes residual Fc gamma receptor binding (L248E). A cysteine residue was also included near the C-terminus of the Fc for chemical coupling purposes (S473C). The modified IgG4 heavy chain constant region sequence is shown in **FIGURE 7**, together with the κ light chain constant region sequence (**FIGURE 8**).

A further VH domain was designed for potential non-binding to CD28 and this sequence is shown in **FIGURE 9**. Analysis of the murine V region sequences suggested (from the extent of somatic mutation of mouse germline V regions) that the VH was likely to the major contributor to CD28 binding. Therefore only a potential non-binding humanized VH variant was designed. This variant does not contain any mouse Fw residues to reconstitute the correct CDR conformations and also contains three mutations in CDRH3 at residues that are likely to be critical for binding (Y100A, Y100aA, Y100bA).

*Example 2: Design of Linkers for Fusion of HLA-A*02:01 to Humanized Antibodies*

Linkers for the fusion of HLA-A*02:01 (IMGT Accession No. HLA00005) to the N-terminus of humanized anti-CD28 antibodies were constructed and incorporated analysis by iTope™ and TCED™ to remove potential immunogenicity.

The iTope™ software predicts favorable interactions between amino acid side chains of a peptide and specific binding pockets (in particular pocket positions; p1, p4, p6, p7 and p9) within the open-ended binding grooves of 34 human MHC class II alleles. These alleles represent the most common HLA-DR alleles found world-wide with no weighting attributed to those found most prevalently in any particular ethnic population. Twenty of the alleles contain the 'open' p1 configuration and fourteen contain the 'closed' configuration where glycine at position 83 is replaced by a valine. The location of key binding residues is achieved by the *in silico* generation of 9mer peptides that overlap by one amino acid spanning the test protein sequence. Comparisons with physical MHC class II binding experiments has shown that iTope™ can be used to successfully discriminate with high accuracy between peptides that either bind or do not bind MHC class II molecules. Any limitations of *in silico* MHC class II binding analysis are reduced using the TCED™ which contains the sequences of a large database of peptides (>10,000 peptides) derived from sequences previously screened in EpiScreen™ *ex vivo* T cell epitope mapping assays. The TCED™ can thus be used to search any test sequence against unrelated antibody and protein sequences to find correlations with actual *ex vivo* immunogenicity.

Analysis of the linker sequences using iTope™ was performed with overlapping 9 mers spanning the linker sequences which were tested against each of the 34 MHC class II alleles. Each 9mer was scored based on the potential 'fit' and interactions with the MHC class II molecules. The peptide scores calculated by the software lie between 0 and 1. Non-germline peptides that produced a high mean binding score (>0.55 in the iTope™ scoring function) were highlighted and, if ≥50% of the MHC class II binding peptides (i.e. 17 out of 34 alleles) had a high binding affinity (score >0.6), such peptides were defined as "promiscuous high affinity" MHC class II binding peptides (which are considered a high risk for containing CD4+ T cell epitopes). Peptides with ≥50% of the MHC class II binding peptides with a score >0.55 (but without a majority >0.6) were

defined as "promiscuous moderate affinity" MHC class II binding peptides. Further analysis of the sequences was performed using the TCED™. The sequences were used to interrogate the TCED™ by BLAST search in order to identify any high sequence homology between peptides (T cell epitopes) from unrelated proteins that stimulated T cell responses in previous EpiScreen™ studies.

The sequences used by Schneck *et al.* incorporated two linkers, one at the N-terminus of HLA-A*02:01 to link with an N-terminal signal sequence and one at the C-terminus for fusion to the anti-CD28 VH domain (See **FIGURE 9** for example). For the N-terminal linker, sequence was analyzed from the signal sequence cleavage site through the linker and including the first 8 amino acids of HLA-A*02:01 mature protein. For the C-terminal linker, sequence was analyzed from the terminal 8 amino acids of HLA-A*02:01 α3 domain, through the linker sequence and up to the first 8 amino acids of the anti-CD28 VH domain.

Peptides with binding scores >0.6 (high affinity) bind to the majority (≥17) of MHC class II alleles (termed promiscuous high affinity binder). Moderate affinity binders with a binding score between 0.55 and 0.6 bind ≥17 MHC class II alleles. The N-terminal linker was found to contain two promiscuous MHC class II binding sequences, one high affinity (with p1 anchor at position 2) and one moderate affinity (with p1 anchor at position 4). The C-terminal linker was found to contain one promiscuous moderate affinity MHC class II binding peptide with p1 anchor at position 11.

A BLAST search of Antitope's T cell epitope database (TCED™) was carried out using the same sequences as used in the iTope™ analysis to determine any homology with previously identified epitopes. The TCED™ is used to search any test sequence against a large (>10,000 peptides) database of peptides derived from unrelated sequences which have been tested in EpiScreen™ T cell epitope mapping assays. Neither of the linker sequences was found to contain any 'hits' in the TCED™.

iTope™ was further used to assess sequence changes to the linkers in order to reduce their propensity for binding to MHC class II. It was noted that the N-terminal

linker could be removed entirely such that the N-terminus of HLA-A*02:01 is fused directly either to the signal sequence provided in the pBFKsr vector or to its natural signal sequence. This would ensure that the N-terminus of the fusion protein would contain only human germline sequence and avoid the risk of T cell epitopes. The recommended linker sequences below were found to reduce MHC class II binding to background residual levels (<5 of the alleles bound by any 9mer), and to provide suitable restriction sites for cloning (although both sequences will require modification of the vector):

N-terminal linker: SEQ ID NO: 32

Q V Q L T R E G S G S H S M R Y F

CAGGTCCAACTGacgcgtGAGGGGTCCGGCTCTCACTCCATGAGGTATTTC SEQ ID NO: 31

Vector | Linker | HLA-A*02:01

C-terminal linker: SEQ ID NO: 34

E G L P K P L T W A R E V S E V K L Q

GAGGGTTTGCCCAAGCCCCTCACCTGGGctcgagAGGTGAGCGAGGTCAAGCTGCAG SEQ ID NO: 33

HLA-A*02:01 | Linker | Anti-CD28

Example 3: Codon optimization of sequences and expression cloning

Codons were optimized using GeneOptimizer®, and optimized sequences were cloned for expression as shown below.

Sequences were engineered with *Pme*I restriction sites, Kozak sequence, and signal peptide for expression in NS0 cells. Translation starts immediately downstream of the Kozak sequence.

The full translated amino acid sequence of the HLA-IgG4HC fusion is shown in **FIGURE 10**.

The translated sequence of LC3 (VK3) is shown in **FIGURE 11**.

The translated sequence for HC1 is shown in **FIGURE 12**.

The translated sequence for HC2 is shown in **FIGURE 13**.

Human β2 microglobulin was also expressed.

Example 4: Expression in NS0 cells

Based on Biacore affinity data and other considerations, the HC1::LC3 and HC2::LC3 heavy chain and light chain combinations were selected as the primary and secondary mAb candidates, respectively, for StableFast-NS0 cell line development.

The final vector map for the pBFksr::HC1::LC3 bicistronic expression vector for STABLEFAST-NS0 cell line generation is depicted in **FIGURE 14**. Construction of pBFksr::HC2::LC3 was done using the same approaches.

Parental NS0 cells were expanded in supplemented serum-free growth medium. Upon establishment of health culture, ten million cells (10×10^6) were transfected with 45 μg linearized (ΔPvuI) expression vector DNA. Cells were allowed to recover for 24 hours in bulk in growth medium. Following recovery, cells were washed in supplemented serum-free selective medium (cholesterol-), resuspended in the selective medium and distributed to 40×96-well plates at 200 μL per well. Actual distribution was 1140 cells/well and 840 cells/well for HC1::LC3 and HC2::LC3, respectively. Plates were incubated at 37°C, 5% CO2 for 1 week and fed with phenol red supplemented selective medium. At two weeks post-transfection, numerous wells were actively growing based on medium color change from red to yellow.

A total of 1,127 wells from the HC1::LC3 transfection were screened for human IgG expression by ELISA. A total of 612 wells from the HC2::LC3 transfection were screened. Based on IgG concentration, a total of 290 and 101 cell lines were scaled up to 24-well plates for HC1::LC3 and HC2::LC3, respectively. A 24-hour productivity assay was used to select best expressers for further analysis. Briefly, 24-well plates were seeded at 5×10^5 cells in 500 μL fresh medium. After 24 hours, supernatants were

screened by ELISA. Based on IgG concentration, a total of 60 and 24 cell lines were scaled up to 6-well plates for HC1::LC3 and HC2::LC3, respectively.

A 3-day specific productivity assay was used to select best expressers for further analysis. Briefly, 6-well plates were seeded at 4×105 cells in 1.5 mL fresh medium. After 3 days, cells were counted and supernatants were screened by ELISA. Based on IgG concentration and growth, the average specific productivity rate or SPR in pg/cell/day can be calculated. Based on relative SPR, a total of 20 and 10 cell lines were scaled up to T-75 flasks for HC1::LC3 and HC2::LC3, respectively. The 3-day SPR assay was repeated at the T-75 scale to select the final cell lines for suspension adaptation and scale up for mAb production.

Five cell lines for each mAb were scaled up to 30-mL shaker culture and re-evaluated for SPR and growth. All suspension lines were banked. The best performing cell line for each mAb was scaled to spinner culture for small scale production.

For the HLA-IgG4 Fusion Protein, the pBFksr::HLA-IgG4::LC3 bicistronic expression vector was constructed for STABLEFAST-NS0 cell line generation. The vector map is shown in **FIGURE 15**. An expression cassette and vector containing the human β2 microglobulin gene was also created for a tricistronic expression vector that encodes all three fusion protein subunits (human HLA-IgG4 heavy chain fusion, a-CD28 light chain [LC3], and human β2 microglobulin). The tricistronic construct is shown in **FIGURE 16**. Expression of all three genes was confirmed in transient HEK293 culture by ELISA and western blot analyses of supernatant.

Example 5: Functional Characterization

The humanized monoclonal antibody against CD28 was tested for its ability to induce expansion of freshly isolated PBMCs on mAb coated plates. As shown in **FIGURE 17**, the humanized anti-CD28 is not a super agonist.

The humanized monoclonal antibody was tested for its ability to stain CD28 on a human T-cell line. The results are shown in **FIGURE 18**. **FIGURE 18(A)** shows

staining with murine anti-human CD8 mAb (clone 9.3, Isotype IgG2a). Black = unstained cells, red = anti-IgG2a FITC, blue= anti-CD28 + anti-IgG2a FITC. **FIGURE 18(B)** shows staining with humanized anti-CD28 (isotype IgG4). Black = unstained cells, red = anti-IgG4 PE, blue = anti-CD28 (35 ng) + anti-IgG4 PE, purple = antiCD28 (1 μg) + anti-IgG4 PE. The staining with humanized anti-CD28 can be blocked with Clone 9.3 mAb (not shown).

After purification of HLA-Ig, the antigen peptide loading efficiency is checked by ELISA using conformation dependent anti-HLA mAb to capture the peptide loaded protein (as described in Current protocols in Immunology Chapter 17.2). Reproducible loading efficiencies of ~90% for specific peptides (i.e. correct MHC restriction) is anticipated, compared to 0% for non-specific peptides (i.e. MHC mis-match).

INCORPORATION BY REFERENCE

All patents and publications referenced herein are hereby incorporated by reference in their entireties.

SEQUENCE LISTING

<110> NEXIMMUNE
MCCREEDY, Bruce
JONES, Timothy David
CARR, Francis Joseph

<120> COMPOSITIONS AND METHODS FOR IMMUNOTHERAPY

<130> NEX-001PC

<140> PCT/US2014/043629
<141> 2014-06-23

<150> US 61/838,547
<151> 2013-06-24

<150> US 61/948,916
<151> 2014-03-06

<160> 34

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<220>
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Glu Val Lys Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                  10                  15

acc ctg tcc ctc act tgt act gtc tct ggg ttt tca tta agc gac tat        96
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asp Tyr
            20                  25                  30

ggt gtt cat tgg gtt cgc cag gct cca gga aag gga ctg gag tgg ctg       144
Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45

gga gta ata tgg gct ggt gga ggc acg aat tat aat tcg gct ctc atg       192
Gly Val Ile Trp Ala Gly Gly Gly Thr Asn Tyr Asn Ser Ala Leu Met
    50                  55                  60

tcc aga aag acc atc agc aaa gac aac tcc aag agc caa gtt ttc tta       240
Ser Arg Lys Thr Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
65                  70                  75                  80

aaa atg aac agt ctg aca gct gct gac aca gcc gtg tat tac tgt gcc       288
Lys Met Asn Ser Leu Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

aga gat aag gga tac tcc tat tac tat tct atg gac tac tgg ggc caa       336
Arg Asp Lys Gly Tyr Ser Tyr Tyr Tyr Ser Met Asp Tyr Trp Gly Gln
            100                 105                 110

ggc acc ctg gtc acc gtc tcc tca                                      360
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Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 2
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 2

Glu Val Lys Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asp Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ala Gly Gly Gly Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

Ser Arg Lys Thr Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
65 70 75 80

Lys Met Asn Ser Leu Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Lys Gly Tyr Ser Tyr Tyr Tyr Ser Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 3
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<213> Artificial Sequence

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<223> Synthetic sequence (Anti-CD28 VH2)

<220>
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<222> (1)..(360)

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Glu Val Lys Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

acc ctg tcc ctc act tgt act gtc tct ggg ttt tca tta agc gac tat 96
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asp Tyr
20 25 30

```
ggt gtt cat tgg gtt cgc cag gct cca gga aag gga ctg gag tgg ctg        144
Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45

gga gta ata tgg gct ggt gga ggc acg aat tat aat tcg gct ctc atg        192
Gly Val Ile Trp Ala Gly Gly Gly Thr Asn Tyr Asn Ser Ala Leu Met
    50                  55                  60

tcc aga aag acc atc agc aaa gac aac tcc aag agc caa gtt tcc tta        240
Ser Arg Lys Thr Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Ser Leu
65                  70                  75                  80

aaa atg agc agt gtg aca gct gct gac aca gcc gtg tat tac tgt gcc        288
Lys Met Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

aga gat aag gga tac tcc tat tac tat tct atg gac tac tgg ggc caa        336
Arg Asp Lys Gly Tyr Ser Tyr Tyr Tyr Ser Met Asp Tyr Trp Gly Gln
            100                 105                 110

ggc acc ctg gtc acc gtc tcc tca                                       360
Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<210> 4
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 4

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1               5                   10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asp Tyr
            20                  25                  30

Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45

Gly Val Ile Trp Ala Gly Gly Gly Thr Asn Tyr Asn Ser Ala Leu Met
    50                  55                  60

Ser Arg Lys Thr Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Ser Leu
65                  70                  75                  80

Lys Met Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Lys Gly Tyr Ser Tyr Tyr Tyr Ser Met Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<210> 5

<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence ((Anti-CD28 VH3)

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<221> CDS
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gag gtg aag ctg cag cag tca gga cct ggc ctg gtg aag ccc tca gag          48
Glu Val Lys Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                   10                  15

acc ctg tcc ctc act tgt act gtc tct ggg ttt tca tta agc gac tat          96
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asp Tyr
            20                  25                  30

ggt gtt cat tgg gtt cgc cag gct cca gga aag gga ctg gag tgg ctg         144
Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45

gga gta ata tgg gct ggt gga ggc acg aat tat aat tcg gct ctc atg         192
Gly Val Ile Trp Ala Gly Gly Gly Thr Asn Tyr Asn Ser Ala Leu Met
    50                  55                  60

tcc aga gtg acc atc agc aaa gac aac tcc aag agc caa gtt tcc tta         240
Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Ser Leu
65                  70                  75                  80

aaa ctg agc agt gtg aca gct gct gac aca gcc gtg tat tac tgt gcc         288
Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

aga gat aag gga tac tcc tat tac tat tct atg gac tac tgg ggc caa         336
Arg Asp Lys Gly Tyr Ser Tyr Tyr Tyr Ser Met Asp Tyr Trp Gly Gln
            100                 105                 110

ggc acc ctg gtc acc gtc tcc tca                                        360
Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<210> 6
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 6

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Glu Val Lys Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asp Tyr
            20                  25                  30

Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45
```

```
Gly Val Ile Trp Ala Gly Gly Gly Thr Asn Tyr Asn Ser Ala Leu Met
    50                  55                  60

Ser Arg Val Thr Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Ser Leu
65                  70                  75                  80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Lys Gly Tyr Ser Tyr Tyr Tyr Ser Met Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<210> 7
<211> 333
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<213> Artificial Sequence

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<223> Synthetic sequence (Anti-CD28 VK1)

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gac atc gag ctc act cag tct cca gat tct ttg gct gtg tct cta ggg          48
Asp Ile Glu Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15

gag aga gcc acc atc aac tgc aga gcc agt gag agt gtt gaa tat tat          96
Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Glu Ser Val Glu Tyr Tyr
            20                  25                  30

gtc aca agt tta atg cag tgg tac cag cag aag cca gga cag cca ccc         144
Val Thr Ser Leu Met Gln Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45

aaa ctc ctc atc ttt gct gca tcc aac gta gaa tct ggg gtc cct gac         192
Lys Leu Leu Ile Phe Ala Ala Ser Asn Val Glu Ser Gly Val Pro Asp
    50                  55                  60

agg ttt agt ggc agt ggg tct ggg aca aac ttc acc ctc acc atc tct         240
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asn Phe Thr Leu Thr Ile Ser
65                  70                  75                  80

tct ctg cag gag gag gat gtt gca atg tat ttc tgt cag caa agt agg         288
Ser Leu Gln Glu Glu Asp Val Ala Met Tyr Phe Cys Gln Gln Ser Arg
                85                  90                  95

aag gtt cct tac acg ttc gga ggg ggg acc aag gtg gaa ata aaa             333
Lys Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110
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<210> 8
<211> 111
<212> PRT
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Asp Ile Glu Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                  10                  15

Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Glu Ser Val Glu Tyr Tyr
            20                  25                  30

Val Thr Ser Leu Met Gln Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45

Lys Leu Leu Ile Phe Ala Ala Ser Asn Val Glu Ser Gly Val Pro Asp
    50                  55                  60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asn Phe Thr Leu Thr Ile Ser
65                  70                  75                  80

Ser Leu Gln Glu Glu Asp Val Ala Met Tyr Phe Cys Gln Gln Ser Arg
                85                  90                  95

Lys Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110
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Asp Ile Glu Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                  10                  15

gag aga gcc acc atc aac tgc aga gcc agt gag agt gtt gaa tat tat          96
Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Glu Ser Val Glu Tyr Tyr
            20                  25                  30

gtc aca agt tta atg cag tgg tac cag cag aag cca gga cag cca ccc         144
Val Thr Ser Leu Met Gln Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45

aaa ctc ctc atc ttt gct gca tcc aac gta gaa tct ggg gtc cct gac         192
Lys Leu Leu Ile Phe Ala Ala Ser Asn Val Glu Ser Gly Val Pro Asp
    50                  55                  60

agg ttt agt ggc agt ggg tct ggg aca aac ttc acc ctc acc atc tct         240
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asn Phe Thr Leu Thr Ile Ser
65                  70                  75                  80

tct ctg cag gcc gag gat gtt gca atg tat ttc tgt cag caa agt agg         288
```

Ser Leu Gln Ala Glu Asp Val Ala Met Tyr Phe Cys Gln Gln Ser Arg
85 90 95

aag gtt cct tac acg ttc gga ggg ggg acc aag gtg gaa ata aaa 333
Lys Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 10
<211> 111
<212> PRT
<213> Artificial Sequence

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Asp Ile Glu Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Glu Ser Val Glu Tyr Tyr
20 25 30

Val Thr Ser Leu Met Gln Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Phe Ala Ala Ser Asn Val Glu Ser Gly Val Pro Asp
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asn Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ala Glu Asp Val Ala Met Tyr Phe Cys Gln Gln Ser Arg
85 90 95

Lys Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 11
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<220>
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Asp Ile Glu Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

gag aga gcc acc atc aac tgc aga gcc agt gag agt gtt gaa tat tat 96
Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Glu Ser Val Glu Tyr Tyr
20 25 30

```
gtc aca agt tta atg cag tgg tac cag cag aag cca gga cag cca ccc        144
Val Thr Ser Leu Met Gln Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45

aaa ctc ctc atc ttt gct gca tcc aac gta gaa tct ggg gtc cct gac        192
Lys Leu Leu Ile Phe Ala Ala Ser Asn Val Glu Ser Gly Val Pro Asp
    50                  55                  60

agg ttt agt ggc agt ggg tct ggg aca gac ttc acc ctc acc atc tct        240
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65                  70                  75                  80

tct ctg cag gcc gag gat gtt gca atg tat ttc tgt cag caa agt agg        288
Ser Leu Gln Ala Glu Asp Val Ala Met Tyr Phe Cys Gln Gln Ser Arg
                85                  90                  95

aag gtt cct tac acg ttc gga ggg ggg acc aag gtg gaa ata aaa            333
Lys Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


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<212>  PRT
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<220>
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            20                  25                  30


Val Thr Ser Leu Met Gln Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45


Lys Leu Leu Ile Phe Ala Ala Ser Asn Val Glu Ser Gly Val Pro Asp
    50                  55                  60


Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65                  70                  75                  80


Ser Leu Gln Ala Glu Asp Val Ala Met Tyr Phe Cys Gln Gln Ser Arg
                85                  90                  95


Lys Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


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agc acc tcc gag agc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac          96
Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30

ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc         144
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45

ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc         192
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60

ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acg aag acc         240
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65                  70                  75                  80

tac acc tgc aat gta gat cac aag ccc agc aac acc aag gtg gac aag         288
Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

aga gtt gag tcc aaa tat ggt ccc cca tgc cca cca tgc cca gca cct         336
Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
            100                 105                 110

gag ttc gag ggg gga cca tca gtc ttc ctg ttc ccc cca aaa ccc aag         384
Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
        115                 120                 125

gac act ctc atg atc tcc cgg acc cct gag gtc acg tgc gtg gtg gtg         432
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
    130                 135                 140

gac gtg agc cag gaa gac ccc gag gtc cag ttc aac tgg tac gtg gat         480
Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145                 150                 155                 160

ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag ttc         528
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
                165                 170                 175

aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac         576
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
            180                 185                 190

tgg ctg aac ggc aag gag tac aag tgc aag gtc tcc aac aaa ggc ctc         624
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
        195                 200                 205

ccg tcc tcc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga         672
Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
    210                 215                 220

gag cca cag gtg tac acc ctg ccc cca tcc cag gag gag atg acc aag         720
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225                 230                 235                 240

aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tac ccc agc gac         768
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
                245                 250                 255
```

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atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag        816
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
            260                 265                 270

acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc        864
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
        275                 280                 285

agg cta acc gtg gac aag agc agg tgg cag gag ggg aat gtc ttc tca        912
Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
    290                 295                 300

tgc tcc gtg atg cat gag gct ctg cac aac cac tac aca cag aag agc        960
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305                 310                 315                 320

ctc tgc ctg tct ctg ggt aaa tga                                       984
Leu Cys Leu Ser Leu Gly Lys
                325
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<210> 14
<211> 327
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 14

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1               5                   10                  15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65                  70                  75                  80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
            100                 105                 110

Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
        115                 120                 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
    130                 135                 140
```

```
Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145                 150                 155                 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
                165                 170                 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
            180                 185                 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
        195                 200                 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
    210                 215                 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225                 230                 235                 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
                245                 250                 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
            260                 265                 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
        275                 280                 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
    290                 295                 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305                 310                 315                 320

Leu Cys Leu Ser Leu Gly Lys
                325
```

<210> 15
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence (constant k Light sequence)

<220>
<221> CDS
<222> (1)..(324)

<400> 15

```
cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag        48
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1               5                   10                  15

cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc        96
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
```

```
            20                  25                  30

tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa        144
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
        35                  40                  45

tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc        192
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
    50                  55                  60

acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag        240
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65                  70                  75                  80

aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg        288
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
                85                  90                  95

ccc gtc aca aag agc ttc aac agg gga gag tgt tag                       324
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
            100                 105


<210>  16
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  16

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1               5                   10                  15

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
            20                  25                  30

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
        35                  40                  45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
    50                  55                  60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65                  70                  75                  80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
                85                  90                  95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
            100                 105


<210>  17
<211>  360
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic sequence (humanized non-CD28-binding variable region)
```

<220>
<221> CDS
<222> (1)..(360)

<400> 17

```
gag gtg aag ctg cag cag tca gga cct ggc ctg gtg aag ccc tca gag          48
Glu Val Lys Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                   10                  15

acc ctg tcc ctc act tgt act gtc tct ggg ttt aca ttc agc gac tat          96
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30

ggt gtt cat tgg att cgc cag cct cca gga aag gga ctg gag tgg atc         144
Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45

gga gta ata tgg gct ggt gga ggc acg aat tat aat tcg gct ctc atg         192
Gly Val Ile Trp Ala Gly Gly Gly Thr Asn Tyr Asn Ser Ala Leu Met
    50                  55                  60

tcc aga gtg acc atc agc gtg gac acc tcc aag aac caa ttt tcc tta         240
Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65                  70                  75                  80

aaa ctg agc agt gtg aca gct gct gac aca gcc gtg tat tac tgt gcc         288
Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

aga gat aag gga tac tcc gct gcc gct tct atg gac tac tgg ggc caa         336
Arg Asp Lys Gly Tyr Ser Ala Ala Ala Ser Met Asp Tyr Trp Gly Gln
            100                 105                 110

ggc acc ctg gtc acc gtc tcc tca                                        360
Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 18
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 18

```
Glu Val Lys Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Thr Phe Ser Asp Tyr
            20                  25                  30

Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45

Gly Val Ile Trp Ala Gly Gly Gly Thr Asn Tyr Asn Ser Ala Leu Met
    50                  55                  60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65                  70                  75                  80
```

```
Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Lys Gly Tyr Ser Ala Ala Ala Ser Met Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  19
<211>  733
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic sequence (humanized HLA-IgG4HC)

<400>  19

Gln Val Gln Leu Thr Arg Glu Gly Ser Gly Ser His Ser Met Arg Tyr
1               5                   10                  15

Phe Phe Thr Ser Val Ser Arg Pro Gly Arg Gly Glu Pro Arg Phe Ile
            20                  25                  30

Ala Val Gly Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp
        35                  40                  45

Ala Ala Ser Gln Arg Met Glu Pro Arg Ala Pro Trp Ile Glu Gln Glu
    50                  55                  60

Gly Pro Glu Tyr Trp Asp Gly Glu Thr Arg Lys Val Lys Ala His Ser
65                  70                  75                  80

Gln Thr His Arg Val Asp Leu Gly Thr Leu Arg Gly Tyr Tyr Asn Gln
                85                  90                  95

Ser Glu Ala Gly Ser His Thr Val Gln Arg Met Tyr Gly Cys Asp Val
            100                 105                 110

Gly Ser Asp Trp Arg Phe Leu Arg Gly Tyr His Gln Tyr Ala Tyr Asp
        115                 120                 125

Gly Lys Asp Tyr Ile Ala Leu Lys Glu Asp Leu Arg Ser Trp Thr Ala
    130                 135                 140

Ala Asp Met Ala Ala Gln Thr Thr Lys His Lys Trp Glu Ala Ala His
145                 150                 155                 160

Val Ala Glu Gln Leu Arg Ala Tyr Leu Glu Gly Thr Cys Val Glu Trp
                165                 170                 175
```

```
Leu Arg Arg Tyr Leu Glu Asn Gly Lys Glu Thr Leu Gln Arg Thr Asp
            180                 185                 190

Ala Pro Lys Thr His Met Thr His His Ala Val Ser Asp His Glu Ala
        195                 200                 205

Thr Leu Arg Cys Trp Ala Leu Ser Phe Tyr Pro Ala Glu Ile Thr Leu
    210                 215                 220

Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp Thr Glu Leu Val
225                 230                 235                 240

Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val
                245                 250                 255

Val Val Pro Ser Gly Gln Glu Gln Arg Tyr Thr Cys His Val Gln His
            260                 265                 270

Glu Gly Leu Pro Lys Pro Leu Thr Trp Ala Arg Glu Val Ser Glu Val
        275                 280                 285

Lys Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu
    290                 295                 300

Ser Leu Thr Cys Thr Val Ser Gly Phe Thr Phe Ser Asp Tyr Gly Val
305                 310                 315                 320

His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Val
                325                 330                 335

Ile Trp Ala Gly Gly Gly Thr Asn Tyr Asn Ser Ala Leu Met Ser Arg
            340                 345                 350

Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu
        355                 360                 365

Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp
    370                 375                 380

Lys Gly Tyr Ser Ala Ala Ala Ser Met Asp Tyr Trp Gly Gln Gly Thr
385                 390                 395                 400

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
                405                 410                 415

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
            420                 425                 430

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
        435                 440                 445
```

```
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
    450                 455                 460

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
465                 470                 475                 480

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
                485                 490                 495

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
            500                 505                 510

Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu
        515                 520                 525

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
    530                 535                 540

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
545                 550                 555                 560

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
                565                 570                 575

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
            580                 585                 590

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
        595                 600                 605

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
    610                 615                 620

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
625                 630                 635                 640

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
                645                 650                 655

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
            660                 665                 670

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
        675                 680                 685

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
    690                 695                 700

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
705                 710                 715                 720
```

His Tyr Thr Gln Lys Ser Leu Cys Leu Ser Leu Gly Lys
725 730

<210> 20
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence (Light Chain 3 (LC3 or Vk3))

<400> 20

Asp Ile Glu Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Glu Ser Val Glu Tyr Tyr
20 25 30

Val Thr Ser Leu Met Gln Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Phe Ala Ala Ser Asn Val Glu Ser Gly Val Pro Asp
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ala Glu Asp Val Ala Met Tyr Phe Cys Gln Gln Ser Arg
85 90 95

Lys Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
180 185 190

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
195 200 205

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 21
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence (Heavy Chain 1 (HC1))

<400> 21

```
Glu Val Lys Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                  10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asp Tyr
            20                  25                  30

Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45

Gly Val Ile Trp Ala Gly Gly Gly Thr Asn Tyr Asn Ser Ala Leu Met
    50                  55                  60

Ser Arg Lys Thr Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
65                  70                  75                  80

Lys Met Asn Ser Leu Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Lys Gly Tyr Ser Tyr Tyr Tyr Ser Met Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
    210                 215                 220
```

```
Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
            260                 265                 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
    290                 295                 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320

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

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            340                 345                 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385                 390                 395                 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
                405                 410                 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430

His Asn His Tyr Thr Gln Lys Ser Leu Cys Leu Ser Leu Gly Lys
        435                 440                 445

<210>  22
<211>  447
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic sequence (Heavy Chain 2 (HC2))

<400>  22

Glu Val Lys Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                   10                  15
```

```
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asp Tyr
            20                  25                  30

Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45

Gly Val Ile Trp Ala Gly Gly Gly Thr Asn Tyr Asn Ser Ala Leu Met
    50                  55                  60

Ser Arg Lys Thr Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Ser Leu
65                  70                  75                  80

Lys Met Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Lys Gly Tyr Ser Tyr Tyr Tyr Ser Met Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
    210                 215                 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
            260                 265                 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285
```

```
Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
    290                 295                 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320

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

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            340                 345                 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385                 390                 395                 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
                405                 410                 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430

His Asn His Tyr Thr Gln Lys Ser Leu Cys Leu Ser Leu Gly Lys
        435                 440                 445
```

<210> 23
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence

<400> 23

```
Asp Tyr Gly Val His
1               5
```

<210> 24
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence

<400> 24

```
Val Ile Trp Ala Gly Gly Gly Thr Asn Tyr Asn Ser Ala Leu Met Ser
1               5                   10                  15
```

<210> 25
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence

<400> 25

Asp Lys Gly Tyr Ser Tyr Tyr Tyr Ser Met Asp Tyr
1 5 10

<210> 26
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence

<400> 26

Arg Ala Ser Glu Ser Val Glu Tyr Tyr Val Thr Ser Leu Met Gln
1 5 10 15

<210> 27
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence

<400> 27

Ala Ala Ser Asn Val Glu Ser
1 5

<210> 28
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence

<400> 28

Gln Gln Ser Arg Lys Val Pro Tyr Thr
1 5

<210> 29
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence

<400> 29

Gly Gly Gly Ser Gly
1 5

<210> 30
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence

<400> 30

Ala Ala Ala Gly Gly
1 5

<210> 31
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence (N-terminal linker)

<220>
<221> CDS
<222> (1)..(51)

<400> 31
cag gtc caa ctg acg cgt gag ggg tcc ggc tct cac tcc atg agg tat 48
Gln Val Gln Leu Thr Arg Glu Gly Ser Gly Ser His Ser Met Arg Tyr
1 5 10 15

ttc 51
Phe

<210> 32
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 32

Gln Val Gln Leu Thr Arg Glu Gly Ser Gly Ser His Ser Met Arg Tyr
1 5 10 15

Phe

<210> 33
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence (C-terminal linker)

<220>
<221> CDS
<222> (1)..(57)

<400> 33
gag ggt ttg ccc aag ccc ctc acc tgg gct cga gag gtg agc gag gtc 48
Glu Gly Leu Pro Lys Pro Leu Thr Trp Ala Arg Glu Val Ser Glu Val
1 5 10 15

aag ctg cag 57
Lys Leu Gln

<210> 34
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 34

Glu Gly Leu Pro Lys Pro Leu Thr Trp Ala Arg Glu Val Ser Glu Val
1 5 10 15

Lys Leu Gln