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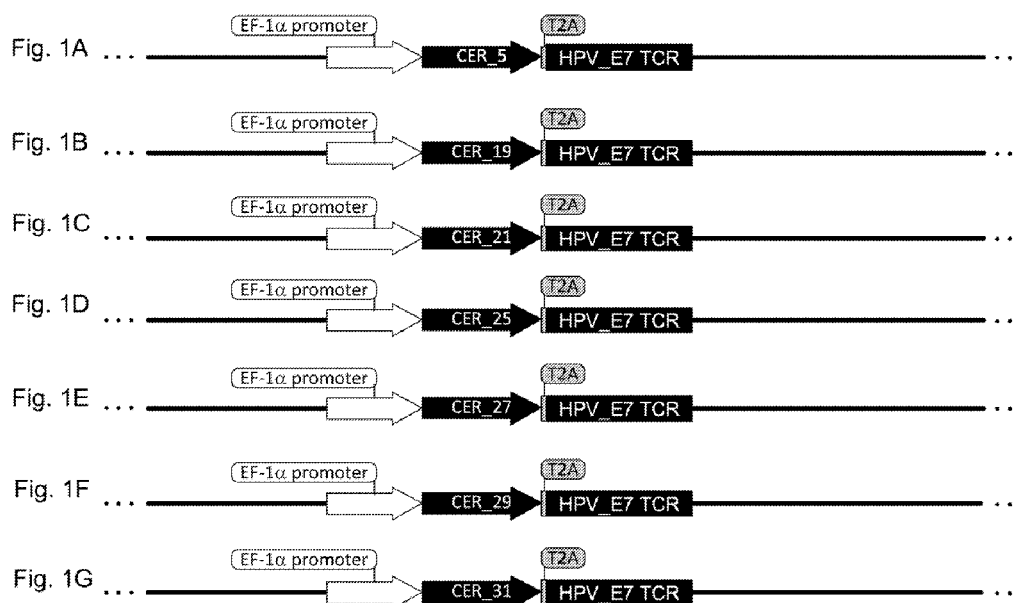
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(54) Title: EXPRESSION VECTORS FOR CHIMERIC ENGULFMENT RECEPTORS, GENETICALLY MODIFIED HOST CELLS, AND USES THEREOF



(57) Abstract: The present disclosure relates to tandem expression cassettes encoding chimeric engulfment receptor molecules and chimeric antigen receptors/or T cell receptor binding proteins, host cells modified to include the tandem expression cassettes, and methods of making and using such receptor molecules and modified cells.



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EXPRESSION VECTORS FOR CHIMERIC ENGULFMENT RECEPTORS, GENETICALLY MODIFIED HOST CELLS, AND USES THEREOF

STATEMENT REGARDING SEQUENCE LISTING

The Sequence Listing associated with this application is provided in text format in lieu of a paper copy, and is hereby incorporated by reference into the specification. The name of the text file containing the Sequence Listing is 200265_406WO_SEQUENCE_LISTING.txt. The text file is 539 KB, was created on March 26, 2019, and is being submitted electronically via EFS-Web.

BACKGROUND

The use of T cells modified with genetically engineered receptors targeted against cancer antigens has demonstrated clinical successes in hematological malignancies (*e.g.*, CD19 specific chimeric antigen receptor therapy in leukemias). A number of clinical trials are underway for adoptive cellular immunotherapy in the treatment of solid tumors, using engineered receptors targeting CEA, GD2, mesothelin, IL13R α , HER2, FAP, and L1CAM, to name a few. Engineered receptors include chimeric antigen receptors (CARs) and enhanced affinity T cell receptors (TCRs). However, treatment of solid tumors presents unique challenges including: trafficking to the tumor site, physical barriers to the tumor microenvironment, a stressful metabolic landscape, and immunosuppressive mechanisms (*e.g.*, expression of immune checkpoint molecules, production of inhibitory cytokines). Efforts to augment T-cell persistence and activity in adoptive immunotherapy treatments are ongoing.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A-G show vector maps for exemplary tandem expression cassettes. The tandem expression cassettes harbor both a human papilloma virus 16 (HPV16) E7 protein specific TCR to induce a tumor (*e.g.*, cervical) specific cytolytic response and a phosphatidylserine specific chimeric engulfment receptor (CER) to elicit tumor specific phagocytic activity upon cytolysis-induced phosphatidylserine exposure.

Figure 1A shows an exemplary tandem expression cassette comprising a polynucleotide encoding a chimeric engulfment receptor 5 (CER5) construct and a polynucleotide encoding a HPV16 E7 specific TCR. CER5 is positioned upstream of the HPV16 E7 specific TCR. The sequences encoding CER5 and HPV16 E7 TCR are operably linked to a EF-1 α promoter and separated by a T2A peptide. CER5 comprises a Tim4 binding domain, a Tim4 transmembrane domain, and a TLR4 engulfment signaling domain. **Figure 1B** shows an exemplary tandem expression cassette comprising a polynucleotide encoding a CER19 construct and a polynucleotide encoding an HPV16 E7 specific TCR. CER19 is positioned upstream of the HPV16 E7 specific TCR. The sequences encoding CER19 and HPV16 E7 TCR are operably linked to a EF-1 α promoter and separated by a T2A peptide. CER19 comprises a Tim4 binding domain, a Tim4 transmembrane domain, and a TLR5 signaling domain. **Figure 1C** shows an exemplary tandem expression cassette comprising a polynucleotide encoding a CER21 construct and a polynucleotide encoding an HPV16 E7 specific TCR. CER21 is positioned upstream of the HPV16 E7 specific TCR. The sequences encoding CER21 and HPV16 E7 TCR are operably linked to an EF-1 α promoter and separated by a T2A peptide. CER21 comprises a Tim4 binding domain, a Tim4 transmembrane domain, and a TLR8 signaling domain. **Figure 1D** shows an exemplary tandem expression cassette comprising a polynucleotide encoding CER25 construct and a polynucleotide encoding an HPV16 E7 specific TCR. CER25 is positioned upstream of the HPV16 E7 specific TCR. The sequences encoding CER25 and HPV16 E7 TCR are operably linked to a EF-1 α promoter and separated by a T2A peptide. CER25 comprises a Tim4 binding domain, a Tim4 transmembrane domain, and a NFAM1 signaling domain. **Figure 1E** shows an exemplary tandem expression cassette comprising a polynucleotide encoding CER27 construct and a polynucleotide encoding an HPV16 E7 specific TCR. CER27 is positioned upstream of the HPV16 E7 specific TCR. The sequences encoding CER27 and HPV E7 TCR are operably linked to a EF-1 α promoter and separated by a T2A peptide. CER27 comprises a Tim4 binding domain, a Tim4 transmembrane domain, and a TLR2 signaling domain. **Figure 1F** shows an exemplary tandem expression cassette comprising a polynucleotide

encoding CER29 construct and a polynucleotide encoding an HPV16 E7 specific TCR. CER29 is positioned upstream of the HPV16 E7 specific TCR. The sequences encoding CER29 and HPV16 E7 TCR are operably linked to a EF-1 α promoter and separated by a T2A peptide. CER29 comprises a Tim4 binding domain, a Tim4 transmembrane domain, and a Traf6 signaling domain. **Figure 1G** shows an exemplary tandem expression cassette comprising a polynucleotide encoding CER31 construct and a polynucleotide encoding an HPV16 E7 specific TCR. CER31 is positioned upstream of the HPV16 E7 specific TCR. The sequences encoding CER31 and HPV16 E7 TCR are operably linked to a EF-1 α promoter and separated by a T2A peptide. CER31 comprises a Tim4 binding domain, a Tim4 transmembrane domain, and a Traf3 signaling domain.

Figure 2 shows cytotoxicity of human primary CD8⁺ T cells modified with tandem expression construct comprising CER21-HPV16 E7 TCR. The images show caspase 3/7 fluorescent indicator dye emitted from HPV16 E7⁺ head and neck squamous cell carcinoma (SCC152) cells taken at various time points (2 hrs, 4 hrs, and 6 hrs). CD8⁺ T cells transduced with CER21-HPV16 E7 TCR tandem expression cassette (top row) were compared to CD8⁺ T cells transduced with HPV16 E7 TCR alone (bottom row) in timed co-culture experiments with SCC152 cells. The tandem expression construct confers both cytolytic and phagocytic activity in the CD8⁺ T cells and enhances killing capacity. Effector CD8⁺ T cells: target SCC152 cells were incubated at a 1:1 ratio.

Figure 3 is a line graph showing Caspase 3/7 induction over time in HPV16 E7⁺ SCC152 cells upon co-culture with human primary CD8⁺ T cells transduced with a lentiviral vector comprising a tandem cassette HPV16 E7 TCR and Chimeric Engulfment Receptor 21 (CER21) separated by a T2A sequence. The tandem expression construct encoding HPV16 E7 TCR and CER21 confers enhanced target cell killing capacity to host CD8⁺ T cells as compared to host CD8⁺ T cells comprising HPV16 E7 TCR alone. Effector CD8⁺ T cells were incubated with target SCC152 cells at a 1:1 ratio. Total caspase 3/7 fluorescence was quantified over time.

Figure 4 is a bar graph showing caspase 3/7 induction in HPV16 E7+ SCC152 cells upon co-culture with CD8+ T cells transduced with a lentiviral vector comprising a tandem cassette HPV16 E7 TCR and CER separated by a T2A sequence, Mock transduced cells were used as a negative control. Labeling of SCC152 cells with the IncuCyte[®] caspase 3/7 red apoptosis reagent enables detection of cells undergoing apoptosis (red fluorescence). Measurements were taken over time from co-culture experiments comparing CD8+ T cells transduced with a tandem CER-HPV16 E7 TCR cassette to CD8+ T cells transduced with HPV16 E7 TCR control.

Figure 5 shows images of caspase 3/7 fluorescent indicator dye emitted from HPV+ head and neck squamous cell carcinoma (SCC152) cells taken 6 hrs after initiation of co-culture. Co-culture with CD8+ T cells transduced with CER-HPV16 E7 TCR tandem expression cassettes was compared to co-culture with CD8+ T cells transduced with HPV16 E7 TCR alone (2nd from top). CD8+ T cells transduced with CER-HPV16 E7 TCR tandem expression cassettes show higher caspase induction than control CD8+ T cells.

Figure 6 is a bar graph showing quantification of phagocytosis after 6 hours of co-culture of CD8+ T cells transduced with HPV16 E7 TCR, CER21-HPV16 E7 TCR tandem expression cassette, CER29-HPV16 E7 TCR tandem expression cassette, or CER31-HPV16 E7 TCR tandem expression cassette. Quantification of phagocytosis was performed by the hybrid capture software in Keyence BZ-X710 imaging system wherein % phagocytosis was determined by identifying the number of red fluorescent targets (SCC152 cells) inside blue stained effector cells (cell trace violet labeled CD8+ T cells transduced with CER-HPV16 E7 TCR tandem expression cassette - # of red internalized/# of blue) x 100.

Figure 7 is a fluorescent micrograph showing CER21-HPV16 E7 TCR tandem expression cassette transduced CD8+ T cells (violet colored) engulfing SCC152 target cells (pHrodo Red labeled). A 1:1 mixture of CER21-HPV16 E7 TCR tandem expression cassette transduced CD8+ T cells to SCC152 target cells were co-cultured for 6 hours and then imaged. Arrows indicate representative images of internalization of SCC152 cells (red) within violet-colored CD8+ T cell endosomal compartments (left

image = bright field overlay, right image = fluorescent overlay). CD8+ T cells engineered with the tandem cassette clearly engulf the SCC152 tumor cell line.

Figure 8 shows that CD8+ T cells transduced with CER21-HPV16 E7 TCR tandem expression cassette engulfed target cells in a Rac1-dependent manner. Activation and membrane recruitment of the small GTP-ase Rac1 triggers phagocytosis. The left image shows engulfment of pH rodo red labeled target cells inside blue labeled CD8+ cells transduced with CER21-HPV16 E7 TCR. The Rac1 inhibitor NSC23766 (50 μ M) was added to co-culture experiments (right image) and *in vitro* phagocytosis/engulfment quantified. Fluorescent micrographs show that inhibition of Rac1 by small molecule abolishes *in vitro* engulfment in CD8+ T cells transduced with CER21-HPV16 E7 TCR tandem expression cassette (right).

Figure 9 shows that CD8+ T cells transduced with CER29-HPV16 E7 TCR tandem expression cassette engulf target cells in a Rac1-dependent manner. Activation and membrane recruitment of the small GTP-ase Rac1 triggers phagocytosis. The left image shows engulfment of pH rodo red labeled target cells inside blue labeled CD8+ cells transduced with CER29-HPV16 E7 TCR. The Rac1 inhibitor NSC23766 (50 μ M) was added to co-culture experiments (right image) and *in vitro* phagocytosis quantified. Fluorescent micrographs show that inhibition of Rac1 by small molecule abolishes *in vitro* phagocytosis in CD8+ T cells transduced with CER29-HPV16 E7 TCR tandem expression cassette (right).

Figure 10 shows that CD8+ T cells transduced with CER31-HPV16 E7 TCR tandem expression cassette engulf target cells in a Rac1-dependent manner. Activation and membrane recruitment of the small GTP-ase Rac1 triggers phagocytosis. The left image shows engulfment of pH rodo red labeled target cells inside blue labeled CD8+ cells transduced with CER31-HPV16 E7 TCR. The Rac1 inhibitor NSC23766 (50 μ M) was added to co-culture experiments (right) and *in vitro* phagocytosis quantified. Fluorescent micrographs show that inhibition of Rac1 by small molecule inhibitor abolishes *in vitro* phagocytosis/engulfment in CD8+ T cells transduced with CER31-HPV16 E7 TCR tandem expression cassette (right).

Figure 11 shows that CD8⁺ T cells transduced with a tandem expression cassette comprising CER21-HPV16 E7 TCR have dual cytolytic and phagocytic functionality. CER21-HPV16 E7 TCR transduced CD8⁺ T cells exhibit phagocytic uptake of phosphatidylserine-coated beads *in vitro*. Streptavidin coated latex beads were bound with biotin-phosphatidylserine and used for phagocytosis assays. After 30 minutes incubation, CER21-HPV16 E7 TCR transduced CD8⁺ T cells exhibited uptake of phosphatidylserine coated beads (white arrows show representative images of engulfment events).

Figure 12 shows a high magnification image of a CER21-HPV16 E7 TCR transduced CD8⁺ T cell exhibiting phagocytic uptake of phosphatidylserine-coated beads *in vitro*.

Figure 13 shows light micrograph of HPV16 E7 TCR transduced CD8⁺ T cells co-cultured with latex beads coated with phosphatidylserine at 30 minutes following incubation. CD8⁺ T cells transduced with HPV16 E7 TCR alone do not exhibit uptake of latex beads coated with phosphatidylserine.

Figure 14 is a 3D bar graph showing cytokine secretion patterns of CD8⁺ T cells transduced with CER21-HPV16 E7 TCR tandem expression cassette or HPV16 E7 TCR alone and co-cultured with SCC152 target cells. To determine cytokine secretion patterns, CER21-HPV16 E7 TCR modified CD8⁺ T cells were co-cultured with SCC152 target cells. Antigen-specific cytokine secretion was determined by measuring cytokine concentrations in the cell supernatants from each co-culture using a mesoscale multi-array cytokine plate. The following cytokines were measured in the assay: IFN γ , IL-2, TNF α , IL-4, IL-6, IL-12b, IL-13, IL-1b, and IL-10. CD8⁺ T cells transduced with CER21-HPV16 E7 TCR tandem expression cassette exhibit antigen specific effector function as shown by cytokine secretion, *e.g.*, IFN γ .

Figures 15A-15B show that phagocytic activity of T cells is specifically induced by CER. Figure 15A shows FACS analysis of phagocytosis assays. CellTrace-violet labeled mock transduced, HPV E7-TCR transduced T cells, and HPV E7-TCR/CER29 tandem expression cassette transduced T cells were co-cultured pHrodo-red labeled HPV⁺ SCC152 head and neck cancer cells. Figure 15B shows

quantification of FACS data, showing no difference in phagocytosis between mock-transduced T cells and E7 TCR transduced T cells. T cells that co-expressed CER29 with the E7 TCR in T cells exhibited phagocytic activity.

DETAILED DESCRIPTION

In one aspect, the present disclosure provides tandem expression cassettes for co-expression of a first transgene encoding a first adoptive immunotherapy molecule and a second transgene encoding a second adoptive immunotherapy molecule in the same host cell. Embodiments of the tandem expression cassettes described herein comprise a polynucleotide encoding a chimeric engulfment receptor (CER); and a polynucleotide encoding a chimeric antigen receptor (CAR) or recombinant T cell receptor (TCR). Tandem expression cassettes of the present disclosure may be used to confer tandem cytolytic and engulfment phenotypes in the same host cell. In certain embodiments, cytotoxic activity of the CAR or TCR specific for a first target antigen induces apoptosis of target cells expressing the first target antigen, thereby exposing a second target antigen; and the co-expressed CER, which is specific for the second target antigen, induces engulfment of target cells or particles expressing the second target antigen. This interaction may be related to separate genetically engineered cells producing the milieu/phosphatidylserine expression associated with the engulfment of target cells from the same cell having different interactions with a defined tumor or tumor cell.

Additionally, cells modified to express tandem expression cassettes of the present disclosure and methods and compositions for delivery of such modified cells to a subject in need thereof are provided.

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

In the present description, any concentration range, percentage range, ratio range, or integer range is to be understood to include the value of any integer within the recited range and, when appropriate, fractions thereof (such as one tenth and one hundredth of an integer), unless otherwise indicated. Also, any number range recited herein relating to any physical feature, such as polymer subunits, size or thickness, are to be understood to include any integer within the recited range, unless

otherwise indicated. As used herein, the term "about" means $\pm 20\%$ of the indicated range, value, or structure, unless otherwise indicated. It should be understood that the terms "a" and "an" as used herein refer to "one or more" of the enumerated components. The use of the alternative (*e.g.*, "or") should be understood to mean either one, both, or any combination thereof of the alternatives. As used herein, the terms "include," "have" and "comprise" are used synonymously, which terms and variants thereof are intended to be construed as non-limiting.

Terms understood by those in the art of antibody technology are each given the meaning acquired in the art, unless expressly defined differently herein. The term "antibody" is used in the broadest sense and includes polyclonal and monoclonal antibodies. An "antibody" may refer to an intact antibody comprising at least two heavy (H) chains and two light (L) chains inter-connected by disulfide bonds, as well as an antigen-binding portion (or antigen-binding domain) of an intact antibody that has or retains the capacity to bind a target molecule. An antibody may be naturally occurring, recombinantly produced, genetically engineered, or modified forms of immunoglobulins, for example intrabodies, peptibodies, nanobodies, single domain antibodies, SMIPs, multispecific antibodies (*e.g.*, bispecific antibodies, diabodies, triabodies, tetrabodies, tandem di-scFv, tandem tri-scFv, ADAPTIR). A monoclonal antibody or antigen-binding portion thereof may be non-human, chimeric, humanized, or human, preferably humanized or human. Immunoglobulin structure and function are reviewed, for example, in Harlow *et al.*, Eds., *Antibodies: A Laboratory Manual*, Chapter 14 (Cold Spring Harbor Laboratory, Cold Spring Harbor, 1988). "Antigen-binding portion" or "antigen-binding domain" of an intact antibody is meant to encompass an "antibody fragment," which indicates a portion of an intact antibody and refers to the antigenic determining variable regions or complementary determining regions of an intact antibody. Examples of antibody fragments include, but are not limited to, Fab, Fab', F(ab')₂, and Fv fragments, Fab'-SH, F(ab')₂, diabodies, linear antibodies, scFv antibodies, VH, and multispecific antibodies formed from antibody fragments. A "Fab" (fragment antigen binding) is a portion of an antibody that binds to antigens and includes the variable region and CH1 of the heavy chain linked to the light chain via an inter-chain disulfide bond. An antibody may be of any class or subclass, including IgG and subclasses thereof (IgG₁, IgG₂, IgG₃, IgG₄), IgM, IgE, IgA, and IgD.

The term "variable region" or "variable domain" in the context of an antibody refers to the domain of an antibody heavy or light chain that is involved in binding of the antibody to antigen. The variable domains of the heavy chain and light chain (VH and VL, respectively) of a native antibody generally have similar structures, with each domain comprising four conserved framework regions (FRs) and three complementary determining regions (CDRs). (*See, e.g.,* Kindt et al. *Kuby Immunology*, 6th ed., W.H. Freeman and Co., page 91 (2007)). A single VH or VL domain may be sufficient to confer antigen-binding specificity. Furthermore, antibodies that bind a particular antigen may be isolated using a VH or VL domain from an antibody that binds the antigen to screen a library of complementary VL or VH domains, respectively. *See, e.g.,* Portolano et al., *J. Immunol.* 150:880-887 (1993); Clarkson et al., *Nature* 352:624-628 (1991).

The terms "complementarity determining region" and "CDR," which are synonymous with "hypervariable region" or "HVR," are known in the art to refer to non-contiguous sequences of amino acids within antibody variable regions, which confer antigen specificity and/or binding affinity. In general, there are three CDRs in each heavy chain variable region (HCDR1, HCDR2, HCDR3) and three CDRs in each light chain variable region (LCDR1, LCDR2, LCDR3).

As used herein, the terms "binding domain", "binding region", and "binding moiety" refer to a molecule, such as a peptide, oligopeptide, polypeptide, or protein that possesses the ability to specifically and non-covalently bind, associate, unite, recognize, or combine with a target molecule (*e.g.,* tumor antigen). A binding domain includes any naturally occurring, synthetic, semi-synthetic, or recombinantly produced binding partner for a biological molecule or other target of interest. In some embodiments, the binding domain is an antigen-binding domain, such as an antibody or functional binding domain or antigen-binding portion thereof. Exemplary binding domains include single chain antibody variable regions (*e.g.,* domain antibodies, sFv, scFv, Fab), receptor ectodomains (*e.g.,* TNF- α), ligands (*e.g.,* cytokines, chemokines), or synthetic polypeptides selected for the specific ability to bind to a biological molecule.

"T cell receptor" (TCR) refers to a molecule found on the surface of T cells (also referred to as T lymphocytes) that is generally responsible for recognizing

antigens bound to major histocompatibility complex (MHC) molecules. The TCR is generally composed of a disulfide-linked heterodimer of the highly variable α and β chains (also known as TCR α and TCR β , respectively) in most T cells. In a small subset of T cells, the TCR is made up of a heterodimer of γ and δ chains (also known as TCR γ and TCR δ , respectively). Each chain of the TCR is a member of the immunoglobulin superfamily and possesses one N-terminal immunoglobulin variable domain, one immunoglobulin constant domain, a transmembrane region, and a short cytoplasmic tail at the C-terminal end (*see Janeway et al., Immunobiology: The Immune System in Health and Disease*, 3rd Ed., Current Biology Publications, p. 4:33, 1997). TCRs of the present disclosure may be from various animal species, including human, mouse, rat, cat, dog, goat, horse, or other mammals. TCRs may be cell-bound (*i.e.*, have a transmembrane region or domain) or in soluble form. TCRs include recombinantly produced, genetically engineered, fusion, or modified forms of TCRs, including for example, scTCRs, soluble TCRs, TCR fusion constructs (TRuCTM; *see*, U.S. Patent Publication No. 2017/0166622).

The term "variable region" or "variable domain" of a TCR α -chain (V_α) and β -chain (V_β), or V_γ and V_δ for $\gamma\delta$ TCRs, are involved in binding of the TCR to antigen. The V_α and V_β of a native TCR generally have similar structures, with each variable domain comprising four conserved FRs and three CDRs. The V_α domain is encoded by two separate DNA segments, the variable gene segment (V gene) and the joining gene segment (J gene); the V_β domain is encoded by three separate DNA segments, the variable gene segment (V gene), the diversity gene segment (D gene), and the joining gene segment (J gene). A single V_α or V_β domain may be sufficient to confer antigen-binding specificity.

"Major histocompatibility complex molecule" (MHC molecule) refers to a glycoprotein that delivers a peptide antigen to a cell surface. MHC class I molecules are heterodimers composed of a membrane spanning α chain (with three α domains) and a non-covalently associated β 2 microglobulin. MHC class II molecules are composed of two transmembrane glycoproteins, α and β , both of which span the membrane. Each chain has two domains. MHC class I molecules deliver peptides originating in the cytosol to the cell surface, where peptide:MHC complex is recognized

by CD8⁺ T cells. MHC class II molecules deliver peptides originating in the vesicular system to the cell surface, where they are recognized by CD4⁺ T cells. An MHC molecule may be from various animal species, including human, mouse, rat, or other mammals.

“Chimeric antigen receptor” (CAR) refers to a chimeric protein comprising two or more distinct domains and can function as a receptor when expressed on the surface of a cell. CARs are generally composed of an extracellular domain comprising a binding domain that binds a target antigen, an optional extracellular spacer domain, a transmembrane domain, and an intracellular signaling domain (*e.g.*, an immunoreceptor tyrosine-based activation motif (ITAM)-containing T cell activating motif, and optionally an intracellular costimulatory domain). In certain embodiments, an intracellular signaling domain of a CAR has an ITAM-containing T cell activating domain (*e.g.*, CD3 ζ) and an intracellular costimulatory domain (*e.g.*, CD28). In certain embodiments, a CAR is synthesized as a single polypeptide chain or is encoded by a nucleic acid molecule as a single chain polypeptide.

A variety of assays are known for identifying binding domains of the present disclosure that specifically bind a particular target, as well as determining binding domain affinities, such as Western blot, ELISA, analytical ultracentrifugation, spectroscopy, surface plasmon resonance (BIAcore®) analysis, and MHC tetramer analysis (*see also, e.g.*, Scatchard *et al.*, *Ann. N.Y. Acad. Sci.* 51:660, 1949; Wilson, *Science* 295:2103, 2002; Wolff *et al.*, *Cancer Res.* 53:2560, 1993; Altman *et al.*, *Science* 274:94-96, 1996; and U.S. Patent Nos. 5,283,173, 5,468,614, or the equivalent). As used herein, “specifically binds” refers to an association or union of a binding domain, or a fusion protein thereof, to a target molecule with an affinity or K_a (*i.e.*, an equilibrium association constant of a particular binding interaction with units of 1/M) equal to or greater than 10^5 M^{-1} , while not significantly associating or uniting with any other molecules or components in a sample.

The terms “antigen” and “Ag” refer to a molecule that is capable of inducing an immune response. The immune response that is induced may involve antibody production, the activation of specific immunologically-competent cells, or both. Macromolecules, including proteins, glycoproteins, and glycolipids, can serve as an antigen. Antigens can be derived from recombinant or genomic DNA. As

contemplated herein, an antigen need not be encoded (i) solely by a full length nucleotide sequence of a gene or (ii) by a “gene” at all. An antigen can be generated or synthesized, or an antigen can be derived from a biological sample. Such a biological sample can include, but is not limited, to a tissue sample, a tumor sample, a cell, or a biological fluid.

The term “epitope” or “antigenic epitope” includes any molecule, structure, amino acid sequence or protein determinant within an antigen that is specifically bound by a cognate immune binding molecule, such as an antibody or fragment thereof (*e.g.*, scFv), T cell receptor (TCR), CAR, chimeric engulfment receptor, or other binding molecule, domain or protein. Epitopic determinants generally contain chemically active surface groupings of molecules, such as amino acids or sugar side chains, and can have specific three dimensional structural characteristics, as well as specific charge characteristics. An epitope may be a linear epitope or a conformational epitope.

As used herein, an “effector domain” is an intracellular portion of a fusion protein or chimeric receptor that can directly or indirectly promote a biological or physiological response in a cell expressing the effector domain when receiving the appropriate signal. In certain embodiments, an effector domain is part of a protein or protein complex that receives a signal when bound. In other embodiments, the effector domain is part of a protein or protein complex that binds directly to a target molecule, which triggers a signal from the effector domain. For example, in response to binding of the CER to a target molecule, the effector domain may transduce a signal to the interior of the host cell, eliciting an effector function, *e.g.*, engulfment, phagolysosome maturation, or secretion of anti-inflammatory, and/or immunosuppressive cytokines. An effector domain may directly promote a cellular response when it contains one or more signaling domains or motifs. In other embodiments, an effector domain will indirectly promote a cellular response by associating with one or more other proteins that directly promote a cellular response.

An “engulfment signaling domain” refers to an intracellular effector domain, which, upon binding of the target molecule (*e.g.*, phosphatidylserine) targeted by the extracellular domain of a CER expressed by a host cell, activates one or more signaling pathways in the host cell resulting in engulfment, including, in specific

embodiments, cytoskeletal rearrangement of the host cell and internalization of the target cell or particle associated with the target antigen. In certain embodiments, an engulfment signaling domain activates one or more signaling pathways resulting in phagocytosis of the target cell or particle. In further embodiments, an engulfment signaling domain comprises a primary engulfment signaling domain and a secondary engulfment signaling domain.

"Junction amino acids" or "junction amino acid residues" refer to one or more (*e.g.*, about 2-20) amino acid residues between two adjacent motifs, regions or domains of a polypeptide. Junction amino acids may result from the construct design of a chimeric protein (*e.g.*, amino acid residues resulting from the use of a restriction enzyme site during the construction of a nucleic acid molecule encoding a fusion protein).

A "disease" is a state of health of a subject wherein the subject cannot maintain homeostasis, and wherein, if the disease is not ameliorated, then the subject's health continues to deteriorate. In contrast, a "disorder" or "undesirable condition" in a subject is a state of health in which the subject is able to maintain homeostasis, but in which the subject's state of health is less favorable than it would be in the absence of the disorder or undesirable condition. Left untreated, a disorder or undesirable condition does not necessarily result in a further decrease in the subject's state of health.

"Nucleic acid molecule" and "polynucleotide" can be in the form of RNA or DNA, which includes cDNA, genomic DNA, and synthetic DNA. A nucleic acid molecule may be composed of naturally occurring nucleotides (such as deoxyribonucleotides and ribonucleotides), analogs of naturally occurring nucleotides (*e.g.*, α -enantiomeric forms of naturally occurring nucleotides), or a combination of both. Modified nucleotides can have "modifications in or replacement of sugar moieties, or pyrimidine or purine base moieties. Nucleic acid monomers can be linked by phosphodiester bonds or analogs of such linkages. Analogs of phosphodiester linkages include phosphorothioate, phosphorodithioate, phosphoroselenoate, phosphorodiselenoate, phosphoroanilothioate, phosphoranilidate, phosphoramidate, and the like. A nucleic acid molecule may be double stranded or single stranded, and if single stranded, may be the coding strand or non-coding (anti-sense strand). A coding

molecule may have a coding sequence identical to a coding sequence known in the art or may have a different coding sequence, which, as the result of the redundancy or degeneracy of the genetic code, or by splicing, can encode the same polypeptide.

“Encoding” refers to the inherent property of specific polynucleotide sequences, such as DNA, cDNA, and mRNA sequences, to serve as templates for synthesis of other polymers and macromolecules in biological processes having either a defined sequence of nucleotides (*i.e.*, rRNA, tRNA and mRNA) or a defined sequence of amino acids and the biological properties resulting therefrom. Thus, a polynucleotide encodes a protein if transcription and translation of mRNA corresponding to that polynucleotide produces the protein in a cell or other biological system. Both a coding strand and a non-coding strand can be referred to as encoding a protein or other product of the polynucleotide. Unless otherwise specified, a “nucleotide sequence encoding an amino acid sequence” includes all nucleotide sequences that are degenerate versions of each other and that encode the same amino acid sequence.

As used herein, the term "endogenous" or "native" refers to a gene, protein, compound, molecule or activity that is normally present in a host or host cell, including naturally occurring variants of the gene, protein, compound, molecule, or activity.

As used herein, "homologous" or "homolog" refers to a molecule or activity from a host cell that is related by ancestry to a second gene or activity, *e.g.*, from the same host cell, from a different host cell, from a different organism, from a different strain, from a different species. For example, a heterologous molecule or heterologous gene encoding the molecule may be homologous to a native host cell molecule or gene that encodes the molecule, respectively, and may optionally have an altered structure, sequence, expression level or any combination thereof.

As used herein, "heterologous" nucleic acid molecule, construct or sequence refers to a nucleic acid molecule or portion of a nucleic acid molecule that is not native to a host cell, but can be homologous to a nucleic acid molecule or portion of a nucleic acid molecule from the host cell. The source of the heterologous nucleic acid molecule, construct or sequence can be from a different genus or species. In some embodiments, the heterologous nucleic acid molecules are not naturally occurring. In

certain embodiments, a heterologous nucleic acid molecule is added (*i.e.*, not endogenous or native) into a host cell or host genome by, for example, conjugation, transformation, transfection, transduction, electroporation, or the like, wherein the added molecule can integrate into the host cell genome or exist as extra-chromosomal genetic material (*e.g.*, as a plasmid or other form of self-replicating vector), and can be present in multiple copies. In addition, "heterologous" refers to a non-native enzyme, protein or other activity encoded by a non-endogenous nucleic acid molecule introduced into the host cell, even if the host cell encodes a homologous protein or activity.

As used herein, the term "engineered," "recombinant," "modified" or "non-natural" refers to an organism, microorganism, cell, nucleic acid molecule, or vector that has been modified by introduction of a heterologous nucleic acid molecule, or refers to a cell or microorganism that has been genetically engineered by human intervention—that is, modified by introduction of a heterologous nucleic acid molecule, or refers to a cell or microorganism that has been altered such that expression of an endogenous nucleic acid molecule or gene is controlled, deregulated or constitutive, where such alterations or modifications can be introduced by genetic engineering. Human-generated genetic alterations can include, for example, modifications introducing nucleic acid molecules (which may include an expression control element, such as a promoter) encoding one or more proteins, chimeric receptors, or enzymes, or other nucleic acid molecule additions, deletions, substitutions, or other functional disruption of or addition to a cell's genetic material. Exemplary modifications include those in coding regions or functional fragments thereof heterologous or homologous polypeptides from a reference or parent molecule. Additional exemplary modifications include, for example, modifications in non-coding regulatory regions in which the modifications alter expression of a gene or operon.

As used here, the term "transgene" refers to a gene or polynucleotide encoding a protein of interest (*e.g.*, CER, CAR, TCR) whose expression is desired in a host cell and that has been transferred by genetic engineering techniques into a cell. A transgene may encode proteins of therapeutic interest as well as proteins that are reporters, tags, markers, suicide proteins, etc. A transgene may be from a natural

source, modification of a natural gene, or a recombinant or synthetic molecule. In certain embodiments, a transgene is a component of a vector.

The term “overexpressed” or “overexpression” of an antigen refers to an abnormally high level of antigen expression in a cell. Overexpressed antigen or overexpression of antigen is often associated with a disease state, such as in hematological malignancies and cells forming a solid tumor within a specific tissue or organ of a subject. Solid tumors or hematological malignancies characterized by overexpression of a tumor antigen can be determined by standard assays known in the art.

As used herein, the terms “peptide,” “polypeptide,” and “protein” are used interchangeably, and refer to a compound comprised of amino acid residues covalently linked by peptide bonds. A protein or peptide must contain at least two amino acids, and no limitation is placed on the maximum number of amino acids that can comprise a protein's or peptide's sequence. Polypeptides include any peptide or protein comprising two or more amino acids joined to each other by peptide bonds. As used herein, the term refers to both short chains, which also commonly are referred to in the art as peptides, oligopeptides and oligomers, for example, and to longer chains, which generally are referred to in the art as proteins, of which there are many types. “Polypeptides” include, for example, biologically active fragments, substantially homologous polypeptides, oligopeptides, homodimers, heterodimers, variants of polypeptides, modified polypeptides, derivatives, analogs, fusion proteins, among others. The polypeptides include natural peptides, recombinant peptides, synthetic peptides, or a combination thereof.

As used herein, the term “mature polypeptide” or “mature protein” refers to a protein or polypeptide that is secreted or localized in the cell membrane or inside certain cell organelles (*e.g.*, the endoplasmic reticulum, golgi, or endosome) and does not include an N-terminal signal peptide.

A “signal peptide”, also referred to as “signal sequence”, “leader sequence”, “leader peptide”, “localization signal” or “localization sequence”, is a short peptide (usually 15-30 amino acids in length) present at the N-terminus of newly synthesized proteins that are destined for the secretory pathway. A signal peptide typically comprises a short stretch of hydrophilic, positively charged amino acids at the

N-terminus, a central hydrophobic domain of 5-15 residues, and a C-terminal region with a cleavage site for a signal peptidase. In eukaryotes, a signal peptide prompts translocation of the newly synthesized protein to the endoplasmic reticulum where it is cleaved by the signal peptidase, creating a mature protein that then proceeds to its appropriate destination.

The "percent identity" between two or more nucleic acid or amino acid sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % identity = number of identical positions/total number of positions x 100), taking into account the number of gaps, and the length of each gap that needs to be introduced to optimize alignment of two or more sequences. The comparison of sequences and determination of percent identity between two or more sequences can be accomplished using a mathematical algorithm, such as BLAST and Gapped BLAST programs at their default parameters (*e.g.*, Altschul *et al.*, *J. Mol. Biol.* 215:403, 1990; see also BLASTN at www.ncbi.nlm.nih.gov/BLAST).

A "conservative substitution" is recognized in the art as a substitution of one amino acid for another amino acid that has similar properties. Exemplary conservative substitutions are well known in the art (*see, e.g.*, WO 97/09433, page 10, published March 13, 1997; Lehninger, *Biochemistry*, Second Edition; Worth Publishers, Inc. NY:NY (1975), pp.71-77; Lewin, *Genes IV*, Oxford University Press, NY and Cell Press, Cambridge, MA (1990), p. 8).

The term "chimeric" refers to any nucleic acid molecule or protein that is not endogenous and comprises a combination of sequences joined or linked together that are not naturally found joined or linked together in nature. For example, a chimeric nucleic acid molecule may comprise nucleic acids encoding various domains from multiple different genes. In another example, a chimeric nucleic acid molecule may comprise regulatory sequences and coding sequences that are derived from different sources, or regulatory sequences and coding sequences that are derived from the same source but arranged in a manner different than that found in nature.

The term "promoter" as used herein is defined as a DNA sequence recognized by the synthetic machinery of the cell, or introduced synthetic machinery, required to initiate the specific transcription of a polynucleotide sequence.

As used herein, the term “promoter/regulatory sequence” means a nucleic acid sequence which is required for expression of a gene product operably linked to the promoter/regulatory sequence. In some instances, this sequence may be the core promoter sequence and in other instances, this sequence may also include an enhancer sequence and other regulatory elements which are required for expression of the gene product. The promoter/regulatory sequence may, for example, be one which expresses the gene product in a tissue specific manner.

A “constitutive” promoter is a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a cell under most or all physiological conditions of the cell.

An “inducible” promoter is a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a cell substantially only when an inducer which corresponds to the promoter is present in the cell.

A “tissue-specific” promoter is a nucleotide sequence which, when operably linked with a polynucleotide encodes or specified by a gene, causes the gene product to be produced in a cell substantially only if the cell is a cell of the tissue type corresponding to the promoter.

The phrase “under transcriptional control” or “operatively linked” as used herein means that a promoter is in the correct location and orientation in relation to a polynucleotide to control the initiation of transcription by RNA polymerase and expression of the polynucleotide.

A “vector” is a nucleic acid molecule that is capable of transporting another nucleic acid. Vectors may be, for example, plasmids, cosmids, viruses, or phage. The term should also be construed to include non-plasmid and non-viral compounds which facilitate transfer of nucleic acid into cells. An “expression vector” is a vector that is capable of directing the expression of a protein encoded by one or more genes carried by the vector when it is present in the appropriate environment.

In certain embodiments, the vector is a viral vector. Examples of viral vectors include, but are not limited to, adenovirus vectors, adeno-associated virus vectors, retrovirus vectors, gammaretrovirus vectors, and lentivirus vectors.

"Retroviruses" are viruses having an RNA genome. "Gammaretrovirus" refers to a genus of the retroviridae family. Examples of gammaretroviruses include mouse stem cell virus, murine leukemia virus, feline leukemia virus, feline sarcoma virus, and avian reticuloendotheliosis viruses. "Lentivirus" refers to a genus of retroviruses that are capable of infecting dividing and non-dividing cells. Examples of lentiviruses include, but are not limited to HIV (human immunodeficiency virus, including HIV type 1 and HIV type 2, equine infectious anemia virus, feline immunodeficiency virus (FIV), bovine immune deficiency virus (BIV), and simian immunodeficiency virus (SIV).

In other embodiments, the vector is a non-viral vector. Examples of non-viral vectors include lipid-based DNA vectors, modified mRNA (modRNA), self-amplifying mRNA, closed-ended linear duplex (CELiD) DNA, and transposon-mediated gene transfer (PiggyBac, Sleeping Beauty). Where a non-viral delivery system is used, the delivery vehicle can be a liposome. Lipid formulations can be used to introduce nucleic acids into a host cell *in vitro*, *ex vivo*, or *in vivo*. The nucleic acid may be encapsulated in the interior of a liposome, interspersed within the lipid bilayer of a liposome, attached to a liposome via a linking molecule that is associated with both the liposome and the nucleic acid, contained or complexed with a micelle, or otherwise associated with a lipid.

As used herein, the term "expression cassette" refers to a distinct component of a vector nucleic acid comprising at least one transgene and regulatory sequences controlling its expression (*e.g.*, promoter, 3'UTR) in a host cell. A tandem expression cassette refers to a component of a vector nucleic acid comprising at least two transgenes under the control of the same set of regulatory sequences for tandem expression of the at least two transgenes. In certain embodiments, the tandem expression cassette comprises at least two transgenes under the control of the same promoter. In certain embodiments, the first transgene and second transgene are separated by an internal ribosome entry site (IRES), furin cleavage site, or self-cleaving viral 2A peptide to allow for co-expression of two proteins from a single mRNA.

A "particle" refers to a fragment of a cell or a small object of at least 10 nm and up to 50 μ m in diameter. A particle may be derived from a living cell or organism, the environment, or synthetic. A particle can be a viral particle, prion particle, protein particle, synthetic particle, small mineral particle, or cellular debris.

As used herein, the term “engulfment” refers to a receptor-mediated process wherein endogenous or exogenous cells or particles greater than 10 nm in diameter are internalized by a phagocyte or host cell of the present disclosure. Engulfment is typically composed of multiple steps: (1) tethering of the target cell or particle via binding of an engulfment receptor to a pro-engulfment marker or antigenic marker directly or indirectly (via a bridging molecule) on a target cell or particle; and (2) internalization or engulfment of the whole target cell or particle, or a portion thereof. In certain embodiments, internalization may occur via cytoskeletal rearrangement of a phagocyte or host cell to form a phagosome, a membrane-bound compartment containing the internalized target. Engulfment may further include maturation of the phagosome, wherein the phagosome becomes increasingly acidic and fuses with lysosomes (to form a phagolysosome), whereupon the engulfed target is degraded (*e.g.*, “phagocytosis”). Alternatively, phagosome-lysosome fusion may not be observed in engulfment. In yet another embodiment, a phagosome may regurgitate or discharge its contents to the extracellular environment before complete degradation. In some embodiments, engulfment refers to phagocytosis. In some embodiments, engulfment includes tethering of the target cell or particle by the phagocyte or host cell of the present disclosure, but not internalization. In some embodiments, engulfment includes tethering of the target cell or particle by the phagocyte or host cell of the present disclosure and internalization of part of the target cell or particle.

As used herein, the term “phagocytosis” refers to an engulfment process of cells or large particles ($\geq 0.5 \mu\text{m}$) wherein tethering of a target cell or particle, engulfment of the target cell or particle, and degradation of the internalized target cell or particle occurs. In certain embodiments, phagocytosis comprises formation of a phagosome that encompasses the internalized target cell or particle and phagosome fusion with a lysosome to form a phagolysosome, wherein the contents therein are degraded. In certain embodiments, following binding of a CER expressed on a host cell of the present disclosure to a target antigen expressed by a target cell or particle, a phagocytic synapse is formed; an actin-rich phagocytic cup is generated at the phagocytic synapse; phagocytic arms are extended around the target cell or particle through cytoskeletal rearrangements; and ultimately, the target cell or particle is pulled into the phagocyte or host cell through force generated by motor proteins. As used

herein, “phagocytosis” includes the process of “efferocytosis”, which specifically refers to the phagocytosis of apoptotic or necrotic cells in a non-inflammatory manner.

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

The term “T cells” refers to cells of T cell lineage. “Cells of T cell lineage” refer to cells that show at least one phenotypic characteristic of a T cell or a precursor or progenitor thereof that distinguishes the cells from other lymphoid cells, and cells of the erythroid or myeloid lineages. Such phenotypic characteristics can include expression of one or more proteins specific for T cells (*e.g.*, CD3⁺, CD4⁺, CD8⁺), or a physiological, morphological, functional, or immunological feature specific for a T cell. For example, cells of the T cell lineage may be progenitor or precursor cells committed to the T cell lineage; CD25⁺ immature and inactivated T cells; cells that have undergone CD4 or CD8 lineage commitment; thymocyte progenitor cells that are CD4⁺CD8⁺ double positive; single positive CD4⁺ or CD8⁺; TCR $\alpha\beta$ or TCR $\gamma\delta$; or mature and functional or activated T cells. The term “T cells” encompasses naïve T cells (CD45 RA⁺, CCR7⁺, CD62L⁺, CD27⁺, CD45RO⁻), central memory T cells (CD45RO⁺, CD62L⁺, CD8⁺), effector memory T cells (CD45RA⁺, CD45RO⁻, CCR7⁻, CD62L⁻, CD27⁻), mucosal-associated invariant T (MAIT) cells, Tregs, natural killer T cells, and tissue resident T cells.

The term “B cells” refers to cells of the B cell lineage. “Cells of B cell lineage” refers to cells that show at least one phenotypic characteristic of a B cell or a precursor or progenitor thereof that distinguishes the cells from other lymphoid cells,

and cells of the erythroid or myeloid lineages. Such phenotypic characteristics can include expression of one or more proteins specific for B cells (*e.g.*, CD19⁺, CD72⁺, CD24⁺, CD20⁺), or a physiological, morphological, functional, or immunological feature specific for a B cell. For example, cells of the B cell lineage may be progenitor or precursor cells committed to the B cell lineage (*e.g.*, pre-pro-B cells, pro-B cells, and pre-B cells); immature and inactivated B cells or mature and functional or activated B cells. Thus, “B cells” encompass naïve B cells, plasma cells, regulatory B cells, marginal zone B cells, follicular B cells, lymphoplasmacytoid cells, plasmablast cells, and memory B cells (*e.g.*, CD27⁺, IgD⁺).

The term “cytotoxic activity,” also referred to as “cytolytic activity,” with respect to a cell (*e.g.*, T cell) that expresses an immune receptor (*e.g.*, TCR) on its surface, means that upon antigen-specific signaling (*e.g.*, via the TCR) the cell induces a target cell to undergo apoptosis. In some embodiments, a cytotoxic cell may induce apoptosis in a target cell via the release of cytotoxins, such as perforin, granzyme, and granulysin, from granules. Perforins insert into the target cell membrane and form pores that allow water and salts to rapidly enter the target cell. Granzymes are serine proteases that induce apoptosis in the target cell. Granulysin is also capable of forming pores in the target cell membrane and is a proinflammatory molecule. In some embodiments, a cytotoxic cell may induce apoptosis in a target cell via interaction of Fas ligand, which is upregulated on T cell following antigen-specific signaling, with Fas molecules expressed on the target cell. Fas is an apoptosis-signaling receptor molecule on the surface of a number of different cells.

A “disease” is a state of health of a subject wherein the subject cannot maintain homeostasis, and wherein, if the disease is not ameliorated, then the subject’s health continues to deteriorate. In contrast, a “disorder” or “undesirable condition” in a subject is a state of health in which the subject is able to maintain homeostasis, but in which the subject’s state of health is less favorable than it would be in the absence of the disorder or undesirable condition. Left untreated, a disorder or undesirable condition does not necessarily result in a further decrease in the subject’s state of health.

The term “cancer” as used herein is defined as disease characterized by the rapid and uncontrolled growth of aberrant cells. The aberrant cells may form solid

tumors or constitute a hematological malignancy. Cancer cells can spread locally or through the bloodstream and lymphatic system to other parts of the body. Examples of various cancers include, but are not limited to, breast cancer, prostate cancer, ovarian cancer, cervical cancer, skin cancer, pancreatic cancer, colorectal cancer, renal cancer, liver cancer, brain cancer, lymphoma, leukemia, lung cancer and the like.

The term “subject,” “patient” and “individual” are used interchangeably herein and are intended to include living organisms in which an immune response can be elicited (*e.g.*, mammals). Examples of subjects include humans, primates, cows, horses, goats, sheep, dogs, cats, mice, rats, rabbits, guinea pigs, pigs, and transgenic species thereof.

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

“Autologous” refers to a graft (*e.g.*, organ, tissue, cells) derived from the same subject to which it is later to be re-introduced.

“Allogeneic” refers to a graft derived from a different subject of the same species.

A “therapeutically effective amount” or “effective amount” of a chimeric protein or cell expressing a chimeric protein of this disclosure (*e.g.*, a tandem expression cassette or a cell expressing a tandem expression cassette) refers to that amount of protein or cells sufficient to result in amelioration of one or more symptoms of the disease, disorder, or undesired condition being treated. When referring to an individual active ingredient or a cell expressing a single active ingredient, administered alone, a therapeutically effective dose refers to the effects of that ingredient or cell expressing that ingredient alone. When referring to a combination, a therapeutically effective dose refers to the combined amounts of active ingredients or combined adjunctive active ingredient with a cell expressing an active ingredient that results in a therapeutic effect, whether administered serially or simultaneously.

"Treat" or "treatment" or "ameliorate" refers to medical management of a disease, disorder, or undesired condition of a subject. In general, an appropriate dose or treatment regimen comprising a host cell expressing a chimeric protein of this disclosure is administered in an amount sufficient to elicit a therapeutic or prophylactic benefit. Therapeutic or prophylactic/preventive benefit includes improved clinical outcome; lessening or alleviation of symptoms associated with a disease, disorder, or undesired condition; decreased occurrence of symptoms; improved quality of life; longer disease-free status; diminishment of extent of disease, disorder, or undesired condition; stabilization of disease state; delay of disease progression; remission; survival; prolonged survival; or any combination thereof.

The term "anti-tumor effect" refers to a biological effect which can be manifested by a decrease in tumor volume, a decrease in the number of tumor cells, a decrease in the number of metastases, an increase in life expectancy, or amelioration of various physiological symptoms associated with a cancerous condition. An "anti-tumor effect" can also be manifested by prevention of a hematological malignancy or tumor formation.

Additional definitions are provided throughout the present disclosure.

Transgenes

Tandem expression cassettes of the present disclosure comprise at least two transgenes encoding a chimeric engulfment receptor (CER) and a chimeric antigen receptor (CAR)/or a T cell receptor (TCR). Certain embodiments of the tandem expression cassettes provided herein comprise: (a) a polynucleotide encoding a CER comprising: an extracellular domain comprising a binding domain that binds to a target antigen; an engulfment signaling domain; and a transmembrane domain positioned between and connecting the extracellular domain and the engulfment signaling domain; and (b) a polynucleotide encoding a CAR comprising an extracellular domain comprising a binding domain that binds to a target antigen; an intracellular signaling domain; and a transmembrane domain positioned between and connecting the extracellular domain and the intracellular signaling domain. Other embodiments of the tandem expression cassettes provided herein comprise: (a) a polynucleotide encoding a CER comprising: an extracellular domain comprising a binding domain that binds to a

target antigen; an engulfment signaling domain; and a transmembrane domain positioned between and connecting the extracellular domain and the engulfment signaling domain; and (b) a polynucleotide encoding a recombinant TCR binding protein. In certain embodiments, the polynucleotide encoding the CER is positioned 5' to the polynucleotide encoding the CAR or TCR. In other embodiments, the polynucleotide encoding the CER is positioned 3' to the polynucleotide encoding the CAR or TCR.

Further aspects of the transgenes and their encoded cellular immunotherapy molecules are provided as follows.

I. Chimeric Engulfment Receptors (CERs)

Tandem expression cassettes of the present disclosure comprise at least one polynucleotide encoding a CER. Chimeric engulfment receptors generally comprise: (a) an extracellular domain comprising a binding domain that binds to a target antigen, (b) an engulfment signaling domain; and (c) a transmembrane domain positioned between and connecting the extracellular domain and the engulfment signaling domain. In certain embodiments, the extracellular domain of the chimeric engulfment receptors described herein optionally includes an extracellular spacer domain positioned between and connecting the binding domain and transmembrane domain.

Chimeric engulfment receptors described herein are capable of conferring an engulfment phenotype that is specific for a target antigen to a host cell that is modified to express said chimeric engulfment receptor. In certain embodiments, expression of a CER as described herein confers an engulfment phenotype to a host cell that does not naturally exhibit an engulfment phenotype. In certain embodiments, the engulfment activity is phagocytic activity. CERs of the present disclosure may be used to redirect engulfment specificity to target cells that express the targeted antigen.

Extracellular Domains

As described herein, a CER comprises an extracellular domain specific to a target antigen. In certain embodiments, the extracellular domain comprises a

binding domain that specifically binds a target antigen (*e.g.*, phosphatidylserine). Binding of a target molecule by the binding domain may block the interaction between the target molecule (*e.g.*, a receptor or a ligand) and another molecule and, for example, interfere with, reduce or eliminate certain functions of the target molecule (*e.g.*, signal transduction). In some embodiments, the binding of a target molecule may induce certain biological pathways or identify the target molecule or cell expressing the target molecule for elimination.

A binding domain suitable for use in a CER of the present disclosure may be any polypeptide or peptide that specifically binds a target molecule of interest, *e.g.*, phosphatidylserine. Sources of binding domains include extracellular domains of receptors, ligands for cell surface receptors or molecules, and antibodies or antigen binding portions, such as antibody variable regions from various species. For example a binding domain may comprise a, sFv, scFv, Fab, scFv-based grababody, VH domain, VL domain, single domain camelid antibody (VHH), or domain antibody. A binding domain may be derived from a human, primate, rodent, avian, or ovine. Additional sources of binding domains include variable regions of antibodies from other species, such as camelid (from camels, dromedaries, or llamas; Ghahroudi *et al.*, *FEBS Lett.* 414:521, 1997; Vincke *et al.*, *J. Biol. Chem.* 284:3273, 2009; Hamers-Casterman *et al.*, *Nature* 363:446, 1993 and Nguyen *et al.*, *J. Mol. Biol.* 275:413, 1998), nurse sharks (Roux *et al.*, *Proc. Nat'l. Acad. Sci. (USA)* 95:11804, 1998), spotted ratfish (Nguyen *et al.*, *Immunogen.* 54:39, 2002), or lamprey (Herrin *et al.*, *Proc. Nat'l. Acad. Sci. (USA)* 105:2040, 2008 and Alder *et al.* *Nat. Immunol.* 9:319, 2008). These antibodies can form antigen-binding regions using only a heavy chain variable region, *i.e.*, these functional antibodies are homodimers of heavy chains only (referred to as "heavy chain antibodies") (Jespers *et al.*, *Nat. Biotechnol.* 22:1161, 2004; Cortez-Retamozo *et al.*, *Cancer Res.* 64:2853, 2004; Baral *et al.*, *Nature Med.* 12:580, 2006; and Barthelemy *et al.*, *J. Biol. Chem.* 283:3639, 2008). In certain embodiments, a binding domain is murine, chimeric, human, or humanized.

In certain embodiments, the CER binding domain comprises an antibody or antigen binding fragment thereof, such as a single chain Fv fragment (scFv) that comprises VH and VL regions, specific for a target disease antigen. In certain

embodiments, the antibody or antigen binding fragment is chimeric, human, or humanized. In further embodiments, the V_H and V_L regions are human or humanized.

A target molecule that is bound by an extracellular domain of a CER of the present disclosure, may be found on or in association with a cell of interest ("target cell"). Exemplary target cells include a cancer cell, a cell associated with an autoimmune disease or disorder or with an inflammatory disease or disorder, an infectious microbe (*e.g.*, bacteria, virus, or fungi), and an infected cell (*e.g.*, virus-infected cell). A cell of an infectious organism, such as a mammalian parasite, is also contemplated as a target cell.

In certain embodiments, the extracellular domain binds to a pro-engulfment marker. As used herein, a pro-engulfment marker is a moiety (*e.g.*, protein, lipid, or polysaccharide) that an apoptotic, necrotic, pyroptotic, or infected cell exhibits on its surface that distinguishes it from a non-apoptotic, non-necrotic, non-pyroptotic, oncotic, or uninfected cell, respectively. A pro-engulfment marker can be an intracellular moiety that is surface exposed on an apoptotic or necrotic cell, a moiety that has altered glycosylation or altered surface charge on an apoptotic or necrotic cell, or a serum moiety that is bound to an apoptotic, necrotic, pyroptotic, or oncotic cell. Examples of pro-engulfment markers for apoptotic cells include phosphatidylserine (PtdSer), ICAM-3, oxidized low density lipoprotein, calreticulin, annexin I, complement C1q, and thrombospondin. Necrotic, oncotic, and pyroptotic cells also expose PtdSer pro-engulfment markers on the cell surface. Engulfment receptors can detect (or bind) a pro-engulfment marker on a target cell (*e.g.*, a damaged, infected, apoptotic, necrotic, pyroptotic, or oncotic cell) directly or indirectly using soluble bridging molecules as intermediaries that bind to the pro-engulfment marker. In certain such embodiments, the pro-engulfment marker targeted by the extracellular domain is phosphatidylserine (PtdSer), ICAM-3, oxidized low density lipoprotein, calreticulin, annexin I, complement C1q, or thrombospondin. Exemplary Tim4 binding domains that bind to phosphatidylserine include amino acid sequences comprising SEQ ID NO:91, SEQ ID NO:96, amino acids 23-279 of SEQ ID NO:91, or amino acids 25-314 of SEQ ID NO:96.

In certain embodiments, the extracellular domain binds to a tumor antigen. Exemplary tumor antigens include CD138, CD38, CD33, CD123, CD72,

CD79a, CD79b, mesothelin, PSMA, BCMA, ROR1, MUC-16, L1CAM, CD22, CD19, CD20, CD23, CD24, CD37, CD30, CA125, CD56, c-Met, EGFR, GD-3, HPV E6, HPV E7, MUC-1, HER2, folate receptor α , CD97, CD171, CD179a, CD44v6, WT1, VEGF- α , VEGFR1, IL-13R α 1, IL-13R α 2, IL-11R α , PSA, FcRH5, NKG2D ligand, NY-ESO-1, TAG-72, CEA, ephrin A2, ephrin B2, Lewis A antigen, Lewis Y antigen, MAGE, MAGE-A1, RAGE-1, folate receptor β , EGFRviii, VEGFR-2, LGR5, SSX2, AKAP-4, FLT3, fucosyl GM1, GM3, o-acetyl-GD2, and GD2.

In certain embodiments, the extracellular domain binds to a viral antigen, bacterial antigen, fungal antigen, protozoan antigen, or parasitic antigen.

In certain embodiments, the extracellular domain optionally comprises an extracellular, non-signaling spacer or linker domain. Where included, such a spacer or linker domain may position the binding domain away from the host cell surface to further enable proper cell to cell contact, binding, and activation. An extracellular spacer domain is generally located between the extracellular binding domain and the transmembrane domain of the CER. The length of the extracellular spacer may be varied to optimize target molecule binding based on the selected target molecule, selected binding epitope, binding domain size and affinity (*see, e.g., Guest et al., J. Immunother.* 28:203-11, 2005; PCT Publication No. WO 2014/031687). In certain embodiments, an extracellular spacer domain is an immunoglobulin hinge region (*e.g., IgG1, IgG2, IgG3, IgG4, IgA, IgD*). An immunoglobulin hinge region may be a wild type immunoglobulin hinge region or an altered wild type immunoglobulin hinge region. An altered IgG₄ hinge region is described in PCT Publication No. WO 2014/031687, which hinge region is incorporated herein by reference in its entirety. In a particular embodiment, an extracellular spacer domain comprises a modified IgG₄ hinge region having an amino acid sequence of ESKYGPPCPPCP (SEQ ID NO:63).

Other examples of hinge regions that may be used in the CERs described herein include the hinge region from the extracellular regions of type 1 membrane proteins, such as CD8a, CD4, CD28 and CD7, which may be wild-type or variants thereof. In further embodiments, an extracellular spacer domain comprises all or a portion of an immunoglobulin Fc domain selected from: a CH1 domain, a CH2 domain, a CH3 domain, or combinations thereof (*see, e.g., PCT Publication WO2014/031687*,

which spacers are incorporated herein by reference in their entirety). In yet further embodiments, an extracellular spacer domain may comprise a stalk region of a type II C-lectin (the extracellular domain located between the C-type lectin domain and the transmembrane domain). Type II C-lectins include CD23, CD69, CD72, CD94, NKG2A, and NKG2D. In yet further embodiments, an extracellular spacer domain may be derived from a toll-like receptor (TLR) juxtamembrane domain. A TLR juxtamembrane domain comprises acidic amino acids lying between the leucine rich repeats (LRRs) and the transmembrane domain of a TLR. In certain embodiments, a TLR juxtamembrane domain is a TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, or TLR9 juxtamembrane domain. An exemplary TLR juxtamembrane domain is a TLR4 juxtamembrane domain comprising an amino acid sequence of SEQ ID NO:1.

Extracellular domains may be derived from any mammalian species, including humans, primates, cows, horses, goats, sheep, dogs, cats, mice, rats, rabbits, guinea pigs, pigs, and transgenic species thereof. In certain embodiments, an extracellular domain is murine, chimeric, human, or humanized.

Engulfment Signaling Domains

The engulfment signaling domain of a CER is an intracellular effector domain and is capable of transmitting functional signals to a cell in response to binding of the extracellular domain of the CER to a target molecule. The engulfment signaling domain may be any portion of an engulfment signaling molecule that retains sufficient signaling activity. In some embodiments, a full length or full length intracellular component of an engulfment signaling molecule is used. In some embodiments, a truncated portion of an engulfment signaling molecule or intracellular component of an engulfment signaling molecule is used, provided that the truncated portion retains sufficient signal transduction activity. In further embodiments, an engulfment signaling domain is a variant of an entire or truncated portion of an engulfment signaling molecule, provided that the variant retains sufficient signal transduction activity (*i.e.*, is a functional variant).

Exemplary engulfment signaling domains that may be used in a CER include a MRC1 signaling domain, a MERTK signaling domain, a Tyro3 signaling

domain, an Axl signaling domain, an ELMO signaling domain, a Traf6 signaling domain, a Syk signaling domain, a MyD88 signaling domain, a PI3K signaling domain, a FcR signaling domain (*e.g.*, FcγR1, FcγR2A, FcγR2C, FcγR2B2, FcγR3A, FcγR2C, FcγR3A, FcεR1, or FcαR1 signaling domain), a B-cell activating factor receptor (BAFF-R) signaling domain, a DAP12 (also referred to as TYRO Protein Tyrosine Kinase Binding Protein (TYROBP)) signaling domain, an NFAT Activating Protein With ITAM Motif 1 (NFAM1) signaling domain, a CD79b signaling domain, a TLR signaling domain (*e.g.*, TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, or TLR9 signaling domain), a Traf2 signaling domain, or a Traf3 signaling domain.

In certain embodiments, the engulfment signaling domain comprises a sequence that has at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5%, or 100% identity to a MRC1 signaling domain comprising an amino acid sequence of SEQ ID NO:2, a MERTK signaling domain comprising an amino acid sequence of SEQ ID NO:3, a Tyro3 signaling domain comprising an amino acid sequence of SEQ ID NO:5, an Axl signaling domain comprising an amino acid sequence of SEQ ID NO:6, an ELMO signaling domain comprising an amino acid sequence of SEQ ID NO:7, a Traf6 signaling domain comprising an amino acid sequence of SEQ ID NO:8, a Syk signaling domain comprising an amino acid sequence of SEQ ID NO:9, a MyD88 signaling domain comprising an amino acid sequence of SEQ ID NO:10, a PI3K signaling domain comprising an amino acid sequence of SEQ ID NO:11, a FcεRIγ signaling domain comprising an amino acid sequence of SEQ ID NO:12, a FcγR1 signaling domain comprising an amino acid sequence of SEQ ID NO:13, a FcγR2A signaling domain comprising an amino acid sequence of SEQ ID NO:14, a FcγR2C signaling domain comprising an amino acid sequence of SEQ ID NO:15, a FcγR3A signaling domain comprising an amino acid sequence of SEQ ID NO:16, a BAFF-R signaling domain comprising an amino acid sequence of SEQ ID NO:17, a DAP12 signaling domain comprising an amino acid sequence of SEQ ID NO:18, a NFAM1 signaling domain comprising an amino acid sequence of SEQ ID NO:19, a CD79b signaling domain comprising an amino acid sequence of SEQ ID NO:21, a TLR1 signaling domain

comprising an amino acid sequence of SEQ ID NO:22, a TLR2 signaling domain comprising an amino acid sequence of SEQ ID NO:23, a TLR3 signaling domain comprising an amino acid sequence of SEQ ID NO:24, a TLR4 signaling domain comprising an amino acid sequence of SEQ ID NO:25, a TLR5 signaling domain comprising an amino acid sequence of SEQ ID NO:26, a TLR6 signaling domain comprising an amino acid sequence of SEQ ID NO:27, a TLR7 signaling domain comprising an amino acid sequence of SEQ ID NO:28, a TLR8 signaling domain comprising an amino acid sequence of SEQ ID NO:29, a TLR9 signaling domain comprising an amino acid sequence of SEQ ID NO:30, a Traf2 signaling domain comprising an amino acid sequence of SEQ ID NO:31, or a Traf3 signaling domain comprising an amino acid sequence of SEQ ID NO:32.

In some embodiments, the engulfment signaling domain is an MRC1 signaling domain comprising or consisting of an amino acid sequence of SEQ ID NO:2, a MERTK signaling domain comprising or consisting of an amino acid sequence of SEQ ID NO:3, a Tyro3 signaling domain comprising or consisting of an amino acid sequence of SEQ ID NO:5, an Axl signaling domain comprising or consisting of an amino acid sequence of SEQ ID NO:6, or an ELMO signaling domain comprising or consisting of an amino acid sequence of SEQ ID NO:7, a Traf6 signaling domain comprising or consisting of an amino acid sequence of SEQ ID NO:8, a Syk signaling domain comprising or consisting of an amino acid sequence of SEQ ID NO:9, a MyD88 signaling domain comprising or consisting of an amino acid sequence of SEQ ID NO:10, a PI3K signaling domain comprising or consisting of an amino acid sequence of SEQ ID NO:11, a FcεRIγ signaling domain comprising or consisting of an amino acid sequence of SEQ ID NO:12, a FcγR1 signaling domain comprising or consisting of an amino acid sequence of SEQ ID NO:13, a FcγR2A signaling domain comprising or consisting of an amino acid sequence of SEQ ID NO:14, a FcγR2C signaling domain comprising or consisting of an amino acid sequence of SEQ ID NO:15, a FcγR3A signaling domain comprising or consisting of an amino acid sequence of SEQ ID NO:16, a BAFF-R signaling domain comprising or consisting of an amino acid sequence of SEQ ID NO:17, a DAP-12 signaling domain comprising or consisting of an

amino acid sequence of SEQ ID NO:18, a NFAM1 signaling domain comprising or consisting of an amino acid sequence of SEQ ID NO:19, a CD79b signaling domain comprising or consisting of an amino acid sequence of SEQ ID NO:21, a TLR1 signaling domain comprising or consisting of an amino acid sequence of SEQ ID NO:22, a TLR2 signaling domain comprising or consisting of an amino acid sequence of SEQ ID NO:23, a TLR3 signaling domain comprising or consisting of an amino acid sequence of SEQ ID NO:24, a TLR4 signaling domain comprising or consisting of an amino acid sequence of SEQ ID NO:25, a TLR5 signaling domain comprising or consisting of an amino acid sequence of SEQ ID NO:26, a TLR6, signaling domain comprising or consisting of an amino acid sequence of SEQ ID NO:27, a TLR7 signaling domain comprising or consisting of an amino acid sequence of SEQ ID NO:28, a TLR8, signaling domain comprising or consisting of an amino acid sequence of SEQ ID NO:29, a TLR9 signaling domain comprising or consisting of an amino acid sequence of SEQ ID NO:30, a Traf2 signaling domain comprising or consisting of an amino acid sequence of SEQ ID NO:31, or a Traf3 signaling domain comprising or consisting of an amino acid sequence of SEQ ID NO:32.

A truncated engulfment signaling domain may be truncated at its N-terminus, its C-terminus, at both the N-terminus and C-terminus. In certain embodiments, the MRC1 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:2; the MERTK engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:3; the Tyro3 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:5; the Axl engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:6; the ELMO engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:7; the Traf6 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:8; the Syk

engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:9; the MyD88 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:10; the PI3K engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:11; the FcεRIγ engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:12; the FcγR1 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:13; the FcγR2A engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:14; the FcγR2C engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:15; the FcγR3A engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:16; the BAFF-R engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:17; the DAP-12 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:18; the NFAM1 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:19; the CD79b engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:21; the TLR1 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:22; the TLR2 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:23; the TLR3 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:24; the TLR4

engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:25; the TLR5 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:26; the TLR6 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:27; the TLR7 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:28; the TLR8 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:29; the TLR9 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:30; the Traf2 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:31; or the Traf3 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its N-terminus corresponding to the amino acid sequence of SEQ ID NO:32.

In certain embodiments, the MRC1 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its C-terminus corresponding to the amino acid sequence of SEQ ID NO:2; the MERTK engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its C-terminus corresponding to the amino acid sequence of SEQ ID NO:3; the Tyro3 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its C-terminus corresponding to the amino acid sequence of SEQ ID NO:5; the Axl engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its C-terminus corresponding to the amino acid sequence of SEQ ID NO:6; the ELMO engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its C-terminus corresponding to the amino acid sequence of SEQ ID NO:7; the Traf6 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its C-terminus corresponding to the amino acid sequence of SEQ ID NO:8; the Syk engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its C-terminus corresponding to the amino acid sequence of SEQ ID NO:9; the MyD88

engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its C-terminus corresponding to the amino acid sequence of SEQ ID NO:10; the PI3K engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its C-terminus corresponding to the amino acid sequence of SEQ ID NO:11; the FcεRIγ engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its C-terminus corresponding to the amino acid sequence of SEQ ID NO:12; the FcγR1 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its C-terminus corresponding to the amino acid sequence of SEQ ID NO:13; the FcγR2A engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its C-terminus corresponding to the amino acid sequence of SEQ ID NO:14; the FcγR2C engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its C-terminus corresponding to the amino acid sequence of SEQ ID NO:15; the FcγR3A engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its C-terminus corresponding to the amino acid sequence of SEQ ID NO:16; the BAFF-R engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its C-terminus corresponding to the amino acid sequence of SEQ ID NO:17; the DAP-12 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its C-terminus corresponding to the amino acid sequence of SEQ ID NO:18; the NFAM1 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its C-terminus corresponding to the amino acid sequence of SEQ ID NO:19; the CD79b engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its C-terminus corresponding to the amino acid sequence of SEQ ID NO:21; the TLR1 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its C-terminus corresponding to the amino acid sequence of SEQ ID NO:22; the TLR2 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its C-terminus corresponding to the amino acid sequence of SEQ ID NO:23; the TLR3 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its C-terminus corresponding to the amino acid sequence of SEQ ID NO:24; the TLR4 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its C-terminus corresponding to the amino acid sequence of SEQ ID NO:25; the TLR5

engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its C-terminus corresponding to the amino acid sequence of SEQ ID NO:26; the TLR6 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its C-terminus corresponding to the amino acid sequence of SEQ ID NO:27; the TLR7 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its C-terminus corresponding to the amino acid sequence of SEQ ID NO:28; the TLR8 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its C-terminus corresponding to the amino acid sequence of SEQ ID NO:29; the TLR9 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its C-terminus corresponding to the amino acid sequence of SEQ ID NO:30; the Traf2 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its C-terminus corresponding to the amino acid sequence of SEQ ID NO:31; or the Traf3 engulfment signaling domain is truncated 1, 2, 3, 4, 5, or more amino acids at its C-terminus corresponding to the amino acid sequence of SEQ ID NO:32.

In certain embodiments, a truncated MyD88 engulfment signaling domain comprises a death domain but lacks a Toll/interleukin-1 receptor (TIR) homology domain. An example of such a truncated MyD88 engulfment signaling domain comprises an amino acid sequence of SEQ ID NO:33. In certain embodiments, a truncated MyD88 engulfment signaling domain comprises a TIR domain. An example of a truncated MyD88 engulfment signaling domain comprising a TIR domain comprises an amino acid sequence of SEQ ID NO:106. An exemplary truncated Traf6 signaling domain comprises an amino acid sequence of SEQ ID NO:34. An exemplary truncated NFAM1 signaling domain comprises an amino acid sequence of SEQ ID NO:35. An exemplary truncated CD79b signaling domain comprises an amino acid sequence of SEQ ID NO:20.

In certain embodiments, a CER comprises a first engulfment signaling domain and a second engulfment signaling domain. In some embodiments, a CER comprises a first engulfment signaling domain and a second engulfment signaling domain that are from the same molecule. In other embodiments, the first engulfment

signaling domain and the second engulfment signaling domain are from different molecules.

Engulfment signaling domains may be derived from a mammalian species, including humans, primates, cows, horses, goats, sheep, dogs, cats, mice, rats, rabbits, guinea pigs, pigs, and transgenic species thereof.

Transmembrane Domains

CERs of the present disclosure comprise a transmembrane domain that connects and is positioned between the extracellular domain and the engulfment signaling domain. The transmembrane domain is a hydrophobic alpha helix that transverses the host cell membrane and anchors the CER in the host cell membrane. The transmembrane domain may be directly fused to the binding domain or to the extracellular spacer domain if present. In certain embodiments, the transmembrane domain is derived from an integral membrane protein (*e.g.*, receptor, cluster of differentiation (CD) molecule, enzyme, transporter, cell adhesion molecule, or the like). The transmembrane domain can be selected from the same molecule as the extracellular domain or the engulfment signaling domain (*e.g.*, a CER comprising a TLR4 engulfment signaling domain and a TLR4 transmembrane domain or a CER comprising a Tim4 binding domain and a Tim4 transmembrane domain). In certain embodiments, the transmembrane domain and the extracellular domain are each selected from different molecules. In other embodiments, the transmembrane domain and the engulfment signaling domain are each selected from different molecules. In yet other embodiments, the transmembrane domain, the extracellular domain, and the engulfment signaling domain are each selected from different molecules.

In certain embodiments, the transmembrane domain comprises a Tim1, Tim4, Tim3, FcR (*e.g.*, FcγR1, FcγR2A, FcγR2B2, FcγR2C, FcγR3A, FcεR1, or FcαR1), CD8a, CD28, MERTK, Axl, Tyro3, CD4, DAP12, MRC1, TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, or TLR9 transmembrane domain.

In certain embodiments, the transmembrane domain comprises a sequence that has at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%,

96%, 97%, 98%, 99%, 99.5%, or 100% identity to a Tim1 transmembrane domain comprising an amino acid sequence of SEQ ID NO:36, Tim4 transmembrane domain comprising an amino acid sequence of SEQ ID NO:37 or 38, Tim3 transmembrane domain comprising an amino acid sequence of SEQ ID NO:39, FcγR1 transmembrane domain comprising an amino acid sequence of SEQ ID NO:40, FcγR2A transmembrane domain comprising an amino acid sequence of SEQ ID NO:41, FcγR2B2 transmembrane domain comprising an amino acid sequence of SEQ ID NO:42, FcγR2C transmembrane domain comprising an amino acid sequence of SEQ ID NO:43, FcγR3A transmembrane domain comprising an amino acid sequence of SEQ ID NO:44, FcεR1 transmembrane domain comprising an amino acid sequence of SEQ ID NO:45, FcαR1 transmembrane domain comprising an amino acid sequence of SEQ ID NO:46, CD8a transmembrane domain comprising an amino acid sequence of SEQ ID NO:47, CD28 transmembrane domain comprising an amino acid sequence of SEQ ID NO:107, MERTK transmembrane domain comprising an amino acid sequence of SEQ ID NO:48, Axl transmembrane domain comprising an amino acid sequence of SEQ ID NO:49, Tyro3 transmembrane domain comprising an amino acid sequence of SEQ ID NO:50, CD4 transmembrane domain comprising an amino acid sequence of SEQ ID NO:51, DAP12 transmembrane domain comprising an amino acid sequence of SEQ ID NO:52, MRC1 transmembrane domain comprising an amino acid sequence of SEQ ID NO:53, TLR1 transmembrane domain comprising an amino acid sequence of SEQ ID NO:54, TLR2 transmembrane domain comprising an amino acid sequence of SEQ ID NO:55, TLR3 transmembrane domain comprising an amino acid sequence of SEQ ID NO:56, TLR4 transmembrane domain comprising an amino acid sequence of SEQ ID NO:57, TLR5 transmembrane domain comprising an amino acid sequence of SEQ ID NO:58, TLR6 transmembrane domain comprising an amino acid sequence of SEQ ID NO:59, TLR7 transmembrane domain comprising an amino acid sequence of SEQ ID NO:60, TLR8 transmembrane domain comprising an amino acid sequence of SEQ ID NO:61, or TLR9 transmembrane domain comprising an amino acid sequence of SEQ ID NO:62.

In certain embodiments, the transmembrane domain is a Tim1 transmembrane domain comprising or consisting of an amino acid sequence of SEQ ID NO:36, Tim4 transmembrane domain comprising or consisting of an amino acid sequence of SEQ ID NO:37 or 38, Tim3 transmembrane domain comprising or consisting of an amino acid sequence of SEQ ID NO:39, FcγR1 transmembrane domain comprising or consisting of an amino acid sequence of SEQ ID NO:40, FcγR2A transmembrane domain comprising or consisting of an amino acid sequence of SEQ ID NO:41, FcγR2B2 transmembrane domain comprising or consisting of an amino acid sequence of SEQ ID NO:42, FcγR2C transmembrane domain comprising or consisting of an amino acid sequence of SEQ ID NO:43, FcγR3A transmembrane domain comprising or consisting of an amino acid sequence of SEQ ID NO:44, FcεR1 transmembrane domain comprising or consisting of an amino acid sequence of SEQ ID NO:45, FcαR1 transmembrane domain comprising or consisting of an amino acid sequence of SEQ ID NO:46, CD8a transmembrane domain comprising or consisting of an amino acid sequence of SEQ ID NO:47, CD28 transmembrane domain comprising or consisting of an amino acid sequence of SEQ ID NO:107, MERTK transmembrane domain comprising or consisting of an amino acid sequence of SEQ ID NO:48, Axl transmembrane domain comprising or consisting of an amino acid sequence of SEQ ID NO:49, Tyro3 transmembrane domain comprising or consisting of an amino acid sequence of SEQ ID NO:50, CD4 transmembrane domain comprising or consisting of an amino acid sequence of SEQ ID NO:51, DAP12 transmembrane domain comprising or consisting of an amino acid sequence of SEQ ID NO:52, MRC1 transmembrane domain comprising or consisting of an amino acid sequence of SEQ ID NO:53, TLR1 transmembrane domain comprising or consisting of an amino acid sequence of SEQ ID NO:54, TLR2 transmembrane domain comprising or consisting of an amino acid sequence of SEQ ID NO:55, TLR3 transmembrane domain comprising or consisting of an amino acid sequence of SEQ ID NO:56, TLR4 transmembrane domain comprising or consisting of an amino acid sequence of SEQ ID NO:57, TLR5 transmembrane domain comprising or consisting of an amino acid sequence of SEQ ID NO:58, TLR6 transmembrane domain comprising or consisting of an amino acid sequence of SEQ ID

NO:59, TLR7 transmembrane domain comprising or consisting of an amino acid sequence of SEQ ID NO:60, TLR8 transmembrane domain comprising or consisting of an amino acid sequence of SEQ ID NO:61, or TLR9 transmembrane domain comprising or consisting of an amino acid sequence of SEQ ID NO:62.

Transmembrane domains may derived from any mammalian species, including humans, primates, cows, horses, goats, sheep, dogs, cats, mice, rats, rabbits, guinea pigs, pigs, and transgenic species thereof.

In certain embodiments, a chimeric engulfment receptor comprises polynucleotide sequences derived from any mammalian species, including humans, primates, cows, horses, goats, sheep, dogs, cats, mice, rats, rabbits, guinea pigs, pigs, transgenic species thereof, or any combination thereof. In certain embodiments, a chimeric engulfment receptor is murine, chimeric, human, or humanized.

It is understood that direct fusion of one domain to another domain of a CER described herein does not preclude the presence of intervening junction amino acids. Junction amino acids may be natural or non-natural (*e.g.*, resulting from the construct design of a chimeric protein).

Embodiments of CERs for use in the tandem expression cassettes of the present disclosure are provided in Table 1 and also described in PCT Application Nos. PCT/2017/053553 and PCT/US2018/52297, each of which is incorporated by reference in its entirety.

Table 1: Exemplary Chimeric Engulfment Receptors

CER Name	Binding Domain	Transmembrane Domain	First Engulfment Signaling Domain	Second Engulfment Signaling Domain	Exemplary Amino Acid Sequences
CER1	Tim4	Tim4	MERTK		SEQ ID NO:109
CER5	Tim4	Tim4	TLR4		SEQ ID NO:97
CER6	Tim4	TLR4	TLR4		SEQ ID NO:110
CER7	Tim4 + TLR juxtamembrane domain	TLR4	TLR4		SEQ ID NO:111
CER8	Tim4	Tim4	Tyro3		SEQ ID NO:112

CER Name	Binding Domain	Transmembrane Domain	First Engulfment Signaling Domain	Second Engulfment Signaling Domain	Exemplary Amino Acid Sequences
CER9	Tim4	Tim4	DAP12		SEQ ID NO:113
CER10	Tim4	DAP12	DAP12		SEQ ID NO:114
CER11	Tim4	Tim4	Axl		SEQ ID NO:115
CER12	Tim4	Tim4	FcRg		SEQ ID NO:116
CER13	Tim4	FcεR1	FcRg		SEQ ID NO:117
CER15	Tim4	Tim4	MyD88		SEQ ID NO:118
CER16	Tim4	Tim4	MyD88_TIR		SEQ ID NO:119
CER17	Tim4	Tim4	TLR_3		SEQ ID NO:120
CER18	Tim4	TLR_3	TLR_3		SEQ ID NO:121
CER19	Tim4	Tim4	TLR_5		SEQ ID NO:98
CER20	Tim4	TLR_5	TLR_5		SEQ ID NO:122
CER21	Tim4	Tim4	TLR_8		SEQ ID NO:99
CER22	Tim4	TLR_8	TLR_8		SEQ ID NO:123
CER23	Tim4	Tim4	TLR_9		SEQ ID NO:124
CER24	Tim4	TLR_9	TLR_9		SEQ ID NO:125
CER25	Tim4	Tim4	NFAM		SEQ ID NO:100
CER26	Tim4	Tim4	TLR_1		SEQ ID NO:126
CER27	Tim4	Tim4	TLR_2		SEQ ID NO:101
CER28	Tim4	Tim4	TLR_7		SEQ ID NO:127
CER29	Tim4	Tim4	TRAF6		SEQ ID NO:102
CER30	Tim4	Tim4	TRAF2		SEQ ID NO:128
CER31	Tim4	Tim4	TRAF3		SEQ ID NO:103
CER85	Tim4	Tim4	MyD88	Baff-R	SEQ ID NO:129
CER86	Tim4	Tim4	MyD88	DAP12	SEQ ID NO:130
CER87	Tim4	Tim4	Baff-R	MyD88	SEQ ID NO:131
CER88	Tim4	Tim4	DAP12	MyD88	SEQ ID NO:132

CER Name	Binding Domain	Transmembrane Domain	First Engulfment Signaling Domain	Second Engulfment Signaling Domain	Exemplary Amino Acid Sequences
CER89	Tim4	Tim4	MyD88	CD79b (185-229)	SEQ ID NO:133
CER90	Tim4	Tim4	MyD88	NFAM1	SEQ ID NO:134
CER91	Tim4	Tim4	MyD88	P2A-Rab	SEQ ID NO:135
CER92	Tim4	Tim4	MERTK	MyD88	SEQ ID NO:136
CER93	Tim4	Tim4	MERTK	Baff-R	SEQ ID NO:137
CER94	Tim4	Tim4	MERTK	DAP12	SEQ ID NO:138
CER95	Tim4	Tim4	MERTK	CD79b (185-229)	SEQ ID NO:139
CER96	Tim4	Tim4	MERTK	NFAM1	SEQ ID NO:140
CER97	Tim4	Tim4	AXL	Dap12	SEQ ID NO:141
CER98	Tim4	Tim4	AXL	CD79b	SEQ ID NO:142
CER99	Tim4	Tim4	AXL	NFAM1	SEQ ID NO:143
CER102	Tim4	Tim4	TLR8	NFAM1	SEQ ID NO:144
CER103A	Tim4	Tim4	TLR8	CD79b (185-229)	SEQ ID NO:145
CER103B	Tim4	Tim4	TLR8	CD79b (185-213)	SEQ ID NO:146
CER104	Tim4	Tim4	TLR8	DAP12	SEQ ID NO:147
CER105	Tim4	Tim4	TLR8	Baff-R	SEQ ID NO:148
CER106	Tim4	Tim4	NFAM1	TLR8	SEQ ID NO:149
CER107	Tim4	Tim4	CD79b (185-213)	TLR8	SEQ ID NO:150
CER108	Tim4	Tim4	DAP12	TLR8	SEQ ID NO:151
CER109	Tim4	Tim4	Baff-R	TLR8	SEQ ID NO:152
CER110	Tim4	Tim4	TRAF6	DAP12	SEQ ID NO:153
CER111A	Tim4	Tim4	TRAF6	CD79b (185-229)	SEQ ID NO:154
CER111B	Tim4	Tim4	TRAF6	CD79b (185-213)	SEQ ID NO:155
CER112	Tim4	Tim4	TRAF6	NFAM1	SEQ ID NO:156
CER113	Tim4	Tim4	TRAF6	Baff-R	SEQ ID NO:157
CER114	Tim4	Tim4	TRAF6	MERTK	SEQ ID NO:158

CER Name	Binding Domain	Transmembrane Domain	First Engulfment Signaling Domain	Second Engulfment Signaling Domain	Exemplary Amino Acid Sequences
CER115	Tim4	Tim4	MERTK	TRAF6	SEQ ID NO:159
CER116	Tim4	Tim4	TRAF6	TLR8	SEQ ID NO:160
CER117	Tim4	Tim4	TLR8	TRAF6	SEQ ID NO:161
CER118	Tim4	Tim4	TLR1	NFAM1	SEQ ID NO:162
CER119A	Tim4	Tim4	TLR1	CD79b (185-229)	SEQ ID NO:183
CER119B	Tim4	Tim4	TLR1	CD79b (185-213)	SEQ ID NO:163
CER120	Tim4	Tim4	TLR1	DAP12	SEQ ID NO:164
CER121	Tim4	Tim4	TLR1	TRAF6	SEQ ID NO:165
CER122	Tim4	Tim4	TLR2	DAP12	SEQ ID NO:171
CER123	Tim4	Tim4	TLR2	TRAF6	SEQ ID NO:172
CER124	Tim4	Tim4	TLR2	NFAM1	SEQ ID NO:173
CER125A	Tim4	Tim4	TLR2	CD79b (185-229)	SEQ ID NO:174
CER125B	Tim4	Tim4	TLR2	CD79b (185-213)	SEQ ID NO:175
CER126	Tim4	Tim4	TLR2	TRAF2	SEQ ID NO:184
CER127	Tim4	Tim4	TRAF2	TLR2	SEQ ID NO:185
CER128	Tim4	Tim4	TRAF2	TLR8	SEQ ID NO:186
CER129	Tim4	Tim4	TLR8	TRAF2	SEQ ID NO:187
hCER21	Tim4	Tim4	TLR8		SEQ ID NO:188
hCER29	Tim4	Tim4	TRAF6		SEQ ID NO:189
hCER104	Tim4	Tim4	TLR8	Dap12	SEQ ID NO:190
hCER116	Tim4	Tim4	TRAF6	TLR8	SEQ ID NO:191
hCER117	Tim4	Tim4	TLR8	TRAF6	SEQ ID NO:192
hCER122	Tim4	Tim4	TLR2	Dap12	SEQ ID NO:193
hCER123	Tim4	Tim4	TLR2	TRAF6	SEQ ID NO:194
hCER126	Tim4	Tim4	TLR2	TRAF2	SEQ ID NO:195

II. Chimeric Antigen Receptors

In certain embodiments, tandem expression cassettes of the present disclosure comprise a transgene encoding a chimeric antigen receptor (CAR). Chimeric antigen receptors are recombinant receptors that generally comprise: an extracellular domain comprising a binding domain that binds to a target antigen; an intracellular signaling domain, and a transmembrane domain positioned between and connecting the extracellular domain and the intracellular signaling domain.

Binding domains suitable for use in CARs of the present disclosure include any antigen-binding polypeptide. A binding domain may comprise an antibody or antigen binding fragment thereof, including for example, a full length heavy chain, Fab fragment, Fab', F(ab')₂, sFv, VH domain, VL domain, dAb, VHH, CDR, and scFv. In certain embodiments, a CAR binding domain is murine, chimeric, human, or humanized.

In certain embodiments, the extracellular domain of CARs provided in the present disclosure optionally comprises an extracellular, non-signaling spacer or linker domain. Where included, such a spacer or linker domain may position the binding domain away from the host cell surface to further enable proper cell to cell contact, binding, and activation. An extracellular spacer domain is generally located between the extracellular binding domain and the transmembrane domain of the CAR. The length of the extracellular spacer may be varied to optimize target molecule binding based on the selected target molecule, selected binding epitope, binding domain size and affinity (*see, e.g., Guest et al., J. Immunother.* 28:203-11, 2005; PCT Publication No. WO 2014/031687). In certain embodiments, an extracellular spacer domain is an immunoglobulin hinge region (*e.g., IgG1, IgG2, IgG3, IgG4, IgA, IgD*). An immunoglobulin hinge region may be a wild type immunoglobulin hinge region or an altered wild type immunoglobulin hinge region. An altered IgG₄ hinge region is described in PCT Publication No. WO 2014/031687, which hinge region is incorporated herein by reference in its entirety. In a particular embodiment, an extracellular spacer domain comprises a modified IgG₄ hinge region having an amino acid sequence of ESKYGPPCPPCP (SEQ ID NO:63).

Other examples of hinge regions that may be used in the CARs described herein include the hinge region from the extracellular regions of type I membrane proteins, such as CD8a, CD4, CD28 and CD7, which may be wild-type or variants thereof. In further embodiments, an extracellular spacer domain comprises all or a portion of an immunoglobulin Fc domain selected from: a CH1 domain, a CH2 domain, a CH3 domain, or combinations thereof (*see, e.g.*, PCT Publication WO2014/031687, which spacers are incorporated herein by reference in their entirety). In yet further embodiments, an extracellular spacer domain may comprise a stalk region of a type II C-lectin (the extracellular domain located between the C-type lectin domain and the transmembrane domain). Type II C-lectins include CD23, CD69, CD72, CD94, NKG2A, and NKG2D.

CARs of the present disclosure comprise a transmembrane domain that connects and is positioned between the extracellular domain and the intracellular signaling domain. The transmembrane domain is a hydrophobic alpha helix that transverses the host cell membrane and anchors the CAR in the host cell membrane. The transmembrane domain may be directly fused to the binding domain or to the extracellular spacer domain if present. In certain embodiments, the transmembrane domain is derived from an integral membrane protein (*e.g.*, receptor, cluster of differentiation (CD) molecule, enzyme, transporter, cell adhesion molecule, or the like). The transmembrane domain can be selected from the same molecule as the extracellular domain or the intracellular signaling domain (*e.g.*, a CAR comprises a CD28 costimulatory signaling domain and a CD28 transmembrane domain). In certain embodiments, the transmembrane domain and the extracellular domain are each selected from different molecules. In other embodiments, the transmembrane domain and the intracellular signaling domain are each selected from different molecules. In yet other embodiments, the transmembrane domain, the extracellular domain, and the intracellular signaling domain are each selected from different molecules.

Exemplary transmembrane domains for use in CARs of the present disclosure include CD28, CD2, CD3 ϵ , CD3 δ , CD3 ζ , CD25, CD27, CD40, CD79A, CD79B, CD80, CD86, CD95 (Fas), CD134 (OX40), CD137 (4-1BB), CD150 (SLAMF1), CD152 (CTLA4), CD200R, CD223 (LAG3), CD270 (HVEM), CD272

(BTLA), CD273 (PD-L2), CD274 (PD-L1), CD278 (ICOS), CD279 (PD-1), CD300, CD357 (GITR), A2aR, DAP10, FcR α , FcR β , FcR γ , Fyn, GAL9, KIR, Lck, LAT, LRP, NKG2D, NOTCH1, NOTCH2, NOTCH3, NOTCH4, PTCH2, ROR2, Ryk, Slp76, SIRP α , pT α , TCR α , TCR β , TIM3, TRIM, LPA5, and Zap70. An exemplary CD28 transmembrane domain comprises an amino acid sequence of SEQ ID NO:107.

The intracellular signaling domain of a CAR is an intracellular effector domain and is capable of transmitting functional signals to a cell in response to binding of the extracellular domain of the CAR to a target molecule. The intracellular signaling domain may be any portion of an intracellular signaling molecule that retains sufficient signaling activity. In some embodiments, a full length or full length intracellular component of an intracellular signaling molecule is used. In some embodiments, a truncated portion of an intracellular signaling molecule or intracellular component of an intracellular signaling molecule is used, provided that the truncated portion retains sufficient signal transduction activity. In further embodiments, an intracellular signaling domain is a variant of an entire or truncated portion of an intracellular signaling molecule, provided that the variant retains sufficient signal transduction activity (*i.e.*, is a functional variant).

In certain embodiments, the intracellular signaling domain of a CAR comprises an immunoreceptor tyrosine-based activation motif (ITAM) containing signaling domain. An ITAM containing signaling domain generally contains at least one (one, two, three, four, or more) ITAMs, which refer to a conserved motif of YXXL/I-X₆₋₈-YXXL/I. An ITAM containing signaling domain may initiate T cell activation signaling following antigen binding or ligand engagement. ITAM-signaling domains include, for example, intracellular signaling domains of CD3 γ , CD3 δ , CD3 ϵ , CD3 ζ , CD5, CD22, CD79a, CD278 (ICOS), DAP10, DAP12, and CD66d. Exemplary CD3 ζ signaling domains that may be used in CARs of the present disclosure comprise an amino acid sequence of SEQ ID NO:166 or 167.

CAR intracellular signaling domains optionally comprise a costimulatory signaling domain, which, when activated in conjunction with a primary or classic (*e.g.*, ITAM-driven) activation signal, promotes or enhances T cell response, such as T cell activation, cytokine production, proliferation, differentiation, survival,

effector function, or combinations thereof. Costimulatory signaling domains for use in CARs include, for example, CD27, CD28, CD40L, GITR, NKG2C, CARD1, CD2, CD7, CD27, CD30, CD40, CD54 (ICAM), CD83, CD134 (OX-40), CD137 (4-1BB), CD150 (SLAMF1), CD152 (CTLA4), CD223 (LAG3), CD226, CD270 (HVEM), CD273 (PD-L2), CD274 (PD-L1), CD278 (ICOS), DAP10, LAT, LFA-1, LIGHT, NKG2C, SLP76, TRIM, ZAP70, or any combination thereof. In a particular embodiment, the costimulatory signaling domain comprises a OX40, CD2, CD27, CD28, ICAM-1, LFA-1 (CD11a/CD18), ICOS (CD278), or 4-1BB (CD137) signaling domain. Exemplary CD28 costimulatory signaling domains that may be used in CARs of the present disclosure comprise an amino acid sequence of SEQ ID NO:169 or 170. An exemplary 4-1BB costimulatory signaling domain comprises an amino acid sequence of SEQ ID NO:168. In certain embodiments, a CAR comprises one, two, or more costimulatory signaling domains.

In certain embodiments, a chimeric antigen receptor comprises polynucleotide sequences derived from any mammalian species, including humans, primates, cows, horses, goats, sheep, dogs, cats, mice, rats, rabbits, guinea pigs, pigs, transgenic species thereof, or any combination thereof. In certain embodiments, chimeric antigen receptor is murine, chimeric, human, or humanized.

In certain embodiments, a CAR is a first generation CAR, a second generation CAR, or a third generation CAR. A first generation CAR generally has an intracellular signaling domain comprising an intracellular signaling domain of CD3 ζ , Fc γ RI, or other ITAM-containing activating domain to provide a T cell activation signal. Second generation CARs further comprise a costimulatory signaling domain (*e.g.*, a costimulatory signaling domain from an endogenous T cell costimulatory receptor, such as CD28, 4-1BB, or ICOS). Third generation CARs comprise an ITAM-containing activating domain, a first costimulatory signaling domain and a second costimulatory signaling domain.

In certain embodiments, a CAR is a T cell receptor-based chimeric antigen receptor (TCR-CAR). A TCR-CAR is a heterodimeric fusion protein generally comprising a soluble TCR (a polypeptide chain comprising a V α domain and C α domain and a polypeptide chain comprising a V β domain and a C β domain), wherein the V β C β polypeptide chain is linked to a transmembrane domain and an intracellular

signaling component (*e.g.*, an ITAM-containing activating domain and optionally a costimulatory signaling domain) (*see, e.g.*, Walseng *et al.*, 2017 Scientific Reports 7:10713).

CARs of the present disclosure may target a variety of antigens, including a viral antigen, bacterial antigen, fungal antigen, parasitic antigen, tumor antigen, autoimmune disease antigen. Exemplary tumor antigens that a CAR may target include CD138, CD38, CD33, CD123, CD72, CD79a, CD79b, mesothelin, PSMA, BCMA, ROR1, MUC-16, L1CAM, CD22, CD19, CD20, CD23, CD24, CD37, CD30, CA125, CD56, c-Met, EGFR, GD-3, HPV E6, HPV E7, MUC-1, HER2, folate receptor α , CD97, CD171, CD179a, CD44v6, WT1, VEGF- α , VEGFR1, IL-13R α 1, IL-13R α 2, IL-11R α , PSA, FcRH5, NKG2D ligand, NY-ESO-1, TAG-72, CEA, ephrin A2, ephrin B2, Lewis A antigen, Lewis Y antigen, MAGE, MAGE-A1, RAGE-1, folate receptor β , EGFRviii, VEGFR-2, LGR5, SSX2, AKAP-4, FLT3, fucosyl GM1, GM3, o-acetyl-GD2, and GD2.

III. T Cell Receptor Binding Proteins

In certain embodiments, tandem expression cassettes of the present disclosure comprise a transgene encoding a recombinant TCR binding protein. Recombinant TCR binding proteins include “traditional” TCRs composed of a heterodimer of α chain polypeptide and β chain polypeptide or a heterodimer of a γ chain polypeptide and a δ chain polypeptide, binding fragments and fusion proteins thereof, including for example, single chain TCRs, single domain TCRs, soluble TCR fusion TCR proteins, and TCR fusion constructs (TRuCTM). In certain embodiments, a tandem expression cassette comprises a polynucleotide encoding a recombinant TCR beta chain comprising a TCR beta variable region and a TCR beta constant region, and a polynucleotide encoding a recombinant TCR alpha chain comprising a TCR alpha variable region and a TCR alpha constant region. In certain embodiments, a recombinant TCR is an enhanced affinity TCR.

In certain embodiments, a recombinant TCR binding protein is a single chain TCR (scTCR) comprising a V α joined to a V β by a flexible linker. In some

embodiments, a scTCR comprises a V α -linker-V β polypeptide. In other embodiments, a scTCR comprises a V β -linker-V α polypeptide.

In certain embodiments, a recombinant TCR binding protein is a single domain TCR (*e.g.*, V β).

In certain embodiments, a recombinant TCR binding protein is a single chain TCR (scTCR) fusion protein. A scTCR fusion protein comprises a binding domain comprising a scTCR (a TCR V α domain linked to a TCR V β domain), an optional extracellular spacer, a transmembrane domain, and an intracellular signaling domain comprising a CD3 ζ ITAM-containing activating domain and optionally a costimulatory signaling domain (*see*, Aggen *et al.*, 2012, *Gene Ther.* 19:365-374; Stone *et al.*, *Cancer Immunol. Immunother.* 2014, 63:1163-76).

In certain embodiments, a recombinant TCR binding protein is a TCR fusion construct (TRuCTM construct) (*see*, U.S. Patent Publication No. 2017/0166622). TRuCTM constructs comprise an antigen-specific binding domain (*e.g.*, scFv) fused at least one component of a TCR complex (CD3 γ , CD3 ϵ , or CD3 δ) to form a TCR complex component fusion protein. A human TCR complex contains the CD3 ϵ polypeptide, the CD3 γ polypeptide, the CD3 δ polypeptide, the CD3 ζ polypeptide, the TCR α chain polypeptide, and the TCR β chain polypeptide. The TCR complex component fusion protein is capable of associating with the other components of the TCR complex to form a functional, complete TCR fusion complex. Unlike TCRs, TRuCTM constructs are capable of binding a target antigen in a MHC independent manner.

In certain embodiments, a TCR binding protein comprises polynucleotide sequences derived from any mammalian species, including humans, primates, cows, horses, goats, sheep, dogs, cats, mice, rats, rabbits, guinea pigs, pigs, transgenic species thereof, or any combination thereof. In certain embodiments, the TCR binding protein is murine, chimeric, human, or humanized.

TCR binding proteins of the present disclosure may bind to a variety of antigens, including tumor antigens, viral antigens, bacterial antigens, fungal antigens, parasitic antigens, and autoimmune disease antigens. Exemplary tumor antigens that a recombinant TCR binding protein may target include WT-1, mesothelin, MART-1, NY-ESO-1, MAGE-A3, HPV E7, survivin, α Fetoprotein, and a tumor-specific neoantigen.

Exemplary HPV16 E7 specific TCRs that may be used in tandem expression cassettes of the present disclosure are provided in PCT Published Application No.

WO2015/184228 (incorporated by reference in its entirety). In certain embodiments, a HPV16 E7 specific TCR comprises an amino acid sequence of SEQ ID NO:90. The amino acid sequence of SEQ ID NO:90 contains a P2A self-cleaving peptide between the TCR β chain sequence and the TCR α chain sequence, which would be cleaved in the host cell to form two polypeptide chains. Thus, in certain embodiments, the TCR represented by SEQ ID NO:90 comprises separate TCR β and TCR α polypeptide chains that are capable dimerizing to form a $\alpha\beta$ TCR. In certain embodiments, a HPV16 E7 specific TCR comprises a V β comprising an amino acid sequence of SEQ ID NO:92. In certain embodiments, a HPV16 E7 specific TCR comprises a V α comprising an amino acid sequence of SEQ ID NO:94. In further embodiments, a HPV16 specific E7 TCR comprises a V β comprising an amino acid sequence of SEQ ID NO:92 and a V α comprising an amino acid sequence of SEQ ID NO:94.

In certain embodiments, a TCR C α domain, a C β domain, or both comprise a cysteine substitution to create an interchain disulfide bond between the two constant domain cysteine residues, which is not present in unmodified TCRs. Such modified TCRs may form more stable heterodimers. In particular embodiments, the C α domain comprises a Thr $\rightarrow$ Cys substitution at position 48 of the wild type protein sequence, and the C β domain comprises a Ser $\rightarrow$ Cys substitution at position 56 of the wild type protein sequence (*see*, PCT Published Application No. WO2015/184228). An exemplary cysteine modified TCR C β constant region comprises an amino acid sequence of SEQ ID NO:93.

In certain embodiments, a TCR comprises substitutions of one, two, or three amino acids in the transmembrane domain of the constant region of one or both of the α and β chains with a hydrophobic amino acid to increase the hydrophobicity of the transmembrane domain. In certain embodiments, one, two, or three of the residues selected from Ser112, Met114, and Gly115 of the TCR α chain are substituted with Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp. An exemplary cysteine modified, "LVL" substituted TCR C α region comprises an amino acid sequence of SEQ ID NO:95.

In certain embodiments, the CER and the CAR/or TCR binding protein encoded by the tandem expression cassette target the same antigen. In other

embodiments, the CER and the CAR/or TCR binding protein encoded by the tandem expression cassette each target different antigens.

Polynucleotides, Expression Cassettes, Vectors, and Modified Host Cells

In certain aspects, the present disclosure provides nucleic acid molecules that encode any one or more of the receptors (*e.g.*, CERs, CARs, and TCR binding proteins) described herein. A nucleic acid may refer to a single- or double-stranded DNA, cDNA, or RNA, and may include a positive and a negative strand of the nucleic acid which complement one another, including antisense DNA, cDNA, and RNA. A nucleic acid may be naturally occurring or synthetic forms of DNA or RNA. The nucleic acid sequences encoding a desired receptor can be obtained or produced using recombinant methods known in the art using standard techniques, such as by screening libraries from cells expressing the desired sequence or a portion thereof, by deriving the sequence from a vector known to include the same, or by isolating the sequence or a portion thereof directly from cells or tissues containing the same as described in, for example, Sambrook *et al.* (1989 and 2001 editions; *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, NY) and Ausubel *et al.* (Current Protocols in Molecular Biology, 2003). Alternatively, the sequence of interest can be produced synthetically, rather than being cloned.

Polynucleotides encoding the receptor compositions provided herein may be derived from any animal, such as humans, primates, cows, horses, sheep, dogs, cats, mice, rats, rabbits, guinea pigs, pigs, or a combination thereof. In certain embodiments, a polynucleotide encoding at least one receptor or both receptors contained in the tandem expression cassette is from the same animal species as the host cell into which the polynucleotide is inserted.

In certain embodiments, a polynucleotide encoding a receptor comprises a sequence encoding a signal peptide (also referred to as leader peptide or signal sequence) at the 5'-end for targeting of the precursor protein to the secretory pathway. The signal peptide is optionally cleaved from the N-terminus of the extracellular domain during cellular processing and localization of the receptor to the host cell membrane. A polypeptide from which a signal peptide sequence has been cleaved or

removed may also be called a mature polypeptide. Examples of signal peptides that may be used in the receptors of the present disclosure include signal peptides derived from endogenous secreted proteins, including, *e.g.*, GM-CSF (amino acid sequence of SEQ ID NO:64) or Tim4 (amino acid sequence of SEQ ID NO:65). As used herein, reference to a polynucleotide or polypeptide sequence of a receptor, *e.g.*, CER, CAR, or TCR binding protein, provided herein may include or exclude the signal sequence. It is understood by persons of skill in the art that for sequences disclosed herein that include a signal peptide sequence, the signal peptide sequence may be replaced with another signal peptide that is capable of trafficking the encoded protein to the extracellular membrane.

In certain embodiments, a receptor encoding polynucleotide of the present disclosure is codon optimized for efficient expression in a target host cell comprising the polynucleotide (*see, e.g.* Scholten *et al.*, *Clin. Immunol.* 119:135-145 (2006)). As used herein, a "codon optimized" polynucleotide comprises a heterologous polynucleotide having codons modified with silent mutations corresponding to the abundances of tRNA in a host cell of interest.

Polynucleotides encoding at least two transgenes (*e.g.*, a CER and CAR, a CER and TCR binding protein) provided in the present disclosure may be used to compose tandem expression cassettes. A tandem expression cassette refers to a component of a vector nucleic acid comprising at least two transgenes under the control of, or operatively linked to, the same set of regulatory sequences for tandem or co-expression of the at least two transgenes. Regulatory sequences that may be used in tandem expression cassettes of the present disclosure include appropriate transcription initiation, termination, promoter and enhancer sequences; efficient RNA processing signals such as splicing and polyadenylation signals; sequences that stabilize cytoplasmic mRNA; sequences that enhance translation efficiency (*i.e.*, Kozak consensus sequences); sequences that enhance protein stability; sequences that enhance protein secretion, or any combination thereof.

In certain embodiments, a tandem expression cassette can be constructed to optimize spatial and temporal control. For example, a tandem expression cassette

can include promoter elements to optimize spatial and temporal control. In some embodiments, a tandem expression cassette includes tissue specific promoters or enhancers that enable specific induction of a tandem expression cassette to an organ, a cell type (*e.g.*, immune cell), or a pathologic microenvironment, such as a tumor or infected tissue. An “enhancer” is an additional promoter element that can function either cooperatively or independently to activate transcription. In certain embodiments, a tandem expression cassette includes a constitutive promoter. An exemplary constitutive promoter for use in tandem expression cassettes of the present disclosure is an EF-1 α promoter. In certain embodiments, a tandem expression cassette includes an inducible promoter. In certain embodiments, a tandem expression cassette includes a tissue specific promoter.

The at least two transgenes contained within the tandem expression cassettes may be in any order. For example, a tandem expression cassette comprising a polynucleotide a CER and a polynucleotide encoding a CAR may be arranged from 5' to 3': CER-CAR, or CAR-CER. In another example, a tandem expression cassette comprising a polynucleotide a CER and a polynucleotide encoding a TCR may be arranged from 5' to 3': CER-TCR, or TCR-CER.

In certain embodiments, receptors that comprise two or more polypeptide chains that associate to form a multimer or complex may be encoded by two or more polynucleotide molecules within a tandem expression construct. Exemplary multimeric receptors contemplated for expression in tandem expression constructs of the present disclosure include multichain CARs, TCRs, TCR-CARs, and TRuCTM constructs. Accordingly, exemplary tandem expression cassette embodiments encoding a CER and a TCR may comprise a polynucleotide encoding a CER, a polynucleotide encoding a TCR α chain polypeptide, and a polynucleotide encoding a TCR β chain polypeptide.

In certain embodiments, tandem expression cassettes of the present disclosure may comprise an internal ribosome entry site (IRES) or peptide cleavage site such as a furin cleavage site or viral 2A peptide, disposed between each polynucleotide contained within the tandem expression cassette to allow for coexpression of multiple proteins from a single mRNA. For example, an IRES, furin cleavage site, or viral 2A

peptide may be disposed between a polynucleotide encoding a CER and a polynucleotide encoding a CAR within a tandem expression cassette. In another example, an IRES, furin cleavage site, or viral 2A peptide may be disposed between each of a polynucleotide encoding a CER, a polynucleotide encoding a TCR α chain polypeptide, and a polynucleotide encoding a TCR β chain polypeptide. In certain embodiments, a viral 2A peptide is a porcine teschovirus-1 (P2A), *Thosea asigna* virus (T2A), equine rhinitis A virus (E2A), foot-and-mouth disease virus (F2A), or variant thereof. An exemplary T2A peptide comprises an amino acid sequence of any one of SEQ ID NOs:67, 68, 69 and 75. An exemplary P2A peptide comprises an amino acid sequence of SEQ ID NO:70 or 71. An exemplary E2A peptide sequence comprises an amino acid sequence of SEQ ID NO:72. An exemplary F2A peptide sequence comprises an amino acid sequence of SEQ ID NO:73.

Certain embodiments of tandem expression cassettes of the present disclosure comprise a polynucleotide encoding a CAR/or TCR specific for a target antigen (*e.g.*, tumor antigen) and a polynucleotide encoding a CER that binds a pro-engulfment marker (*e.g.*, an apoptosis marker such as phosphatidylserine). Upon binding a target cell expressing the target antigen by the CAR/or TCR, a cell modified to express such a tandem expression cassette induces apoptosis of the target cell. Apoptosis induces exposure of pro-engulfment markers on the target cell, such as phosphatidylserine, which may then target the damaged or apoptotic cells for engulfment by the CER.

An exemplary tandem expression cassette of the present disclosure comprises: (a) a polynucleotide encoding a CER comprising: an extracellular domain comprising a Tim4 binding domain that binds to phosphatidylserine; a TLR4 engulfment signaling domain; a Tim4 transmembrane domain positioned between and connecting the extracellular domain and the engulfment signaling domain; (b) a polynucleotide encoding a HPV-E7 specific recombinant T cell receptor (TCR) beta chain comprising a TCR beta variable region and a TCR beta constant region; and (c) a polynucleotide encoding a HPV-E7 specific recombinant TCR alpha chain comprising a TCR alpha variable region and a TCR alpha constant region (*see* Figure 1A). In certain embodiments, the tandem expression cassette comprises a 2A peptide sequence interspersed between the polynucleotide encoding the CER, the polynucleotide

encoding the TCR β chain, and the polynucleotide encoding the TCR α chain. In certain embodiments, the tandem expression cassette comprises an EF-1 α promoter operably linked to the CER and TCR polynucleotides. In certain embodiments, such an exemplary tandem expression cassette (“CER5-HPV16 E7 TCR”) comprises CER5 comprising an amino acid sequence of SEQ ID NO:97 and HPV16 E7 TCR comprising an amino acid sequence of SEQ ID NO:90.

Another exemplary tandem expression cassette of the present disclosure comprises: (a) a polynucleotide encoding a CER comprising: an extracellular domain comprising a Tim4 binding domain that binds to phosphatidylserine; a TLR5 engulfment signaling domain; a Tim4 transmembrane domain positioned between and connecting the extracellular domain and the engulfment signaling domain; (b) a polynucleotide encoding a HPV-E7 specific recombinant T cell receptor (TCR) beta chain comprising a TCR beta variable region and a TCR beta constant region; and (c) a polynucleotide encoding a HPV-E7 specific recombinant TCR alpha chain comprising a TCR alpha variable region and a TCR alpha constant region (*see* Figure 1B). In certain embodiments, the tandem expression cassette comprises a 2A peptide sequence interspersed between the polynucleotide encoding the CER, the polynucleotide encoding the TCR β chain, and the polynucleotide encoding the TCR α chain. In certain embodiments, the tandem expression cassette comprises an EF-1 α promoter operably linked to the CER and TCR polynucleotides. In certain embodiments, such an exemplary tandem expression cassette (“CER19-HPV16 E7 TCR”) comprises CER19 comprising an amino acid sequence of SEQ ID NO:98 and HPV16 E7 TCR comprising an amino acid sequence of SEQ ID NO:90.

Another exemplary tandem expression cassette of the present disclosure comprises: (a) a polynucleotide encoding a CER comprising: an extracellular domain comprising a Tim4 binding domain; a TLR8 engulfment signaling domain; a Tim4 transmembrane domain positioned between and connecting the extracellular domain and the engulfment signaling domain; (b) a polynucleotide encoding a HPV-E7 specific recombinant T cell receptor (TCR) beta chain comprising a TCR beta variable region and a TCR beta constant region; and (c) a polynucleotide encoding a HPV-E7 specific recombinant TCR alpha chain comprising a TCR alpha variable region and a TCR alpha constant region (*see* Figure 1C). In certain embodiments, the tandem expression

cassette comprises a 2A peptide sequence interspersed between the polynucleotide encoding the CER, the polynucleotide encoding the TCR β chain, and the polynucleotide encoding the TCR α chain. In certain embodiments, the tandem expression cassette comprises an EF-1 α promoter operably linked to the CER and TCR polynucleotides. In certain embodiments, such an exemplary tandem expression cassette (“CER21-HPV16 E7 TCR”) comprises CER21 comprising an amino acid sequence of SEQ ID NO:99 and HPV16 E7 TCR comprising an amino acid sequence of SEQ ID NO:90.

Another exemplary tandem expression cassette of the present disclosure comprises: (a) a polynucleotide encoding a CER comprising: an extracellular domain comprising a Tim4 binding domain that binds to phosphatidylserine; a NFAM1 engulfment signaling domain; a Tim4 transmembrane domain positioned between and connecting the extracellular domain and the engulfment signaling domain; (b) a polynucleotide encoding a HPV-E7 specific recombinant T cell receptor (TCR) beta chain comprising a TCR beta variable region and a TCR beta constant region; and (c) a polynucleotide encoding a HPV-E7 specific recombinant TCR alpha chain comprising a TCR alpha variable region and a TCR alpha constant region (*see* Figure 1D). In certain embodiments, the tandem expression cassette comprises a 2A peptide sequence interspersed between the polynucleotide encoding the CER, the polynucleotide encoding the TCR β chain, and the polynucleotide encoding the TCR α chain. In certain embodiments, the tandem expression cassette comprises an EF-1 α promoter operably linked to the CER and TCR polynucleotides. In certain embodiments, such an exemplary tandem expression cassette (“CER25-HPV16 E7 TCR”) comprises CER25 comprising an amino acid sequence of SEQ ID NO:100 and HPV16 E7 TCR comprising an amino acid sequence of SEQ ID NO:90.

Another exemplary tandem expression cassette of the present disclosure comprises: (a) a polynucleotide encoding a CER comprising: an extracellular domain comprising a Tim4 binding domain that binds to phosphatidylserine; a TLR2 engulfment signaling domain; a Tim4 transmembrane domain positioned between and connecting the extracellular domain and the engulfment signaling domain; (b) a polynucleotide encoding a HPV-E7 specific recombinant T cell receptor (TCR) beta chain comprising a TCR beta variable region and a TCR beta constant region; and (c) a

polynucleotide encoding a HPV-E7 specific recombinant TCR alpha chain comprising a TCR alpha variable region and a TCR alpha constant region (*see* Figure 1E). In certain embodiments, the tandem expression cassette comprises a 2A peptide sequence interspersed between the polynucleotide encoding the CER, the polynucleotide encoding the TCR β chain, and the polynucleotide encoding the TCR α chain. In certain embodiments, the tandem expression cassette comprises an EF-1 α promoter operably linked to the CER and TCR polynucleotides. In certain embodiments, such an exemplary tandem expression cassette (“CER27-HPV16 E7 TCR”) CER27 comprising an amino acid sequence of SEQ ID NO:101 and HPV16 E7 TCR comprising an amino acid sequence of SEQ ID NO:90.

Another exemplary tandem expression cassette of the present disclosure comprises: (a) a polynucleotide encoding a CER comprising: an extracellular domain comprising a Tim4 binding domain that binds to phosphatidylserine; a Traf6 engulfment signaling domain; a Tim4 transmembrane domain positioned between and connecting the extracellular domain and the engulfment signaling domain; (b) a polynucleotide encoding a HPV-E7 specific recombinant T cell receptor (TCR) beta chain comprising a TCR beta variable region and a TCR beta constant region; and (c) a polynucleotide encoding a HPV-E7 specific recombinant TCR alpha chain comprising a TCR alpha variable region and a TCR alpha constant region (*see* Figure 1F). In certain embodiments, the tandem expression cassette comprises a 2A peptide sequence interspersed between the polynucleotide encoding the CER, the polynucleotide encoding the TCR β chain, and the polynucleotide encoding the TCR α chain. In certain embodiments, the tandem expression cassette comprises an EF-1 α promoter operably linked to the CER and TCR polynucleotides. In certain embodiments, such an exemplary tandem expression cassette (“CER29-HPV16 E7 TCR”) comprises CER29 comprising an amino acid sequence of SEQ ID NO:102 and HPV16 E7 TCR comprising an amino acid sequence of SEQ ID NO:90.

Yet another exemplary tandem expression cassette of the present disclosure comprises: (a) a polynucleotide encoding a CER comprising: an extracellular domain comprising a Tim4 binding domain that binds to phosphatidylserine; a Traf3 engulfment signaling domain; a Tim4 transmembrane domain positioned between and connecting the extracellular domain and the engulfment

signaling domain; (b) a polynucleotide encoding a HPV-E7 specific recombinant T cell receptor (TCR) beta chain comprising a TCR beta variable region and a TCR beta constant region; and (c) a polynucleotide encoding a HPV-E7 specific recombinant TCR alpha chain comprising a TCR alpha variable region and a TCR alpha constant region (*see* Figure 1G). In certain embodiments, the tandem expression cassette comprises a 2A peptide sequence interspersed between the polynucleotide encoding the CER, the polynucleotide encoding the TCR β chain, and the polynucleotide encoding the TCR α chain. In certain embodiments, the tandem expression cassette comprises an EF-1 α promoter operably linked to the CER and TCR polynucleotides. In certain embodiments, such an exemplary tandem expression cassette ("CER31-HPV16 E7 TCR") comprises CER31 comprising an amino acid sequence of SEQ ID NO:103 and HPV16 E7 TCR comprising an amino acid sequence of SEQ ID NO:90.

A polynucleotide encoding a desired tandem expression cassette can be inserted into an appropriate vector, *e.g.*, a viral vector, non-viral plasmid vector, and non-viral vectors, such as lipid-based DNA vectors, modified mRNA (modRNA), self-amplifying mRNA, CELiD, and transposon-mediated gene transfer (PiggyBac, Sleeping Beauty), for introduction into a host cell of interest (*e.g.*, an immune cell). Polynucleotides encoding a tandem expression cassette of the present disclosure can be cloned into any suitable vector, such as an expression vector, a replication vector, a probe generation vector, or a sequencing vector. In certain embodiments, a polynucleotide encoding the CER, and a polynucleotide encoding the CAR or TCR binding protein are joined together into a single polynucleotide and then inserted into a vector. In other embodiments, a polynucleotide encoding the CER, and a polynucleotide encoding the CAR or TCR binding protein may be inserted separately into a vector such that the expressed amino acid sequence produces a functional CER and CAR/or TCR. A vector that encodes a tandem expression cassette is referred to herein as a "tandem expression vector."

In certain embodiments, a vector comprises a polynucleotide encoding a tandem expression cassette. In certain embodiments, a vector comprises a tandem expression cassette encoding a CER and a CAR/or TCR binding protein.

In certain embodiments, vectors that allow long-term integration of a tandem expression cassette and propagation to daughter cells are utilized. Examples include viral vectors such as, adenovirus, adeno-associated virus, vaccinia virus, herpes viruses, cytomegalovirus, pox virus, or retroviral vectors, such as lentiviral vectors. Vectors derived from lentivirus can be used to achieve long-term gene transfer and have added advantages over vectors including the ability to transduce non-proliferating cells, such as hepatocytes, and low immunogenicity.

In certain embodiments, non-integrating vectors that remain episomal are used for the tandem expression cassettes of the present disclosure. Examples of non-integrating viral vectors include adenoviral vectors and integrating viral vectors that have been mutated to be non-integrating, such as non-integrating lentiviral vectors and non-integrating foamy virus vectors.

A vector that encodes a core virus is referred to herein as a "viral vector." There are a large number of available viral vectors suitable for use with the compositions of the instant disclosure, including those identified for human gene therapy applications (*see Pfeifer and Verma, Ann. Rev. Genomics Hum. Genet.* 2:177, 2001). Suitable viral vectors include vectors based on RNA viruses, such as retrovirus-derived vectors, *e.g.*, Moloney murine leukemia virus (MLV)-derived vectors, and include more complex retrovirus-derived vectors, *e.g.*, lentivirus-derived vectors. HIV-1-derived vectors belong to this category. Other examples include lentivirus vectors derived from HIV-2, FIV, equine infectious anemia virus, SIV, and Maedi-Visna virus (ovine lentivirus). Methods of using retroviral and lentiviral viral vectors and packaging cells for transducing mammalian host cells with viral particles containing chimeric receptor transgenes are known in the art and have been previously described, for example, in U.S. Patent 8,119,772; Walchli *et al.*, *PLoS One* 6:327930, 2011; Zhao *et al.*, *J. Immunol.* 174:4415, 2005; Engels *et al.*, *Hum. Gene Ther.* 14:1155, 2003; Frecha *et al.*, *Mol. Ther.* 18:1748, 2010; Verhoeven *et al.*, *Methods Mol. Biol.* 506:97, 2009. Retroviral and lentiviral vector constructs and expression systems are also commercially available.

In certain embodiments, a viral vector is used to introduce a non-endogenous polynucleotide encoding a tandem expression cassette to a host cell. A viral vector may be a retroviral vector or a lentiviral vector. A viral vector may also include a nucleic acid sequence encoding a marker for transduction. Transduction markers for viral vectors are known in the art and include selection markers, which may confer drug resistance, or detectable markers, such as fluorescent markers or cell surface proteins that can be detected by methods such as flow cytometry. In particular embodiments, a viral vector further comprises a gene marker for transduction comprising a fluorescent protein (*e.g.*, green, yellow), an extracellular domain of human CD2, or a truncated human EGFR (EGFRt or tEGFR; *see Wang et al., Blood 118*:1255, 2011). An exemplary tEGFR sequence comprises an amino acid sequence of SEQ ID NO:82.

Other viral vectors also can be used for polynucleotide delivery including DNA viral vectors, including, for example adenovirus-based vectors and adeno-associated virus (AAV)-based vectors; vectors derived from herpes simplex viruses (HSVs), including amplicon vectors, replication-defective HSV and attenuated HSV (Krisky *et al., Gene Ther. 5*: 1517, 1998).

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

Where temporal control is desired, a tandem expression cassette vector may include an element that allows for inducible depletion of transduced cells. For example, such a vector may include an inducible suicide gene. A suicide gene may be an apoptotic gene or a gene that confers sensitivity to an agent (*e.g.*, a drug). Exemplary suicide genes include chemically inducible caspase 9 (iCASP9) (U.S. Patent Publication No. 2013/0071414), chemically inducible Fas, or Herpes simplex virus thymidine kinase (HSV-TK), which confers sensitivity to ganciclovir. In further

embodiments, a tandem expression cassette vector can be designed to express a known cell surface antigen that, upon infusion of an associated antibody, enables depletion of transduced cells. Examples of cell surface antigens and their associated antibodies that may be used for depletion of transduced cells include CD20 and Rituximab, RQR8 (combined CD34 and CD20 epitopes, allowing CD34 selection and anti-CD20 deletion) and Rituximab, and EGFR and Cetuximab.

Inducible vector systems, such as the tetracycline (Tet)-On vector system which activates transgene expression with doxycycline (Heinz et al., Hum. Gene Ther. 2011, 22:166-76) may also be used for inducible expression of tandem expression cassettes. Small molecule responsive transcription factors may also be used to regulate expression. Inducible expression of tandem expression cassettes may be also accomplished via retention using a selective hook (RUSH) system based on streptavidin anchored to the membrane of the endoplasmic reticulum through a hook and a streptavidin binding protein introduced into the CER and CAR/or TCR structure, where addition of biotin to the system leads to the release of the CER and CAR/or TCR from the endoplasmic reticulum (Agaugue et al., 2015, Mol. Ther. 23(Suppl. 1):S88).

In certain embodiments, a tandem expression cassette modified host cell may also be modified to co-express one or more small GTPases. Rho GTPases, a family of small (~21 k Da) signaling G proteins and also a subfamily of the Ras superfamily, regulate actin cytoskeleton organization in various cell types and promote pseudopod extension and phagosome closure during phagocytosis (*see, e.g.*, Castellano et al., 2000, J. Cell Sci. 113:2955-2961). Engulfment requires F-actin recruitment beneath tethered cells or particles, and F-actin rearrangement to allow membrane extension resulting in cell or particle internalization. RhoGTPases include RhoA, Rac1, Rac2, RhoG, and CDC42. Other small GTPases, such as Rap1, is involved in regulation of complement mediated phagocytosis. Co-expression of a small GTPase with the tandem expression cassette encoding a CER may promote or enhance target cell or particle internalization and/or phagosome formation by the host cell. In some embodiments, a recombinant nucleic acid molecule encoding a GTPase is encoded on a separate vector than the tandem expression cassette-containing vector. In other

embodiments, a recombinant nucleic acid molecule encoding a GTPase is encoded on the same vector as the tandem expression cassette. The GTPase and tandem expression may be expressed under the regulation of different promoters on the same vector (*e.g.*, at different multiple cloning sites). Alternatively, the tandem expression cassette and GTPase may be expressed under the regulation of one promoter in a multicistronic vector.

Examples of GTPases that may be co-expressed with a tandem expression cassette include Rac1, Rac2, Rab5 (also referred to as Rab5a), Rab7, Rap1, RhoA, RhoG, CDC42, or any combination thereof. In specific embodiments, the GTPase comprises or is a sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identical to a Rac1 amino acid sequence of SEQ ID NO:83, a Rab5 amino acid sequence of SEQ ID NO:84, a Rab7 amino acid sequence of SEQ ID NO:85, a Rap1 amino acid sequence of SEQ ID NO:86, a RhoA amino acid sequence of SEQ ID NO:87, a CDC42 amino acid sequence of SEQ ID NO:108, or any combination thereof. In certain embodiments, expression of the GTPase is induced or regulated in a host cell such that following a sufficient amount of time for the CER encoded by the tandem expression cassette to have bound its target antigen, the expression of GTPase is switched on. In further embodiments, expression of the GTPase may be switched off following a sufficient amount of time for CER mediated engulfment of the cells expressing the target antigen.

In certain embodiments, a cell, such as an immune cell, obtained from a subject may be genetically modified into a non-natural or recombinant cell (*e.g.*, a non-natural or recombinant immune cell) by introducing a tandem expression cassette as described herein and whereby the cell expresses a cell surface localized CER and CAR/or TCR. In certain embodiments, a host cell is an immune cell, such as a myeloid progenitor cell or a lymphoid progenitor cell. Exemplary immune cells that may be modified to comprise a tandem expression cassette or a vector comprising a tandem expression cassette include a T cell, a natural killer cell, a B cell, a lymphoid precursor

cell, an antigen presenting cell, a dendritic cell, a Langerhans cell, a myeloid precursor cell, a mature myeloid cell, a monocyte, or a macrophage.

In certain embodiments, a B cell is genetically modified to express a tandem expression cassette of the present disclosure. B cells possess certain properties that may be advantageous as host cells, including: trafficking to sites of inflammation, capable of internalizing and presenting antigen, capable of costimulating T cells, highly proliferative, and self-renewing (persist for life). In certain embodiments, a tandem expression cassette modified B cell is capable of digesting an engulfed target cell or engulfed target particle into smaller peptides and presenting them to T cells via an MHC molecule. Antigen presentation by a tandem expression cassette modified B cell may contribute to antigen spreading of the immune response to non-targeted antigens. B cells include progenitor or precursor cells committed to the B cell lineage (*e.g.*, pre-pro-B cells, pro-B cells, and pre-B cells); immature and inactivated B cells; or mature and functional or activated B cells. In certain embodiments, B cells may be naïve B cells, plasma cells, regulatory B cells, marginal zone B cells, follicular B cells, lymphoplasmacytoid cell, plasmablast cell, memory B cells, or any combination thereof. Memory B cells may be distinguished from naïve B cells by expression of CD27, which is absent on naïve B cells. In certain embodiments, the B cells can be primary cells or cell lines derived from human, mouse, rat, or other mammals. B cell lines are well known in the art. If obtained from a mammal, a B cell can be obtained from numerous sources, including blood, bone marrow, spleen, lymph node, or other tissues or fluids. A B cell composition may be enriched or purified.

In certain embodiments, a T cell is genetically modified to express a tandem expression cassette of the present disclosure. Exemplary T cells include CD4⁺ helper, CD8⁺ effector (cytotoxic), naïve (CD45 RA⁺, CCR7⁺, CD62L⁺, CD27⁺, CD45RO⁻), central memory (CD45RO⁺, CD62L⁺, CD8⁺), effector memory (CD45RA⁺, CD45RO⁻, CCR7⁻, CD62L⁻, CD27⁻), T memory stem, regulatory, mucosal-associated invariant (MAIT), $\gamma\delta$ (gd), tissue resident T cells, natural killer T cells, or any combination thereof. In certain embodiments, the T cells can be primary cells or cell lines derived from human, mouse, rat, or other mammals. If obtained from a mammal,

a T cell can be obtained from numerous sources, including blood, bone marrow, lymph node, thymus, or other tissues or fluids. A T cell composition may be enriched or purified. T cell lines are well known in the art, some of which are described in Sandberg *et al.*, *Leukemia* 21:230, 2000. In certain embodiments, the T cells lack endogenous expression of a TCR α gene, TCR β gene, or both. Such T cells may naturally lack endogenous expression of TCR α and β chains, or may have been modified to block expression (*e.g.*, T cells from a transgenic mouse that does not express TCR α and β chains or cells that have been manipulated to inhibit expression of TCR α and β chains) or to knockout a TCR α chain, a TCR β chain, or both genes.

In certain embodiments, host cells expressing a tandem expression cassette of the present disclosure are not T cells or cells of a T cell lineage, but cells that are progenitor cells, stem cells or cells that have been modified to express cell surface anti-CD3.

In certain embodiments, gene editing methods are used to modify the host cell genome to comprise a tandem expression cassette of the present disclosure. Gene editing, or genome editing, is a method of genetic engineering wherein DNA is inserted, replaced, or removed from a host cell's genome using genetically engineered endonucleases. The nucleases create specific double-stranded breaks at targeted loci in the genome. The host cell's endogenous DNA repair pathways then repair the induced break(s), *e.g.*, by non-homologous ending joining (NHEJ) and homologous recombination. Exemplary endonucleases useful for gene editing include a zinc finger nuclease (ZFN), a transcription activator-like effector (TALE) nuclease, a clustered regularly interspaced short palindromic repeats (CRISPR)/Cas nuclease system (*e.g.*, CRISPR-Cas9), a meganuclease, or combinations thereof. Methods of disrupting genes or gene expression in immune cells including B cells and T cells, using gene editing endonucleases are known in the art and described, for example, in PCT Publication Nos. WO 2015/066262; WO 2013/074916; WO 2014/059173; Cheong *et al.*, *Nat. Comm.* 2016 7:10934; Chu *et al.*, *Proc. Natl. Acad. Sci. USA* 2016 113:12514-12519; methods from each of which are incorporated herein by reference in their entirety.

In certain embodiments, expression of an endogenous gene of the host cell is inhibited, knocked down, or knocked out. Examples of endogenous genes that may be inhibited, knocked down, or knocked out in a B cell include IGH, IG κ , IG λ , or any combination thereof. Examples of endogenous genes that may be inhibited, knocked down, or knocked out in a T cell include a TCR gene (TRA or TRB), an HLA gene (HLA class I gene or HLA class II gene), an immune checkpoint molecule (PD-L1, PD-L2, CD80, CD86, B7-H3, B7-H4, HVEM, adenosine, GAL9, VISTA, CEACAM-1, CEACAM-3, CEACAM-5, PVRL2, PD-1, CTLA-4, BTLA, KIR, LAG3, TIM3, A2aR, CD244/2B4, CD160, TIGIT, LAIR-1, or PVRIG/CD112R), or any combination thereof. Expression of an endogenous gene may be inhibited, knocked down, or knocked out at the gene level, transcriptional level, translational level, or a combination thereof. Methods of inhibiting, knocking down, or knocking out an endogenous gene may be accomplished, for example, by an RNA interference agent (*e.g.*, siRNA, shRNA, miRNA, etc.) or an engineered endonuclease (*e.g.*, CRISPR/Cas nuclease system, a zinc finger nuclease (ZFN), a Transcription Activator Like Effector nuclease (TALEN), a meganuclease), or any combination thereof. In certain embodiments, an endogenous B cell gene (*e.g.*, IGH, IG κ , or IG λ) is knocked out by insertion of a tandem expression cassette of the present disclosure into the locus of the endogenous B cell gene, such as via an engineered endonuclease. In certain embodiments, an endogenous T cell gene (*e.g.*, a TCR gene, an HLA gene, or an immune checkpoint molecule gene) is knocked out by insertion of a polynucleotide encoding a tandem expression cassette of the present disclosure into the locus of the endogenous T cell gene, such as via an engineered endonuclease.

The present disclosure also provides a composition comprising a population of tandem expression cassette modified host cells. In certain embodiments, the population of tandem expression cassette modified host cells may be a population of B cells, a population of T cells, a population of natural killer cells, a population of lymphoid precursor cells, a population of antigen presenting cells, a population of dendritic cells, a population of Langerhans cells, a population of myeloid precursor cells, a population of mature myeloid cells, or any combination thereof. Furthermore, a

population of tandem expression cassette modified host cells of a particular cell type may be composed of one or more subtypes. For example, a population of B cells may be composed of tandem expression cassette modified naïve B cells, plasma cells, regulatory B cells, marginal zone B cells, follicular B cells, lymphoplasmacytoid cell, plasmablast cell, memory B cells, or any combination thereof. In another example, a population of T cells may be composed of tandem expression cassette modified CD4⁺ helper T cells, CD8⁺ effector (cytotoxic) T cells, naïve (CD45 RA⁺, CCR7⁺, CD62L⁺, CD27⁺, CD45RO⁻) T cells, central memory (CD45RO⁺, CD62L⁺, CD8⁺) T cells, effector memory (CD45RA⁺, CD45RO⁻, CCR7⁻, CD62L⁻, CD27⁻) T cells, T memory stem cells, regulatory T cells, mucosal-associated invariant T cells (MAIT), $\gamma\delta$ (gd), tissue resident T cells, natural killer T cells, or any combination thereof.

In certain embodiments, a population of host cells is composed of cells that each express the same tandem expression cassette. In other embodiments, a population of host cells is composed of a mixture of two or more subpopulation of host cells, wherein each subpopulation expresses a different tandem expression cassette.

In certain embodiments, when preparing tandem expression cassette modified host cells, *e.g.*, B cells or T cells, one or more growth factor cytokines that promote proliferation of the host cells, *e.g.*, B cells or T cells, may be added to the cell culture. The cytokines may be human or non-human. Exemplary growth factor cytokines that may be used to promote T cell proliferation include IL-2, IL-15, or the like. Exemplary growth factor cytokines that may be used to promote B cell proliferation include CD40L, IL-2, IL-4, IL-15, IL-21, BAFF, or the like.

Prior to genetic modification of the host cells with a tandem expression cassette vector, a source of host cells (*e.g.*, T cells, B cells, natural killer cells, etc.) is obtained from a subject (*e.g.*, whole blood, peripheral blood mononuclear cells, bone marrow, lymph node tissue, cord blood, thymus tissue, tissue from a site of infection, ascites, pleural effusion, spleen tissue), from which host cells are isolated using methods known in the art. Specific host cell subsets can be collected in accordance with known techniques and enriched or depleted by known techniques, such as affinity binding to antibodies, flow cytometry and/or immunomagnetic selection. After

enrichment and/or depletion steps and introduction of a tandem expression cassette, *in vitro* expansion of the desired modified host cells can be carried out in accordance with known techniques, or variations thereof that will be apparent those skilled in the art.

The expression of receptors encoded by tandem expression cassettes on host cells may be functionally characterized according to any of a large number of art-accepted methodologies for assaying host cell (*e.g.*, T cell) activity, including determination of T cell binding, activation or induction and also including determination of T cell responses that are antigen-specific. Examples include determination of T cell proliferation, T cell cytokine release, antigen-specific T cell stimulation, CTL activity (*e.g.*, by detecting ^{51}Cr or Europium release from pre-loaded target cells, induction of caspase activity in target cells, extracellular release of lactate dehydrogenase by target cells), changes in T cell phenotypic marker expression, and other measures of T cell functions. Procedures for performing these and similar assays are may be found, for example, in Lefkovits (*Immunology Methods Manual: The Comprehensive Sourcebook of Techniques*, 1998). *See, also, Current Protocols in Immunology*; Weir, *Handbook of Experimental Immunology*, Blackwell Scientific, Boston, MA (1986); Mishell and Shigii (eds.) *Selected Methods in Cellular Immunology*, Freeman Publishing, San Francisco, CA (1979); Green and Reed, *Science* 281:1309 (1998) and references cited therein. Cytokine levels may be determined according to methods known in the art, including for example, ELISA, ELISPOT, intracellular cytokine staining, flow cytometry, and any combination thereof (*e.g.*, intracellular cytokine staining and flow cytometry). Immune cell proliferation and clonal expansion resulting from an antigen-specific elicitation or stimulation of an immune response may be determined by isolating lymphocytes, such as circulating lymphocytes in samples of peripheral blood cells or cells from lymph nodes, stimulating the cells with antigen, and measuring cytokine production, cell proliferation and/or cell viability, such as by incorporation of tritiated thymidine or non-radioactive assays, such as MTT assays and the like.

In certain embodiments, a tandem expression cassette modified host cell comprising a CER has a phagocytic index of about 20 to about 1,500 for a target cell.

A “phagocytic index” is a measure of phagocytic activity of the transduced host cell as determined by counting the number of target cells or particles ingested per tandem expression cassette modified host cell during a set period of incubation of a suspension of target cells or particles and tandem expression cassette modified host cells in media. Phagocytic index may be calculated by multiplying [total number of engulfed target cells/total number of counted tandem expression cassette modified cells (*e.g.*, phagocytic frequency)] x [average area of target cell or particle staining per tandem expression cassette⁺ host cell x 100 (*e.g.*, hybrid capture)] or [total number of engulfed particles/total number of counted tandem expression cassette modified host cells] x [number of tandem expression cassette modified host cells containing engulfed particles/ total number of counted tandem expression cassette⁺ cells] x 100. In certain embodiments, a tandem expression cassette modified cell has a phagocytic index of about 30 to about 1,500; about 40 to about 1,500; about 50 to about 1,500; about 75 to about 1,500; about 100 to about 1,500; about 200 to about 1,500; about 300 to about 1,500; about 400 to about 1,500; about 500 to about 1,500; about 20 to about 1,400; about 30 to about 1,400; about 40 to about 1,400; about 50 to about 1,400; about 100 to about 1,400; about 200 to about 1,400; about 300 to about 1,400; about 400 to about 1,400; about 500 to about 1,400; about 20 to about 1,300; about 30 to about 1,300; about 40 to about 1,300; about 50 to about 1,300; about 100 to about 1,300; about 200 to about 1,300; about 300 to about 1,300; about 400 to about 1,300; about 500 to about 1,300; about 20 to about 1,200; about 30 to about 1,200; about 40 to about 1,200; about 50 to about 1,200; about 100 to about 1,200; about 200 to about 1,200; about 300 to about 1,200; about 400 to about 1,200; about 500 to about 1,200; about 20 to about 1,100; about 30 to about 1,100; about 40 to about 1,100; about 50 to about 1,100; about 100 to about 1,100; about 200 to about 1,100; about 300 to about 1,100; about 400 to about 1,100; or about 500 to about 1,100; about 20 to about 1,000; about 30 to about 1,000; about 40 to about 1,000; about 50 to about 1,000; about 100 to about 1,000; about 200 to about 1,000; about 300 to about 1,000; about 400 to about 1,000; or about 500 to about 1,000; about 20 to about 750; about 30 to about 750; about 40 to about 750; about 50 to about 750; about 100 to about 750; about 200 to about 750; about 300

to about 750; about 400 to about 750; or about 500 to about 750; about 20 to about 500; about 30 to about 500; about 40 to about 500; about 50 to about 500; about 100 to about 500; about 200 to about 500; or about 300 to about 500. In further embodiments, the incubation time is from about 2 hours to about 4 hours, *e.g.*, about 2 hours, about 3 hours, or about 4 hours. In yet further embodiments, a tandem expression cassette modified cell exhibits phagocytic index that is statistically significantly higher than a control cell transduced with truncated EGFR. Phagocytic index may be calculated using methods known in the art and as further described in the Examples and PCT Application No. PCT/US2017/053553 (incorporated herein by reference in its entirety), including quantification by flow cytometry or fluorescence microscopy.

Host cells may be from an animal, such as a human, primate, cow, horse, sheep, dog, cat, mouse, rat, rabbit, guinea pig, pig, or a combination thereof. In a preferred embodiment, the animal is a human. Host cells may be obtained from a healthy subject or a subject having a disease associated with expression or overexpression of an antigen.

Methods of Use

In one aspect, the present disclosure provides methods for conferring antigen specific cytolytic activity and engulfment activity to a cell comprising introducing into a host cell a tandem expression cassette according to any of the embodiments described herein; and expressing the CER and CAR/or TCR binding protein in the host cell. In certain embodiments, the CER and CAR/or TCR binding protein bind to the same target antigen. In some embodiments, the CER and CAR/or TCR bind to different target antigens. In certain embodiments, host cells modified with tandem expression cassettes of the present disclosure are capable of engulfing target cells or portions of target cells. Thus, cells modified with tandem expression cassettes of the present disclosure may possess targeted cell killing capacity via multiple modalities: cytolysis of the target cell, engulfment of the whole target cell, engulfment of parts of the target cell, or any combination thereof.

In another aspect, the present disclosure provides methods for enhancing antigen-specific cytotoxic activity of a cell comprising introducing into a host cell a tandem expression cassette according to any of the embodiments described herein; and expressing the CER and CAR/or TCR binding protein in the host cell, wherein the expression of the tandem expression cassette enhances cytotoxic activity of the host cell as compared to a host cell that expresses the CAR/or TCR binding protein alone. In certain embodiments, the cytotoxic activity of the host cell is increased at least about 10%, 15%, 20%, 25%, 30%, 35%, 40%, 50%, 55%, 60%, 65%, 70%, 75%, 80% , 85%, 90%, 95%, 100%, 110%, 120%, 130%, 140%, 150%, 160%, 170%, 180%, 190%, 200% or more as compared to the host cell expressing the CAR/or TCR alone. In further embodiments, the tandem expression cassette confers a synergistic cytotoxic response. In some embodiments, the host cell is a T cell or an NK cell. Methods of measuring cytotoxic activity of host cells, particularly immune cells such as T cells and NK cells, include a chromium (^{51}Cr)-release assay, a β -gal or firefly luciferase release assay, flow cytometric methods of measuring target cell death and effector cell activity (*see, e.g.*, Expert Rev. Vaccines, 2010, 9:601-616). In certain embodiments, cytotoxic activity of host cells may be measured by detecting target cell apoptosis following exposure to the host cell, *e.g.*, caspase 3/7 activity, lactate dehydrogenase release.

In another aspect, a tandem expression cassette according to any of the embodiments provided herein may be used in a method of treating a subject suffering from a disease, disorder or undesired condition. Embodiments of these methods include administering to a subject a therapeutically effective amount of a pharmaceutical composition including one or more tandem expression cassettes, polynucleotides encoding one or more tandem expression cassettes, vectors comprising one or more tandem expression cassettes, or a population of host cells genetically modified to express one or more tandem expression cassettes according to the present description.

Diseases that may be treated with cells expressing tandem expression cassette provided in the present disclosure include cancer, autoimmune diseases, and infectious diseases (viral, bacterial, fungal, protozoan infections). Adoptive immune and gene therapies are promising treatments for various types of cancer (Morgan *et al.*,

Science 314:126, 2006; Schmitt *et al.*, *Hum. Gene Ther.* 20:1240, 2009; June, *J. Clin. Invest.* 117:1466, 2007) and infectious disease (Kitchen *et al.*, *PLoS One* 4:38208, 2009; Rossi *et al.*, *Nat. Biotechnol.* 25:1444, 2007; Zhang *et al.*, *PLoS Pathog.* 6:e1001018, 2010; Luo *et al.*, *J. Mol. Med.* 89:903, 2011).

A wide variety of cancers, including solid tumors and leukemias are amenable to treatment using the tandem expression cassette compositions provided herein. Exemplary cancers that may be treated using the receptors, modified host cells, and composition described herein include adenocarcinoma of the breast, prostate, and colon; all forms of bronchogenic carcinoma of the lung; myeloid leukemia; melanoma; hepatoma; neuroblastoma; papilloma; apudoma; choristoma; branchioma; malignant carcinoid syndrome; carcinoid heart disease; and carcinoma (*e.g.*, Walker, basal cell, basosquamous, Brown-Pearce, ductal, Ehrlich tumor, Krebs 2, Merkel cell, mucinous, non-small cell lung, oat cell, papillary, scirrhous, bronchiolar, bronchogenic, squamous cell, and transitional cell). Additional types of cancers that may be treated using the receptors, modified host cells, and composition described herein include histiocytic disorders; malignant histiocytosis; leukemia; Hodgkin's disease; immunoproliferative small; non-Hodgkin's lymphoma; plasmacytoma; multiple myeloma; plasmacytoma; reticuloendotheliosis; melanoma; chondroblastoma; chondroma; chondrosarcoma; fibroma; fibrosarcoma; giant cell tumors; histiocytoma; lipoma; liposarcoma; mesothelioma; myxoma; myxosarcoma; osteoma; osteosarcoma; chordoma; craniopharyngioma; dysgerminoma; hamartoma; mesenchymoma; mesonephroma; myosarcoma; ameloblastoma; cementoma; odontoma; teratoma; thymoma; trophoblastic tumor. Further, the following types of cancers are also contemplated as amenable to treatment using the receptors, modified host cells, and composition described herein: adenoma; cholangioma; cholesteatoma; cyclindroma; cystadenocarcinoma; cystadenoma; granulosa cell tumor; gynandroblastoma; hepatoma; hidradenoma; islet cell tumor; Leydig cell tumor; papilloma; sertoli cell tumor; theca cell tumor; leiomyoma; leiomyosarcoma; myoblastoma; myomma; myosarcoma; rhabdomyoma; rhabdomyosarcoma; ependymoma; ganglioneuroma; glioma; medulloblastoma; meningioma; neurilemmoma; neuroblastoma; neuroepithelioma;

neurofibroma; neuroma; paraganglioma; paraganglioma nonchromaffin. The types of cancers that may be treated also include angiokeratoma; angiolymphoid hyperplasia with eosinophilia; angioma sclerosing; angiomatosis; glomangioma; hemangioendothelioma; hemangioma; hemangiopericytoma; hemangiosarcoma; lymphangioma; lymphangiomyoma; lymphangiosarcoma; pinealoma; carcinosarcoma; chondrosarcoma; cystosarcoma phyllodes; fibrosarcoma; hemangiosarcoma; leiomyosarcoma; leukosarcoma; liposarcoma; lymphangiosarcoma; myosarcoma; myxosarcoma; ovarian carcinoma; rhabdomyosarcoma; sarcoma; neoplasms; neurofibromatosis; and cervical dysplasia.

Examples of hyperproliferative disorders amenable to therapy using the tandem expression cassette compositions described herein include B-cell cancers, including B-cell lymphomas (such as various forms of Hodgkin's disease, non-Hodgkins lymphoma (NHL) or central nervous system lymphomas), leukemias (such as acute lymphoblastic leukemia (ALL), chronic lymphocytic leukemia (CLL), Hairy cell leukemia, B cell blast transformation of chronic myeloid leukemia) and myelomas (such as multiple myeloma). Additional B cell cancers that may be treated using the receptors, modified host cells, and composition described herein include small lymphocytic lymphoma, B-cell prolymphocytic leukemia, lymphoplasmacytic lymphoma, splenic marginal zone lymphoma, plasma cell myeloma, solitary plasmacytoma of bone, extraosseous plasmacytoma, extra-nodal marginal zone B-cell lymphoma of mucosa-associated (MALT) lymphoid tissue, nodal marginal zone B-cell lymphoma, follicular lymphoma, mantle cell lymphoma, diffuse large B-cell lymphoma, mediastinal (thymic) large B-cell lymphoma, intravascular large B-cell lymphoma, primary effusion lymphoma, Burkitt's lymphoma/leukemia, B-cell proliferations of uncertain malignant potential, lymphomatoid granulomatosis, and post-transplant lymphoproliferative disorder.

Infectious diseases include those associated with infectious agents and include any of a variety of bacteria (*e.g.*, pathogenic *E. coli*, *S. typhimurium*, *P. aeruginosa*, *B. anthracis*, *C. botulinum*, *C. difficile*, *C. perfringens*, *H. pylori*, *V. cholerae*, *Listeria spp.*, *Rickettsia spp.*, *Chlamydia spp.*, and the like), mycobacteria,

and parasites (including any known parasitic member of the Protozoa). Infectious viruses include eukaryotic viruses, such as adenovirus, bunyavirus, herpesvirus, papovavirus, papillomavirus (*e.g.*, HPV), paramyxovirus, picornavirus, rhabdovirus (*e.g.*, Rabies), orthomyxovirus (*e.g.*, influenza), poxvirus (*e.g.*, Vaccinia), reovirus, retrovirus, lentivirus (*e.g.*, HIV), flavivirus (*e.g.*, HCV, HBV) or the like. In certain embodiments, a composition comprising a tandem expression cassette according to the present disclosure is used for treating infection with a microbe capable of establishing a persistent infection in a subject.

Methods of treating a subject comprise administering an effective amount of tandem expression cassette modified cells (*i.e.*, recombinant cells that express tandem expression cassettes). The tandem expression cassette modified cells may be xenogeneic, syngeneic, allogeneic, or autologous to the subject.

Pharmaceutical compositions including tandem expression cassette modified cells may be administered in a manner appropriate to the disease or condition to be treated (or prevented) as determined by persons skilled in the medical art. An appropriate dose, suitable duration, and frequency of administration of the compositions will be determined by such factors as the condition of the patient, size, weight, body surface area, age, sex, type and severity of the disease, particular therapy to be administered, particular form of the active ingredient, time and the method of administration, and other drugs being administered concurrently. The present disclosure provides pharmaceutical compositions comprising tandem expression cassette modified cells and a pharmaceutically acceptable carrier, diluent, or excipient. Suitable excipients include water, saline, dextrose, glycerol, or the like and combinations thereof. Other suitable infusion medium can be any isotonic medium formulation, including saline, Normosol R (Abbott), Plasma-Lyte A (Baxter), 5% dextrose in water, or Ringer's lactate.

A treatment effective amount of cells in a pharmaceutical composition is at least one cell (for example, one tandem expression cassette modified T cell) or is more typically greater than 10^2 cells, for example, up to 10^6 , up to 10^7 , up to 10^8 cells, up to 10^9 cells, up to 10^{10} cells, or up to 10^{11} cells or more. In certain embodiments, the

cells are administered in a range from about 10^6 to about 10^{10} cells/m², preferably in a range of about 10^7 to about 10^9 cells/m². In a specific embodiment, the tandem expression cassette modified cells are administered in an amount of at least about 1×10^6 cells, 2×10^6 cells, 3×10^6 cells, 4×10^6 cells, 5×10^6 cells, 6×10^6 cells, 7×10^6 cells, 8×10^6 cells, 9×10^6 cells, 1×10^7 cells, 2×10^7 cells, 3×10^7 cells, 4×10^7 cells, 5×10^7 cells, 6×10^7 cells, 7×10^7 cells, 8×10^7 cells, 9×10^7 cells, 1×10^8 cells, 2×10^8 cells, 3×10^8 cells, 4×10^8 cells, 5×10^8 cells, 6×10^8 cells, 7×10^8 cells, 8×10^8 cells, 9×10^8 cells, 1×10^9 cells, 2×10^9 cells, 3×10^9 cells, 4×10^9 cells, 5×10^9 cells, 6×10^9 cells, 7×10^9 cells, 8×10^9 cells, 9×10^9 cells, 1×10^{10} cells, 2×10^{10} cells, 3×10^{10} cells, 4×10^{10} cells, 5×10^{10} cells, 6×10^{10} cells, 7×10^{10} cells, 8×10^{10} cells, 9×10^{10} cells, 1×10^{11} cells, 2×10^{11} cells, 3×10^{11} cells, 4×10^{11} cells, 5×10^{11} cells, 6×10^{11} cells, 7×10^{11} cells, 8×10^{11} cells, or 9×10^{11} cells. The number of cells will depend upon the ultimate use for which the composition is intended as well the type of cells included therein. For example, a composition comprising cells modified to contain a tandem expression cassette will comprise a cell population containing from about 5% to about 95% or more of such cells. In certain embodiments, a composition comprising tandem expression cassette modified cells comprises a cell population comprising at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more of such cells. For uses provided herein, the cells are generally in a volume of a liter or less, 500 mls or less, 250 mls or less, or 100 mls or less. Hence the density of the desired cells is typically greater than 10^4 cells/ml and generally is greater than 10^7 cells/ml, generally 10^8 cells/ml or greater. The cells may be administered as a single infusion or in multiple infusions over a range of time. Repeated infusions of tandem expression cassette modified cells may be separated by days, weeks, months, or even years if relapses of disease or disease activity are present. A clinically relevant number of immune cells can be apportioned into multiple infusions that cumulatively equal or exceed 10^6 , 10^7 , 10^8 , 10^9 , 10^{10} , or 10^{11} cells. A preferred dose for administration of a host cell comprising a recombinant expression vector as described herein is about 10^7 cells/m², about 5×10^7 cells/m², about 10^8

cells/m², about 5 x 10⁸ cells/m², about 10⁹ cells/m², about 5 x 10⁹ cells/m², about 10¹⁰ cells/m², about 5 x 10¹⁰ cells/m², or about 10¹¹ cells/m².

Compositions comprising tandem expression cassettes, vectors comprising tandem expression cassettes, or tandem expression cassette modified cells as described herein may be administered intravenously, intraperitoneally, intranasally, intratumorally, into the bone marrow, into the lymph node, and /or into cerebrospinal fluid.

Tandem expression cassette compositions may be administered to a subject in combination with one or more additional therapeutic agents. Examples of therapeutic agents that may be administered in combination with a tandem expression cassette compositions according to the present description include radiation therapy, genetically engineered cellular immunotherapy (e.g., T cell, dendritic cell, natural killer cell, macrophage, chimeric antigen receptor therapy), antibody therapy, immune checkpoint molecule inhibitor therapy, UV light therapy, electric pulse therapy, high intensity focused ultrasound therapy, oncolytic virus therapy, or a pharmaceutical therapy, such as a chemotherapeutic agent, a therapeutic peptide, a hormone, an aptamer, antibiotic, anti-viral agent, anti-fungal agent, anti-inflammatory agent, a small molecule therapy.

Radiation therapy includes external beam radiation therapy (e.g., conventional external beam radiation therapy, stereotactic radiation, 3-dimensional conformal radiation therapy, intensity-modulated radiation therapy, volumetric modulated arc therapy, particle therapy, proton therapy, and auger therapy), brachytherapy, systemic radioisotope therapy, intraoperative radiotherapy, or any combination thereof.

Exemplary antibodies for use in conjunction with the tandem expression cassette compositions described herein include rituxmab, pertuzumab, trastuzumab, alemtuzumab, Ibritumomab tiuxetan, Brentuximab vedotin, cetuximab, bevacizumab, abciximab, adalimumab, alefacept, basilizimab, belimumab, bezlotoxumab, canakinumab, certolizumab pegol, daclizumab, denosumab, efalizumab, golimumab, olaratumab, palivizumab, panitumumab, and tocilizumab.

Exemplary inhibitors of immune checkpoint molecules that may be for use in conjunction with the tandem expression cassette compositions described herein include checkpoint inhibitors targeting PD-L1, PD-L2, CD80, CD86, B7-H3, B7-H4, HVEM, adenosine, GAL9, VISTA, CEACAM-1, CEACAM-3, CEACAM-5, PVRL2, PD-1, CTLA-4, BTLA, KIR, LAG3, TIM3, A2aR, CD244/2B4, CD160, TIGIT, LAIR-1, PVRIG/CD112R, or any combination thereof. In certain embodiments, an immune checkpoint inhibitor may be an antibody, a peptide, an RNAi agent, or a small molecule. An antibody specific for CTLA-4 may be ipilimumab or tremelimumab. An antibody specific for PD-1 may be pidilizumab, nivolumab, or pembrolizumab. An antibody specific for PD-L1 may be durvalumab, atezolizumab, or avelumab.

A chemotherapeutic includes non-specific cytotoxic agents that inhibit mitosis or cell division, as well as molecularly targeted therapy that blocks the growth and spread of cancer cells by targeting specific molecules that are involved in tumor growth, progression, and metastasis (e.g., oncogenes). Exemplary non-specific chemotherapeutics for use in conjunction with the tandem expression cassette compositions described herein may include an alkylating agent, a platinum based agent, a cytotoxic agent, an inhibitor of chromatin function, a topoisomerase inhibitor, a microtubule inhibiting drug, a DNA damaging agent, an antimetabolite (such as folate antagonists, pyrimidine analogs, purine analogs, and sugar-modified analogs), a DNA synthesis inhibitor, a DNA interactive agent (such as an intercalating agent), and a DNA repair inhibitor.

Examples of chemotherapeutic agents considered for use in combination therapies contemplated herein include vemurafenib, dabrafenib, trametinib, cobimetinib, anastrozole (Arimidex®), bicalutamide (Casodex®), bleomycin sulfate (Blenoxane®), busulfan (Myleran®), busulfan injection (Busulfex®), capecitabine (Xeloda®), N4-pentoxycarbonyl-5-deoxy-5-fluorocytidine, carboplatin (Paraplatin®), carmustine (BiCNU®), chlorambucil (Leukeran®), cisplatin (Platinol®), cladribine (Leustatin®), cyclophosphamide (Cytosan® or Neosar®), cytarabine, cytosine arabinoside (Cytosar-U®), cytarabine liposome injection (DepoCyt®), dacarbazine (DTIC-Dome®), dactinomycin (Actinomycin D, Cosmegen), daunorubicin

hydrochloride (Cerubidine®), daunorubicin citrate liposome injection (DaunoXome®), dexamethasone, docetaxel (Taxotere®), doxorubicin hydrochloride (Adriamycin®, Rubex®), etoposide (Vepesid®), fludarabine phosphate (Fludara®), 5-fluorouracil (Acrucil®, Efudex®), flutamide (Eulexin®), tezacitibine, Gemcitabine (difluorodeoxycytidine), hydroxyurea (Hydrea®), Idarubicin (Idamycin®), ifosfamide (IFEX®), irinotecan (Camptosar®), L-asparaginase (ELSPAR®), leucovorin calcium, melphalan (Alkeran®), 6-mercaptopurine (Purinethol®), methotrexate (Folex®), mitoxantrone (Novantrone®), mylotarg, paclitaxel (Taxol®), phoenix (Yttrium90/MX-DTPA), pentostatin, polifeprosan 20 with carmustine implant (Gliadel®), fdabra tamoxifen citrate (Nolvadex®), teniposide (Vumon®), 6-thioguanine, thiotepa, tirapazamine (Tirazone®), topotecan hydrochloride for injection (Hycamptin®), vinblastine (Velban®), vincristine (Oncovin®), ibrutinib, venetoclax, crizotinib, alectinib, brigatinib, ceritinib, and vinorelbine (Navelbine®).

Exemplary alkylating agents for use in combination therapies contemplated herein include nitrogen mustards, ethylenimine derivatives, alkyl sulfonates, nitrosoureas and triazenes): uracil mustard (Aminouracil Mustard®, Chlorethaminacil®, Demethyldopan®, Desmethyldopan®, Haemanthamine®, Nordopan®, Uracil nitrogen Mustard®, Uracillost®, Uracilmostaza®, Uramustin®, Uramustine®), chlormethine (Mustargen®), cyclophosphamide (Cytosan®, Neosar®, Clafen®, Endoxan®, Procytox®, Revimmune™), ifosfamide (Mitoxana®), melphalan (Alkeran®), Chlorambucil (Leukeran®), pipobroman (Amedel®, Vercyte®), triethylenemelamine (Hemel®, Hexalen®, Hexastat®), triethylenethiophosphoramine, Temozolomide (Temodar®), thiotepa (Thioplex®), busulfan (Busilvex®, Myleran®), carmustine (BiCNU®), lomustine (CeeNU®), streptozocin (Zanosar®), and Dacarbazine (DTIC-Dome®). Additional exemplary alkylating agents for use in combination therapies contemplated herein include, without limitation, Oxaliplatin (Eloxatin®); Temozolomide (Temodar® and Temodal®); Dactinomycin (also known as actinomycin-D, Cosmegen®); Melphalan (also known as L-PAM, L-sarcolysin, and phenylalanine mustard, Alkeran®); Altretamine (also known as hexamethylmelamine (HMM), Hexalen®); Carmustine (BiCNU®); Bendamustine (Treanda®); Busulfan

(Busulfex® and Myleran®); Carboplatin (Paraplatin®); Lomustine (also known as CCNU, CeeNU®); Cisplatin (also known as CDDP, Platinol® and Platinol®-AQ); Chlorambucil (Leukeran®); Cyclophosphamide (Cytosan® and Neosar®); Dacarbazine (also known as DTIC, DIC and imidazole carboxamide, DTIC-Dome®); Altretamine (also known as hexamethylmelamine (HMM), Hexalen®); Ifosfamide (Ifex®); Prednimustine; Procarbazine (Matulane®); Mechlorethamine (also known as nitrogen mustard, mustine and mechloroethamine hydrochloride, Mustargen®); Streptozocin (Zanosar®); Thiotepa (also known as thiophosphoamide, TESP and TSPA, Thioplex®); Cyclophosphamide (Endoxan®, Cytosan®, Neosar®, Procytox®, Revimmune®); and Bendamustine HCl (Treanda®).

Exemplary platinum based agents for use in combination therapies contemplated herein include carboplatin, cisplatin, oxaliplatin, nedaplatin, picoplatin, satraplatin, phenanthriplatin, and triplatin tetranitrate.

Exemplary molecularly targeted inhibitors for use in conjunction with the tandem expression cassette compositions described herein include small molecules that target molecules involved in cancer cell growth and survival, including for example, hormone antagonists, signal transduction inhibitors, gene expression inhibitors (*e.g.*, translation inhibitors), apoptosis inducers, angiogenesis inhibitors (*e.g.*, a VEGF pathway inhibitor), tyrosine kinase inhibitors (*e.g.*, an EGF/EGFR pathway inhibitor), growth factor inhibitors, GTPase inhibitors, serine/threonine kinase inhibitors, transcription factor inhibitors, inhibitors of driver mutations associated with cancer, B-Raf inhibitors, a MEK inhibitors, mTOR inhibitors, adenosine pathway inhibitors, EGFR inhibitors, PI3K inhibitors, BCL2 inhibitors, VEGFR inhibitors, MET inhibitors, MYC inhibitors, BCR-ABL inhibitors, HER2 inhibitors, H-RAS inhibitors, K-RAS inhibitors, PDGFR inhibitors, ALK inhibitors, ROS1 inhibitors, and BTK inhibitors. In certain embodiments, use of molecularly targeted therapy comprises administering a molecularly targeted therapy specific for the molecular target to a subject identified as having a tumor that possesses the molecular target (*e.g.*, driver oncogene). In certain embodiments, the molecular target has an activating mutation. In certain embodiments, use of tandem expression cassette modified cells in combination

with a molecularly targeted inhibitor increases the magnitude of anti-tumor response, the durability of anti-tumor response, or both. In certain embodiments, a lower than typical dose of molecularly targeted therapy is used in combination with tandem expression cassette modified cells.

Exemplary angiogenesis inhibitors for use in conjunction with tandem expression cassette compositions described herein may include, without limitation A6 (Angstrom Pharmaceuticals), ABT-510 (Abbott Laboratories), ABT-627 (Atrasentan) (Abbott Laboratories/Xinlay), ABT-869 (Abbott Laboratories), Actimid (CC4047, Pomalidomide) (Celgene Corporation), AdGVPEDF.11D (GenVec), ADH-1 (Exherin) (Adherex Technologies), AEE788 (Novartis), AG-013736 (Axitinib) (Pfizer), AG3340 (Prinomastat) (Agouron Pharmaceuticals), AGX1053 (AngioGenex), AGX51 (AngioGenex), ALN-VSP (ALN-VSP O2) (Alnylam Pharmaceuticals), AMG 386 (Amgen), AMG706 (Amgen), Apatinib (YN968D1) (Jiangsu Hengrui Medicine), AP23573 (Ridaforolimus/MK8669) (Ariad Pharmaceuticals), AQ4N (Novavea), ARQ 197 (ArQule), ASA404 (Novartis/Antisoma), Atiprimod (Callisto Pharmaceuticals), ATN-161 (Attenuon), AV-412 (Aveo Pharmaceuticals), AV-951 (Aveo Pharmaceuticals), Avastin (Bevacizumab) (Genentech), AZD2171 (Cediranib/Recentin) (AstraZeneca), BAY 57-9352 (Telatinib) (Bayer), BEZ235 (Novartis), BIBF1120 (Boehringer Ingelheim Pharmaceuticals), BIBW 2992 (Boehringer Ingelheim Pharmaceuticals), BMS-275291 (Bristol-Myers Squibb), BMS-582664 (Brivanib) (Bristol-Myers Squibb), BMS-690514 (Bristol-Myers Squibb), Calcitriol, CCI-779 (Torisel) (Wyeth), CDP-791 (ImClone Systems), Ceflatonin (Homoharringtonine/HHT) (ChemGenex Therapeutics), Celebrex (Celecoxib) (Pfizer), CEP-7055 (Cephalon/Sanofi), CHIR-265 (Chiron Corporation), NGR-TNF, COL-3 (Metastat) (Collagenex Pharmaceuticals), Combretastatin (Oxigene), CP-751,871 (Figitumumab) (Pfizer), CP-547,632 (Pfizer), CS-7017 (Daiichi Sankyo Pharma), CT-322 (Angiocept) (Adnexus), Curcumin, Dalteparin (Fragmin) (Pfizer), Disulfiram (Antabuse), E7820 (Eisai Limited), E7080 (Eisai Limited), EMD 121974 (Cilengitide) (EMD Pharmaceuticals), ENMD-1198 (EntreMed), ENMD-2076 (EntreMed), Endostar (Simcere), Erbitux (ImClone/Bristol-Myers Squibb), EZN-2208 (Enzon

Pharmaceuticals), EZN-2968 (Enzon Pharmaceuticals), GC1008 (Genzyme), Genistein, GSK1363089(Foretinib) (GlaxoSmithKline), GW786034 (Pazopanib) (GlaxoSmithKline), GT-111 (Vascular Biogenics Ltd.), IMC-1121B (Ramucirumab) (ImClone Systems), IMC-18F1 (ImClone Systems), IMC-3G3 (ImClone LLC), INCB007839 (Incyte Corporation), INGN 241 (Introgen Therapeutics), Iressa (ZD1839/Gefitinib), LBH589 (Faridak/Panobinostat) (Novartis), Lucentis (Ranibizumab) (Genentech/Novartis), LY317615 (Enzastaurin) (Eli Lilly and Company), Macugen (Pegaptanib) (Pfizer), MEDI522 (Abrigin) (MedImmune), MLN518(Tandutinib) (Millennium), Neovastat (AE941/Benefin) (Aeterna Zentaris), Nexavar (Bayer/Onyx), NM-3 (Genzyme Corporation), Noscapine (Cougar Biotechnology), NPI-2358 (Nereus Pharmaceuticals), OSI-930 (OSI), Palomid 529 (Paloma Pharmaceuticals, Inc.), Panzem Capsules (2ME2) (EntreMed), Panzem NCD (2ME2) (EntreMed), PF-02341066 (Pfizer), PF-04554878 (Pfizer), PI-88 (Progen Industries/Medigen Biotechnology), PKC412 (Novartis), Polyphenon E (Green Tea Extract) (Polypheno E International, Inc), PPI-2458 (Praecis Pharmaceuticals), PTC299 (PTC Therapeutics), PTK787 (Vatalanib) (Novartis), PXD101 (Belinostat) (CuraGen Corporation), RAD001 (Everolimus) (Novartis), RAF265 (Novartis), Regorafenib (BAY73-4506) (Bayer), Revlimid (Celgene), Retaane (Alcon Research), SN38 (Liposomal) (Neopharm), SNS-032 (BMS-387032) (Sunesis), SOM230(Pasireotide) (Novartis), Squalamine (Genaera), Suramin, Sutent (Pfizer), Tarceva (Genentech), TB-403 (Thrombogenics), Temozolastin (Collard Biopharmaceuticals), Tetrathiomolybdate (Sigma-Aldrich), TG100801 (TargeGen), Thalidomide (Celgene Corporation), Tinzaparin Sodium, TKI258 (Novartis), TRC093 (Tacon Pharmaceuticals Inc.), VEGF Trap (Aflibercept) (Regeneron Pharmaceuticals), VEGF Trap-Eye (Regeneron Pharmaceuticals), Veglin (VasGene Therapeutics), Bortezomib (Millennium), XL184 (Exelixis), XL647 (Exelixis), XL784 (Exelixis), XL820 (Exelixis), XL999 (Exelixis), ZD6474 (AstraZeneca), Vorinostat (Merck), and ZSTK474.

Exemplary Vascular Endothelial Growth Factor (VEGF) receptor inhibitors for use in conjunction with the tandem expression cassette compositions described herein may include, but are not limited to, Bevacizumab (Avastin®), axitinib

(Inlyta®); Brivanib alaninate (BMS-582664, (S)—((R)-1-(4-(4-Fluoro-2-methyl-1H-indol-5-yloxy)-5-methylpyrrolo[2,1-f][1,2,4]triazin-6-yloxy)propan-2-yl)2-aminopropanoate); Sorafenib (Nexavar®); Pazopanib (Votrient®); Sunitinib malate (Sutent®); Cediranib (AZD2171, CAS 288383-20-1); Vargatef (BIBF1120, CAS 928326-83-4); Foretinib (GSK1363089); Telatinib (BAY57-9352, CAS 332012-40-5); Apatinib (YN968D1, CAS 811803-05-1); Imatinib (Gleevec®); Ponatinib (AP24534, CAS 943319-70-8); Tivozanib (AV951, CAS 475108-18-0); Regorafenib (BAY73-4506, CAS 755037-03-7); Vatalanib dihydrochloride (PTK787, CAS 212141-51-0); Brivanib (BMS-540215, CAS 649735-46-6); Vandetanib (Caprelsa® or AZD6474); Motesanib diphosphate (AMG706, CAS 857876-30-3, N-(2,3-dihydro-3,3-dimethyl-1H-indol-6-yl)-2-[(4-pyridinylmethyl)amino]-3-pyridinecarboxamide, described in PCT Publication No. WO 02/066470); Dovitinib dilactic acid (TKI258, CAS 852433-84-2); Linfanib (ABT869, CAS 796967-16-3); Cabozantinib (XL184, CAS 849217-68-1); Lestaurtinib (CAS 111358-88-4); N-[5-[[[5-(1,1-Dimethylethyl)-2-oxazolyl]methyl]thio]-2-thiazolyl]-4-piperidinecarboxamide (BMS38703, CAS 345627-80-7); (3R,4R)-4-Amino-1-((4-((3-methoxyphenyl)amino)pyrrolo[2,1-f][1,2,4]triazin-5-yl)methyl)piperidin-3-ol (BMS690514); N-(3,4-Dichloro-2-fluorophenyl)-6-methoxy-7-[[[(3 α ,5 β ,6 α)-octahydro-2-methylcyclopenta[c]pyrrol-5-yl]methoxy]-4-quinazolinamine (XL647, CAS 781613-23-8); 4-Methyl-3-[[1-methyl-6-(3-pyridinyl)-1H-pyrazolo[3,4-d]pyrimidin-4-yl]amino]-N-[3-(trifluoromethyl)phenyl]-benzamide (BHG712, CAS 940310-85-0); and Aflibercept (Eylea®).

Exemplary EGF pathway inhibitors for use in conjunction with the tandem expression cassette compositions described herein may include, without limitation tyrphostin 46, EKB-569, erlotinib (Tarceva®), gefitinib (Iressa®), erbitux, nimotuzumab, lapatinib (Tykerb®), cetuximab (anti-EGFR mAb), ¹⁸⁸Re-labeled nimotuzumab (anti-EGFR mAb), and those compounds that are generically and specifically disclosed in WO 97/02266, EP 0 564 409, WO 99/03854, EP 0 520 722, EP 0 566 226, EP 0 787 722, EP 0 837 063, U.S. Pat. No. 5,747,498, WO 98/10767, WO 97/30034, WO 97/49688, WO 97/38983 and WO 96/33980. Exemplary EGFR antibodies include, but are not limited to, Cetuximab (Erbix®); Panitumumab

(Vectibix®); Matuzumab (EMD-72000); Trastuzumab (Herceptin®); Nimotuzumab (hR3); Zalutumumab; TheraCIM h-R3; MDX0447 (CAS 339151-96-1); and ch806 (mAb-806, CAS 946414-09-1). Exemplary Epidermal growth factor receptor (EGFR) inhibitors include, but not limited to, Osimertinib (Tagrisso®), Erlotinib hydrochloride (Tarceva®), Gefitinib (Iressa®); N-[4-[(3-Chloro-4-fluorophenyl)amino]-7-[(3''S'')-tetrahydro-3-furanyl]oxy]-6-quinazolinyl]-4(dimethylamino)-2-butenamide, Tovok®; Vandetanib (Caprelsa®); Lapatinib (Tykerb®); (3R,4R)-4-Amino-1-((4-((3-methoxyphenyl)amino)pyrrolo[2,1-f][1,2,4]triazin-5-yl)methyl)piperidin-3-ol (BMS690514); Canertinib dihydrochloride (CI-1033); 6-[4-[(4-Ethyl-1-piperazinyl)methyl]phenyl]-N-[(1R)-1-phenylethyl]-7H-Pyrrolo[2,3-d]pyrimidin-4-amine (AEE788, CAS 497839-62-0); Mubritinib (TAK165); Pelitinib (EKB569); Afatinib (BIBW2992); Neratinib (HKI-272); N-[4-[[1-[(3-Fluorophenyl)methyl]-1H-indazol-5-yl]amino]-5-methylpyrrolo[2,1-f][1,2,4]triazin-6-yl]-carbamic acid, (3S)-3-morpholinylmethyl ester (BMS599626); N-(3,4-Dichloro-2-fluorophenyl)-6-methoxy-7-[[[(3 α ,5 β ,6 α)-octahydro-2-methylcyclopenta[c]pyrrol-5-yl]methoxy]-4-quinazolinamine (XL647, CAS 781613-23-8); and 4-[4-[(1R)-1-Phenylethyl]amino]-7H-pyrrolo[2,3-d]pyrimidin-6-yl]-phenol (PKI166, CAS 187724-61-4).

Exemplary mTOR inhibitors for use in conjunction with the tandem expression cassette compositions described herein may include, without limitation, rapamycin (Rapamune®), and analogs and derivatives thereof; SDZ-RAD; Temsirolimus (Torisel®; also known as CCI-779); Ridaforolimus (formally known as deferolimus, (1R,2R,4S)-4-[(2R)-2[(1R,9S,12S,15R,16E,18R,19R,21R,23S,24E,26E,28Z,30S,32S,35R)-1,18-dihydroxy-19,30-dimethoxy-15,17,21,23,29,35-hexamethyl-2,3,10,14,20-pentaoxo-11,36-dioxo-4-azatricyclo[30.3.1.0^{4,9}]hexatriaconta-16,24,26,28-tetraen-12-yl]propyl]-2-methoxycyclohexyl dimethylphosphinate, also known as AP23573 and MK8669, and described in PCT Publication No. WO 03/064383); Everolimus (Afinitor® or RAD001); Rapamycin (AY22989, Sirolimus®); Simapimod (CAS 164301-51-3); (5-{2,4-Bis[(3S)-3-methylmorpholin-4-yl]pyrido[2,3-d]pyrimidin-7-yl}-2-methoxyphenyl)methanol (AZD8055); 2-Amino-8-[trans-4-(2-

hydroxyethoxy)cyclohexyl]-6-(6-methoxy-3-pyridinyl)-4-methyl-pyrido[2,3-d]pyrimidin-7(8H)-one (PF04691502, CAS 1013101-36-4); and N²-[1,4-dioxo-[[4-(4-oxo-8-phenyl-4H-1-benzopyran-2-yl)morpholinium-4-yl]methoxy]butyl]-L-arginylglycyl-L- α -aspartyl-L-serine-, inner salt (SF1126, CAS 936487-67-1).

Exemplary Phosphoinositide 3-kinase (PI3K) inhibitors for use in conjunction with the tandem expression cassette compositions described herein may include, but are not limited to, 4-[2-(1H-Indazol-4-yl)-6-[[4-(methylsulfonyl)piperazin-1-yl]methyl]thieno[3,2-d]pyrimidin-4-yl]morpholine (also known as GDC 0941 and described in PCT Publication Nos. WO 09/036082 and WO 09/055730); 2-Methyl-2-[4-[3-methyl-2-oxo-8-(quinolin-3-yl)-2,3-dihydroimidazo[4,5-c]quinolin-1-yl]phenyl]propionitrile (also known as BEZ 235 or NVP-BEZ 235, and described in PCT Publication No. WO 06/122806); 4-(trifluoromethyl)-5-(2,6-dimorpholinopyrimidin-4-yl)pyridin-2-amine (also known as BKM120 or NVP-BKM120, and described in PCT Publication No. WO2007/084786); Tozasertib (VX680 or MK-0457, CAS 639089-54-6); (5Z)-5-[[4-(4-Pyridinyl)-6-quinolinyl]methylene]-2,4-thiazolidinedione (GSK1059615, CAS 958852-01-2); (1E,4S,4aR,5R,6aS,9aR)-5-(Acetyloxy)-1-[(di-2-propenylamino)methylene]-4,4a,5,6,6a,8,9,9a-octahydro-11-hydroxy-4-(methoxymethyl)-4a,6a-dimethyl-cyclopenta[5,6]naphtho[1,2-c]pyran-2,7,10(1H)-trione (PX866, CAS 502632-66-8); and 8-Phenyl-2-(morpholin-4-yl)-chromen-4-one (LY294002, CAS 154447-36-6). Exemplary Protein Kinase B (PKB) or AKT inhibitors include, but are not limited to, 8-[4-(1-Aminocyclobutyl)phenyl]-9-phenyl-1,2,4-triazolo[3,4-f][1,6]naphthyridin-3(2H)-one (MK-2206, CAS 1032349-93-1); Perifosine (KRX0401); 4-Dodecyl-N-1,3,4-thiadiazol-2-yl -benzenesulfonamide (PHT-427, CAS 1191951-57-1); 4-[2-(4-Amino-1,2,5-oxadiazol-3-yl)-1-ethyl-7-[(3S)-3-piperidinylmethoxy]-1H-imidazo[4,5-c]pyridin-4-yl]-2-methyl-3-butyn-2-ol (GSK690693, CAS 937174-76-0); 8-(1-Hydroxyethyl)-2-methoxy-3-[(4-methoxyphenyl)methoxy]-6H-dibenzo[b,d]pyran-6-one (palomid 529, P529, or SG-00529); Tricirbine (6-Amino-4-methyl-8-(β -D-ribofuranosyl)-4H,8H-pyrrolo[4,3,2-de]pyrimido[4,5-c]pyridazine); (α S)- α -[[[5-(3-Methyl-1H-indazol-5-yl)-3-pyridinyl]oxy]methyl]-benzeneethanamine (A674563, CAS 552325-73-2); 4-[(4-

Chlorophenyl)methyl]-1-(7H-pyrrolo[2,3-d]pyrimidin-4-yl)-4-piperidinamine (CCT128930, CAS 885499-61-6); 4-(4-Chlorophenyl)-4-[4-(1H pyrazol-4-yl)phenyl]-piperidine (AT7867, CAS 857531-00-1); and Archexin (RX-0201, CAS 663232-27-7).

In certain embodiments, a tyrosine kinase inhibitor used in combination with CER modified cells is an anaplastic lymphoma kinase (ALK) inhibitor. Exemplary ALK inhibitors include crizotinib, ceritinib, alectinib, brigatinib, dalantercept, entrectinib, and lorlatinib.

In certain embodiments where tandem expression cassette modified cells are administered in combination with one or more additional therapies, the one or more additional therapies may be administered at a dose that might otherwise be considered subtherapeutic if administered as a monotherapy. In such embodiments, the tandem expression cassette may provide an additive or synergistic effect such that the one or more additional therapies can be administered at a lower dose. Combination therapy includes administration of a tandem expression cassette composition as described herein before an additional therapy (*e.g.*, 1 day to 30 days or more before the additional therapy), concurrently with an additional therapy (on the same day), or after an additional therapy (*e.g.*, 1 day – 30 days or more after the additional therapy). In certain embodiments, the tandem expression cassette modified cells are administered after administration of the one or more additional therapies. In further embodiments, the tandem expression cassette modified cells are administered 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 days after administration of the one or more additional therapies. In still further embodiments, the tandem expression cassette modified cells are administered within 4 weeks, within 3 weeks, within 2 weeks, or within 1 week after administration of the one or more additional therapies. Where the one or more additional therapies involves multiple doses, the tandem expression cassette modified cells may be administered after the initial dose of the one or more additional therapies, after the final dose of the one or more additional therapies, or in between multiple doses of the one or more additional therapies.

In certain embodiments, methods of the present disclosure include a depletion step. A depletion step to remove tandem expression cassette modified cells from the subject may occur after a sufficient amount of time for therapeutic benefit in order to mitigate toxicity to a subject. In such embodiments, a vector comprising the tandem expression cassette may include an inducible suicide gene, such as iCASP9, inducible Fas, or HSV-TK. Similarly, the vector may be designed for expression of a known cell surface antigen such as CD20 or truncated EGFR (SEQ ID NO:82) that facilitates depletion of transduced cells through infusion of an associated monoclonal antibody (mAb), for example, Rituximab for CD20 or Cetuximab for EGFR. Alemtuzumab, which targets CD52 present on the surface of mature lymphocytes, may also be used to deplete transduced B cells, T cells, or natural killer cells.

Subjects that can be treated by the compositions and methods of the present disclosure include animals, such as humans, primates, cows, horses, sheep, dogs, cats, mice, rats, rabbits, guinea pigs, or pigs. The subject may be male or female, and can be any suitable age, including infant, juvenile, adolescent, adult, and geriatric subjects.

EXAMPLES

EXAMPLE 1: CONSTRUCTION OF TANDEM EXPRESSION CASSETTES

A polynucleotide comprising the extracellular domain of the phosphatidylserine binding protein Tim4 and Tim4 transmembrane domain was fused to the intracellular signaling domain of TLR4 to create chimeric engulfment receptor “CER5” encoding an amino acid sequence of SEQ ID NO:97. A polynucleotide comprising the extracellular domain of the phosphatidylserine binding protein Tim4 and Tim4 transmembrane domain was fused to the intracellular signaling domain of TLR5 to create chimeric engulfment receptor “CER19” encoding an amino acid sequence of SEQ ID NO:98. A polynucleotide comprising the extracellular domain of the phosphatidylserine binding protein Tim4 and Tim4 transmembrane domain and TLR8 intracellular signaling domain to create chimeric engulfment receptor “CER21”

encoding an amino acid sequence of SEQ ID NO:99. A polynucleotide comprising the extracellular domain of the phosphatidylserine binding protein Tim4 and Tim4 transmembrane domain was fused to the intracellular signaling domain of NFAM1 to create chimeric engulfment receptor “CER25” encoding an amino acid sequence of SEQ ID NO:100. A polynucleotide comprising the extracellular domain of the phosphatidylserine binding protein Tim4 and Tim4 transmembrane domain was fused to the intracellular signaling domain of TLR2 to create chimeric engulfment receptor “CER27” encoding an amino acid sequence of SEQ ID NO:101. A polynucleotide comprising the extracellular domain of the phosphatidylserine binding protein Tim4 and Tim4 transmembrane domain was fused to the intracellular signaling domain of Traf6 to create chimeric engulfment receptor “CER29” encoding an amino acid sequence of SEQ ID NO:102. A polynucleotide comprising the extracellular domain of the phosphatidylserine binding protein Tim4 and Tim4 transmembrane domain was fused to the intracellular signaling domain of Traf3 to create chimeric engulfment receptor “CER31” encoding an amino acid sequence of SEQ ID NO:103.

A polynucleotide encoding a TCR β chain and a polynucleotide encoding a TCR α of an HPV16 E7 specific TCR (*see*, PCT Publication No. WO2015/184228) were fused using a sequence for P2A self-cleaving peptide therebetween. The TCR V α domain comprises an amino acid sequence of SEQ ID NO:94, and the TCR V β region comprises an amino acid sequence of SEQ ID NO:92. The C α domain comprises a cysteine substitution and LVL substitutions at positions 12, 14, and 15 and comprises an amino acid sequence of SEQ ID NO:95. The C β also comprises a cysteine substitution and comprises an amino acid sequence of SEQ ID NO:93. The encoded HPV16 E7 specific TCR comprises an amino acid sequence of SEQ ID NO:90. Amino acid sequences for the tandem expression constructs described in this example are provided in Table 2.

Table 2: Exemplary Tandem Expression Cassettes

Name	Amino Acid Sequence	SEQ ID NO:#
CER5_T2A_HP16 E7 TCR	MSKGLLLLWLVTLEWWLYLTPAASEDTIIGF LGQPVTLPCHYLSWSQSRNSMCWGKGSCPN	SEQ ID NO:176

Name	Amino Acid Sequence	SEQ ID NO:#
	SKCNAELLRTDGTIRSRKSTKYTLLGKVQFG EVSLTISNTNRGDSGVYCCRIEVPWFNDVK KNRLELRRATTTKKPTTTTRPTTTPYVTTTT PELLPTTVMTTSVLPTTTPPQTLATTAFASTAV TTCPSTTPGSFSQETTKGSAFTTESETLPASN SQRSMMTISTDIAVLRPTGSNPGILPSTSQT QKTTLTTSSESLQKTTKSHQINSRQTILIIACCV GFVLMVLLFLAFLKFYFHLMLLAGCIKYGRG ENIYDAFVIYSSQDEDWVRNELVKNLEEGVP PFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVI VVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGI IFIVLQKVEKTLLRQQVELYRLLSRNTYLEW EDSVLGRHIFWRRLRKALLDGKSWNPEGTV GTGCNWQEATSILEGGGEGRGSLTTCGDVEE NPGPMAPGLLCWALLCLLGAGLVDAGVTQS PTHLIKTRGQQVTLRCSPKSGHDTVSWYQQ ALGQGPQFIFQYYEEEEERQGNFPDRFSGHQ FPNYSSELNVNALLLGDSALYLCASSLGWRG GRYNEQFFGPGTRLTVLEDLRNVTPPKVSLF EPSKAEIANKQKATLVCLARGFFPDHVELSW WVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRCQVQFHGLSEEDKW PEGSPKPVTQNISAEAWGRADCGITSASYQQ GVLSATILYEILLGKATLYAVLVSTLVVMAM VKRKNSRAKRSGSGATNFSLLKQAGDVEEN PGPWVGVFLLYVSMKMGGTTGQNIDQPT MTATEGAIVQINCTYQTSGFNGLFWYQQHA GEAPTFLSYNVLDGLEEKGRFSSFLSRKGY YLLKELQMKDSASYLCASVDGNNRLAFGK GNQVVVIPNIQNPEPAVYQLKDPRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKA MDSKSNGAIAWSNQTSTFCQDIFKETNATYP SSDVPCDATLTEKSFETDMNLFQNLLVIVL RILLKLVAGFNLLMTLRLWSS	
CER19_T2A_HP16 E7 TCR	MSKGLLLLWLVTCLWWLYLTPAASEDTIIGF LGQPVTLPCHYLSWSQSRNSMCWGKGSCPN SKCNAELLRTDGTIRSRKSTKYTLLGKVQFG EVSLTISNTNRGDSGVYCCRIEVPWFNDVK KNRLELRRATTTKKPTTTTRPTTTPYVTTTT PELLPTTVMTTSVLPTTTPPQTLATTAFASTAV TTCPSTTPGSFSQETTKGSAFTTESETLPASN SQRSMMTISTDIAVLRPTGSNPGILPSTSQT QKTTLTTSSESLQKTTKSHQINSRQTILIIACCV GFVLMVLLFLAFLTKFRGFCFICYKTAQRLV FKDHPQGTEPDMYKYDAYLCFSSKDFTWVQ NALLKHLDTQYSDQNRNLCFEERDFVPGEN RIANIQDAIWNRSRKIVCLVSRHFLRDGWCLE AFSYAQGRCLSDLNSALIMVVVGSLSQYQL MKHQISIRGFVQKQYLRWPEDFQDVGWFL HKLSQQILKKEKEKKKDNNIPLQTVATISLEG GGEGRGSLTTCGDVEENPGPMAPGLLCWAL LCLLGAGLVDAGVTQSPTHLIKTRGQQVTLR CSPKSGHDTVSWYQQALGQGPQFIFQYYEE ERQGNFPDRFSGHQFPNYSSELNVNALLLG	SEQ ID NO:177

Name	Amino Acid Sequence	SEQ ID NO:#
	DSALYLCASSLGWRGGRYNEQFFGPGTRLT VLEDLRNVTPPKVSLFEPKAEIANKQKATL VCLARGFFPDHVELSWVWNGKEVHSGVCT DPQAYKESNYSYCLSSRLRVSATFWHNPRN HFRCQVQFHGLSEEDKWPEGSPKPVTQNISAEAW GRADCGITSASYQQGVLSATILYEILLGKATL YAVLVSTLVVMAMVKRKNRAKRSGSGAT NFSLLKQAGDVEENPGPMWGVFLLYVSMK MGGTTGQNIDQPTMTATEGAIVQINCTYQT SGFNGLFWYQQHAGEAPTFLSYNVLDGLEE KGRFSSFLSRKGYSYLLKELQMKDSASYL CASVDGNNRLAFGKGNQVVIPNIQNPEPAV YQLKDPRSQDSTLCLFTDFDSQINVPKTMES GTFITDKCVLDMKAMDSKNGAIAWSNQTS FTCQDIFKETNATYPSSDVPCDATLTEKSFET DMNLNFQNLLVIVLRILLKLVAGFNLLMTLR LWSS	
CER21_T2A_HP16 E7 TCR	MSKGLLLLWLVTLEWWLYLTPAASEDTIIGF LGQPVTLPCHYLSWSQSRNSMCWGKGSCPN SKCNAELLRTDGTIRSRKSTKYTLGKVQFG EVSLTISNTNRGDSGVYCCRIEVPWFNDVK KNRLELRRATTTKKPTTTTRPTTTPYVTTTT PELLPTTVMTTSVLPTTTPPQTLATTAFASTAV TTCPSTTPGSFSQETTKGSAFTTESETLPASNH SQRSMMTISTDIAVLRPTGSNPGILPSTSQLTT QKTTLTTSESLQKTTKSHQINSRQTILIIACCV GFVLMVLLFLAFLHHLFYWDVWFIYNVCLA KVKGYRSLSTSQTIFYDAYISYDTKDASVTD WVINELRYHLEESRDKNVLLCLEERDWDPG LAIIDNLMQSINQSKKTVFVLTKKYAKSWNF KTAFLALQRLMDENMDVIIFILLEPVLQHS QYLRLRQRICKSSILQWPDNPKAEGFLFWQTL RNVVLTENDSRYNMYVDSIKQYLEGGGEG RGSLTCDGVEENPGPMAPGLLCWALLCCL GAGLVDAAGVTQSPTHLIKTRGQQVTLRCSPK SGHDTVSWYQQALGQGPQFIFQYEEEEERQ RGNFPDRFSGHQFPNYSSELNVNALLLGDSA LYLCASSLGWRGGRYNEQFFGPGTRLT VLEDLRNVTPPKVSLFEPKAEIANKQKATL VCLARGFFPDHVELSWVWNGKEVHSGVCTDPQ AYKESNYSYCLSSRLRVSATFWHNPRNHFRC QVQFHGLSEEDKWPEGSPKPVTQNISAEAW GRADCGITSASYQQGVLSATILYEILLGKATL YAVLVSTLVVMAMVKRKNRAKRSGSGAT NFSLLKQAGDVEENPGPMWGVFLLYVSMK MGGTTGQNIDQPTMTATEGAIVQINCTYQT SGFNGLFWYQQHAGEAPTFLSYNVLDGLEE KGRFSSFLSRKGYSYLLKELQMKDSASYL CASVDGNNRLAFGKGNQVVIPNIQNPEPAV YQLKDPRSQDSTLCLFTDFDSQINVPKTMES GTFITDKCVLDMKAMDSKNGAIAWSNQTS FTCQDIFKETNATYPSSDVPCDATLTEKSFET DMNLNFQNLLVIVLRILLKLVAGFNLLMTLR LWSS	SEQ ID NO:178

Name	Amino Acid Sequence	SEQ ID NO:#
CER25_T2A_HP16 E7 TCR	MSKGLLLLWLVTLEWWLYLTPAASEDTIIGF LGQPVTLPCHYLSWSQSRNSMCWGKGSCPN SKCNAELLRTDGTIRISRKSTKYTLLGKVQFG EVSLTISNTNRGDSGVYCCRIEVPWFNDVK KNVRLELRRATTTKKPTTTTRPTTTPYVTTTT PELLPTTVMTTSVLPTTTPPQTLATTAFASTAV TTCPSTTPGSFSQETTKGSAFTTESETLPASNH SQSRMMTISTDIAVLRPTGSNPGILPSTSQT QKTTLTTSESLQKTTKSHQINSRQTILIIACCV GFVLMVLLFLAFLWLNKKMRMRGPGKDPTRK CPDPRSASSPKQHPSESVYTALQRRETEVYA CIENEDGSSPTAKQSPLSQERPHRFEDDGELN LVYENLLEGGEGRGSLTTCGDVEENPGPM APGLLCWALLCLLGAGLVDAGVTQSPHLLIK TRGQQVTLRCSPKSGHDTVSWYQQALGQGP QFIFQYEEEEERQGRNFPDRFSGHQFPNYSSE LNVNALLLGDSALYLCASSLGWRGGRYNEQ FFGPGTRLTVLEDLRNVTPPKVSLFEPSKAEI ANKQKATLVCLARGFFPDHVELSWWVNGK EVHSGVCTDPQAYKESNYSYCLSSRLRVSAT FWHNPRNHFRCQVQFHGLSEEDKWPEGSPK PVTQNISAEAWGRADCGITSASYQQGVLSAT ILYEILLGKATLYAVLVSTLVMMAMVKRKN SRAKRSGSGATNFSLLKQAGDVEENPGPMW GVFLLYVSMKMGTTGQNIQDQPTMTATEG AIVQINCTYQTSGFNGLFWYQQHAGEAPTFL SYNVLDGLEEKGRFSSFLSRKGYSYLLLLKE LQMKDSASYLCASVDGNNRLAFGKGNQVV VIPNIQNPEPAVYQLKDPQRSQDSTLCLFTDFD SQINVPKTMESGTFITDKCVLDMKAMDSKSN GAIAWSNQTSTFCQDIFKETNATYPSSDVPC DATLTEKSFETDMNLFQNLVIVLRILLKLV AGFNLLMTLRLWSS	SEQ ID NO:179
CER27_T2A_HP16 E7 TCR	MSKGLLLLWLVTLEWWLYLTPAASEDTIIGF LGQPVTLPCHYLSWSQSRNSMCWGKGSCPN SKCNAELLRTDGTIRISRKSTKYTLLGKVQFG EVSLTISNTNRGDSGVYCCRIEVPWFNDVK KNVRLELRRATTTKKPTTTTRPTTTPYVTTTT PELLPTTVMTTSVLPTTTPPQTLATTAFASTAV TTCPSTTPGSFSQETTKGSAFTTESETLPASNH SQSRMMTISTDIAVLRPTGSNPGILPSTSQT QKTTLTTSESLQKTTKSHQINSRQTILIIACCV GFVLMVLLFLAFLHRFHGLWYMKMMWAW LQAKRKPRKAPSRNICYDAFVSYSERDAYW VENLMVQELFNPPFKLCLHKRDFIPGKWII DNIIDSIEKSHKTVFVLSNFVKSEWCKYELD FSHFRLFDENNDAAAILILLEPIEKKAIPQRFC LRKIMNTKTYLEWPMDEAQREGFWVNLRA AIKSLEGGEGRGSLTTCGDVEENPGPMAPG LLCWALLCLLGAGLVDAGVTQSPHLLIKTRG QQVTLRCSPKSGHDTVSWYQQALGQGPQFIF QYEEEEERQGRNFPDRFSGHQFPNYSSELNV NALLLGDSALYLCASSLGWRGGRYNEQFFG PGTRLTVLEDLRNVTPPKVSLFEPSKAEIANK	SEQ ID NO:180

Name	Amino Acid Sequence	SEQ ID NO:#
	QKATLVCLARGFFPDHVELSWWVNGKEVHS GVCTDPQAYKESNYSYCLSSRLRVSATFWH NPRNHFRCQVQFHGLSEEDKWPEGSPKPVT QNISAEAWGRADCGITSASYQQGVLSATILY EILLGKATLYAVLVSTLVVMAMVKRKSRA KRSGSGATNFSLLKQAGDVEENPGPMWGVF LLYVSMKMGTTGQNIDQPTMTATEGAIV QINCTYQTSGFNGLFWYQQHAGEAPTFLSYN VLDGLEEKGRFSSFLSRSGYSYLLKELQ KDSASYLCASVDGNNRLAFGKGNQVVVIPNI QNPEPAVYQLKDPRSQDSTLCLFTDFDSQIN VPKTMESGTFITDKCVLDMKAMDSSKNGAI AWSNQTSFTCQDIFKETNATYPSSDVPDAT LTEKSFETDMNLFQNLVIVLRILLKLVAGF NLLMTLRLWSS	
CER29_T2A_HP16 E7 TCR	MSKGLLLLWLVTLEWWLYLTPAASEDTIIGF LGQPVTLPCHYLSWSQSRNSMCWGKSCPN SKCNAELLRTDGTIRISRKSTKYTLGKVQFG EVSLTISNTNRGDSGVYCCRIEVPWFNDVK KNVRLELRRTTTKKPTTTTRPTTTPYVTTTT PELLPTTVMTTSVLPTTTPPQTLATTAFTAV TTCPSTTPGSFSQETTKGSAFTTESETLPASN SQRSMMTISTDIAVLRPTGSPGILPSTSQLTT QKTTLTTSESLQKTTKSHQINSRQTILIIACCV GFVLMVLLFLAFLMSLLNCENSCGSSQSESD CCVAMASSCSAVTKDDSVGGTASTGNLSSSF MEEIQGYDVEFDPPLESKYECPICLMALREA VQTPCGHRFCKACIIKSIRDAGHKCPVDNEIL LENQLFPDNFAKREILSLMVKCPNEGCLHKM ELRHLEDHQAHCFAALMDCPQCQRPFQKFHI NIHILKDCPRRQVSCDNCAASMAFEDKEIHD QNCPLANVICEYCNILIREQMPNHYDLDCP TAPICTFSTFGCHEKMQRNHLARHLQENTQ SHMRMLALEGGGEGRGSLTTCGDVEENPGP MAPGLLCWALLCLLGAGLVDAVGTQSPHTL IKTRGQQVTLRCSPKSGHDTVSWYQQALGQ GPQFIFQYEEEEERQGNFPDRFSGHQFPNYS SELNVNALLLGDSALYLCASSLGWRGGRYN EQFFGPGTRLTVLEDLRNVTPPKVSLFEPSKA EIANKQKATLVCLARGFFPDHVELSWWVNG KEVHSGVCTDPQAYKESNYSYCLSSRLRVSA TFWHNPRNHFRCQVQFHGLSEEDKWPEGSP KPVTQNISAEAWGRADCGITSASYQQGVLSA TILYEILLGKATLYAVLVSTLVVMAMVKRK NSRAKRSGSGATNFSLLKQAGDVEENPGPM WGVFLLYVSMKMGTTGQNIDQPTMTATE GAIVQINCTYQTSGFNGLFWYQQHAGEAPTF LSYNVLDGLEEKGRFSSFLSRSGYSYLLK ELQMKDSASYLCASVDGNNRLAFGKGNQV VVIPNIQNPEPAVYQLKDPRSQDSTLCLFTDF DSQINVPKTMESGTFITDKCVLDMKAMDSSK NGAIAWSNQTSFTCQDIFKETNATYPSSDVP CDATLTEKSFETDMNLFQNLVIVLRILLK VAGFNLLMTLRLWSS	SEQ ID NO:181

Name	Amino Acid Sequence	SEQ ID NO:#
CER31_T2A_HP16 E7 TCR	MSKGLLLLWLVTLEWWLYLTPAASEDTIIGF LGQPVTLPCHYLSWSQSRNSMCWGKGSCPN SKCNAELLRTDGTIRISRKSTKYTLLGKVQFG EVSLTISNTNRGDSGVYCCRIEVPWFNDVK KNVRLELRRATTTKKPTTTTRPTTTPYVTTTT PELLPTTVMTTSVLPTTTPPQTLATTAFASTAV TTCPSTTPGSFSQETTKGSAFTTESETLPASNH SQSRMMTISTDIAVLRPTGSNPGILPSTSQLT QKTTLTTSLSLQKTTKSHQINSRQTILIIACCV GFVLMVLLFLAFLMESSKKMDSPGALQTNPP LKLHTDRSAGTPVFVPEQGGYKEKFVKTV DKYKCEKCHLVLCSPKQTECGHRFCESMA ALLSSSSPKCTACQESIVKDKVFKDNCKREI LALQIYCRNESRGCAEQLMLGHLLVHLKND CHFEELPCVRPDCKEVLRLKDLRDHVEKAC KYREATCSHCKSQVPMIALQKHEDTDCPCV VVSCPHKCSVQTLRLSELSEHLSECVNAPST CSFKRYGCVFQGTNQQIKAHEASSAVQHV LLKEWSNSLEKKVLEGGEGRGSLTCDGV EENPGPMAPGLLCWALLCLLGLVLDAGVT QSPTHLIKTRGQVTLRCSPKSGHDTVSWYQ QALGQGPQFIFQYEEEEERQGNFPDRFSGH QFPNYSSELNVNALLLGDSALYLCASSLGWR GGRYNEQFFGPGTRLTVLEDLRNVTPPKVSL FEPSKAEIANKQKATLVCLARGFFPDHVELS WWVNGKEVHSGVCTDPQAYKESNYSYCLS SRLRVSATFWHNPNNHFRQVQFHGLSEED KWPEGSPKPVTONISAEAWGRADCGITSASY QQGVLSATILYEILLGKATLYAVLVSTLVVM AMVKRKNSRAKRSRSGATNFSLLKQAGDVE ENPGPMWGVFLLYVSMKMGTTGQNDQPT EMTATEGAIVQINCTYQTSGFNGLFWYQQH AGEAPTFLSYNVLDGLEEKGRFSSFLSRSG YSYLLKELQMKDSASYLCASVDGNNRLAF GKGNQVVVIPNIQNPEPAVYQLKDPQSQDST LCLFTDFDSQINVPKTMESGTFITDKCVLDM KAMDSSNGAIAWSNQTSFTCQDIFKETNAT YPSSDVPCDATLTEKSFETDMNLFQNLVI VLRILLKLVAGFNLLMTLRLWSS	SEQ ID NO:182

A selected CER polynucleotide and the HPV16 E7 TCR polynucleotide were inserted into the same pLenti lentiviral vector with a T2A sequence (encoding an amino acid sequence of SEQ ID NO:68) therebetween. (*see*, Figs. 1A-1G). Peripheral blood was collected by venipuncture from a human donor, and human peripheral blood mononuclear cells (PBMCs) were isolated by density gradient centrifugation using lymphocyte separation media. CD8⁺ T cells were enriched from PBMCs using a commercially available isolation kit and activated with anti-CD3 and anti-CD28 in

Complete Cell Growth Media. 50 μ l of viral vector expressing the CER-HPV16 E7 TCR combination were diluted in 0.5 ml Complete Cell Growth Media and added to the CD8⁺ T cells. The transduced CD8⁺ T cells were then centrifuged at 270 x g rpm for 1 hour in a 32°C pre-warmed centrifuge. The CD8⁺ T cells were incubated for 24 hours at 37°C. T cells were expanded for another 72 hours in Complete Cell Growth Media, de-beaded, and allowed to expand for 5 days prior to being utilized for functional assays.

EXAMPLE 2: CD8 T CELLS TRANSDUCED WITH CER-TCR TANDEM EXPRESSION CASSETTE EXHIBIT ANTIGEN SPECIFIC CYTOLYTIC AND PHAGOCYtic ACTIVITY

Cytotoxic activity of tandem expression cassette transduced CD8⁺ T cells was detected using a caspase 3/7 apoptosis reagent (IncuCyte®) that couples the activated caspase 3/7 recognition motif with a red reagent that fluoresces upon cleavage. The fluorescent signal was measured using fluorescent microscopy. Transduced CD8⁺ T cells were co-cultured with HPV16 E7⁺ head and neck squamous cell carcinoma cells (SCC152) at a 1:1 ratio, and caspase 3/7 apoptosis reagent was added to the co-culture. CD8⁺ T cells comprising CER21-HPV16 E7 TCR tandem expression cassette exhibit cytotoxic activity toward SCC152 cells (see, Figure 2). The cytotoxic response by the CD8⁺ T cells transduced with CER21-HPV16 E7 TCR tandem expression cassette appears to be exponentially higher than the CD8⁺ T cells comprising HPV16 E7 TCR alone by 6 hours (see, Figure 3). CD8⁺ T cells transduced with CER21-HPV16 E7 TCR tandem expression cassette, CER29-HPV16 E7 TCR tandem expression cassette, or CER31-HPV16 E7 TCR tandem expression cassette were co-cultured with SCC152 cells at a target:effector cell ratio of 1:1. The caspase 3/7 apoptosis reagent was added to the co-culture, and cytotoxic activity was measured over time by measuring fluorescence (see, Figures 4 and 5). Control samples were CD8⁺ T cells transduced with HPV16 E7 TCR alone or mock transduced T cells.

Phagocytic activity of tandem expression cassette transduced CD8⁺ T cells was detected by co-culturing tandem expression cassette transduced CD8⁺ T cells with SCC152 cells for 6 hours at a 1:1 ratio. Phagocytic events were visualized and

quantified using KEYENCE BZ-X710 fluorescence microscope, 20X objective and hybrid capture software. CD8⁺ T cells transduced with CER21-HPV16 E7 TCR, CER29-HPV16 E7 TCR, or CER31-HPV16 E7 TCR tandem cassettes were capable of phagocytosing SCC152 cells (see, Figures 6 and 7). Rac1 inhibitor NSC23766 (50 μ M) was also added to co-culture experiments and *in vitro* phagocytosis was measured. Treatment with Rac1 inhibitor revealed that the engulfment of SCC152 cells by the CER21-HPV16 E7 TCR, CER29-HPV16 E7 TCR, or CER31-HPV16 E7 TCR transduced T cells occurred in a Rac1-dependent manner (see, Figures 8-10). Figures 11 and 12 show that CD8⁺ T cells transduced with CER21-HPV16 E7 TCR tandem expression cassette engulfed streptavidin coated latex beads, to which were coated with biotin-conjugated phosphatidylserine. After about 30 minutes of incubation, the phosphatidylserine coated beads could be visualized inside the CER21-HPV16 E7 TCR⁺ T cells.

Cytokine response of CD8⁺ T cells transduced with CER21-HPV16 E7 TCR tandem expression cassette was measured during co-culture experiments with SCC152 cells by sampling the cellular supernatants and showed that CER21-HPV16 E7 TCR⁺ T cells exhibit antigen specific effector function as measured by IFN γ response (see, Figure 14).

EXAMPLE 3: PHAGOCYTIC ACTIVITY OF T CELLS SPECIFICALLY INDUCED BY CER

The ability of CER modified-T cells to engulf target cells and recapitulate engulfment-signaling events was evaluated in co-culture assays. T cells were transduced with a nucleic acid encoding HPV E7 specific TCR (polypeptide sequence comprising SEQ ID NO:158) or tandem expression cassette encoding HPV E7 specific TCR + CER29 (polypeptide sequence comprising SEQ ID NO:169). pHrodo-labeled HPV⁺ SCC152 head and neck cancer cells were co-incubated with mock transduced T cells, HPV E7 TCR transduced T cells, or HPV E7 TCR/CER29-transduced T cells. Phagocytosis was analyzed by FACS, which showed large populations of cell-trace violet-labeled E7 TCR/CER29-T cells doubly stained with

pHrodo positive (see Figure 15A). Quantification of FACS data showed no difference between mock-transduced T cells and E7 TCR-transduced T cells (see Figure 15B).

The various embodiments described above can be combined to provide further embodiments. All of the U.S. patents, U.S. patent application publications, U.S. patent applications, foreign patents, foreign patent applications and non-patent publications referred to in this specification and/or listed in the Application Data Sheet including but not limited to U.S. Provisional Patent Application No. 62/649,499, filed March 28, 2018, are incorporated herein by reference, in their entirety. Aspects of the embodiments can be modified, if necessary to employ concepts of the various patents, applications and publications to provide yet further embodiments.

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

CLAIMS

1. An expression cassette comprising:

(a) a polynucleotide encoding a chimeric engulfment receptor (CER)

comprising:

an extracellular domain comprising a binding domain that binds to a first target antigen;

an engulfment signaling domain;

a transmembrane domain positioned between and connecting the extracellular domain and the engulfment signaling domain; and

(b) a polynucleotide encoding a chimeric antigen receptor (CAR) comprising:

an extracellular domain comprising a binding domain that binds to a second target antigen;

an intracellular signaling domain; and

a transmembrane domain positioned between and connecting the extracellular domain and the intracellular signaling domain.

2. An expression cassette comprising:

(a) a polynucleotide encoding a chimeric engulfment receptor (CER)

comprising:

an extracellular domain comprising a binding domain that binds to a first target antigen;

an engulfment signaling domain;

a transmembrane domain positioned between and connecting the extracellular domain and the engulfment signaling domain;

(b) a polynucleotide encoding a recombinant T cell receptor (TCR) binding protein beta chain comprising a TCR beta variable region and a TCR beta constant region; and

(c) a polynucleotide encoding a recombinant TCR alpha chain comprising a TCR alpha variable region and a TCR alpha constant region.

3. The expression cassette of claim 1 or 2, wherein the CER binding domain comprises a scFv, receptor ectodomain, or a ligand.
4. The expression cassette of any one of claims 1-3, wherein the CER extracellular domain further comprises a spacer domain.
5. The expression cassette of any one of claims 1-4, wherein the CER transmembrane domain comprises a Tim1, Tim4, Tim3, FcR, CD8, CD28, MERTK, Axl, Tyro3, BAI1, CD4, DAP12, MRC1, FcR, TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, or TLR9 transmembrane domain.
6. The expression cassette of any one of claims 1-5, wherein the CER engulfment signaling domain comprises a MERTK, Tyro3, ItgB5, MRC1, BAI1, ELMO, Axl, Syk, MyD88, Zap70, FcγR1, FcγR2A, FcγR2B2, FcγR2C, FcγR3A, FcεR1, FcαR1, BAFF-R, DAP12, NFAM1, CD79b, TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9, Traf6, Traf2, or Traf3 signaling domain.
7. The expression cassette of any one of claims 1-6, wherein the CER engulfment signaling domain comprises a primary engulfment signaling domain and a secondary engulfment signaling domain.
8. The expression cassette of any one of claims 1-7, wherein the CER primary and secondary engulfment signaling domains are different.
9. The expression cassette of any one of claims 1-8, wherein the CER primary and secondary engulfment signaling domains are each independently selected from MERTK, Tyro3, ItgB5, MRC1, BAI1, ELMO, Axl, Syk, MyD88, Zap70, FcγR1, FcγR2A, FcγR2B2, FcγR2C, FcγR3A, FcεR1, FcαR1, BAFF-R, DAP12, NFAM1, CD79b, TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9, Traf6, Traf2, and Traf3 signaling domain.

10. The expression cassette of any one of claims, 1-9, wherein the first target antigen of the CER is a pro-engulfment marker, tumor antigen, viral antigen, or parasite antigen.
11. The expression cassette of claim 10, wherein the pro-engulfment marker is phosphatidylserine.
12. The expression cassette of claim 11, wherein the CER binding domain comprises a Tim4 binding domain that binds phosphatidylserine.
13. The expression cassette of any one of claims 1 and 3-12, wherein the CAR binding domain comprises a scFv.
14. The expression cassette of any one of claims 1 and 3-13, wherein the CAR extracellular domain further comprises a spacer domain.
15. The expression cassette of any one of claims 1 and 3-14, wherein the CAR transmembrane domain comprises a CD28, CD2, CD4, CD8, CD3 ϵ , CD3 δ , CD3 ζ , CD25, CD27, CD40, CD79A, CD79B, CD80, CD86, CD95 (Fas), CD134 (OX40), CD137 (4-1BB), CD150 (SLAMF1), CD152 (CTLA4), CD200R, CD223 (LAG3), CD270 (HVEM), CD272 (BTLA), CD273 (PD-L2), CD274 (PD-L1), CD278 (ICOS), CD279 (PD-1), CD300, CD357 (GITR), A2aR, DAP10, FcR α , FcR β , FcR γ , Fyn, GAL9, KIR, Lck, LAT, LRP, NKG2D, NOTCH1, NOTCH2, NOTCH3, NOTCH4, PTCH2, ROR2, Ryk, Slp76, SIRP α , pT α , TCR α , TCR β , TIM3, TRIM, LPA5, or Zap70 transmembrane domain.
16. The expression cassette of any one of claims 1 and 3-15, wherein the CAR intracellular signaling domain comprises an ITAM-containing activating signaling domain selected from CD3 ζ , CD3 γ , CD3 δ , CD3 ϵ , CD5, CD22, CD79a, CD278 (ICOS), DAP10, DAP12, CD79b, FcR, and CD66d signaling domains.
17. The expression cassette of any one of claims 1 and 3-16, wherein the CAR intracellular signaling domain comprises a first costimulatory signaling domain selected

from CD27, CD28, 4-1BB, OX40, CD30, CD40, PD-1, ICOS, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, LIGHT, NKG2C, and B7-H3 signaling domain.

18. The expression cassette of any one of claims 1 and 3-17, wherein the CAR intracellular signaling domain comprises a second costimulatory signaling domain selected from CD27, CD28, 4-1BB, OX40, CD30, CD40, PD-1, ICOS, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, LIGHT, NKG2C, and B7-H3 signaling domain.

19. The expression cassette of any one of claims 1 and 3-18, wherein the CAR is a first generation CAR, second generation CAR, third generation CAR, or TCR-CAR.

20. The expression cassette of any one of claims 1 and 3-19, wherein the second target antigen of the CAR is a tumor antigen, viral antigen, or parasite antigen.

21. The expression cassette of any one of claims 20, wherein the second target antigen of the CAR is a tumor antigen selected from CD138, CD38, CD33, CD123, CD72, CD79a, CD79b, mesothelin, PSMA, BCMA, ROR1, MUC-16, L1CAM, CD22, CD19, CD20, CD23, CD24, CD37, CD30, CA125, CD56, c-Met, EGFR, GD-3, HPV E6, HPV E7, MUC-1, HER2, folate receptor α , CD97, CD171, CD179a, CD44v6, WT1, VEGF- α , VEGFR1, IL-13R α 1, IL-13R α 2, IL-11R α , PSA, FcRH5, NKG2D ligand, NY-ESO-1, TAG-72, CEA, ephrin A2, ephrin B2, Lewis A antigen, Lewis Y antigen, MAGE, MAGE-A1, RAGE-1, folate receptor β , EGFRviii, VEGFR-2, LGR5, SSX2, AKAP-4, FLT3, fucosyl GM1, GM3, o-acetyl-GD2, or GD2.

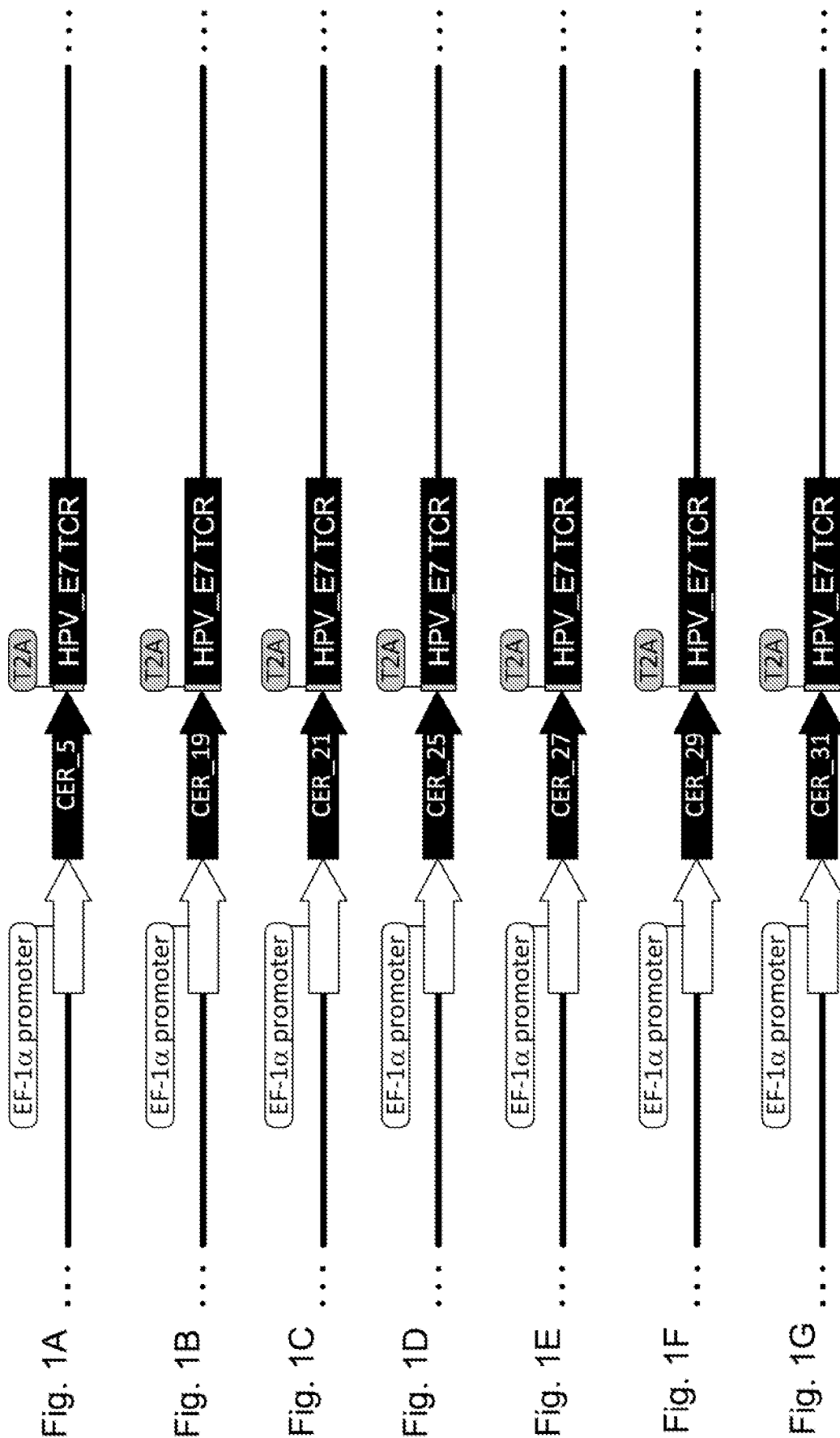
22. The expression cassette of any one of claims 2-12, wherein the second target antigen of the recombinant TCR is WT-1, mesothelin, MART-1, NY-ESO-1, MAGE-A3, HPV E7, survivin, α Fetoprotein, or a tumor neoantigen.

23. The expression cassette of any one of claims 2-12 and 22, wherein the TCR alpha chain comprises an LVL substitution at positions 12, 14, and 15.

24. The expression cassette of any one of claims 2-12, 22, and 23, wherein the TCR beta chain constant region comprises a cysteine substitution at position 56, TCR alpha chain constant region comprises a cysteine substitution at position 48, or both.
25. The expression cassette of any one of claims 1-24, wherein the polynucleotide encoding the CER is upstream of the polynucleotide encoding the CAR or TCR.
26. The expression cassette of any one of claims 1, 3-21, and 25, further comprising a polynucleotide encoding an IRES element or 2A peptide between the polynucleotide encoding the CER and the polynucleotide encoding the CAR.
27. The expression cassette of any one of claims 2-12, 22-24, and 25, wherein the polynucleotides encoding the CER, TCR alpha chain, and TCR beta chain are separated from each other by a first polynucleotide encoding IRES element or 2A peptide and a second polynucleotide encoding a IRES element or 2A peptide.
28. The expression cassette of any one of claims 26 or 27, wherein the 2A peptide comprises a T2A, P2A, E2A, or F2A peptide.
29. The expression cassette of claim 2, wherein:
- (a) the CER comprises an amino acid sequence of any one of the SEQ ID NOs listed in Table 1; and
 - (b) the TCR comprises an amino acid sequence of SEQ ID NO:90.
30. The expression cassette of any one of claims 1-29, further comprising a promoter operably linked to the expression cassette.
31. A vector comprising the expression cassette of any one of claims 1-30.
32. The vector of claim 31, wherein the vector is a viral vector.

33. The vector of claim 32, wherein the viral vector is a retroviral vector or a lentiviral vector.
34. A host cell comprising the vector of any one of claims 31-33.
35. The host cell of claim 34, wherein the host cell is a T cell.
36. The host cell of claim 35, wherein the T cell is a CD4 T cell, CD8 T cell, or both.
37. The host cell of claim 35 or 36, wherein the T cell is a naïve T cell, central memory T cell, effector T cell, or any combination thereof.
38. The host cell of any one of claims 34-37, wherein the host cell is human.
39. The host cell of any one of claims 34-38, wherein the host cell exhibits cytolytic activity towards a cell expressing the antigen targeted by the CAR or TCR and phagocytic activity towards a cell expressing the antigen targeted by the CER.
40. A method of treating a disease in a subject comprising administering an effective amount of the host cell of any one of claims 34-39.
41. The method of claim 40, wherein the disease is a cancer, viral infection, bacterial infection, or parasitic infection.
42. The method of claim 41, wherein the cancer is a solid tumor, melanoma, non-small cell lung cancer, renal cell carcinoma, renal cancer, a hematological cancer, prostate cancer, castration-resistant prostate cancer, colon cancer, rectal cancer, gastric cancer, esophageal cancer, bladder cancer, head and neck cancer, thyroid cancer, breast cancer, triple-negative breast cancer, ovarian cancer, cervical cancer, lung cancer, urothelial cancer, pancreatic cancer, glioblastoma, hepatocellular cancer, myeloma, multiple myeloma, leukemia, Hodgkin's lymphoma, non-Hodgkin's lymphoma, myelodysplastic syndrome, brain cancer, CNS cancer, or malignant glioma.

43. The method of any one of claims 39-42, wherein the host cell is autologous or allogeneic to the subject.
44. The method of any one of claims 39-43, wherein the host cell is administered to the subject in combination with an additional therapeutic agent.
45. The method of claim 44, wherein the additional therapeutic agent is an antibody, radiation therapy, chemotherapeutic agent, small molecule therapy, cellular immunotherapy, oncolytic virus, electropulse therapy, UV light therapy, high frequency ultrasound therapy, antibiotic, anti-fungal agent, or anti-viral agent.
46. The method of claim 44 or 45, wherein the additional therapeutic agent is administered at a subtherapeutic dose.



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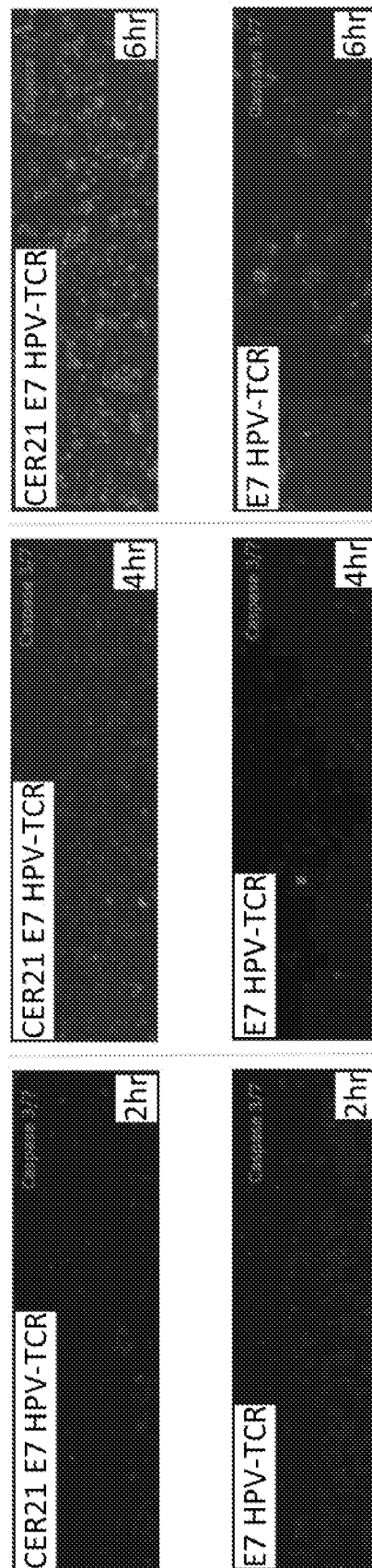


Fig. 2

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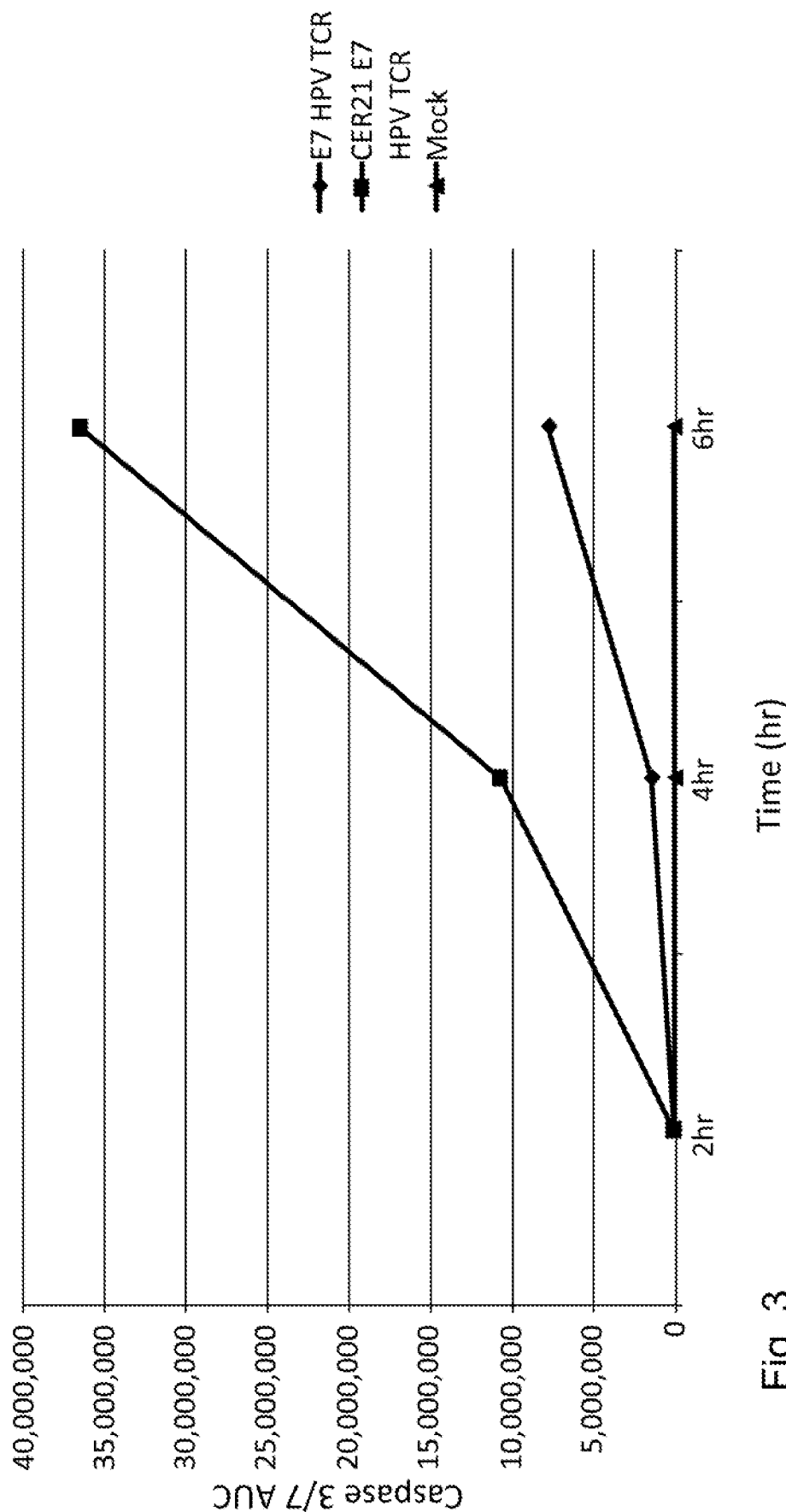


Fig. 3

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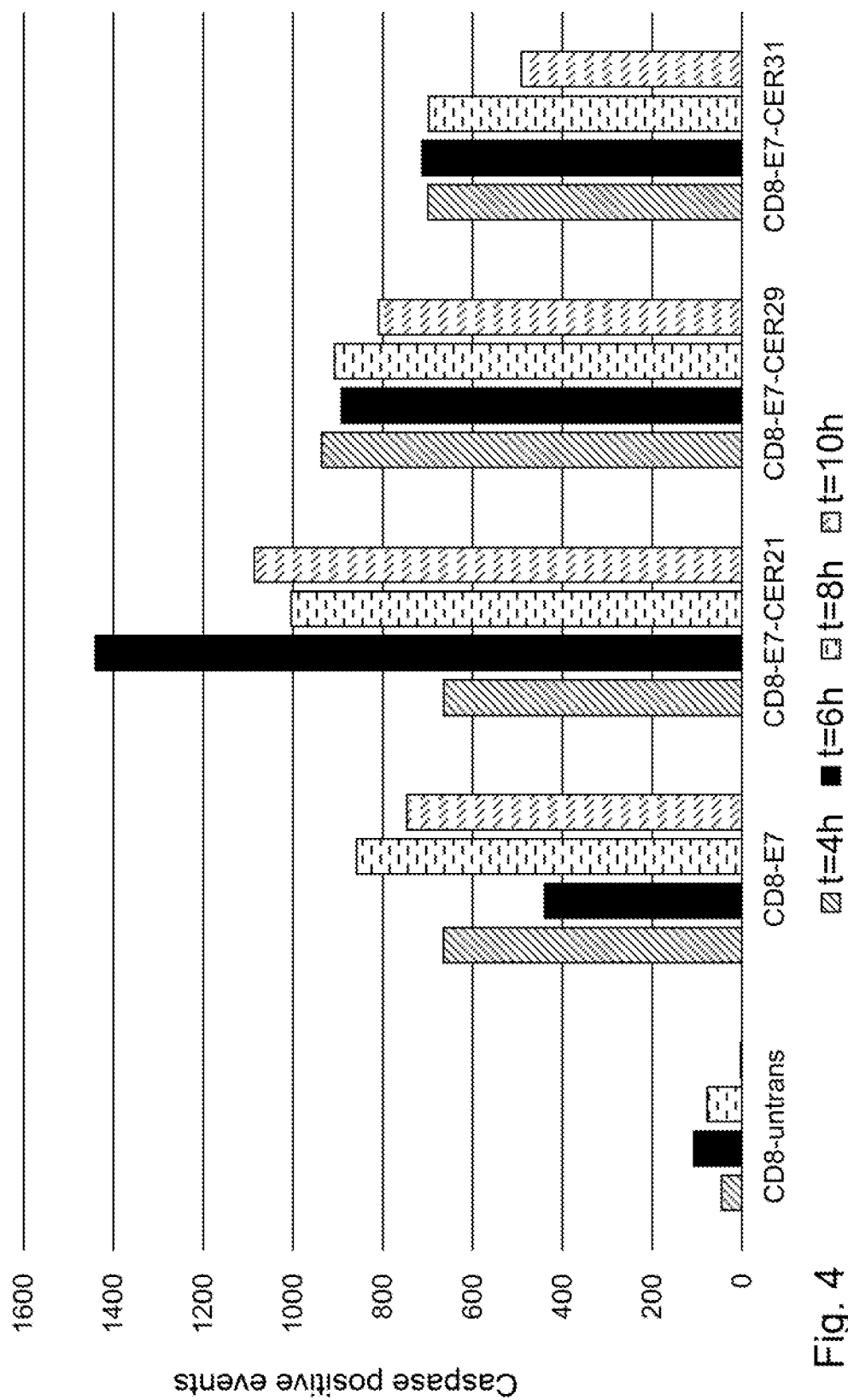
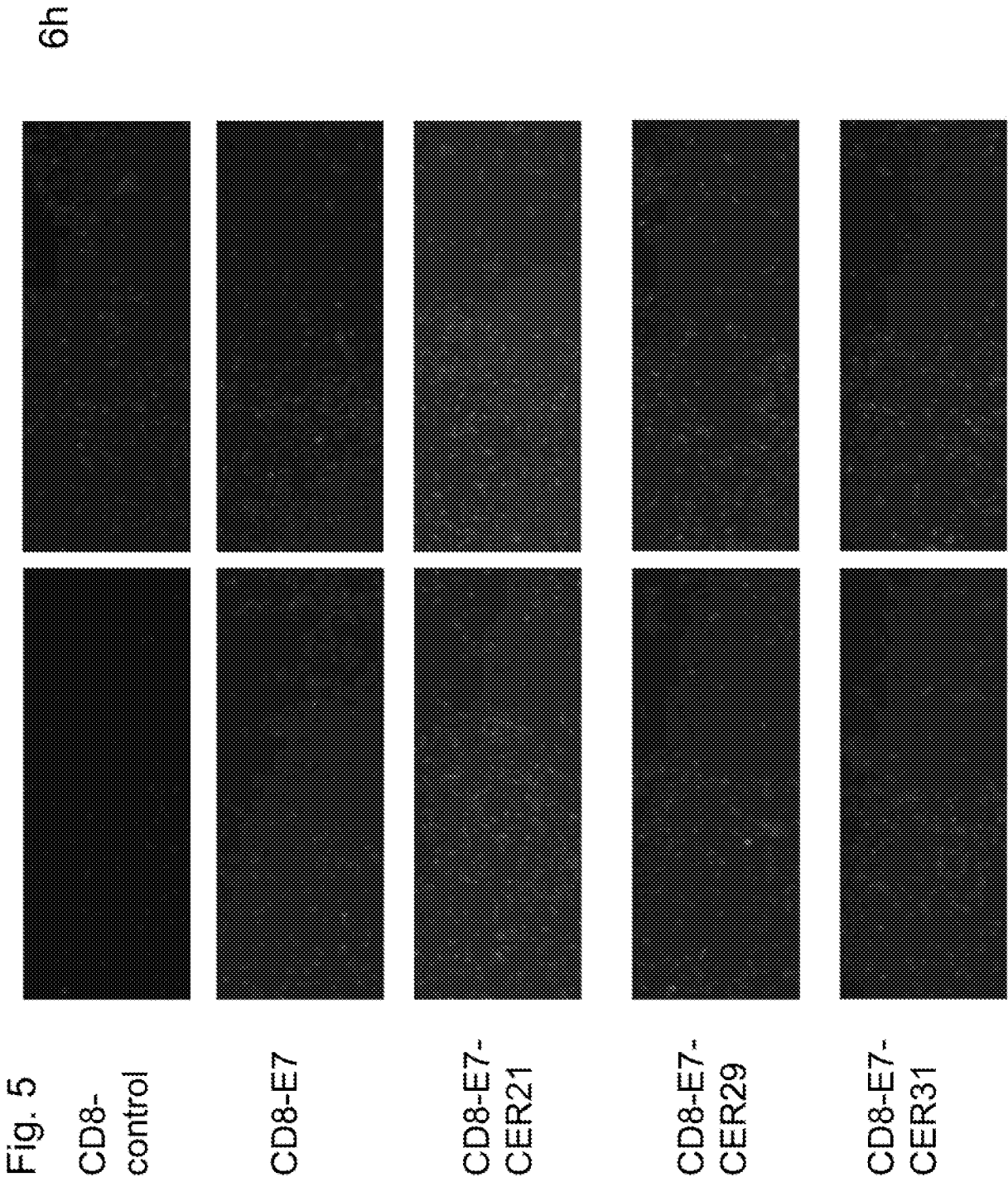


Fig. 4



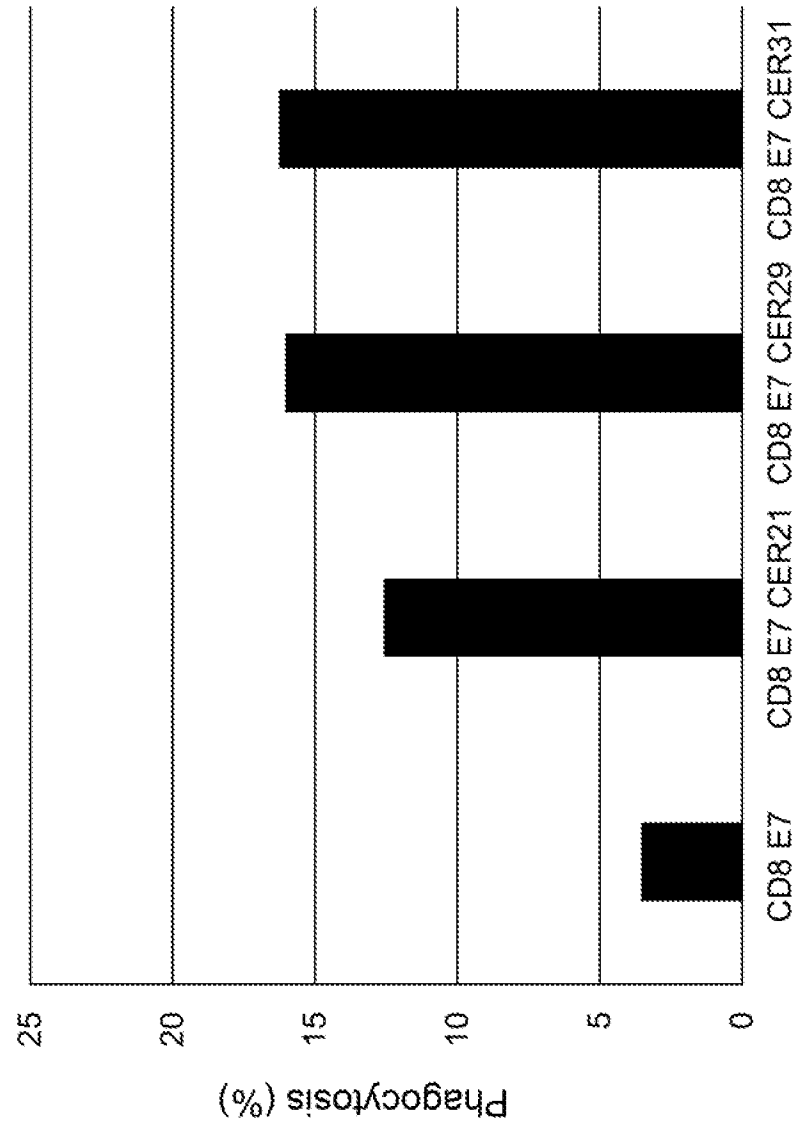
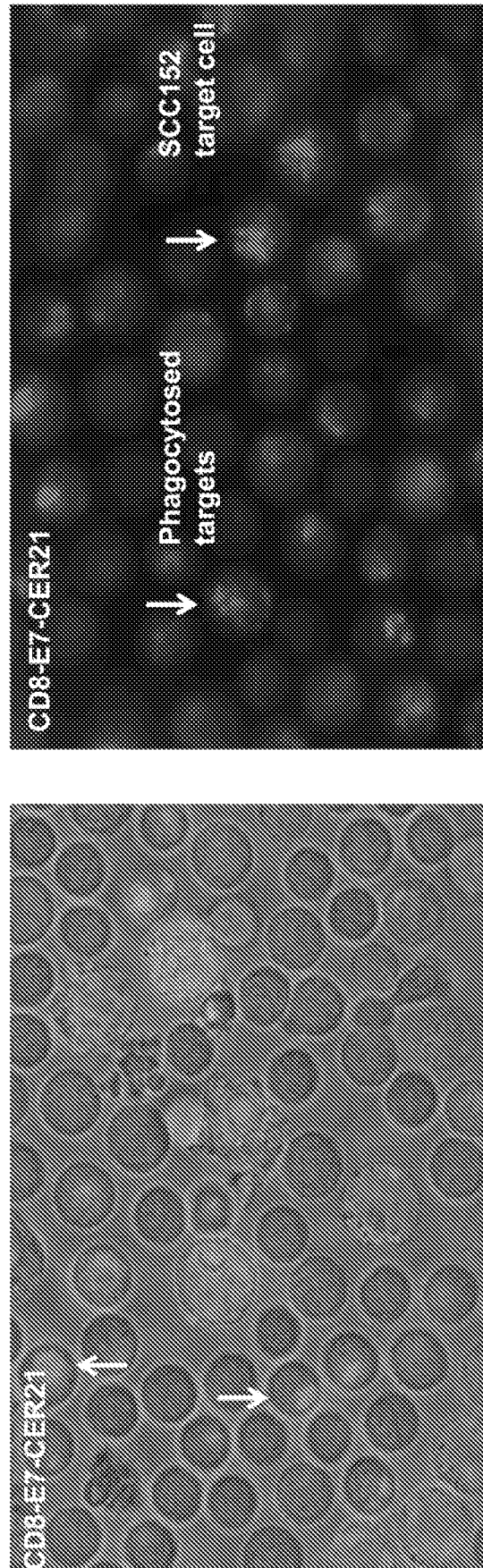


Fig. 6

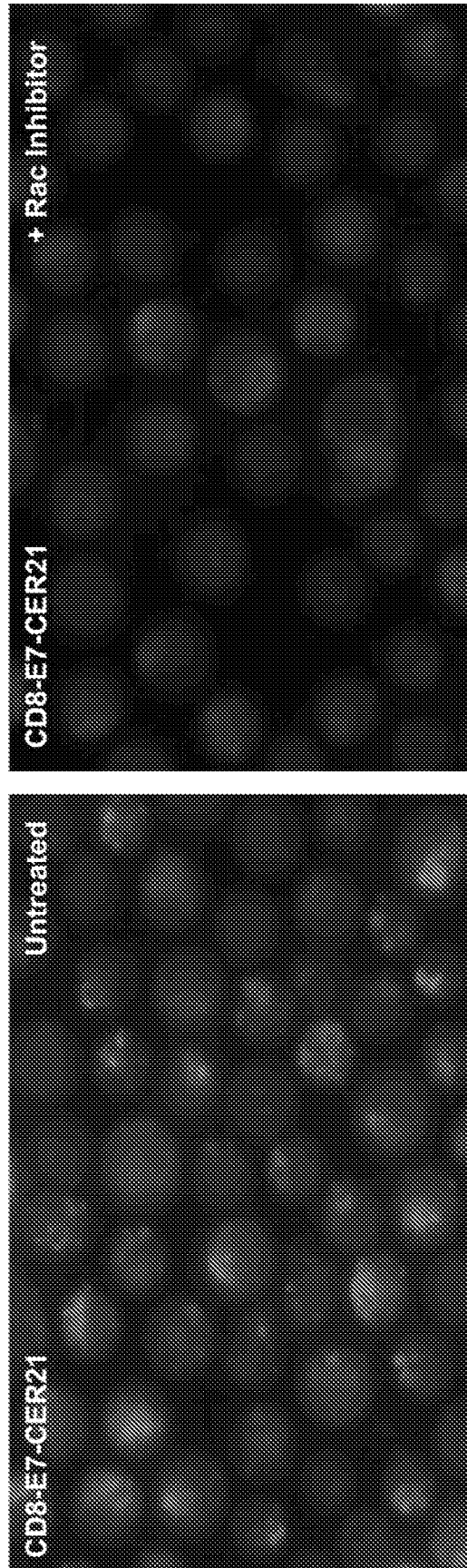
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Fig. 7

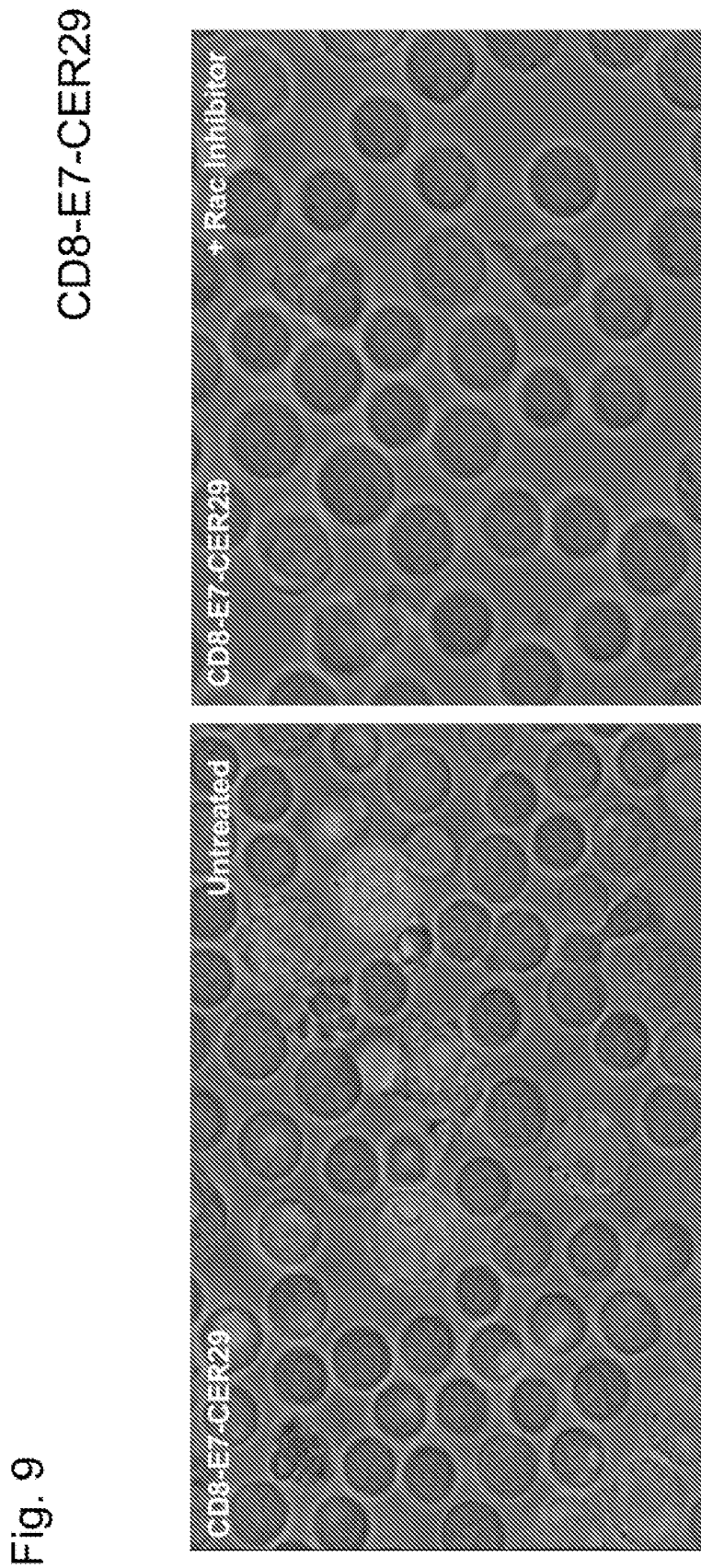


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Fig. 8



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CD8-E7-CER31

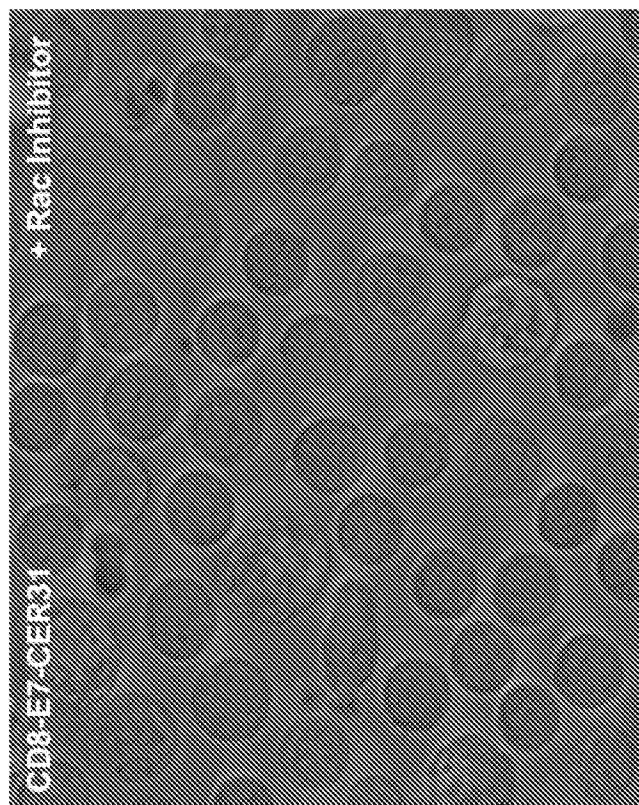
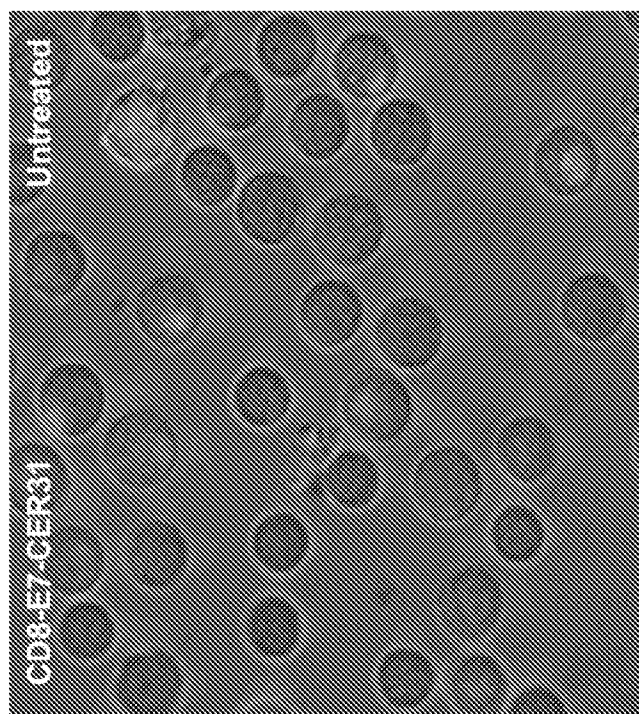


Fig. 10



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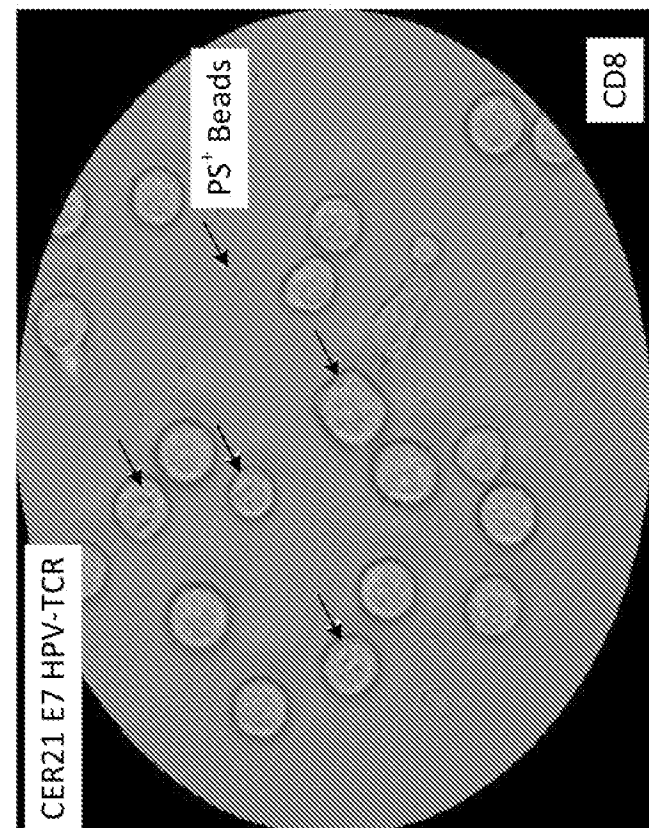
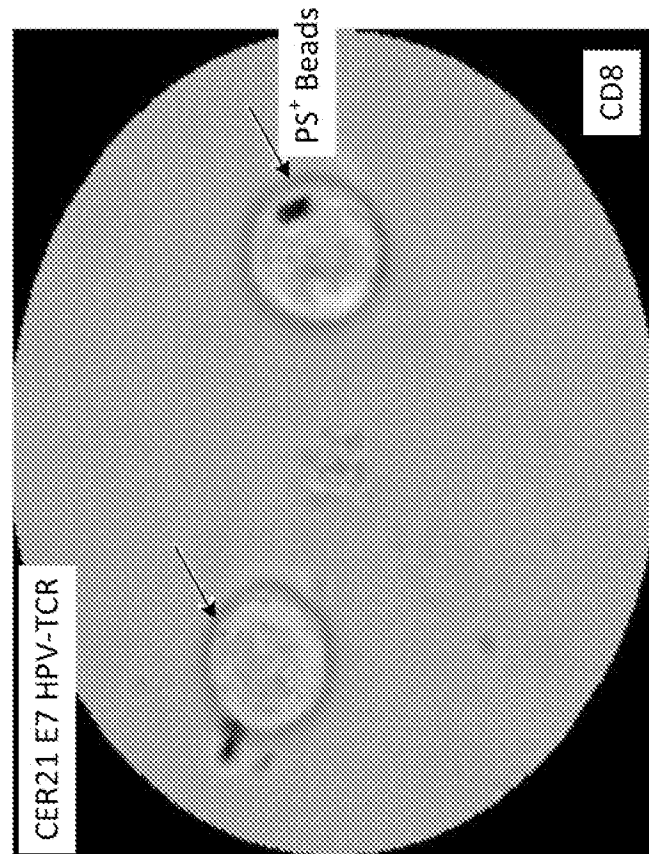


Fig. 11

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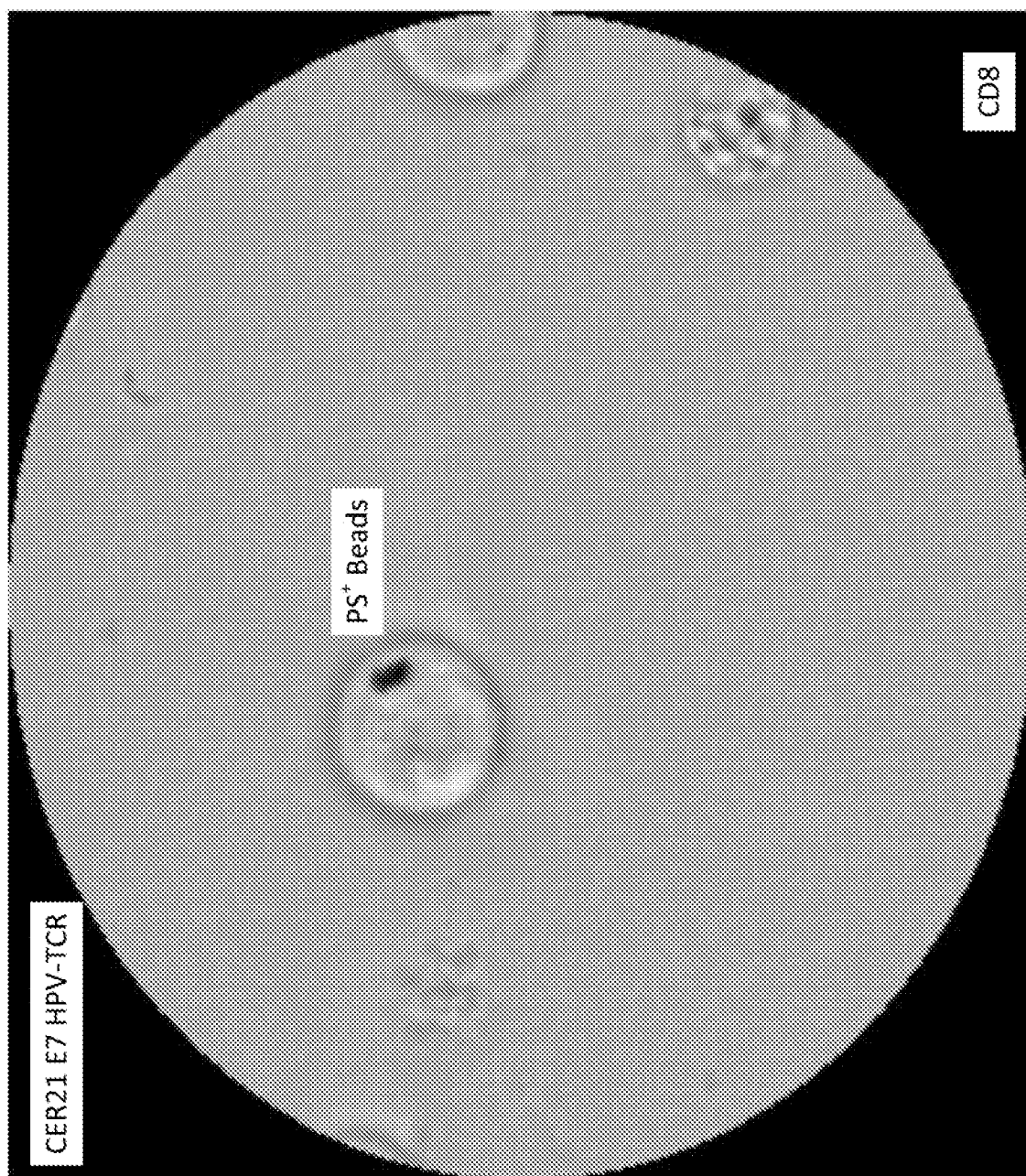


Fig. 12

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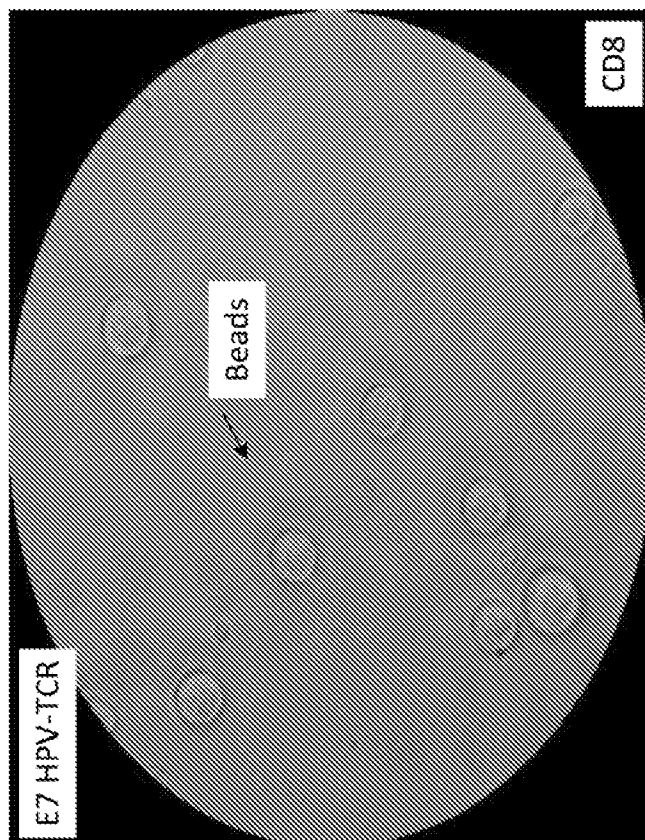
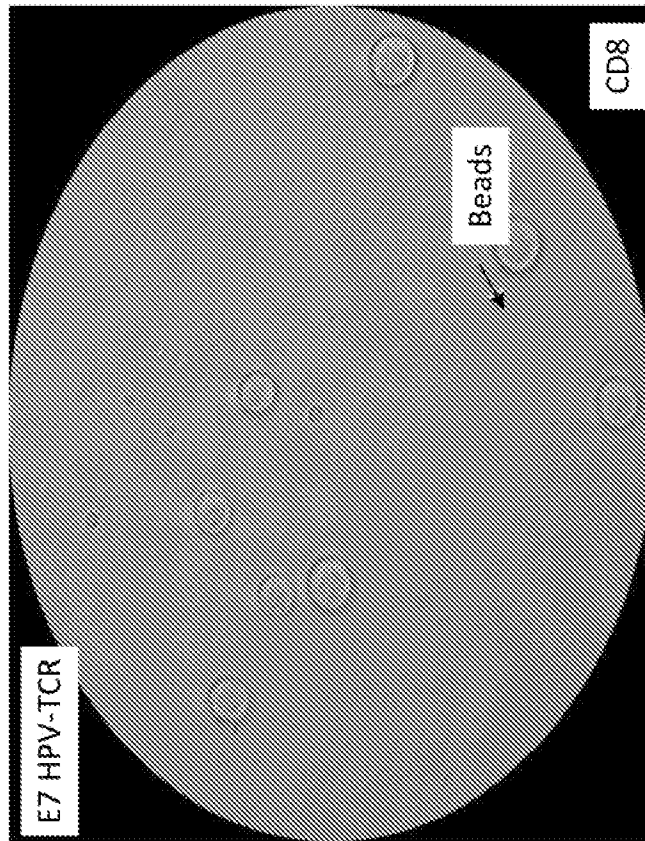
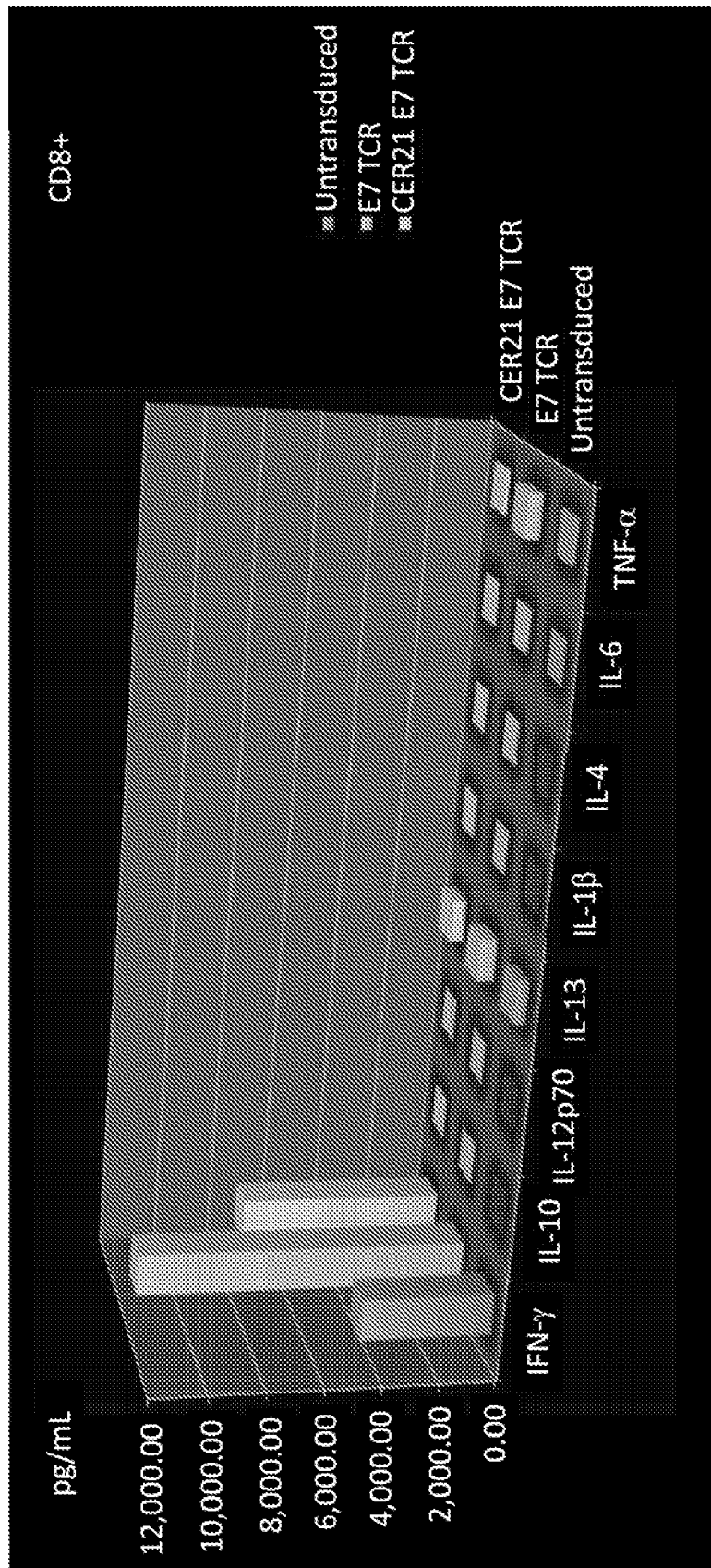


Fig. 13

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Fig. 14



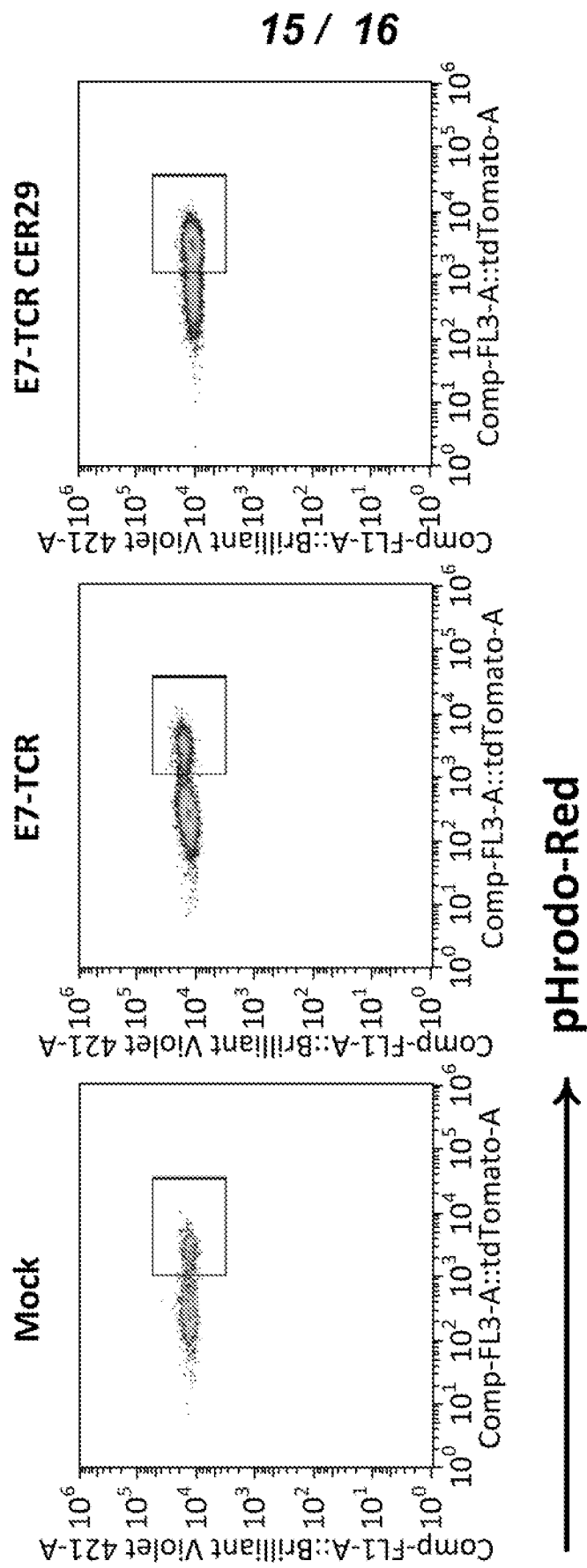


Fig. 15A

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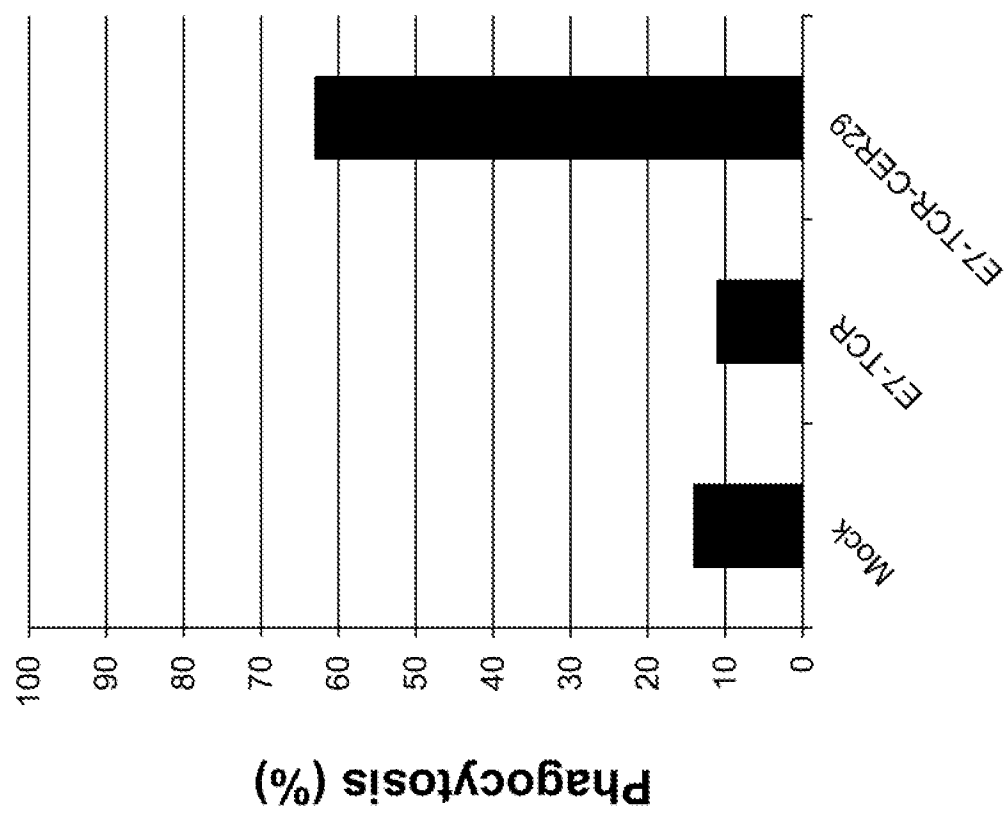


Fig. 15B

200265_406WO_SEQUENCE_LISTING.TXT

SEQUENCE LISTING

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Corey, Daniel Mark
Ibarra, Ingrid

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RECEPTORS, GENETICALLY MODIFIED HOST CELLS,
AND USES THEREOF

<130> 200265.406WO

<140> PCT

<141> 2019-03-27

<150> US 62/649,499

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<210> 2

<211> 46

<212> PRT

<213> Homo sapiens

<220>

<223> MRC1 signaling domain

<400> 2

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

200265_406WO_SEQUENCE_LISTING.TXT

Asp Leu Val Gly Asn Ile Glu Gln Asn Glu His Ser Val Ile
 35 40 45

<210> 3

<211> 473

<212> PRT

<213> Homo sapiens

<220>

<223> MERTK signaling domain

<400> 3

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

200265_406WO_SEQUENCE_LISTING.TXT

```

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

```

<210> 4

<211> 476

<212> PRT

<213> Mus musculus

<220>

<223> MERTK signaling domain

<400> 4

```

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

```

200265_406WO_SEQUENCE_LISTING.TXT

```

Ser Glu Ala Ala Cys Met Lys Asp Phe Asn His Pro Asn Val Ile Arg
   115                               120               125
Leu Leu Gly Val Cys Ile Glu Leu Ser Ser Gln Gly Ile Pro Lys Pro
   130                               135               140
Met Val Ile Leu Pro Phe Met Lys Tyr Gly Asp Leu His Thr Phe Leu
  145                               150               155               160
Leu Tyr Ser Arg Leu Asn Thr Gly Pro Lys Tyr Ile His Leu Gln Thr
   165                               170               175
Leu Leu Lys Phe Met Met Asp Ile Ala Gln Gly Met Glu Tyr Leu Ser
   180                               185               190
Asn Arg Asn Phe Leu His Arg Asp Leu Ala Ala Arg Asn Cys Met Leu
   195                               200               205
Arg Asp Asp Met Thr Val Cys Val Ala Asp Phe Gly Leu Ser Lys Lys
   210                               215               220
Ile Tyr Ser Gly Asp Tyr Tyr Arg Gln Gly Arg Ile Ala Lys Met Pro
  225                               230               235               240
Val Lys Trp Ile Ala Ile Glu Ser Leu Ala Asp Arg Val Tyr Thr Ser
   245                               250               255
Lys Ser Asp Val Trp Ala Phe Gly Val Thr Met Trp Glu Ile Thr Thr
   260                               265               270
Arg Gly Met Thr Pro Tyr Pro Gly Val Gln Asn His Glu Met Tyr Asp
   275                               280               285
Tyr Leu Leu His Gly His Arg Leu Lys Gln Pro Glu Asp Cys Leu Asp
   290                               295               300
Glu Leu Tyr Asp Ile Met Tyr Ser Cys Trp Ser Ala Asp Pro Leu Asp
  305                               310               315               320
Arg Pro Thr Phe Ser Val Leu Arg Leu Gln Leu Glu Lys Leu Ser Glu
   325                               330               335
Ser Leu Pro Asp Ala Gln Asp Lys Glu Ser Ile Ile Tyr Ile Asn Thr
   340                               345               350
Gln Leu Leu Glu Ser Cys Glu Gly Ile Ala Asn Gly Pro Ser Leu Thr
   355                               360               365
Gly Leu Asp Met Asn Ile Asp Pro Asp Ser Ile Ile Ala Ser Cys Thr
   370                               375               380
Pro Gly Ala Ala Val Ser Val Val Thr Ala Glu Val His Glu Asn Asn
  385                               390               395               400
Leu Arg Glu Glu Arg Tyr Ile Leu Asn Gly Gly Asn Glu Glu Trp Glu
   405                               410               415
Asp Val Ser Ser Thr Pro Phe Ala Ala Val Thr Pro Glu Lys Asp Gly
   420                               425               430
Val Leu Pro Glu Asp Arg Leu Thr Lys Asn Gly Val Ser Trp Ser His
   435                               440               445
His Ser Thr Leu Pro Leu Gly Ser Pro Ser Pro Asp Glu Leu Leu Phe
   450                               455               460
Val Asp Asp Ser Leu Glu Asp Ser Glu Val Leu Met
  465                               470               475

```

<210> 5

200265_406WO_SEQUENCE_LISTING.TXT

<211> 440

<212> PRT

<213> Homo sapiens

<220>

<223> Tyro3 signaling domain

<400> 5

```

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

```


200265_406WO_SEQUENCE_LISTING.TXT

Ala	Asp	Pro	Lys	Gln	Arg	Pro	Ser	Phe	Thr	Cys	Leu	Arg	Met	Glu	Leu
				325					330					335	
Glu	Asn	Ile	Leu	Gly	Gln	Leu	Ser	Val	Leu	Ser	Ala	Ser	Gln	Asp	Pro
			340					345					350		
Leu	Tyr	Ile	Asn	Ile	Glu	Arg	Ala	Glu	Glu	Pro	Thr	Ala	Gly	Gly	Ser
		355					360					365			
Leu	Glu	Leu	Pro	Gly	Arg	Asp	Gln	Pro	Tyr	Ser	Gly	Ala	Gly	Asp	Gly
	370					375					380				
Ser	Gly	Met	Gly	Ala	Val	Gly	Gly	Thr	Pro	Ser	Asp	Cys	Arg	Tyr	Ile
385					390					395					400
Leu	Thr	Pro	Gly	Gly	Leu	Ala	Glu	Gln	Pro	Gly	Gln	Ala	Glu	His	Gln
			405					410						415	
Pro	Glu	Ser	Pro	Leu	Asn	Glu	Thr	Gln	Arg	Leu	Leu	Leu	Leu	Gln	Gln
			420					425					430		
Gly	Leu	Leu	Pro	His	Ser	Ser	Cys								
		435					440								

<210> 6

<211> 422

<212> PRT

<213> Homo sapiens

<220>

<223> Axl signaling domain

<400> 6

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

200265_406WO_SEQUENCE_LISTING.TXT

```

Leu Val Lys Phe Met Ala Asp Ile Ala Ser Gly Met Glu Tyr Leu Ser
    180                      185                      190
Thr Lys Arg Phe Ile His Arg Asp Leu Ala Ala Arg Asn Cys Met Leu
    195                      200                      205
Asn Glu Asn Met Ser Val Cys Val Ala Asp Phe Gly Leu Ser Lys Lys
    210                      215                      220
Ile Tyr Asn Gly Asp Tyr Tyr Arg Gln Gly Arg Ile Ala Lys Met Pro
    225                      230                      235                      240
Val Lys Trp Ile Ala Ile Glu Ser Leu Ala Asp Arg Val Tyr Thr Ser
    245                      250                      255
Lys Ser Asp Val Trp Ser Phe Gly Val Thr Met Trp Glu Ile Ala Thr
    260                      265                      270
Arg Gly Gln Thr Pro Tyr Pro Gly Val Glu Asn Ser Glu Ile Tyr Asp
    275                      280                      285
Tyr Leu Arg Gln Gly Asn Arg Leu Lys Gln Pro Ala Asp Cys Leu Asp
    290                      295                      300
Gly Leu Tyr Ala Leu Met Ser Arg Cys Trp Glu Leu Asn Pro Gln Asp
    305                      310                      315                      320
Arg Pro Ser Phe Thr Glu Leu Arg Glu Asp Leu Glu Asn Thr Leu Lys
    325                      330                      335
Ala Leu Pro Pro Ala Gln Glu Pro Asp Glu Ile Leu Tyr Val Asn Met
    340                      345                      350
Asp Glu Gly Gly Gly Tyr Pro Glu Pro Pro Gly Ala Ala Gly Gly Ala
    355                      360                      365
Asp Pro Pro Thr Gln Pro Asp Pro Lys Asp Ser Cys Ser Cys Leu Thr
    370                      375                      380
Ala Ala Glu Val His Pro Ala Gly Arg Tyr Val Leu Cys Pro Ser Thr
    385                      390                      395                      400
Thr Pro Ser Pro Ala Gln Pro Ala Asp Arg Gly Ser Pro Ala Ala Pro
    405                      410                      415
Gly Gln Glu Asp Gly Ala
    420

```

<210> 7

<211> 727

<212> PRT

<213> Homo sapiens

<220>

<223> ELMO signaling domain

<400> 7

```

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

```

200265_406WO_SEQUENCE_LISTING.TXT

Phe	Ala	Leu	Gln	His	Ala	Asp	Ser	Ser	Asn	Phe	Tyr	Ile	Thr	Glu	Lys
50						55				60					
Asn	Arg	Asn	Glu	Ile	Lys	Asn	Gly	Thr	Ile	Leu	Arg	Leu	Thr	Thr	Ser
65					70				75						80
Pro	Ala	Gln	Asn	Ala	Gln	Gln	Leu	His	Glu	Arg	Ile	Gln	Ser	Ser	Ser
				85					90					95	
Met	Asp	Ala	Lys	Leu	Glu	Ala	Leu	Lys	Asp	Leu	Ala	Ser	Leu	Ser	Arg
			100					105					110		
Asp	Val	Thr	Phe	Ala	Gln	Glu	Phe	Ile	Asn	Leu	Asp	Gly	Ile	Ser	Leu
		115					120					125			
Leu	Thr	Gln	Met	Val	Glu	Ser	Gly	Thr	Glu	Arg	Tyr	Gln	Lys	Leu	Gln
						135					140				
Lys	Ile	Met	Lys	Pro	Cys	Phe	Gly	Asp	Met	Leu	Ser	Phe	Thr	Leu	Thr
145					150					155					160
Ala	Phe	Val	Glu	Leu	Met	Asp	His	Gly	Ile	Val	Ser	Trp	Asp	Thr	Phe
				165					170					175	
Ser	Val	Ala	Phe	Ile	Lys	Lys	Ile	Ala	Ser	Phe	Val	Asn	Lys	Ser	Ala
			180					185					190		
Ile	Asp	Ile	Ser	Ile	Leu	Gln	Arg	Ser	Leu	Ala	Ile	Leu	Glu	Ser	Met
		195					200						205		
Val	Leu	Asn	Ser	His	Asp	Leu	Tyr	Gln	Lys	Val	Ala	Gln	Glu	Ile	Thr
	210					215				220					
Ile	Gly	Gln	Leu	Ile	Pro	His	Leu	Gln	Gly	Ser	Asp	Gln	Glu	Ile	Gln
225					230					235					240
Thr	Tyr	Thr	Ile	Ala	Val	Ile	Asn	Ala	Leu	Phe	Leu	Lys	Ala	Pro	Asp
				245					250					255	
Glu	Arg	Arg	Gln	Glu	Met	Ala	Asn	Ile	Leu	Ala	Gln	Lys	Gln	Leu	Arg
			260					265					270		
Ser	Ile	Ile	Leu	Thr	His	Val	Ile	Arg	Ala	Gln	Arg	Ala	Ile	Asn	Asn
		275					280					285			
Glu	Met	Ala	His	Gln	Leu	Tyr	Val	Leu	Gln	Val	Leu	Thr	Phe	Asn	Leu
	290					295					300				
Leu	Glu	Asp	Arg	Met	Met	Thr	Lys	Met	Asp	Pro	Gln	Asp	Gln	Ala	Gln
305					310					315					320
Arg	Asp	Ile	Ile	Phe	Glu	Leu	Arg	Arg	Ile	Ala	Phe	Asp	Ala	Glu	Ser
				325					330					335	
Glu	Pro	Asn	Asn	Ser	Ser	Gly	Ser	Met	Glu	Lys	Arg	Lys	Ser	Met	Tyr
			340					345					350		
Thr	Arg	Asp	Tyr	Lys	Lys	Leu	Gly	Phe	Ile	Asn	His	Val	Asn	Pro	Ala
		355					360					365			
Met	Asp	Phe	Thr	Gln	Thr	Pro	Pro	Gly	Met	Leu	Ala	Leu	Asp	Asn	Met
					375						380				
Leu	Tyr	Phe	Ala	Lys	His	His	Gln	Asp	Ala	Tyr	Ile	Arg	Ile	Val	Leu
385					390					395					400
Glu	Asn	Ser	Ser	Arg	Glu	Asp	Lys	His	Glu	Cys	Pro	Phe	Gly	Arg	Ser
				405					410					415	
Ser	Ile	Glu	Leu	Thr	Lys	Met	Leu	Cys	Glu	Ile	Leu	Lys	Val	Gly	Glu
			420					425					430		

200265_406WO_SEQUENCE_LISTING.TXT

```

Leu Pro Ser Glu Thr Cys Asn Asp Phe His Pro Met Phe Phe Thr His
    435                440                445
Asp Arg Ser Phe Glu Glu Phe Phe Cys Ile Cys Ile Gln Leu Leu Asn
    450                455                460
Lys Thr Trp Lys Glu Met Arg Ala Thr Ser Glu Asp Phe Asn Lys Val
    465                470                475                480
Met Gln Val Val Lys Glu Gln Val Met Arg Ala Leu Thr Thr Lys Pro
    485                490                495
Ser Ser Leu Asp Gln Phe Lys Ser Lys Leu Gln Asn Leu Ser Tyr Thr
    500                505                510
Glu Ile Leu Lys Ile Arg Gln Ser Glu Arg Met Asn Gln Glu Asp Phe
    515                520                525
Gln Ser Arg Pro Ile Leu Glu Leu Lys Glu Lys Ile Gln Pro Glu Ile
    530                535                540
Leu Glu Leu Ile Lys Gln Gln Arg Leu Asn Arg Leu Val Glu Gly Thr
    545                550                555                560
Cys Phe Arg Lys Leu Asn Ala Arg Arg Arg Gln Asp Lys Phe Trp Tyr
    565                570                575
Cys Arg Leu Ser Pro Asn His Lys Val Leu His Tyr Gly Asp Leu Glu
    580                585                590
Glu Ser Pro Gln Gly Glu Val Pro His Asp Ser Leu Gln Asp Lys Leu
    595                600                605
Pro Val Ala Asp Ile Lys Ala Val Val Thr Gly Lys Asp Cys Pro His
    610                615                620
Met Lys Glu Lys Gly Ala Leu Lys Gln Asn Lys Glu Val Leu Glu Leu
    625                630                635                640
Ala Phe Ser Ile Leu Tyr Asp Ser Asn Cys Gln Leu Asn Phe Ile Ala
    645                650                655
Pro Asp Lys His Glu Tyr Cys Ile Trp Thr Asp Gly Leu Asn Ala Leu
    660                665                670
Leu Gly Lys Asp Met Met Ser Asp Leu Thr Arg Asn Asp Leu Asp Thr
    675                680                685
Leu Leu Ser Met Glu Ile Lys Leu Arg Leu Leu Asp Leu Glu Asn Ile
    690                695                700
Gln Ile Pro Asp Ala Pro Pro Pro Ile Pro Lys Glu Pro Ser Asn Tyr
    705                710                715                720
Asp Phe Val Tyr Asp Cys Asn
    725

```

<210> 8

<211> 522

<212> PRT

<213> Homo sapiens

<220>

<223> Traf6 signaling domain - full length

<400> 8

200265_406WO_SEQUENCE_LISTING.TXT

```

Met Ser Leu Leu Asn Cys Glu Asn Ser Cys Gly Ser Ser Gln Ser Glu
 1           5           10           15
Ser Asp Cys Cys Val Ala Met Ala Ser Ser Cys Ser Ala Val Thr Lys
           20           25           30
Asp Asp Ser Val Gly Gly Thr Ala Ser Thr Gly Asn Leu Ser Ser Ser
 35           40           45
Phe Met Glu Glu Ile Gln Gly Tyr Asp Val Glu Phe Asp Pro Pro Leu
 50           55           60
Glu Ser Lys Tyr Glu Cys Pro Ile Cys Leu Met Ala Leu Arg Glu Ala
 65           70           75           80
Val Gln Thr Pro Cys Gly His Arg Phe Cys Lys Ala Cys Ile Ile Lys
           85           90           95
Ser Ile Arg Asp Ala Gly His Lys Cys Pro Val Asp Asn Glu Ile Leu
 100          105          110
Leu Glu Asn Gln Leu Phe Pro Asp Asn Phe Ala Lys Arg Glu Ile Leu
 115          120          125
Ser Leu Met Val Lys Cys Pro Asn Glu Gly Cys Leu His Lys Met Glu
 130          135          140
Leu Arg His Leu Glu Asp His Gln Ala His Cys Glu Phe Ala Leu Met
 145          150          155          160
Asp Cys Pro Gln Cys Gln Arg Pro Phe Gln Lys Phe His Ile Asn Ile
           165          170          175
His Ile Leu Lys Asp Cys Pro Arg Arg Gln Val Ser Cys Asp Asn Cys
 180          185          190
Ala Ala Ser Met Ala Phe Glu Asp Lys Glu Ile His Asp Gln Asn Cys
 195          200          205
Pro Leu Ala Asn Val Ile Cys Glu Tyr Cys Asn Thr Ile Leu Ile Arg
 210          215          220
Glu Gln Met Pro Asn His Tyr Asp Leu Asp Cys Pro Thr Ala Pro Ile
 225          230          235          240
Pro Cys Thr Phe Ser Thr Phe Gly Cys His Glu Lys Met Gln Arg Asn
           245          250          255
His Leu Ala Arg His Leu Gln Glu Asn Thr Gln Ser His Met Arg Met
 260          265          270
Leu Ala Gln Ala Val His Ser Leu Ser Val Ile Pro Asp Ser Gly Tyr
 275          280          285
Ile Ser Glu Val Arg Asn Phe Gln Glu Thr Ile His Gln Leu Glu Gly
 290          295          300
Arg Leu Val Arg Gln Asp His Gln Ile Arg Glu Leu Thr Ala Lys Met
 305          310          315          320
Glu Thr Gln Ser Met Tyr Val Ser Glu Leu Lys Arg Thr Ile Arg Thr
           325          330          335
Leu Glu Asp Lys Val Ala Glu Ile Glu Ala Gln Gln Cys Asn Gly Ile
 340          345          350
Tyr Ile Trp Lys Ile Gly Asn Phe Gly Met His Leu Lys Cys Gln Glu
 355          360          365
Glu Glu Lys Pro Val Val Ile His Ser Pro Gly Phe Tyr Thr Gly Lys
 370          375          380

```

200265_406WO_SEQUENCE_LISTING.TXT

```

Pro Gly Tyr Lys Leu Cys Met Arg Leu His Leu Gln Leu Pro Thr Ala
385          390          395          400
Gln Arg Cys Ala Asn Tyr Ile Ser Leu Phe Val His Thr Met Gln Gly
          405          410          415
Glu Tyr Asp Ser His Leu Pro Trp Pro Phe Gln Gly Thr Ile Arg Leu
          420          425          430
Thr Ile Leu Asp Gln Ser Glu Ala Pro Val Arg Gln Asn His Glu Glu
          435          440          445
Ile Met Asp Ala Lys Pro Glu Leu Leu Ala Phe Gln Arg Pro Thr Ile
          450          455          460
Pro Arg Asn Pro Lys Gly Phe Gly Tyr Val Thr Phe Met His Leu Glu
465          470          475          480
Ala Leu Arg Gln Arg Thr Phe Ile Lys Asp Asp Thr Leu Leu Val Arg
          485          490          495
Cys Glu Val Ser Thr Arg Phe Asp Met Gly Ser Leu Arg Arg Glu Gly
          500          505          510
Phe Gln Pro Arg Ser Thr Asp Ala Gly Val
          515          520

```

<210> 9

<211> 261

<212> PRT

<213> Homo sapiens

<220>

<223> Syk signaling domain

<400> 9

```

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

```

200265_406WO_SEQUENCE_LISTING.TXT

His	Gly	Lys	Trp	Pro	Val	Lys	Trp	Tyr	Ala	Pro	Glu	Cys	Ile	Asn	Tyr
				165					170					175	
Tyr	Lys	Phe	Ser	Ser	Lys	Ser	Asp	Val	Trp	Ser	Phe	Gly	Val	Leu	Met
			180					185					190		
Trp	Glu	Ala	Phe	Ser	Tyr	Gly	Gln	Lys	Pro	Tyr	Arg	Gly	Met	Lys	Gly
		195					200					205			
Ser	Glu	Val	Thr	Ala	Met	Leu	Glu	Lys	Gly	Glu	Arg	Met	Gly	Cys	Pro
	210					215					220				
Ala	Gly	Cys	Pro	Arg	Glu	Met	Tyr	Asp	Leu	Met	Asn	Leu	Cys	Trp	Thr
225					230					235					240
Tyr	Asp	Val	Glu	Asn	Arg	Pro	Gly	Phe	Ala	Ala	Val	Glu	Leu	Arg	Leu
				245					250					255	
Arg	Asn	Tyr	Tyr	Tyr											
			260												

<210> 10

<211> 296

<212> PRT

<213> Homo sapiens

<220>

<223> MyD88 signaling domain

<400> 10

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

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Val	Ser	Asp	Arg	Asp	Val	Leu	Pro	Gly	Thr	Cys	Val	Trp	Ser	Ile	Ala
		195					200					205			
Ser	Glu	Leu	Ile	Glu	Lys	Arg	Cys	Arg	Arg	Met	Val	Val	Val	Val	Ser
	210					215					220				
Asp	Asp	Tyr	Leu	Gln	Ser	Lys	Glu	Cys	Asp	Phe	Gln	Thr	Lys	Phe	Ala
225					230					235					240
Leu	Ser	Leu	Ser	Pro	Gly	Ala	His	Gln	Lys	Arg	Leu	Ile	Pro	Ile	Lys
				245					250					255	
Tyr	Lys	Ala	Met	Lys	Lys	Glu	Phe	Pro	Ser	Ile	Leu	Arg	Phe	Ile	Thr
			260					265					270		
Val	Cys	Asp	Tyr	Thr	Asn	Pro	Cys	Thr	Lys	Ser	Trp	Phe	Trp	Thr	Arg
		275					280					285			
Leu	Ala	Lys	Ala	Leu	Ser	Leu	Pro								
	290					295									

<210> 11

<400> 11
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<210> 12

<211> 42

<212> PRT

<213> Homo sapiens

<220>

<223> FcepsilonR1gamma signaling domain

<400> 12

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

<210> 13

<211> 61

<212> PRT

<213> Homo sapiens

<220>

<223> FcgammaR1 signaling domain

<400> 13

Arg	Lys	Glu	Leu	Lys	Arg	Lys	Lys	Lys	Trp	Asp	Leu	Glu	Ile	Ser	Leu
1				5				10						15	
Asp	Ser	Gly	His	Glu	Lys	Lys	Val	Ile	Ser	Ser	Leu	Gln	Glu	Asp	Arg

200265_406WO_SEQUENCE_LISTING.TXT

			20					25					30				
His	Leu	Glu	Glu	Glu	Leu	Lys	Cys	Gln	Glu	Gln	Lys	Glu	Glu	Gln	Leu		
		35					40						45				
Gln	Glu	Gly	Val	His	Arg	Lys	Glu	Pro	Gln	Gly	Ala	Thr					
	50					55					60						

<210> 14

<211> 77

<212> PRT

<213> Homo sapiens

<220>

<223> FcgammaR2A signaling domain

<400> 14

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

<210> 15

<211> 77

<212> PRT

<213> Homo sapiens

<220>

<223> FcgammaR2c signaling domain

<400> 15

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

<210> 16

<211> 25

200265_406WO_SEQUENCE_LISTING.TXT

<212> PRT

<213> Homo sapiens

<220>

<223> FcgammaR3A signaling domain

<400> 16

Lys	Thr	Asn	Ile	Arg	Ser	Ser	Thr	Arg	Asp	Trp	Lys	Asp	His	Lys	Phe
1				5					10					15	
Lys	Trp	Arg	Lys	Asp	Pro	Gln	Asp	Lys							
			20					25							

<210> 17

<211> 85

<212> PRT

<213> Homo sapiens

<220>

<223> BAFF-R signaling domain

<400> 17

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

<210> 18

<211> 52

<212> PRT

<213> Homo sapiens

<220>

<223> DAP12 signaling domain

<400> 18

Tyr	Phe	Leu	Gly	Arg	Leu	Val	Pro	Arg	Gly	Arg	Gly	Ala	Ala	Glu	Ala
1				5					10					15	
Ala	Thr	Arg	Lys	Gln	Arg	Ile	Thr	Glu	Thr	Glu	Ser	Pro	Tyr	Gln	Glu
			20					25					30		
Leu	Gln	Gly	Gln	Arg	Ser	Asp	Val	Tyr	Ser	Asp	Leu	Asn	Thr	Gln	Arg

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35
Pro Tyr Tyr Lys
50

40

45

<210> 19
<211> 86
<212> PRT
<213> Homo sapiens

<220>
<223> NFAM1 signaling domain

<400> 19
Leu Trp Asn Lys Lys Arg Met Arg Gly Pro Gly Lys Asp Pro Thr Arg
1 5 10 15
Lys Cys Pro Asp Pro Arg Ser Ala Ser Ser Pro Lys Gln His Pro Ser
20 25 30
Glu Ser Val Tyr Thr Ala Leu Gln Arg Arg Glu Thr Glu Val Tyr Ala
35 40 45
Cys Ile Glu Asn Glu Asp Gly Ser Ser Pro Thr Ala Lys Gln Ser Pro
50 55 60
Leu Ser Gln Glu Arg Pro His Arg Phe Glu Asp Asp Gly Glu Leu Asn
65 70 75 80
Leu Val Tyr Glu Asn Leu
85

<210> 20
<211> 29
<212> PRT
<213> Homo sapiens

<220>
<223> CD79b signaling domain (amino acids 185-229)

<400> 20
Asp Ser Lys Ala Gly Met Glu Glu Asp His Thr Tyr Glu Gly Leu Asp
1 5 10 15
Ile Asp Gln Thr Ala Thr Tyr Glu Asp Ile Val Thr Leu
20 25

<210> 21
<211> 45
<212> PRT
<213> Homo sapiens

<220>
<223> CD79b signaling domain (amino acids 185-213)

200265_406WO_SEQUENCE_LISTING.TXT

<400> 21

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

<210> 22

<211> 185

<212> PRT

<213> Homo sapiens

<220>

<223> TLR1 signaling domain

<400> 22

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

<210> 23

<211> 175

<212> PRT

<213> Homo sapiens

<220>

200265_406WO_SEQUENCE_LISTING.TXT

<223> TLR2 signaling domain

<400> 23

```

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

```

<210> 24

<211> 179

<212> PRT

<213> Homo sapiens

<220>

<223> TLR3 signaling domain

<400> 24

```

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

```

200265 406W0 SEQUENCE LISTING.TXT

[illegible]

<210> 25

<211> 187

<212> PRT

<213> Homo sapiens

 $\langle 220 \rangle$

<223> TLR4 signaling domain

<400> 25

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

<210> 26

<211> 198

200265_406WO_SEQUENCE_LISTING.TXT

<212> PRT

<213> Homo sapiens

<220>

<223> TLR5 signaling domain

<400> 26

```

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

```

<210> 27

<211> 189

<212> PRT

<213> Homo sapiens

<220>

<223> TLR6 signaling domain

<400> 27

```

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

```

200265_406WO_SEQUENCE_LISTING.TXT

```

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

```

<210> 28

<211> 189

<212> PRT

<213> Homo sapiens

<220>

<223> TLR7 signaling domain

<400> 28

```

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

```


145						150						155						160
Ala	His	Pro	Tyr	Phe	Trp	Gln	Cys	Leu	Lys	Asn	Ala	Leu	Ala	Thr	Asp			
				165						170						175		
Asn	His	Val	Ala	Tyr	Ser	Gln	Val	Phe	Lys	Glu	Thr	Val						
			180						185									

<213> Homo sapiens

<223> TLR8 signaling domain

[illegible]

<213> Homo sapiens

$\langle 220 \rangle$

200265_406WO_SEQUENCE_LISTING.TXT

<223> TLR9 signaling domain

<400> 30

```

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

```

<210> 31

<211> 303

<212> PRT

<213> Homo sapiens

<220>

<223> TRAF2 signaling domain

<400> 31

```

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

```

200265_406WO_SEQUENCE_LISTING.TXT

```

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

```

<210> 32

<211> 274

<212> PRT

<213> Homo sapiens

<220>

<223> TRAF3 signaling domain

<400> 32

```

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

```

200265_406WO_SEQUENCE_LISTING.TXT

```

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

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<210> 33

<211> 155

<212> PRT

<213> Homo sapiens

<220>

<223> truncated MyD88 signaling domain without TIR
domain

<400> 33

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

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200265_406WO_SEQUENCE_LISTING.TXT

Arg Pro Gly Ala Ser Val Gly Arg Leu Leu Glu Leu Leu Thr Lys Leu
85 90 95
Gly Arg Asp Asp Val Leu Leu Glu Leu Gly Pro Ser Ile Glu Glu Asp
100 105 110
Cys Gln Lys Tyr Ile Leu Lys Gln Gln Gln Glu Glu Ala Glu Lys Pro
115 120 125
Leu Gln Val Ala Ala Val Asp Ser Ser Val Pro Arg Thr Ala Glu Leu
130 135 140
Ala Gly Ile Thr Thr Leu Asp Asp Pro Leu Gly
145 150 155

<210> 34

<211> 274

<212> PRT

<213> Homo sapiens

<220>

<223> truncated TRAF6 signaling domain

<400> 34

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

200265_406WO_SEQUENCE_LISTING.TXT

Glu Gln Met Pro Asn His Tyr Asp Leu Asp Cys Pro Thr Ala Pro Ile
 225 230 235 240
 Pro Cys Thr Phe Ser Thr Phe Gly Cys His Glu Lys Met Gln Arg Asn
 245 250 255
 His Leu Ala Arg His Leu Gln Glu Asn Thr Gln Ser His Met Arg Met
 260 265 270
 Leu Ala

<210> 35
 <211> 29
 <212> PRT
 <213> Homo sapiens

<220>
 <223> truncated NFAM1 signaling domain

<400> 35
 Ser Ser Pro Lys Gln His Pro Ser Glu Ser Val Tyr Thr Ala Leu Gln
 1 5 10 15
 Arg Arg Glu Thr Glu Val Tyr Ala Cys Ile Glu Asn Glu
 20 25

<210> 36
 <211> 21
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Tim1 transmembrane domain

<400> 36
 Ile Tyr Ala Gly Val Cys Ile Ser Val Leu Val Leu Leu Ala Leu Leu
 1 5 10 15
 Gly Val Ile Ile Ala
 20

<210> 37
 <211> 21
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Tim4 transmembrane domain

<400> 37
 Leu Leu Met Ile Ile Ala Pro Ser Leu Gly Phe Val Leu Phe Ala Leu
 1 5 10 15

200265_406WO_SEQUENCE_LISTING.TXT

Phe Val Ala Phe Leu
20

<210> 38
<211> 21
<212> PRT
<213> Mus musculus

<220>
<223> Tim4 transmembrane domain

<400> 38
Ile Leu Ile Ile Ala Cys Cys Val Gly Phe Val Leu Met Val Leu Leu
1 5 10 15
Phe Leu Ala Phe Leu
20

<210> 39
<211> 21
<212> PRT
<213> Homo sapiens

<220>
<223> Tim3 transmembrane domain

<400> 39
Ile Tyr Ile Gly Ala Gly Ile Cys Ala Gly Leu Ala Leu Ala Leu Ile
1 5 10 15
Phe Gly Ala Leu Ile
20

<210> 40
<211> 21
<212> PRT
<213> Homo sapiens

<220>
<223> FcgammaR1 transmembrane domain

<400> 40
Val Leu Phe Tyr Leu Ala Val Gly Ile Met Phe Leu Val Asn Thr Val
1 5 10 15
Leu Trp Val Thr Ile
20

<210> 41
<211> 23
<212> PRT

200265_406WO_SEQUENCE_LISTING.TXT

<213> Homo sapiens

<220>

<223> FcgammaR2A transmembrane domain

<400> 41

Ile	Ile	Val	Ala	Val	Val	Ile	Ala	Thr	Ala	Val	Ala	Ala	Ile	Val	Ala
1				5					10				15		
Ala	Val	Val	Ala	Leu	Ile	Tyr									
				20											

<210> 42

<211> 23

<212> PRT

<213> Homo sapiens

<220>

<223> FcgammaR2B2 transmembrane domain

<400> 42

Ser	Ser	Ser	Pro	Met	Gly	Ile	Ile	Val	Ala	Val	Val	Thr	Gly	Ile	Ala
1				5					10					15	
Val	Ala	Ala	Ile	Val	Ala	Ala									
				20											

<210> 43

<211> 23

<212> PRT

<213> Homo sapiens

<220>

<223> FcgammaR2C transmembrane domain

<400> 43

Ile	Ile	Val	Ala	Val	Val	Thr	Gly	Ile	Ala	Val	Ala	Ala	Ile	Val	Ala
1				5					10				15		
Ala	Val	Val	Ala	Leu	Ile	Tyr									
				20											

<210> 44

<211> 21

<212> PRT

<213> Homo sapiens

<220>

<223> FcgammaR3A transmembrane domain

<400> 44

200265_406WO_SEQUENCE_LISTING.TXT

Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp Thr Gly
 1 5 10 15
 Leu Tyr Phe Ser Val
 20

<210> 45
 <211> 21
 <212> PRT
 <213> Homo sapiens

<220>
 <223> FcepsilonR1 transmembrane domain

<400> 45
 Leu Cys Tyr Ile Leu Asp Ala Ile Leu Phe Leu Tyr Gly Ile Val Leu
 1 5 10 15
 Thr Leu Leu Tyr Cys
 20

<210> 46
 <211> 19
 <212> PRT
 <213> Homo sapiens

<220>
 <223> FcalphaR1 transmembrane domain

<400> 46
 Leu Ile Arg Met Ala Val Ala Gly Leu Val Leu Val Ala Leu Leu Ala
 1 5 10 15
 Ile Leu Val

<210> 47
 <211> 21
 <212> PRT
 <213> Homo sapiens

<220>
 <223> CD8 transmembrane domain

<400> 47
 Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
 1 5 10 15
 Ser Leu Val Ile Thr
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<210> 48

200265_406W0_SEQUENCE_LISTING.TXT

<211> 21

<212> PRT

<213> Homo sapiens

<220>

<223> MERTK transmembrane domain

<400> 48

Phe	Gly	Cys	Phe	Cys	Gly	Phe	Ile	Leu	Ile	Gly	Leu	Ile	Leu	Tyr	Ile
1				5				10						15	
Ser	Leu	Ala	Ile	Arg											
			20												

<210> 49

<211> 21

<212> PRT

<213> Homo sapiens

<220>

<223> Axl transmembrane domain

<400> 49

Tyr	Val	Leu	Leu	Gly	Ala	Val	Val	Ala	Ala	Ala	Cys	Val	Leu	Ile	Leu
1				5				10						15	
Ala	Leu	Phe	Leu	Val											
			20												

<210> 50

<211> 21

<212> PRT

<213> Homo sapiens

<220>

<223> Tyro3 transmembrane domain

<400> 50

Val	Pro	Val	Val	Leu	Gly	Val	Leu	Thr	Ala	Leu	Val	Thr	Ala	Ala	Ala
1				5				10						15	
Leu	Ala	Leu	Ile	Leu											
			20												

<210> 51

<211> 22

<212> PRT

<213> Homo sapiens

<220>

<223> CD4 transmembrane domain

200265_406WO_SEQUENCE_LISTING.TXT

<400> 51

Met Ala Leu Ile Val Leu Gly Gly Val Ala Gly Leu Leu Leu Phe Ile
 1 5 10 15
 Gly Leu Gly Ile Phe Phe
 20

<210> 52

<211> 21

<212> PRT

<213> Homo sapiens

<220>

<223> DAP12 transmembrane domain

<400> 52

Gly Val Leu Ala Gly Ile Val Met Gly Asp Leu Val Leu Thr Val Leu
 1 5 10 15
 Ile Ala Leu Ala Val
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<210> 53

<211> 21

<212> PRT

<213> Homo sapiens

<220>

<223> MRC1 transmembrane domain

<400> 53

Gly Val Val Ile Ile Val Ile Leu Leu Ile Leu Thr Gly Ala Gly Leu
 1 5 10 15
 Ala Ala Tyr Phe Phe
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<210> 54

<211> 21

<212> PRT

<213> Homo sapiens

<220>

<223> TLR1 transmembrane domain

<400> 54

Leu Leu Ile Val Thr Ile Val Ala Thr Met Leu Val Leu Ala Val Thr
 1 5 10 15
 Val Thr Ser Leu Cys
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200265_406WO_SEQUENCE_LISTING.TXT

<210> 55

<211> 21

<212> PRT

<213> Homo sapiens

<220>

<223> TLR2 transmembrane domain

<400> 55

Ala	Leu	Val	Ser	Gly	Met	Cys	Cys	Ala	Leu	Phe	Leu	Leu	Ile	Leu	Leu
1				5				10					15		
Thr	Gly	Val	Leu	Cys											
			20												

<210> 56

<211> 21

<212> PRT

<213> Homo sapiens

<220>

<223> TLR3 Transmembrane domain

<400> 56

Phe	Phe	Met	Ile	Asn	Thr	Ser	Ile	Leu	Leu	Ile	Phe	Ile	Phe	Ile	Val
1				5				10					15		
Leu	Leu	Ile	His	Phe											
			20												

<210> 57

<211> 21

<212> PRT

<213> Homo sapiens

<220>

<223> TLR4 transmembrane domain

<400> 57

Thr	Ile	Ile	Gly	Val	Ser	Val	Leu	Ser	Val	Leu	Val	Val	Ser	Val	Val
1				5				10					15		
Ala	Val	Leu	Val	Tyr											
			20												

<210> 58

<211> 21

<212> PRT

<213> Homo sapiens

200265_406WO_SEQUENCE_LISTING.TXT

<220>

<223> TLR5 transmembrane domain

<400> 58

Phe	Ser	Leu	Phe	Ile	Val	Cys	Thr	Val	Thr	Leu	Thr	Leu	Phe	Leu	Met
1				5					10					15	
Thr	Ile	Leu	Thr	Val											
				20											

<210> 59

<211> 21

<212> PRT

<213> Homo sapiens

<220>

<223> TLR6 transmembrane domain

<400> 59

Ala	Leu	Val	Ser	Gly	Met	Cys	Cys	Ala	Leu	Phe	Leu	Leu	Ile	Leu	Leu
1				5					10					15	
Thr	Gly	Val	Leu	Cys											
				20											

<210> 60

<211> 21

<212> PRT

<213> Homo sapiens

<220>

<223> TLR7 transmembrane domain

<400> 60

Leu	Ile	Leu	Phe	Ser	Leu	Ser	Ile	Ser	Val	Ser	Leu	Phe	Leu	Met	Val
1				5					10					15	
Met	Met	Thr	Ala	Ser											
				20											

<210> 61

<211> 21

<212> PRT

<213> Homo sapiens

<220>

<223> TLR8 transmembrane domain

<400> 61

Ala	Val	Ile	Leu	Phe	Phe	Phe	Thr	Phe	Phe	Ile	Thr	Thr	Met	Val	Met
1				5					10					15	

200265_406WO_SEQUENCE_LISTING.TXT

Leu Ala Ala Leu Ala
20

<210> 62
<211> 21
<212> PRT
<213> Homo sapiens

<220>
<223> TLR9 transmembrane domain

<400> 62
Phe Ala Leu Ser Leu Leu Ala Val Ala Leu Gly Leu Gly Val Pro Met
1 5 10 15
Leu His His Leu Cys
20

<210> 63
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> modified IgG4 hinge

<400> 63
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
1 5 10

<210> 64
<211> 22
<212> PRT
<213> Homo sapiens

<220>
<223> GM-CSF signal peptide

<400> 64
Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15
Ala Phe Leu Leu Ile Pro
20

<210> 65
<211> 24
<212> PRT
<213> Homo sapiens

200265_406WO_SEQUENCE_LISTING.TXT

<220>

<223> Tim4 signal peptide

<400> 65

Met	Ser	Lys	Glu	Pro	Leu	Ile	Leu	Trp	Leu	Met	Ile	Glu	Phe	Trp	Trp
1				5				10					15		
Leu	Tyr	Leu	Thr	Pro	Val	Thr	Ser								
			20												

<210> 66

<211> 22

<212> PRT

<213> Mus musculus

<220>

<223> Tim4 signal peptide

<400> 66

Met	Ser	Lys	Gly	Leu	Leu	Leu	Leu	Trp	Leu	Val	Thr	Glu	Leu	Trp	Trp
1				5				10					15		
Leu	Tyr	Leu	Thr	Pro	Ala										
			20												

<210> 67

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> T2A self-cleaving peptide

<400> 67

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

<210> 68

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> T2A self-cleaving peptide variant

<400> 68

Leu	Glu	Gly	Gly	Gly	Glu	Gly	Arg	Gly	Ser	Leu	Leu	Thr	Cys	Gly	Asp
1				5				10					15		

200265_406WO_SEQUENCE_LISTING.TXT

Val Glu Glu Asn Pro Gly Pro
20

<210> 69
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> T2A self-cleaving peptide variant

<400> 69
Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
1 5 10 15
Gly Pro Arg

<210> 70
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> P2A self-cleaving peptide

<400> 70
Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn
1 5 10 15
Pro Gly Pro

<210> 71
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> P2A self-cleaving peptide variant

<400> 71
Arg Ala Lys Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys
1 5 10 15
Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro
20 25

<210> 72
<211> 20
<212> PRT

<213> Artificial Sequence

<220>

<223> E2A self-cleaving peptide

<400> 72

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

<210> 73

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> F2A self-cleaving peptide

<400> 73

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

<210> 74

<400> 74

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<210> 75

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> T2A self-cleaving peptide variant

<400> 75

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

<210> 76

<400> 76

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200265_406WO_SEQUENCE_LISTING.TXT

<210> 77

<400> 77
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<210> 78

<400> 78
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<210> 79

<400> 79
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<210> 80

<400> 80
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<210> 81

<400> 81
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<210> 82

<211> 285

<212> PRT

<213> Homo sapiens

<220>

<223> truncated EGFR

<400> 82

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

200265 406W0 SEQUENCE LISTING.TXT

[illegible]

<210> 83

<211> 192

<212> PRT

<213> Homo sapiens

 $\langle 220 \rangle$

<223> Rac1

<400> 83

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

200265_406WO_SEQUENCE_LISTING.TXT

115	120	125													
Leu	Lys	Glu	Lys	Lys	Leu	Thr	Pro	Ile	Thr	Tyr	Pro	Gln	Gly	Leu	Ala
130						135					140				
Met	Ala	Lys	Glu	Ile	Gly	Ala	Val	Lys	Tyr	Leu	Glu	Cys	Ser	Ala	Leu
145					150					155					160
Thr	Gln	Arg	Gly	Leu	Lys	Thr	Val	Phe	Asp	Glu	Ala	Ile	Arg	Ala	Val
				165					170					175	
Leu	Cys	Pro	Pro	Pro	Val	Lys	Lys	Arg	Lys	Arg	Lys	Cys	Leu	Leu	Leu
			180					185					190		

<210> 84
 <211> 215
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Rab5

<400> 84

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

200265_406WO_SEQUENCE_LISTING.TXT

<210> 85
 <211> 207
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Rab7

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

<210> 86
 <211> 184
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Rap1

<400> 86
 Met Arg Glu Tyr Lys Leu Val Val Leu Gly Ser Gly Gly Val Gly Lys
 1 5 10 15
 Ser Ala Leu Thr Val Gln Phe Val Gln Gly Ile Phe Val Glu Lys Tyr

200265_406WO_SEQUENCE_LISTING.TXT

```

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

```

<210> 87

<211> 193

<212> PRT

<213> Homo sapiens

<220>

<223> RhoA

<400> 87

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

```

200265_406WO_SEQUENCE_LISTING.TXT

130		135		140	
Arg	Asp	Met	Ala	Asn	Arg
145		150		155	
Ala	Lys	Thr	Lys	Asp	Gly
		165		170	
Ala	Ala	Leu	Gln	Ala	Arg
		180		185	
Leu				190	

<210> 88

<400> 88
000

<210> 89

<400> 89
000

<210> 90

<211> 598

<212> PRT

<213> Artificial Sequence

<220>

<223> HPV16 E7 TCRbeta chain-P2A-TCRalpha chain

<400> 90

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

200265_406WO_SEQUENCE_LISTING.TXT

145					150					155				160	
Lys	Ala	Thr	Leu	Val	Cys	Leu	Ala	Arg	Gly	Phe	Phe	Pro	Asp	His	Val
				165					170					175	
Glu	Leu	Ser	Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Cys
			180					185					190		
Thr	Asp	Pro	Gln	Ala	Tyr	Lys	Glu	Ser	Asn	Tyr	Ser	Tyr	Cys	Leu	Ser
		195				200					205				
Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	His	Asn	Pro	Arg	Asn	His
	210					215					220				
Phe	Arg	Cys	Gln	Val	Gln	Phe	His	Gly	Leu	Ser	Glu	Glu	Asp	Lys	Trp
225					230					235				240	
Pro	Glu	Gly	Ser	Pro	Lys	Pro	Val	Thr	Gln	Asn	Ile	Ser	Ala	Glu	Ala
				245					250					255	
Trp	Gly	Arg	Ala	Asp	Cys	Gly	Ile	Thr	Ser	Ala	Ser	Tyr	Gln	Gln	Gly
			260					265					270		
Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr
		275					280					285			
Leu	Tyr	Ala	Val	Leu	Val	Ser	Thr	Leu	Val	Val	Met	Ala	Met	Val	Lys
	290					295					300				
Arg	Lys	Asn	Ser	Arg	Ala	Lys	Arg	Ser	Gly	Ser	Gly	Ala	Thr	Asn	Phe
305					310					315					320
Ser	Leu	Leu	Lys	Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met
			325						330					335	
Trp	Gly	Val	Phe	Leu	Leu	Tyr	Val	Ser	Met	Lys	Met	Gly	Gly	Thr	Thr
			340					345					350		
Gly	Gln	Asn	Ile	Asp	Gln	Pro	Thr	Glu	Met	Thr	Ala	Thr	Glu	Gly	Ala
		355					360						365		
Ile	Val	Gln	Ile	Asn	Cys	Thr	Tyr	Gln	Thr	Ser	Gly	Phe	Asn	Gly	Leu
	370					375					380				
Phe	Trp	Tyr	Gln	Gln	His	Ala	Gly	Glu	Ala	Pro	Thr	Phe	Leu	Ser	Tyr
385					390					395					400
Asn	Val	Leu	Asp	Gly	Leu	Glu	Glu	Lys	Gly	Arg	Phe	Ser	Ser	Phe	Leu
			405						410					415	
Ser	Arg	Ser	Lys	Gly	Tyr	Ser	Tyr	Leu	Leu	Leu	Lys	Glu	Leu	Gln	Met
			420					425					430		
Lys	Asp	Ser	Ala	Ser	Tyr	Leu	Cys	Ala	Ser	Val	Asp	Gly	Asn	Asn	Arg
		435					440					445			
Leu	Ala	Phe	Gly	Lys	Gly	Asn	Gln	Val	Val	Val	Ile	Pro	Asn	Ile	Gln
	450					455					460				
Asn	Pro	Glu	Pro	Ala	Val	Tyr	Gln	Leu	Lys	Asp	Pro	Arg	Ser	Gln	Asp
465					470					475					480
Ser	Thr	Leu	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Ile	Asn	Val	Pro
			485						490					495	
Lys	Thr	Met	Glu	Ser	Gly	Thr	Phe	Ile	Thr	Asp	Lys	Cys	Val	Leu	Asp
			500					505					510		
Met	Lys	Ala	Met	Asp	Ser	Lys	Ser	Asn	Gly	Ala	Ile	Ala	Trp	Ser	Asn
	515						520					525			
Gln	Thr	Ser	Phe	Thr	Cys	Gln	Asp	Ile	Phe	Lys	Glu	Thr	Asn	Ala	Thr

200265_406WO_SEQUENCE_LISTING.TXT

```

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

```

<210> 91

<211> 279

<212> PRT

<213> Mus musculus

<220>

<223> Tim4 binding domain, amino acids 1-22 are signal peptide

<400> 91

```

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

```

200265_406WO_SEQUENCE_LISTING.TXT

Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
 225 230 235 240
 Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
 245 250 255
 Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
 260 265 270
 Gln Ile Asn Ser Arg Gln Thr
 275

<210> 92
 <211> 135
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR Vbeta region

<400> 92
 Met Ala Pro Gly Leu Leu Cys Trp Ala Leu Leu Cys Leu Leu Gly Ala
 1 5 10 15
 Gly Leu Val Asp Ala Gly Val Thr Gln Ser Pro Thr His Leu Ile Lys
 20 25 30
 Thr Arg Gly Gln Gln Val Thr Leu Arg Cys Ser Pro Lys Ser Gly His
 35 40 45
 Asp Thr Val Ser Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Gln Phe
 50 55 60
 Ile Phe Gln Tyr Tyr Glu Glu Glu Glu Arg Gln Arg Gly Asn Phe Pro
 65 70 75 80
 Asp Arg Phe Ser Gly His Gln Phe Pro Asn Tyr Ser Ser Glu Leu Asn
 85 90 95
 Val Asn Ala Leu Leu Leu Gly Asp Ser Ala Leu Tyr Leu Cys Ala Ser
 100 105 110
 Ser Leu Gly Trp Arg Gly Gly Arg Tyr Asn Glu Gln Phe Phe Gly Pro
 115 120 125
 Gly Thr Arg Leu Thr Val Leu
 130 135

<210> 93
 <211> 173
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR Cbeta region, Cys-substituted

<400> 93
 Glu Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser Leu Phe Glu Pro
 1 5 10 15

200265_406WO_SEQUENCE_LISTING.TXT

```

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

```

<210> 94

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR Valpha region

<400> 94

```

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

```

<210> 95

200265_406WO_SEQUENCE_LISTING.TXT

<211> 137

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR Calpha region, Cys-substituted, LVL substituted

<400> 95

```

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

```

<210> 96

<211> 314

<212> PRT

<213> Homo sapiens

<220>

<223> Tim4 binding domain, amino acids 1-24 signal peptide

<400> 96

```

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

```

200265_406WO_SEQUENCE_LISTING.TXT

```

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

```

<210> 97

<211> 487

<212> PRT

<213> Artificial Sequence

<220>

<223> CER5, amino acids 1-22 are signal peptide

<400> 97

```

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

```

200265_406WO_SEQUENCE_LISTING.TXT

```

Asn Ala Glu Leu Leu Arg Thr Asp Gly Thr Arg Ile Ile Ser Arg Lys
65      70      75      80
Ser Thr Lys Tyr Thr Leu Leu Gly Lys Val Gln Phe Gly Glu Val Ser
      85      90      95
Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr Cys Cys
100      105      110
Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn Val Arg
115      120      125
Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr Thr Thr
130      135      140
Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
145      150      155      160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
165      170      175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
180      185      190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
195      200      205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
210      215      220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
225      230      235      240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
245      250      255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
260      265      270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
275      280      285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Lys Phe Tyr Phe
290      295      300
His Leu Met Leu Leu Ala Gly Cys Ile Lys Tyr Gly Arg Gly Glu Asn
305      310      315      320
Ile Tyr Asp Ala Phe Val Ile Tyr Ser Ser Gln Asp Glu Asp Trp Val
325      330      335
Arg Asn Glu Leu Val Lys Asn Leu Glu Gly Val Pro Pro Phe Gln
340      345      350
Leu Cys Leu His Tyr Arg Asp Phe Ile Pro Gly Val Ala Ile Ala Ala
355      360      365
Asn Ile Ile His Glu Gly Phe His Lys Ser Arg Lys Val Ile Val Val
370      375      380
Val Ser Gln His Phe Ile Gln Ser Arg Trp Cys Ile Phe Glu Tyr Glu
385      390      395      400
Ile Ala Gln Thr Trp Gln Phe Leu Ser Ser Arg Ala Gly Ile Ile Phe
405      410      415
Ile Val Leu Gln Lys Val Glu Lys Thr Leu Leu Arg Gln Gln Val Glu
420      425      430
Leu Tyr Arg Leu Leu Ser Arg Asn Thr Tyr Leu Glu Trp Glu Asp Ser
435      440      445

```

200265_406WO_SEQUENCE_LISTING.TXT

Val Leu Gly Arg His Ile Phe Trp Arg Arg Leu Arg Lys Ala Leu Leu
 450 455 460
 Asp Gly Lys Ser Trp Asn Pro Glu Gly Thr Val Gly Thr Gly Cys Asn
 465 470 475 480
 Trp Gln Glu Ala Thr Ser Ile
 485

<210> 98

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> CER19, amino acids 1-22 are signal peptide

<400> 98

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

200265_406WO_SEQUENCE_LISTING.TXT

```

Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
    260                265                270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
    275                280                285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Thr Lys Phe Arg
    290                295                300
Gly Phe Cys Phe Ile Cys Tyr Lys Thr Ala Gln Arg Leu Val Phe Lys
    305                310                315                320
Asp His Pro Gln Gly Thr Glu Pro Asp Met Tyr Lys Tyr Asp Ala Tyr
    325                330                335
Leu Cys Phe Ser Ser Lys Asp Phe Thr Trp Val Gln Asn Ala Leu Leu
    340                345                350
Lys His Leu Asp Thr Gln Tyr Ser Asp Gln Asn Arg Phe Asn Leu Cys
    355                360                365
Phe Glu Glu Arg Asp Phe Val Pro Gly Glu Asn Arg Ile Ala Asn Ile
    370                375                380
Gln Asp Ala Ile Trp Asn Ser Arg Lys Ile Val Cys Leu Val Ser Arg
    385                390                395                400
His Phe Leu Arg Asp Gly Trp Cys Leu Glu Ala Phe Ser Tyr Ala Gln
    405                410                415
Gly Arg Cys Leu Ser Asp Leu Asn Ser Ala Leu Ile Met Val Val Val
    420                425                430
Gly Ser Leu Ser Gln Tyr Gln Leu Met Lys His Gln Ser Ile Arg Gly
    435                440                445
Phe Val Gln Lys Gln Gln Tyr Leu Arg Trp Pro Glu Asp Phe Gln Asp
    450                455                460
Val Gly Trp Phe Leu His Lys Leu Ser Gln Gln Ile Leu Lys Lys Glu
    465                470                475                480
Lys Glu Lys Lys Lys Asp Asn Asn Ile Pro Leu Gln Thr Val Ala Thr
    485                490                495
Ile Ser

```

<210> 99

<211> 493

<212> PRT

<213> Artificial Sequence

<220>

<223> CER21, amino acids 1-22 are signal peptide

<400> 99

```

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

```


200265_406WO_SEQUENCE_LISTING.TXT

```

Arg Asn Ser Met Cys Trp Gly Lys Gly Ser Cys Pro Asn Ser Lys Cys
 50      55      60
Asn Ala Glu Leu Leu Arg Thr Asp Gly Thr Arg Ile Ile Ser Arg Lys
 65      70      75      80
Ser Thr Lys Tyr Thr Leu Leu Gly Lys Val Gln Phe Gly Glu Val Ser
      85      90      95
Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr Cys Cys
      100      105      110
Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn Val Arg
      115      120      125
Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr Thr Thr
      130      135      140
Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
 145      150      155      160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
      165      170      175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
      180      185      190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
      195      200      205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
 210      215      220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
 225      230      235      240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
      245      250      255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
      260      265      270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
      275      280      285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu His His Leu Phe
      290      295      300
Tyr Trp Asp Val Trp Phe Ile Tyr Asn Val Cys Leu Ala Lys Val Lys
 305      310      315      320
Gly Tyr Arg Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile
      325      330      335
Ser Tyr Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu
      340      345      350
Leu Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu Cys
      355      360      365
Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp Asn Leu
      370      375      380
Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val Leu Thr Lys
 385      390      395      400
Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe Tyr Leu Ala Leu
      405      410      415
Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile Ile Phe Ile Leu Leu
      420      425      430

```

200265_406WO_SEQUENCE_LISTING.TXT

Glu Pro Val Leu Gln His Ser Gln Tyr Leu Arg Leu Arg Gln Arg Ile
 435 440 445
 Cys Lys Ser Ser Ile Leu Gln Trp Pro Asp Asn Pro Lys Ala Glu Gly
 450 455 460
 Leu Phe Trp Gln Thr Leu Arg Asn Val Val Leu Thr Glu Asn Asp Ser
 465 470 475 480
 Arg Tyr Asn Asn Met Tyr Val Asp Ser Ile Lys Gln Tyr
 485 490

<210> 100

<211> 386

<212> PRT

<213> Artificial Sequence

<220>

<223> CER25; amino acids 1-22 are signal peptide

<400> 100

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

200265_406WO_SEQUENCE_LISTING.TXT

```

Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
      245                250                255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
      260                265                270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
      275                280                285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Leu Trp Asn Lys
      290                295                300
Lys Arg Met Arg Gly Pro Gly Lys Asp Pro Thr Arg Lys Cys Pro Asp
305                310                315                320
Pro Arg Ser Ala Ser Ser Pro Lys Gln His Pro Ser Glu Ser Val Tyr
      325                330                335
Thr Ala Leu Gln Arg Arg Glu Thr Glu Val Tyr Ala Cys Ile Glu Asn
      340                345                350
Glu Asp Gly Ser Ser Pro Thr Ala Lys Gln Ser Pro Leu Ser Gln Glu
      355                360                365
Arg Pro His Arg Phe Glu Asp Asp Gly Glu Leu Asn Leu Val Tyr Glu
      370                375                380
Asn Leu
385

```

<210> 101

<211> 475

<212> PRT

<213> Artificial Sequence

<220>

<223> CER27, amino acids 1-22 are signal peptide

<400> 101

```

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

```

200265_406WO_SEQUENCE_LISTING.TXT

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

<210> 102

<211> 574

<212> PRT

<213> Artificial Sequence

200265_406WO_SEQUENCE_LISTING.TXT

<220>

<223> CER29, amino acids 1-22 are signal peptide

<400> 102

```

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

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200265_406WO_SEQUENCE_LISTING.TXT

```

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

```

<210> 103

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> CER31, amino acids 1-22 are signal peptide

<400> 103

```

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

```

200265_406WO_SEQUENCE_LISTING.TXT

```

Ser Thr Lys Tyr Thr Leu Leu Gly Lys Val Gln Phe Gly Glu Val Ser
      85                      90                      95
Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr Cys Cys
      100                    105                    110
Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn Val Arg
      115                    120                    125
Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr Thr Thr
      130                    135                    140
Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
      145                    150                    155                    160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
      165                    170                    175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
      180                    185                    190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
      195                    200                    205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
      210                    215                    220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
      225                    230                    235                    240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
      245                    250                    255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
      260                    265                    270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
      275                    280                    285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Met Glu Ser Ser
      290                    295                    300
Lys Lys Met Asp Ser Pro Gly Ala Leu Gln Thr Asn Pro Pro Leu Lys
      305                    310                    315                    320
Leu His Thr Asp Arg Ser Ala Gly Thr Pro Val Phe Val Pro Glu Gln
      325                    330                    335
Gly Gly Tyr Lys Glu Lys Phe Val Lys Thr Val Glu Asp Lys Tyr Lys
      340                    345                    350
Cys Glu Lys Cys His Leu Val Leu Cys Ser Pro Lys Gln Thr Glu Cys
      355                    360                    365
Gly His Arg Phe Cys Glu Ser Cys Met Ala Ala Leu Leu Ser Ser Ser
      370                    375                    380
Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Val Lys Asp Lys Val
      385                    390                    395                    400
Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala Leu Gln Ile Tyr
      405                    410                    415
Cys Arg Asn Glu Ser Arg Gly Cys Ala Glu Gln Leu Met Leu Gly His
      420                    425                    430
Leu Leu Val His Leu Lys Asn Asp Cys His Phe Glu Glu Leu Pro Cys
      435                    440                    445
Val Arg Pro Asp Cys Lys Glu Lys Val Leu Arg Lys Asp Leu Arg Asp
      450                    455                    460

```

200265_406WO_SEQUENCE_LISTING.TXT

```

His Val Glu Lys Ala Cys Lys Tyr Arg Glu Ala Thr Cys Ser His Cys
465                               470                     475           480
Lys Ser Gln Val Pro Met Ile Ala Leu Gln Lys His Glu Asp Thr Asp
                               485                     490           495
Cys Pro Cys Val Val Val Ser Cys Pro His Lys Cys Ser Val Gln Thr
                               500                     505           510
Leu Leu Arg Ser Glu Leu Ser Ala His Leu Ser Glu Cys Val Asn Ala
                               515                     520           525
Pro Ser Thr Cys Ser Phe Lys Arg Tyr Gly Cys Val Phe Gln Gly Thr
                               530                     535           540
Asn Gln Gln Ile Lys Ala His Glu Ala Ser Ser Ala Val Gln His Val
545                               550                     555           560
Asn Leu Leu Lys Glu Trp Ser Asn Ser Leu Glu Lys Lys Val
                               565                     570

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<210> 104

<211> 70

<212> PRT

<213> Homo sapiens

<220>

<223> FcgammaR2B2 signaling domain

<400> 104

```

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

```

<210> 105

<211> 41

<212> PRT

<213> Homo sapiens

<220>

<223> FcalphaR1 signaling domain

<400> 105

```

Glu Asn Trp His Ser His Thr Ala Leu Asn Lys Glu Ala Ser Ala Asp
 1                               5                     10           15
Val Ala Glu Pro Ser Trp Ser Gln Gln Met Cys Gln Pro Gly Leu Thr
                               20                     25           30

```


200265_406W0_SEQUENCE_LISTING.TXT

Phe Ala Arg Thr Pro Ser Val Cys Lys
35 40

<210> 106
<211> 141
<212> PRT
<213> Homo sapiens

<220>
<223> MyD88 TIR domain

<400> 106
His Met Pro Glu Arg Phe Asp Ala Phe Ile Cys Tyr Cys Pro Ser Asp
1 5 10 15
Ile Gln Phe Val Gln Glu Met Ile Arg Gln Leu Glu Gln Thr Asn Tyr
20 25 30
Arg Leu Lys Leu Cys Val Ser Asp Arg Asp Val Leu Pro Gly Thr Cys
35 40 45
Val Trp Ser Ile Ala Ser Glu Leu Ile Glu Lys Arg Cys Arg Arg Met
50 55 60
Val Val Val Val Ser Asp Asp Tyr Leu Gln Ser Lys Glu Cys Asp Phe
65 70 75 80
Gln Thr Lys Phe Ala Leu Ser Leu Ser Pro Gly Ala His Gln Lys Arg
85 90 95
Leu Ile Pro Ile Lys Tyr Lys Ala Met Lys Lys Glu Phe Pro Ser Ile
100 105 110
Leu Arg Phe Ile Thr Val Cys Asp Tyr Thr Asn Pro Cys Thr Lys Ser
115 120 125
Trp Phe Trp Thr Arg Leu Ala Lys Ala Leu Ser Leu Pro
130 135 140

<210> 107
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<223> CD28 transmembrane domain

<400> 107
Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
1 5 10 15
Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
20 25

<210> 108
<211> 191
<212> PRT

200265_406WO_SEQUENCE_LISTING.TXT

<213> Homo sapiens

<220>

<223> CDC42

<400> 108

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

<210> 109

<211> 776

<212> PRT

<213> Artificial Sequence

<220>

<223> CER1, amino acids 1-22 are signal peptide

<400> 109

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

200265_406WO_SEQUENCE_LISTING.TXT

```

Asn Ala Glu Leu Leu Arg Thr Asp Gly Thr Arg Ile Ile Ser Arg Lys
65      70      75      80
Ser Thr Lys Tyr Thr Leu Leu Gly Lys Val Gln Phe Gly Glu Val Ser
      85      90      95
Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr Cys Cys
      100      105      110
Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn Val Arg
      115      120      125
Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr Thr Thr
      130      135      140
Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
145      150      155      160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
      165      170      175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
      180      185      190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
      195      200      205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
      210      215      220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
225      230      235      240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
      245      250      255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
      260      265      270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
      275      280      285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Ala Leu Arg Arg
      290      295      300
Arg Val Gln Glu Thr Lys Phe Gly Gly Ala Phe Ser Glu Glu Asp Ser
305      310      315      320
Gln Leu Val Val Asn Tyr Arg Ala Lys Lys Ser Phe Cys Arg Arg Ala
      325      330      335
Ile Glu Leu Thr Leu Gln Ser Leu Gly Val Ser Glu Glu Leu Gln Asn
      340      345      350
Lys Leu Glu Asp Val Val Ile Asp Arg Asn Leu Leu Val Leu Gly Lys
      355      360      365
Val Leu Gly Glu Gly Glu Phe Gly Ser Val Met Glu Gly Asn Leu Lys
      370      375      380
Gln Glu Asp Gly Thr Ser Gln Lys Val Ala Val Lys Thr Met Lys Leu
385      390      395      400
Asp Asn Phe Ser Gln Arg Glu Ile Glu Glu Phe Leu Ser Glu Ala Ala
      405      410      415
Cys Met Lys Asp Phe Asn His Pro Asn Val Ile Arg Leu Leu Gly Val
      420      425      430
Cys Ile Glu Leu Ser Ser Gln Gly Ile Pro Lys Pro Met Val Ile Leu
      435      440      445

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200265_406WO_SEQUENCE_LISTING.TXT

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Pro Phe Met Lys Tyr Gly Asp Leu His Thr Phe Leu Leu Tyr Ser Arg
450          455          460
Leu Asn Thr Gly Pro Lys Tyr Ile His Leu Gln Thr Leu Leu Lys Phe
465          470          475          480
Met Met Asp Ile Ala Gln Gly Met Glu Tyr Leu Ser Asn Arg Asn Phe
          485          490          495
Leu His Arg Asp Leu Ala Ala Arg Asn Cys Met Leu Arg Asp Asp Met
          500          505          510
Thr Val Cys Val Ala Asp Phe Gly Leu Ser Lys Lys Ile Tyr Ser Gly
          515          520          525
Asp Tyr Tyr Arg Gln Gly Arg Ile Ala Lys Met Pro Val Lys Trp Ile
          530          535          540
Ala Ile Glu Ser Leu Ala Asp Arg Val Tyr Thr Ser Lys Ser Asp Val
          545          550          555          560
Trp Ala Phe Gly Val Thr Met Trp Glu Ile Thr Thr Arg Gly Met Thr
          565          570          575
Pro Tyr Pro Gly Val Gln Asn His Glu Met Tyr Asp Tyr Leu Leu His
          580          585          590
Gly His Arg Leu Lys Gln Pro Glu Asp Cys Leu Asp Glu Leu Tyr Asp
          595          600          605
Ile Met Tyr Ser Cys Trp Ser Ala Asp Pro Leu Asp Arg Pro Thr Phe
          610          615          620
Ser Val Leu Arg Leu Gln Leu Glu Lys Leu Ser Glu Ser Leu Pro Asp
          625          630          635          640
Ala Gln Asp Lys Glu Ser Ile Ile Tyr Ile Asn Thr Gln Leu Leu Glu
          645          650          655
Ser Cys Glu Gly Ile Ala Asn Gly Pro Ser Leu Thr Gly Leu Asp Met
          660          665          670
Asn Ile Asp Pro Asp Ser Ile Ile Ala Ser Cys Thr Pro Gly Ala Ala
          675          680          685
Val Ser Val Val Thr Ala Glu Val His Glu Asn Asn Leu Arg Glu Glu
          690          695          700
Arg Tyr Ile Leu Asn Gly Gly Asn Glu Glu Trp Glu Asp Val Ser Ser
          705          710          715          720
Thr Pro Phe Ala Ala Val Thr Pro Glu Lys Asp Gly Val Leu Pro Glu
          725          730          735
Asp Arg Leu Thr Lys Asn Gly Val Ser Trp Ser His His Ser Thr Leu
          740          745          750
Pro Leu Gly Ser Pro Ser Pro Asp Glu Leu Leu Phe Val Asp Asp Ser
          755          760          765
Leu Glu Asp Ser Glu Val Leu Met
          770          775

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<210> 110

<211> 487

<212> PRT

<213> Artificial Sequence

200265_406WO_SEQUENCE_LISTING.TXT

<220>

<223> CER6, amino acids 1-22 are signal peptide

<400> 110

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

200265_406WO_SEQUENCE_LISTING.TXT

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Leu Cys Leu His Tyr Arg Asp Phe Ile Pro Gly Val Ala Ile Ala Ala
  355                      360                      365
Asn Ile Ile His Glu Gly Phe His Lys Ser Arg Lys Val Ile Val Val
  370                      375                      380
Val Ser Gln His Phe Ile Gln Ser Arg Trp Cys Ile Phe Glu Tyr Glu
385                      390                      395                      400
Ile Ala Gln Thr Trp Gln Phe Leu Ser Ser Arg Ala Gly Ile Ile Phe
      405                      410                      415
Ile Val Leu Gln Lys Val Glu Lys Thr Leu Leu Arg Gln Gln Val Glu
      420                      425                      430
Leu Tyr Arg Leu Leu Ser Arg Asn Thr Tyr Leu Glu Trp Glu Asp Ser
      435                      440                      445
Val Leu Gly Arg His Ile Phe Trp Arg Arg Leu Arg Lys Ala Leu Leu
      450                      455                      460
Asp Gly Lys Ser Trp Asn Pro Glu Gly Thr Val Gly Thr Gly Cys Asn
465                      470                      475                      480
Trp Gln Glu Ala Thr Ser Ile
      485

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<210> 111

<211> 500

<212> PRT

<213> Artificial Sequence

<220>

<223> CER7, amino acids 1-22 are signal peptide

<400> 111

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

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200265_406WO_SEQUENCE_LISTING.TXT

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

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<210> 112

<211> 740

<212> PRT

<223> CER8, amino acids 1-22 are signal peptide

Met 1	Ser	Lys	Gly	Leu 5	Leu	Leu	Leu	Trp	Leu 10	Val	Thr	Glu	Leu	Trp 15	Trp
Leu	Tyr	Leu	Thr	Pro	Ala	Ala	Ser	Glu	Asp	Thr	Ile	Ile	Gly	Phe	Leu
Gly	Gln	Pro	Val	Thr	Leu	Pro	Cys	His	Tyr	Leu	Ser	Trp	Ser	Gln	Ser
Arg	Asn	Ser	Met	Cys	Trp	Gly	Lys	Gly	Ser	Cys	Pro	Asn	Ser	Lys	Cys
Asn	Ala	Glu	Leu	Leu	Arg	Thr	Asp	Gly	Thr	Arg	Ile	Ile	Ser	Arg	Lys
65					70					75					80
Ser	Thr	Lys	Tyr	Thr	Leu	Leu	Gly	Lys	Val	Gln	Phe	Gly	Glu	Val	Ser
Leu	Thr	Ile	Ser	Asn	Thr	Asn	Arg	Gly	Asp	Ser	Gly	Val	Tyr	Cys	Cys
Arg	Ile	Glu	Val	Pro	Gly	Trp	Phe	Asn	Asp	Val	Lys	Lys	Asn	Val	Arg
Leu	Glu	Leu	Arg	Arg	Ala	Thr	Thr	Thr	Lys	Lys	Pro	Thr	Thr	Thr	Thr
Arg	Pro	Thr	Thr	Thr	Pro	Tyr	Val	Thr	Thr	Thr	Thr	Pro	Glu	Leu	Leu
145					150					155					160
Pro	Thr	Thr	Val	Met	Thr	Thr	Ser	Val	Leu	Pro	Thr	Thr	Thr	Pro	Pro
Gln	Thr	Leu	Ala	Thr	Thr	Ala	Phe	Ser	Thr	Ala	Val	Thr	Thr	Cys	Pro
Ser	Thr	Thr	Pro	Gly	Ser	Phe	Ser	Gln	Glu	Thr	Thr	Lys	Gly	Ser	Ala
Phe	Thr	Thr	Glu	Ser	Glu	Thr	Leu	Pro	Ala	Ser	Asn	His	Ser	Gln	Arg
Ser	Met	Met	Thr	Ile	Ser	Thr	Asp	Ile	Ala	Val	Leu	Arg	Pro	Thr	Gly
225					230					235					240
Ser	Asn	Pro	Gly	Ile	Leu	Pro	Ser	Thr	Ser	Gln	Leu	Thr	Thr	Gln	Lys
Thr	Thr	Leu	Thr	Thr	Ser	Glu	Ser	Leu	Gln	Lys	Thr	Thr	Lys	Ser	His
Gln	Ile	Asn	Ser	Arg	Gln	Thr	Ile	Leu	Ile	Ile	Ala	Cys	Cys	Val	Gly
Phe	Val	Leu	Met	Val	Leu	Leu	Phe	Leu	Ala	Phe	Leu	Leu	Arg	Lys	Arg
Arg	Lys	Glu	Thr	Arg	Phe	Gly	Gln	Ala	Phe	Asp	Ser	Val	Met	Ala	Arg
305					310					315					320
Gly	Glu	Pro	Ala	Val	His	Phe	Arg	Ala	Ala	Arg	Ser	Phe	Asn	Arg	Glu
				325					330					335	

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Arg	Pro	Glu	Arg	Ile	Glu	Ala	Thr	Leu	Asp	Ser	Leu	Gly	Ile	Ser	Asp	340	345	350	
Glu	Leu	Lys	Glu	Lys	Leu	Glu	Asp	Val	Leu	Ile	Pro	Glu	Gln	Gln	Phe	355	360	365	
Thr	Leu	Gly	Arg	Met	Leu	Gly	Lys	Gly	Glu	Phe	Gly	Ser	Val	Arg	Glu	370	375	380	
Ala	Gln	Leu	Lys	Gln	Glu	Asp	Gly	Ser	Phe	Val	Lys	Val	Ala	Val	Lys	385	390	395	400
Met	Leu	Lys	Ala	Asp	Ile	Ile	Ala	Ser	Ser	Asp	Ile	Glu	Glu	Phe	Leu	405	410	415	
Arg	Glu	Ala	Ala	Cys	Met	Lys	Glu	Phe	Asp	His	Pro	His	Val	Ala	Lys	420	425	430	
Leu	Val	Gly	Val	Ser	Leu	Arg	Ser	Arg	Ala	Lys	Gly	Arg	Leu	Pro	Ile	435	440	445	
Pro	Met	Val	Ile	Leu	Pro	Phe	Met	Lys	His	Gly	Asp	Leu	His	Ala	Phe	450	455	460	
Leu	Leu	Ala	Ser	Arg	Ile	Gly	Glu	Asn	Pro	Phe	Asn	Leu	Pro	Leu	Gln	465	470	475	480
Thr	Leu	Ile	Arg	Phe	Met	Val	Asp	Ile	Ala	Cys	Gly	Met	Glu	Tyr	Leu	485	490	495	
Ser	Ser	Arg	Asn	Phe	Ile	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Cys	Met	500	505	510	
Leu	Ala	Glu	Asp	Met	Thr	Val	Cys	Val	Ala	Asp	Phe	Gly	Leu	Ser	Arg	515	520	525	
Lys	Ile	Tyr	Ser	Gly	Asp	Tyr	Tyr	Arg	Gln	Gly	Cys	Ala	Ser	Lys	Leu	530	535	540	
Pro	Val	Lys	Trp	Leu	Ala	Leu	Glu	Ser	Leu	Ala	Asp	Asn	Leu	Tyr	Thr	545	550	555	560
Val	Gln	Ser	Asp	Val	Trp	Ala	Phe	Gly	Val	Thr	Met	Trp	Glu	Ile	Met	565	570	575	
Thr	Arg	Gly	Gln	Thr	Pro	Tyr	Ala	Gly	Ile	Glu	Asn	Ala	Glu	Ile	Tyr	580	585	590	
Asn	Tyr	Leu	Ile	Gly	Gly	Asn	Arg	Leu	Lys	Gln	Pro	Pro	Glu	Cys	Met	595	600	605	
Glu	Asp	Val	Tyr	Asp	Leu	Met	Tyr	Gln	Cys	Trp	Ser	Ala	Asp	Pro	Lys	610	615	620	
Gln	Arg	Pro	Ser	Phe	Thr	Cys	Leu	Arg	Met	Glu	Leu	Glu	Asn	Ile	Leu	625	630	635	640
Gly	Gln	Leu	Ser	Val	Leu	Ser	Ala	Ser	Gln	Asp	Pro	Leu	Tyr	Ile	Asn	645	650	655	
Ile	Glu	Arg	Ala	Glu	Glu	Pro	Thr	Ala	Gly	Gly	Ser	Leu	Glu	Leu	Pro	660	665	670	
Gly	Arg	Asp	Gln	Pro	Tyr	Ser	Gly	Ala	Gly	Asp	Gly	Ser	Gly	Met	Gly	675	680	685	
Ala	Val	Gly	Gly	Thr	Pro	Ser	Asp	Cys	Arg	Tyr	Ile	Leu	Thr	Pro	Gly	690	695	700	
Gly	Leu	Ala	Glu	Gln	Pro	Gly	Gln	Ala	Glu	His	Gln	Pro	Glu	Ser	Pro	705	710	715	720

200265_406WO_SEQUENCE_LISTING.TXT

Leu Asn Glu Thr Gln Arg Leu Leu Leu Leu Gln Gln Gly Leu Leu Pro
725 730 735
His Ser Ser Cys
740

<210> 113
<211> 352
<212> PRT
<213> Artificial Sequence

<220>
<223> CER9, amino acids 1-22 are signal peptide

<400> 113
Met Ser Lys Gly Leu Leu Leu Leu Trp Leu Val Thr Glu Leu Trp Trp
1 5 10 15
Leu Tyr Leu Thr Pro Ala Ala Ser Glu Asp Thr Ile Ile Gly Phe Leu
20 25 30
Gly Gln Pro Val Thr Leu Pro Cys His Tyr Leu Ser Trp Ser Gln Ser
35 40 45
Arg Asn Ser Met Cys Trp Gly Lys Gly Ser Cys Pro Asn Ser Lys Cys
50 55 60
Asn Ala Glu Leu Leu Arg Thr Asp Gly Thr Arg Ile Ile Ser Arg Lys
65 70 75 80
Ser Thr Lys Tyr Thr Leu Leu Gly Lys Val Gln Phe Gly Glu Val Ser
85 90 95
Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr Cys Cys
100 105 110
Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn Val Arg
115 120 125
Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr Thr Thr
130 135 140
Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
145 150 155 160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
165 170 175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
180 185 190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
195 200 205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
210 215 220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
225 230 235 240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
245 250 255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
260 265 270

200265_406WO_SEQUENCE_LISTING.TXT

Gln	Ile	Asn	Ser	Arg	Gln	Thr	Ile	Leu	Ile	Ile	Ala	Cys	Cys	Val	Gly
		275					280					285			
Phe	Val	Leu	Met	Val	Leu	Leu	Phe	Leu	Ala	Phe	Leu	Tyr	Phe	Leu	Gly
		290					295				300				
Arg	Leu	Val	Pro	Arg	Gly	Arg	Gly	Ala	Ala	Glu	Ala	Ala	Thr	Arg	Lys
305					310					315					320
Gln	Arg	Ile	Thr	Glu	Thr	Glu	Ser	Pro	Tyr	Gln	Glu	Leu	Gln	Gly	Gln
				325					330					335	
Arg	Ser	Asp	Val	Tyr	Ser	Asp	Leu	Asn	Thr	Gln	Arg	Pro	Tyr	Tyr	Lys
			340					345					350		

<210> 114

<211> 352

<212> PRT

<213> Artificial Sequence

<220>

<223> CER10, amino acids 1-22 are signal peptide

<400> 114

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

200265_406WO_SEQUENCE_LISTING.TXT

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Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
225                230                235                240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
                245                250                255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
                260                265                270
Gln Ile Asn Ser Arg Gln Thr Gly Val Leu Ala Gly Ile Val Met Gly
                275                280                285
Asp Leu Val Leu Thr Val Leu Ile Ala Leu Ala Val Tyr Phe Leu Gly
                290                295                300
Arg Leu Val Pro Arg Gly Arg Gly Ala Ala Glu Ala Ala Thr Arg Lys
305                310                315                320
Gln Arg Ile Thr Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln
                325                330                335
Arg Ser Asp Val Tyr Ser Asp Leu Asn Thr Gln Arg Pro Tyr Tyr Lys
                340                345                350

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<210> 115

<211> 722

<212> PRT

<213> Artificial Sequence

<220>

<223> CER11, amino acids 1-22 are signal peptide

<400> 115

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

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200265_406WO_SEQUENCE_LISTING.TXT

Gln	Thr	Leu	Ala	Thr	Thr	Ala	Phe	Ser	Thr	Ala	Val	Thr	Thr	Cys	Pro	180	185	190
Ser	Thr	Thr	Pro	Gly	Ser	Phe	Ser	Gln	Glu	Thr	Thr	Lys	Gly	Ser	Ala	195	200	205
Phe	Thr	Thr	Glu	Ser	Glu	Thr	Leu	Pro	Ala	Ser	Asn	His	Ser	Gln	Arg	210	215	220
Ser	Met	Met	Thr	Ile	Ser	Thr	Asp	Ile	Ala	Val	Leu	Arg	Pro	Thr	Gly	225	230	235
Ser	Asn	Pro	Gly	Ile	Leu	Pro	Ser	Thr	Ser	Gln	Leu	Thr	Thr	Gln	Lys	245	250	255
Thr	Thr	Leu	Thr	Thr	Ser	Glu	Ser	Leu	Gln	Lys	Thr	Thr	Lys	Ser	His	260	265	270
Gln	Ile	Asn	Ser	Arg	Gln	Thr	Ile	Leu	Ile	Ile	Ala	Cys	Cys	Val	Gly	275	280	285
Phe	Val	Leu	Met	Val	Leu	Leu	Phe	Leu	Ala	Phe	Leu	His	Arg	Arg	Lys	290	295	300
Lys	Glu	Thr	Arg	Tyr	Gly	Glu	Val	Phe	Glu	Pro	Thr	Val	Glu	Arg	Gly	305	310	315
Glu	Leu	Val	Val	Arg	Tyr	Arg	Val	Arg	Lys	Ser	Tyr	Ser	Arg	Arg	Thr	325	330	335
Thr	Glu	Ala	Thr	Leu	Asn	Ser	Leu	Gly	Ile	Ser	Glu	Glu	Leu	Lys	Glu	340	345	350
Lys	Leu	Arg	Asp	Val	Met	Val	Asp	Arg	His	Lys	Val	Ala	Leu	Gly	Lys	355	360	365
Thr	Leu	Gly	Glu	Gly	Glu	Phe	Gly	Ala	Val	Met	Glu	Gly	Gln	Leu	Asn	370	375	380
Gln	Asp	Asp	Ser	Ile	Leu	Lys	Val	Ala	Val	Lys	Thr	Met	Lys	Ile	Ala	385	390	395
Ile	Cys	Thr	Arg	Ser	Glu	Leu	Glu	Asp	Phe	Leu	Ser	Glu	Ala	Val	Cys	405	410	415
Met	Lys	Glu	Phe	Asp	His	Pro	Asn	Val	Met	Arg	Leu	Ile	Gly	Val	Cys	420	425	430
Phe	Gln	Gly	Ser	Glu	Arg	Glu	Ser	Phe	Pro	Ala	Pro	Val	Val	Ile	Leu	435	440	445
Pro	Phe	Met	Lys	His	Gly	Asp	Leu	His	Ser	Phe	Leu	Leu	Tyr	Ser	Arg	450	455	460
Leu	Gly	Asp	Gln	Pro	Val	Tyr	Leu	Pro	Thr	Gln	Met	Leu	Val	Lys	Phe	465	470	475
Met	Ala	Asp	Ile	Ala	Ser	Gly	Met	Glu	Tyr	Leu	Ser	Thr	Lys	Arg	Phe	485	490	495
Ile	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Cys	Met	Leu	Asn	Glu	Asn	Met	500	505	510
Ser	Val	Cys	Val	Ala	Asp	Phe	Gly	Leu	Ser	Lys	Lys	Ile	Tyr	Asn	Gly	515	520	525
Asp	Tyr	Tyr	Arg	Gln	Gly	Arg	Ile	Ala	Lys	Met	Pro	Val	Lys	Trp	Ile	530	535	540
Ala	Ile	Glu	Ser	Leu	Ala	Asp	Arg	Val	Tyr	Thr	Ser	Lys	Ser	Asp	Val	545	550	555

200265_406WO_SEQUENCE_LISTING.TXT

```

Trp Ser Phe Gly Val Thr Met Trp Glu Ile Ala Thr Arg Gly Gln Thr
      565                      570                      575
Pro Tyr Pro Gly Val Glu Asn Ser Glu Ile Tyr Asp Tyr Leu Arg Gln
      580                      585                      590
Gly Asn Arg Leu Lys Gln Pro Ala Asp Cys Leu Asp Gly Leu Tyr Ala
      595                      600                      605
Leu Met Ser Arg Cys Trp Glu Leu Asn Pro Gln Asp Arg Pro Ser Phe
      610                      615                      620
Thr Glu Leu Arg Glu Asp Leu Glu Asn Thr Leu Lys Ala Leu Pro Pro
      625                      630                      635                      640
Ala Gln Glu Pro Asp Glu Ile Leu Tyr Val Asn Met Asp Glu Gly Gly
      645                      650                      655
Gly Tyr Pro Glu Pro Pro Gly Ala Ala Gly Gly Ala Asp Pro Pro Thr
      660                      665                      670
Gln Pro Asp Pro Lys Asp Ser Cys Ser Cys Leu Thr Ala Ala Glu Val
      675                      680                      685
His Pro Ala Gly Arg Tyr Val Leu Cys Pro Ser Thr Thr Pro Ser Pro
      690                      695                      700
Ala Gln Pro Ala Asp Arg Gly Ser Pro Ala Ala Pro Gly Gln Glu Asp
      705                      710                      715                      720
Gly Ala

```

<210> 116

<211> 342

<212> PRT

<213> Artificial Sequence

<220>

<223> CER12, amino acids 1-22 are signal peptide

<400> 116

```

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

```

200265_406WO_SEQUENCE_LISTING.TXT

```

Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr Thr Thr
 130          135          140
Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
145          150          155          160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
          165          170          175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
          180          185          190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
          195          200          205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
          210          215          220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
225          230          235          240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
          245          250          255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
          260          265          270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
          275          280          285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Arg Leu Lys Ile
          290          295          300
Gln Val Arg Lys Ala Ala Ile Thr Ser Tyr Glu Lys Ser Asp Gly Val
305          310          315          320
Tyr Thr Gly Leu Ser Thr Arg Asn Gln Glu Thr Tyr Glu Thr Leu Lys
          325          330          335
His Glu Lys Pro Pro Gln
          340

```

<210> 117

<211> 342

<212> PRT

<213> Artificial Sequence

<220>

<223> CER13, amino acids 1-22 are signal peptide

<400> 117

```

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

```

200265_406WO_SEQUENCE_LISTING.TXT

```

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

```

<210> 118

<211> 455

<212> PRT

<213> Artificial Sequence

<220>

<223> CER15, amino acids 1-22 are signal peptide

<400> 118

```

Met Ser Lys Gly Leu Leu Leu Leu Trp Leu Val Thr Glu Leu Trp Trp
  1          5          10          15
Leu Tyr Leu Thr Pro Ala Ala Ser Glu Asp Thr Ile Ile Gly Phe Leu
      20          25          30

```


200265_406WO_SEQUENCE_LISTING.TXT

Gly	Gln	Pro	Val	Thr	Leu	Pro	Cys	His	Tyr	Leu	Ser	Trp	Ser	Gln	Ser		
		35					40					45					
Arg	Asn	Ser	Met	Cys	Trp	Gly	Lys	Gly	Ser	Cys	Pro	Asn	Ser	Lys	Cys		
	50					55					60						
Asn	Ala	Glu	Leu	Leu	Arg	Thr	Asp	Gly	Thr	Arg	Ile	Ile	Ser	Arg	Lys		
65					70					75					80		
Ser	Thr	Lys	Tyr	Thr	Leu	Leu	Gly	Lys	Val	Gln	Phe	Gly	Glu	Val	Ser		
			85						90					95			
Leu	Thr	Ile	Ser	Asn	Thr	Asn	Arg	Gly	Asp	Ser	Gly	Val	Tyr	Cys	Cys		
			100					105					110				
Arg	Ile	Glu	Val	Pro	Gly	Trp	Phe	Asn	Asp	Val	Lys	Lys	Asn	Val	Arg		
		115					120						125				
Leu	Glu	Leu	Arg	Arg	Ala	Thr	Thr	Thr	Lys	Lys	Pro	Thr	Thr	Thr	Thr		
	130					135					140						
Arg	Pro	Thr	Thr	Thr	Pro	Tyr	Val	Thr	Thr	Thr	Thr	Pro	Glu	Leu	Leu		
145					150						155				160		
Pro	Thr	Thr	Val	Met	Thr	Thr	Ser	Val	Leu	Pro	Thr	Thr	Thr	Pro	Pro		
			165						170					175			
Gln	Thr	Leu	Ala	Thr	Thr	Ala	Phe	Ser	Thr	Ala	Val	Thr	Thr	Cys	Pro		
		180					185							190			
Ser	Thr	Thr	Pro	Gly	Ser	Phe	Ser	Gln	Glu	Thr	Thr	Lys	Gly	Ser	Ala		
	195					200						205					
Phe	Thr	Thr	Glu	Ser	Glu	Thr	Leu	Pro	Ala	Ser	Asn	His	Ser	Gln	Arg		
	210					215					220						
Ser	Met	Met	Thr	Ile	Ser	Thr	Asp	Ile	Ala	Val	Leu	Arg	Pro	Thr	Gly		
225					230					235					240		
Ser	Asn	Pro	Gly	Ile	Leu	Pro	Ser	Thr	Ser	Gln	Leu	Thr	Thr	Gln	Lys		
			245							250				255			
Thr	Thr	Leu	Thr	Thr	Ser	Glu	Ser	Leu	Gln	Lys	Thr	Thr	Lys	Ser	His		
		260						265						270			
Gln	Ile	Asn	Ser	Arg	Gln	Thr	Ile	Leu	Ile	Ile	Ala	Cys	Cys	Val	Gly		
		275					280					285					
Phe	Val	Leu	Met	Val	Leu	Leu	Phe	Leu	Ala	Phe	Leu	Met	Ala	Ala	Gly		
	290					295					300						
Gly	Pro	Gly	Ala	Gly	Ser	Ala	Ala	Pro	Val	Ser	Ser	Thr	Ser	Ser	Leu		
305					310					315					320		
Pro	Leu	Ala	Ala	Leu	Asn	Met	Arg	Val	Arg	Arg	Arg	Leu	Ser	Leu	Phe		
			325						330					335			
Leu	Asn	Val	Arg	Thr	Gln	Val	Ala	Ala	Asp	Trp	Thr	Ala	Leu	Ala	Glu		
			340					345					350				
Glu	Met	Asp	Phe	Glu	Tyr	Leu	Glu	Ile	Arg	Gln	Leu	Glu	Thr	Gln	Ala		
		355					360					365					
Asp	Pro	Thr	Gly	Arg	Leu	Leu	Asp	Ala	Trp	Gln	Gly	Arg	Pro	Gly	Ala		
	370					375					380						
Ser	Val	Gly	Arg	Leu	Leu	Glu	Leu	Leu	Thr	Lys	Leu	Gly	Arg	Asp	Asp		
385					390					395					400		
Val	Leu	Leu	Glu	Leu	Gly	Pro	Ser	Ile	Glu	Glu	Asp	Cys	Gln	Lys	Tyr		
			405						410					415			

200265_406WO_SEQUENCE_LISTING.TXT

Ile Leu Lys Gln Gln Gln Glu Glu Ala Glu Lys Pro Leu Gln Val Ala
 420 425 430
 Ala Val Asp Ser Ser Val Pro Arg Thr Ala Glu Leu Ala Gly Ile Thr
 435 440 445
 Thr Leu Asp Asp Pro Leu Gly
 450 455

<210> 119

<211> 441

<212> PRT

<213> Artificial Sequence

<220>

<223> CER16, amino acids 1-22 are signal peptide

<400> 119

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

200265_406WO_SEQUENCE_LISTING.TXT

```

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

```

<210> 120

<211> 479

<212> PRT

<213> Artificial Sequence

<220>

<223> CER17, amino acids 1-22 are signal peptide

<400> 120

```

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

```

200265_406WO_SEQUENCE_LISTING.TXT

```

Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn Val Arg
   115               120               125
Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr Thr Thr
   130               135               140
Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
  145               150               155               160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
           165               170               175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
   180               185               190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
   195               200               205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
  210               215               220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
  225               230               235               240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
           245               250               255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
           260               265               270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
   275               280               285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Glu Gly Trp Arg
  290               295               300
Ile Ser Phe Tyr Trp Asn Val Ser Val His Arg Val Leu Gly Phe Lys
  305               310               315               320
Glu Ile Asp Arg Gln Thr Glu Gln Phe Glu Tyr Ala Ala Tyr Ile Ile
           325               330               335
His Ala Tyr Lys Asp Lys Asp Trp Val Trp Glu His Phe Ser Ser Met
   340               345               350
Glu Lys Glu Asp Gln Ser Leu Lys Phe Cys Leu Glu Glu Arg Asp Phe
   355               360               365
Glu Ala Gly Val Phe Glu Leu Glu Ala Ile Val Asn Ser Ile Lys Arg
  370               375               380
Ser Arg Lys Ile Ile Phe Val Ile Thr His His Leu Leu Lys Asp Pro
  385               390               395               400
Leu Cys Lys Arg Phe Lys Val His His Ala Val Gln Gln Ala Ile Glu
           405               410               415
Gln Asn Leu Asp Ser Ile Ile Leu Val Phe Leu Glu Glu Ile Pro Asp
   420               425               430
Tyr Lys Leu Asn His Ala Leu Cys Leu Arg Arg Gly Met Phe Lys Ser
   435               440               445
His Cys Ile Leu Asn Trp Pro Val Gln Lys Glu Arg Ile Gly Ala Phe
   450               455               460
Arg His Lys Leu Gln Val Ala Leu Gly Ser Lys Asn Ser Val His
  465               470               475

```

<210> 121

200265_406WO_SEQUENCE_LISTING.TXT

<211> 479

<212> PRT

<213> Artificial Sequence

<220>

<223> CER18, amino acids 1-22 are signal peptide

<400> 121

```

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

```

200265_406WO_SEQUENCE_LISTING.TXT

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

<210> 122

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> CER20, amino acids 1-22 are signal peptide

<400> 122

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

200265_406WO_SEQUENCE_LISTING.TXT

```

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

```

<210> 123

200265_406WO_SEQUENCE_LISTING.TXT

<211> 493

<212> PRT

<213> Artificial Sequence

<220>

<223> CER22, amino acids 1-22 are signal peptide

<400> 123

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

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200265_406WO_SEQUENCE_LISTING.TXT

```

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

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<210> 124

<211> 493

<212> PRT

<213> Artificial Sequence

<220>

<223> CER23, amino acids 1-22 are signal peptide

<400> 124

```

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

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200265_406WO_SEQUENCE_LISTING.TXT

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Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr Thr Thr
130      135      140
Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
145      150      155      160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
165      170      175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
180      185      190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
195      200      205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
210      215      220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
225      230      235      240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
245      250      255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
260      265      270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
275      280      285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Gly Trp Asp Leu
290      295      300
Trp Tyr Cys Phe His Leu Cys Leu Ala Trp Leu Pro Trp Arg Gly Arg
305      310      315      320
Gln Ser Gly Arg Asp Glu Asp Ala Leu Pro Tyr Asp Ala Phe Val Val
325      330      335
Phe Asp Lys Thr Gln Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu
340      345      350
Arg Gly Gln Leu Glu Glu Cys Arg Gly Arg Trp Ala Leu Arg Leu Cys
355      360      365
Leu Glu Glu Arg Asp Trp Leu Pro Gly Lys Thr Leu Phe Glu Asn Leu
370      375      380
Trp Ala Ser Val Tyr Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His
385      390      395      400
Thr Asp Arg Val Ser Gly Leu Leu Arg Ala Ser Phe Leu Leu Ala Gln
405      410      415
Gln Arg Leu Leu Glu Asp Arg Lys Asp Val Val Val Leu Val Ile Leu
420      425      430
Ser Pro Asp Gly Arg Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu
435      440      445
Cys Arg Gln Ser Val Leu Leu Trp Pro His Gln Pro Ser Gly Gln Arg
450      455      460
Ser Phe Trp Ala Gln Leu Gly Met Ala Leu Thr Arg Asp Asn His His
465      470      475      480
Phe Tyr Asn Arg Asn Phe Cys Gln Gly Pro Thr Ala Glu
485      490

```

<210> 125

200265_406WO_SEQUENCE_LISTING.TXT

<211> 493

<212> PRT

<213> Artificial Sequence

<220>

<223> CER24, amino acids 1-22 are signal peptide

<400> 125

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

200265_406WO_SEQUENCE_LISTING.TXT

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

```

<210> 126

<211> 485

<212> PRT

<213> Artificial Sequence

<220>

<223> CER26, amino acids 1-22 are signal peptide

<400> 126

```

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

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200265_406WO_SEQUENCE_LISTING.TXT

```

Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr Thr Thr
 130          135          140
Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
145          150          155          160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
          165          170          175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
          180          185          190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
          195          200          205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
          210          215          220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
225          230          235          240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
          245          250          255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
          260          265          270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
          275          280          285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Ser Tyr Leu Asp
          290          295          300
Leu Pro Trp Tyr Leu Arg Met Val Cys Gln Trp Thr Gln Thr Arg Arg
305          310          315          320
Arg Ala Arg Asn Ile Pro Leu Glu Glu Leu Gln Arg Asn Leu Gln Phe
          325          330          335
His Ala Phe Ile Ser Tyr Ser Gly His Asp Ser Phe Trp Val Lys Asn
          340          345          350
Glu Leu Leu Pro Asn Leu Glu Lys Glu Gly Met Gln Ile Cys Leu His
          355          360          365
Glu Arg Asn Phe Val Pro Gly Lys Ser Ile Val Glu Asn Ile Ile Thr
          370          375          380
Cys Ile Glu Lys Ser Tyr Lys Ser Ile Phe Val Leu Ser Pro Asn Phe
385          390          395          400
Val Gln Ser Glu Trp Cys His Tyr Glu Leu Tyr Phe Ala His His Asn
          405          410          415
Leu Phe His Glu Gly Ser Asn Ser Leu Ile Leu Ile Leu Leu Glu Pro
          420          425          430
Ile Pro Gln Tyr Ser Ile Pro Ser Ser Tyr His Lys Leu Lys Ser Leu
          435          440          445
Met Ala Arg Arg Thr Tyr Leu Glu Trp Pro Lys Glu Lys Ser Lys Arg
          450          455          460
Gly Leu Phe Trp Ala Asn Leu Arg Ala Ala Ile Asn Ile Lys Leu Thr
465          470          475          480
Glu Gln Ala Lys Lys
          485

```

<210> 127

200265_406WO_SEQUENCE_LISTING.TXT

<211> 489

<212> PRT

<213> Artificial Sequence

<220>

<223> CER28, amino acids 1-22 are signal peptide

<400> 127

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

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200265_406WO_SEQUENCE_LISTING.TXT

```

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

```

<210> 128

<211> 603

<212> PRT

<213> Artificial Sequence

<220>

<223> CER30, amino acids 1-22 are signal peptide

<400> 128

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

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200265_406WO_SEQUENCE_LISTING.TXT

Leu	Glu	Leu	Arg	Arg	Ala	Thr	Thr	Thr	Lys	Lys	Pro	Thr	Thr	Thr	Thr	130	135	140
Arg	Pro	Thr	Thr	Thr	Pro	Tyr	Val	Thr	Thr	Thr	Thr	Pro	Glu	Leu	Leu	145	150	155
Pro	Thr	Thr	Val	Met	Thr	Thr	Ser	Val	Leu	Pro	Thr	Thr	Thr	Pro	Pro	165	170	175
Gln	Thr	Leu	Ala	Thr	Thr	Ala	Phe	Ser	Thr	Ala	Val	Thr	Thr	Cys	Pro	180	185	190
Ser	Thr	Thr	Pro	Gly	Ser	Phe	Ser	Gln	Glu	Thr	Thr	Lys	Gly	Ser	Ala	195	200	205
Phe	Thr	Thr	Glu	Ser	Glu	Thr	Leu	Pro	Ala	Ser	Asn	His	Ser	Gln	Arg	210	215	220
Ser	Met	Met	Thr	Ile	Ser	Thr	Asp	Ile	Ala	Val	Leu	Arg	Pro	Thr	Gly	225	230	235
Ser	Asn	Pro	Gly	Ile	Leu	Pro	Ser	Thr	Ser	Gln	Leu	Thr	Thr	Gln	Lys	245	250	255
Thr	Thr	Leu	Thr	Thr	Ser	Glu	Ser	Leu	Gln	Lys	Thr	Thr	Lys	Ser	His	260	265	270
Gln	Ile	Asn	Ser	Arg	Gln	Thr	Ile	Leu	Ile	Ile	Ala	Cys	Cys	Val	Gly	275	280	285
Phe	Val	Leu	Met	Val	Leu	Leu	Phe	Leu	Ala	Phe	Leu	Met	Ala	Ala	Ala	290	295	300
Ser	Val	Thr	Pro	Pro	Gly	Ser	Leu	Glu	Leu	Leu	Gln	Pro	Gly	Phe	Ser	305	310	315
Lys	Thr	Leu	Leu	Gly	Thr	Lys	Leu	Glu	Ala	Lys	Tyr	Leu	Cys	Ser	Ala	325	330	335
Cys	Arg	Asn	Val	Leu	Arg	Arg	Pro	Phe	Gln	Ala	Gln	Cys	Gly	His	Arg	340	345	350
Tyr	Cys	Ser	Phe	Cys	Leu	Ala	Ser	Ile	Leu	Ser	Ser	Gly	Pro	Gln	Asn	355	360	365
Cys	Ala	Ala	Cys	Val	His	Glu	Gly	Ile	Tyr	Glu	Glu	Gly	Ile	Ser	Ile	370	375	380
Leu	Glu	Ser	Ser	Ser	Ala	Phe	Pro	Asp	Asn	Ala	Ala	Arg	Arg	Glu	Val	385	390	395
Glu	Ser	Leu	Pro	Ala	Val	Cys	Pro	Ser	Asp	Gly	Cys	Thr	Trp	Lys	Gly	405	410	415
Thr	Leu	Lys	Glu	Tyr	Glu	Ser	Cys	His	Glu	Gly	Arg	Cys	Pro	Leu	Met	420	425	430
Leu	Thr	Glu	Cys	Pro	Ala	Cys	Lys	Gly	Leu	Val	Arg	Leu	Gly	Glu	Lys	435	440	445
Glu	Arg	His	Leu	Glu	His	Glu	Cys	Pro	Glu	Arg	Ser	Leu	Ser	Cys	Arg	450	455	460
His	Cys	Arg	Ala	Pro	Cys	Cys	Gly	Ala	Asp	Val	Lys	Ala	His	His	Glu	465	470	475
Val	Cys	Pro	Lys	Phe	Pro	Leu	Thr	Cys	Asp	Gly	Cys	Gly	Lys	Lys	Lys	485	490	495
Ile	Pro	Arg	Glu	Lys	Phe	Gln	Asp	His	Val	Lys	Thr	Cys	Gly	Lys	Cys	500	505	510

200265_406W0_SEQUENCE_LISTING.TXT

```

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

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<210> 129

<211> 540

<212> PRT

<213> Artificial Sequence

<220>

<223> CER85, amino acids 1-22 are signal peptide

<400> 129

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

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200265_406WO_SEQUENCE_LISTING.TXT

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

<210> 130

<211> 507

<212> PRT

<213> Artificial Sequence

200265_406WO_SEQUENCE_LISTING.TXT

<220>

<223> CER86, amino acids 1-22 are signal peptide

<400> 130

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

200265_406WO_SEQUENCE_LISTING.TXT

Glu Met Asp Phe Glu Tyr Leu Glu Ile Arg Gln Leu Glu Thr Gln Ala
 355 360 365
 Asp Pro Thr Gly Arg Leu Leu Asp Ala Trp Gln Gly Arg Pro Gly Ala
 370 375 380
 Ser Val Gly Arg Leu Leu Glu Leu Leu Thr Lys Leu Gly Arg Asp Asp
 385 390 395 400
 Val Leu Leu Glu Leu Gly Pro Ser Ile Glu Glu Asp Cys Gln Lys Tyr
 405 410 415
 Ile Leu Lys Gln Gln Gln Glu Glu Ala Glu Lys Pro Leu Gln Val Ala
 420 425 430
 Ala Val Asp Ser Ser Val Pro Arg Thr Ala Glu Leu Ala Gly Ile Thr
 435 440 445
 Thr Leu Asp Asp Pro Leu Gly Tyr Phe Leu Gly Arg Leu Val Pro Arg
 450 455 460
 Gly Arg Gly Ala Ala Glu Ala Ala Thr Arg Lys Gln Arg Ile Thr Glu
 465 470 475 480
 Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg Ser Asp Val Tyr
 485 490 495
 Ser Asp Leu Asn Thr Gln Arg Pro Tyr Tyr Lys
 500 505

<210> 131

<211> 540

<212> PRT

<213> Artificial Sequence

<220>

<223> CER87, amino acids 1-22 are signal peptide

<400> 131

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

200265_406WO_SEQUENCE_LISTING.TXT

Arg	Pro	Thr	Thr	Thr	Pro	Tyr	Val	Thr	Thr	Thr	Thr	Pro	Glu	Leu	Leu
145					150					155					160
Pro	Thr	Thr	Val	Met	Thr	Thr	Ser	Val	Leu	Pro	Thr	Thr	Thr	Pro	Pro
				165					170						175
Gln	Thr	Leu	Ala	Thr	Thr	Ala	Phe	Ser	Thr	Ala	Val	Thr	Thr	Cys	Pro
			180					185						190	
Ser	Thr	Thr	Pro	Gly	Ser	Phe	Ser	Gln	Glu	Thr	Thr	Lys	Gly	Ser	Ala
			195				200					205			
Phe	Thr	Thr	Glu	Ser	Glu	Thr	Leu	Pro	Ala	Ser	Asn	His	Ser	Gln	Arg
			210				215				220				
Ser	Met	Met	Thr	Ile	Ser	Thr	Asp	Ile	Ala	Val	Leu	Arg	Pro	Thr	Gly
225					230					235					240
Ser	Asn	Pro	Gly	Ile	Leu	Pro	Ser	Thr	Ser	Gln	Leu	Thr	Thr	Gln	Lys
				245						250					255
Thr	Thr	Leu	Thr	Thr	Ser	Glu	Ser	Leu	Gln	Lys	Thr	Thr	Lys	Ser	His
			260					265						270	
Gln	Ile	Asn	Ser	Arg	Gln	Thr	Ile	Leu	Ile	Ile	Ala	Cys	Cys	Val	Gly
			275				280					285			
Phe	Val	Leu	Met	Val	Leu	Leu	Phe	Leu	Ala	Phe	Leu	Ser	Trp	Arg	Arg
			290				295				300				
Arg	Gln	Arg	Arg	Leu	Arg	Gly	Ala	Ser	Ser	Ala	Glu	Ala	Pro	Asp	Gly
305					310					315					320
Asp	Lys	Asp	Ala	Pro	Glu	Pro	Leu	Asp	Lys	Val	Ile	Ile	Leu	Ser	Pro
				325					330						335
Gly	Ile	Ser	Asp	Ala	Thr	Ala	Pro	Ala	Trp	Pro	Pro	Pro	Gly	Glu	Asp
			340					345					350		
Pro	Gly	Thr	Thr	Pro	Pro	Gly	His	Ser	Val	Pro	Val	Pro	Ala	Thr	Glu
			355				360						365		
Leu	Gly	Ser	Thr	Glu	Leu	Val	Thr	Thr	Lys	Thr	Ala	Gly	Pro	Glu	Gln
	370					375					380				
Gln	Met	Ala	Ala	Gly	Gly	Pro	Gly	Ala	Gly	Ser	Ala	Ala	Pro	Val	Ser
385					390					395					400
Ser	Thr	Ser	Ser	Leu	Pro	Leu	Ala	Ala	Leu	Asn	Met	Arg	Val	Arg	Arg
				405					410					415	
Arg	Leu	Ser	Leu	Phe	Leu	Asn	Val	Arg	Thr	Gln	Val	Ala	Ala	Asp	Trp
			420					425					430		
Thr	Ala	Leu	Ala	Glu	Glu	Met	Asp	Phe	Glu	Tyr	Leu	Glu	Ile	Arg	Gln
			435				440					445			
Leu	Glu	Thr	Gln	Ala	Asp	Pro	Thr	Gly	Arg	Leu	Leu	Asp	Ala	Trp	Gln
	450					455					460				
Gly	Arg	Pro	Gly	Ala	Ser	Val	Gly	Arg	Leu	Leu	Glu	Leu	Leu	Thr	Lys
465					470					475					480
Leu	Gly	Arg	Asp	Asp	Val	Leu	Leu	Glu	Leu	Gly	Pro	Ser	Ile	Glu	Glu
				485					490					495	
Asp	Cys	Gln	Lys	Tyr	Ile	Leu	Lys	Gln	Gln	Gln	Glu	Glu	Ala	Glu	Lys
			500					505					510		
Pro	Leu	Gln	Val	Ala	Ala	Val	Asp	Ser	Ser	Val	Pro	Arg	Thr	Ala	Glu
			515				520					525			

200265_406WO_SEQUENCE_LISTING.TXT

Leu Ala Gly Ile Thr Thr Leu Asp Asp Pro Leu Gly
530 535 540

<210> 132

<211> 507

<212> PRT

<213> Artificial Sequence

<220>

<223> CER88, amino acids 1-22 are signal peptide

<400> 132

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

200265_406WO_SEQUENCE_LISTING.TXT

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Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Tyr Phe Leu Gly
290                295                300
Arg Leu Val Pro Arg Gly Arg Gly Ala Ala Glu Ala Ala Thr Arg Lys
305                310                315                320
Gln Arg Ile Thr Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln
                325                330                335
Arg Ser Asp Val Tyr Ser Asp Leu Asn Thr Gln Arg Pro Tyr Tyr Lys
                340                345                350
Met Ala Ala Gly Gly Pro Gly Ala Gly Ser Ala Ala Pro Val Ser Ser
                355                360                365
Thr Ser Ser Leu Pro Leu Ala Ala Leu Asn Met Arg Val Arg Arg Arg
                370                375                380
Leu Ser Leu Phe Leu Asn Val Arg Thr Gln Val Ala Ala Asp Trp Thr
385                390                395                400
Ala Leu Ala Glu Glu Met Asp Phe Glu Tyr Leu Glu Ile Arg Gln Leu
                405                410                415
Glu Thr Gln Ala Asp Pro Thr Gly Arg Leu Leu Asp Ala Trp Gln Gly
                420                425                430
Arg Pro Gly Ala Ser Val Gly Arg Leu Leu Glu Leu Leu Thr Lys Leu
                435                440                445
Gly Arg Asp Asp Val Leu Leu Glu Leu Gly Pro Ser Ile Glu Glu Asp
450                455                460
Cys Gln Lys Tyr Ile Leu Lys Gln Gln Gln Glu Glu Ala Glu Lys Pro
465                470                475                480
Leu Gln Val Ala Ala Val Asp Ser Ser Val Pro Arg Thr Ala Glu Leu
                485                490                495
Ala Gly Ile Thr Thr Leu Asp Asp Pro Leu Gly
                500                505

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<210> 133

<211> 500

<212> PRT

<213> Artificial Sequence

<220>

<223> CER89, amino acids 1-22 are signal peptide

<400> 133

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

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200265_406WO_SEQUENCE_LISTING.TXT

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Ser Thr Lys Tyr Thr Leu Leu Gly Lys Val Gln Phe Gly Glu Val Ser
      85                      90                      95
Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr Cys Cys
      100                    105                    110
Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn Val Arg
      115                    120                    125
Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr Thr Thr
      130                    135                    140
Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
      145                    150                    155                    160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
      165                    170                    175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
      180                    185                    190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
      195                    200                    205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
      210                    215                    220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
      225                    230                    235                    240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
      245                    250                    255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
      260                    265                    270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
      275                    280                    285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Met Ala Ala Gly
      290                    295                    300
Gly Pro Gly Ala Gly Ser Ala Ala Pro Val Ser Ser Thr Ser Ser Leu
      305                    310                    315                    320
Pro Leu Ala Ala Leu Asn Met Arg Val Arg Arg Arg Leu Ser Leu Phe
      325                    330                    335
Leu Asn Val Arg Thr Gln Val Ala Ala Asp Trp Thr Ala Leu Ala Glu
      340                    345                    350
Glu Met Asp Phe Glu Tyr Leu Glu Ile Arg Gln Leu Glu Thr Gln Ala
      355                    360                    365
Asp Pro Thr Gly Arg Leu Leu Asp Ala Trp Gln Gly Arg Pro Gly Ala
      370                    375                    380
Ser Val Gly Arg Leu Leu Glu Leu Leu Thr Lys Leu Gly Arg Asp Asp
      385                    390                    395                    400
Val Leu Leu Glu Leu Gly Pro Ser Ile Glu Glu Asp Cys Gln Lys Tyr
      405                    410                    415
Ile Leu Lys Gln Gln Gln Glu Glu Ala Glu Lys Pro Leu Gln Val Ala
      420                    425                    430
Ala Val Asp Ser Ser Val Pro Arg Thr Ala Glu Leu Ala Gly Ile Thr
      435                    440                    445
Thr Leu Asp Asp Pro Leu Gly Asp Ser Lys Ala Gly Met Glu Glu Asp
      450                    455                    460

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200265_406WO_SEQUENCE_LISTING.TXT

His Thr Tyr Glu Gly Leu Asp Ile Asp Gln Thr Ala Thr Tyr Glu Asp
 465 470 475 480
 Ile Val Thr Leu Arg Thr Gly Glu Val Lys Trp Ser Val Gly Glu His
 485 490 495
 Pro Gly Gln Glu
 500

<210> 134

<211> 541

<212> PRT

<213> Artificial Sequence

<220>

<223> CER90, amino acids 1-22 are signal peptide

<400> 134

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

200265_406WO_SEQUENCE_LISTING.TXT

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

<210> 135

<211> 692

<212> PRT

<213> Artificial Sequence

<220>

<223> CER91, amino acids 1-22 are signal peptide

<400> 135

Met	Ser	Lys	Gly	Leu	Leu	Leu	Leu	Trp	Leu	Val	Thr	Glu	Leu	Trp	Trp
1				5					10					15	

200265_406WO_SEQUENCE_LISTING.TXT

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Leu Tyr Leu Thr Pro Ala Ala Ser Glu Asp Thr Ile Ile Gly Phe Leu
    20          25          30
Gly Gln Pro Val Thr Leu Pro Cys His Tyr Leu Ser Trp Ser Gln Ser
    35          40          45
Arg Asn Ser Met Cys Trp Gly Lys Gly Ser Cys Pro Asn Ser Lys Cys
    50          55          60
Asn Ala Glu Leu Leu Arg Thr Asp Gly Thr Arg Ile Ile Ser Arg Lys
    65          70          75          80
Ser Thr Lys Tyr Thr Leu Leu Gly Lys Val Gln Phe Gly Glu Val Ser
    85          90          95
Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr Cys Cys
    100         105         110
Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn Val Arg
    115         120         125
Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr Thr Thr
    130         135         140
Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
    145         150         155         160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
    165         170         175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
    180         185         190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
    195         200         205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
    210         215         220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
    225         230         235         240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
    245         250         255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
    260         265         270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
    275         280         285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Met Ala Ala Gly
    290         295         300
Gly Pro Gly Ala Gly Ser Ala Ala Pro Val Ser Ser Thr Ser Ser Leu
    305         310         315         320
Pro Leu Ala Ala Leu Asn Met Arg Val Arg Arg Arg Leu Ser Leu Phe
    325         330         335
Leu Asn Val Arg Thr Gln Val Ala Ala Asp Trp Thr Ala Leu Ala Glu
    340         345         350
Glu Met Asp Phe Glu Tyr Leu Glu Ile Arg Gln Leu Glu Thr Gln Ala
    355         360         365
Asp Pro Thr Gly Arg Leu Leu Asp Ala Trp Gln Gly Arg Pro Gly Ala
    370         375         380
Ser Val Gly Arg Leu Leu Glu Leu Leu Thr Lys Leu Gly Arg Asp Asp
    385         390         395         400

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200265_406WO_SEQUENCE_LISTING.TXT

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Val Leu Leu Glu Leu Gly Pro Ser Ile Glu Glu Asp Cys Gln Lys Tyr
      405                      410                      415
Ile Leu Lys Gln Gln Gln Glu Glu Ala Glu Lys Pro Leu Gln Val Ala
      420                      425                      430
Ala Val Asp Ser Ser Val Pro Arg Thr Ala Glu Leu Ala Gly Ile Thr
      435                      440                      445
Thr Leu Asp Asp Pro Leu Gly Gly Ser Gly Ala Thr Asn Phe Ser Leu
      450                      455                      460
Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Ser
465      470                      475                      480
Arg Gly Ala Thr Arg Pro Asn Gly Pro Asn Thr Gly Asn Lys Ile Cys
      485                      490                      495
Gln Phe Lys Leu Val Leu Leu Gly Glu Ser Ala Val Gly Lys Ser Ser
      500                      505                      510
Leu Val Leu Arg Phe Val Lys Gly Gln Phe His Glu Phe Gln Glu Ser
      515                      520                      525
Thr Ile Gly Ala Ala Phe Leu Thr Gln Thr Val Cys Leu Asp Asp Thr
      530                      535                      540
Thr Val Lys Phe Glu Ile Trp Asp Thr Ala Gly Gln Glu Arg Tyr His
545      550                      555                      560
Ser Leu Ala Pro Met Tyr Tyr Arg Gly Ala Gln Ala Ala Ile Val Val
      565                      570                      575
Tyr Asp Ile Thr Asn Glu Glu Ser Phe Ala Arg Ala Lys Asn Trp Val
      580                      585                      590
Lys Glu Leu Gln Arg Gln Ala Ser Pro Asn Ile Val Ile Ala Leu Ser
      595                      600                      605
Gly Asn Lys Ala Asp Leu Ala Asn Lys Arg Ala Val Asp Phe Gln Glu
      610                      615                      620
Ala Gln Ser Tyr Ala Asp Asp Asn Ser Leu Leu Phe Met Glu Thr Ser
625      630                      635                      640
Ala Lys Thr Ser Met Asn Val Asn Glu Ile Phe Met Ala Ile Ala Lys
      645                      650                      655
Lys Leu Pro Lys Asn Glu Pro Gln Asn Pro Gly Ala Asn Ser Ala Arg
      660                      665                      670
Gly Arg Gly Val Asp Leu Thr Glu Pro Thr Gln Pro Thr Arg Asn Gln
      675                      680                      685
Cys Cys Ser Asn
      690

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<210> 136

<211> 931

<212> PRT

<213> Artificial Sequence

<220>

<223> CER92, amino acids 1-22 are signal peptide

<400> 136

200265_406WO_SEQUENCE_LISTING.TXT

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Met Ser Lys Gly Leu Leu Leu Leu Trp Leu Val Thr Glu Leu Trp Trp
 1          5          10          15
Leu Tyr Leu Thr Pro Ala Ala Ser Glu Asp Thr Ile Ile Gly Phe Leu
 20          25          30
Gly Gln Pro Val Thr Leu Pro Cys His Tyr Leu Ser Trp Ser Gln Ser
 35          40          45
Arg Asn Ser Met Cys Trp Gly Lys Gly Ser Cys Pro Asn Ser Lys Cys
 50          55          60
Asn Ala Glu Leu Leu Arg Thr Asp Gly Thr Arg Ile Ile Ser Arg Lys
 65          70          75          80
Ser Thr Lys Tyr Thr Leu Leu Gly Lys Val Gln Phe Gly Glu Val Ser
 85          90          95
Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr Cys Cys
100          105          110
Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn Val Arg
115          120          125
Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr Thr Thr
130          135          140
Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
145          150          155          160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
165          170          175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
180          185          190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
195          200          205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
210          215          220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
225          230          235          240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
245          250          255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
260          265          270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
275          280          285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Ala Leu Arg Arg
290          295          300
Arg Val Gln Glu Thr Lys Phe Gly Gly Ala Phe Ser Glu Glu Asp Ser
305          310          315          320
Gln Leu Val Val Asn Tyr Arg Ala Lys Lys Ser Phe Cys Arg Arg Ala
325          330          335
Ile Glu Leu Thr Leu Gln Ser Leu Gly Val Ser Glu Glu Leu Gln Asn
340          345          350
Lys Leu Glu Asp Val Val Ile Asp Arg Asn Leu Leu Val Leu Gly Lys
355          360          365
Val Leu Gly Glu Gly Glu Phe Gly Ser Val Met Glu Gly Asn Leu Lys
370          375          380

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200265_406WO_SEQUENCE_LISTING.TXT

Gln	Glu	Asp	Gly	Thr	Ser	Gln	Lys	Val	Ala	Val	Lys	Thr	Met	Lys	Leu	385	390	395	400
Asp	Asn	Phe	Ser	Gln	Arg	Glu	Ile	Glu	Glu	Phe	Leu	Ser	Glu	Ala	Ala	405	410	415	
Cys	Met	Lys	Asp	Phe	Asn	His	Pro	Asn	Val	Ile	Arg	Leu	Leu	Gly	Val	420	425	430	
Cys	Ile	Glu	Leu	Ser	Ser	Gln	Gly	Ile	Pro	Lys	Pro	Met	Val	Ile	Leu	435	440	445	
Pro	Phe	Met	Lys	Tyr	Gly	Asp	Leu	His	Thr	Phe	Leu	Leu	Tyr	Ser	Arg	450	455	460	
Leu	Asn	Thr	Gly	Pro	Lys	Tyr	Ile	His	Leu	Gln	Thr	Leu	Leu	Lys	Phe	465	470	475	480
Met	Met	Asp	Ile	Ala	Gln	Gly	Met	Glu	Tyr	Leu	Ser	Asn	Arg	Asn	Phe	485	490	495	
Leu	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Cys	Met	Leu	Arg	Asp	Asp	Met	500	505	510	
Thr	Val	Cys	Val	Ala	Asp	Phe	Gly	Leu	Ser	Lys	Lys	Ile	Tyr	Ser	Gly	515	520	525	
Asp	Tyr	Tyr	Arg	Gln	Gly	Arg	Ile	Ala	Lys	Met	Pro	Val	Lys	Trp	Ile	530	535	540	
Ala	Ile	Glu	Ser	Leu	Ala	Asp	Arg	Val	Tyr	Thr	Ser	Lys	Ser	Asp	Val	545	550	555	560
Trp	Ala	Phe	Gly	Val	Thr	Met	Trp	Glu	Ile	Thr	Thr	Arg	Gly	Met	Thr	565	570	575	
Pro	Tyr	Pro	Gly	Val	Gln	Asn	His	Glu	Met	Tyr	Asp	Tyr	Leu	Leu	His	580	585	590	
Gly	His	Arg	Leu	Lys	Gln	Pro	Glu	Asp	Cys	Leu	Asp	Glu	Leu	Tyr	Asp	595	600	605	
Ile	Met	Tyr	Ser	Cys	Trp	Ser	Ala	Asp	Pro	Leu	Asp	Arg	Pro	Thr	Phe	610	615	620	
Ser	Val	Leu	Arg	Leu	Gln	Leu	Glu	Lys	Leu	Ser	Glu	Ser	Leu	Pro	Asp	625	630	635	640
Ala	Gln	Asp	Lys	Glu	Ser	Ile	Ile	Tyr	Ile	Asn	Thr	Gln	Leu	Leu	Glu	645	650	655	
Ser	Cys	Glu	Gly	Ile	Ala	Asn	Gly	Pro	Ser	Leu	Thr	Gly	Leu	Asp	Met	660	665	670	
Asn	Ile	Asp	Pro	Asp	Ser	Ile	Ile	Ala	Ser	Cys	Thr	Pro	Gly	Ala	Ala	675	680	685	
Val	Ser	Val	Val	Thr	Ala	Glu	Val	His	Glu	Asn	Asn	Leu	Arg	Glu	Glu	690	695	700	
Arg	Tyr	Ile	Leu	Asn	Gly	Gly	Asn	Glu	Glu	Trp	Glu	Asp	Val	Ser	Ser	705	710	715	720
Thr	Pro	Phe	Ala	Ala	Val	Thr	Pro	Glu	Lys	Asp	Gly	Val	Leu	Pro	Glu	725	730	735	
Asp	Arg	Leu	Thr	Lys	Asn	Gly	Val	Ser	Trp	Ser	His	His	Ser	Thr	Leu	740	745	750	
Pro	Leu	Gly	Ser	Pro	Ser	Pro	Asp	Glu	Leu	Leu	Phe	Val	Asp	Asp	Ser	755	760	765	

200265_406WO_SEQUENCE_LISTING.TXT

```

Leu Glu Asp Ser Glu Val Leu Met Met Ala Ala Gly Gly Pro Gly Ala
 770          775          780
Gly Ser Ala Ala Pro Val Ser Ser Thr Ser Ser Leu Pro Leu Ala Ala
 785          790          795          800
Leu Asn Met Arg Val Arg Arg Arg Leu Ser Leu Phe Leu Asn Val Arg
          805          810          815
Thr Gln Val Ala Ala Asp Trp Thr Ala Leu Ala Glu Glu Met Asp Phe
          820          825          830
Glu Tyr Leu Glu Ile Arg Gln Leu Glu Thr Gln Ala Asp Pro Thr Gly
          835          840          845
Arg Leu Leu Asp Ala Trp Gln Gly Arg Pro Gly Ala Ser Val Gly Arg
          850          855          860
Leu Leu Glu Leu Leu Thr Lys Leu Gly Arg Asp Asp Val Leu Leu Glu
 865          870          875          880
Leu Gly Pro Ser Ile Glu Glu Asp Cys Gln Lys Tyr Ile Leu Lys Gln
          885          890          895
Gln Gln Glu Glu Ala Glu Lys Pro Leu Gln Val Ala Ala Val Asp Ser
          900          905          910
Ser Val Pro Arg Thr Ala Glu Leu Ala Gly Ile Thr Thr Leu Asp Asp
          915          920          925
Pro Leu Gly
 930

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<210> 137

<211> 861

<212> PRT

<213> Artificial Sequence

<220>

<223> CER93, amino acids 1-22 are signal peptide

<400> 137

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

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200265_406WO_SEQUENCE_LISTING.TXT

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Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr Thr Thr
130      135      140
Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
145      150      155      160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
165      170      175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
180      185      190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
195      200      205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
210      215      220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
225      230      235      240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
245      250      255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
260      265      270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
275      280      285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Ala Leu Arg Arg
290      295      300
Arg Val Gln Glu Thr Lys Phe Gly Gly Ala Phe Ser Glu Glu Asp Ser
305      310      315      320
Gln Leu Val Val Asn Tyr Arg Ala Lys Lys Ser Phe Cys Arg Arg Ala
325      330      335
Ile Glu Leu Thr Leu Gln Ser Leu Gly Val Ser Glu Glu Leu Gln Asn
340      345      350
Lys Leu Glu Asp Val Val Ile Asp Arg Asn Leu Leu Val Leu Gly Lys
355      360      365
Val Leu Gly Glu Gly Glu Phe Gly Ser Val Met Glu Gly Asn Leu Lys
370      375      380
Gln Glu Asp Gly Thr Ser Gln Lys Val Ala Val Lys Thr Met Lys Leu
385      390      395      400
Asp Asn Phe Ser Gln Arg Glu Ile Glu Glu Phe Leu Ser Glu Ala Ala
405      410      415
Cys Met Lys Asp Phe Asn His Pro Asn Val Ile Arg Leu Leu Gly Val
420      425      430
Cys Ile Glu Leu Ser Ser Gln Gly Ile Pro Lys Pro Met Val Ile Leu
435      440      445
Pro Phe Met Lys Tyr Gly Asp Leu His Thr Phe Leu Leu Tyr Ser Arg
450      455      460
Leu Asn Thr Gly Pro Lys Tyr Ile His Leu Gln Thr Leu Leu Lys Phe
465      470      475      480
Met Met Asp Ile Ala Gln Gly Met Glu Tyr Leu Ser Asn Arg Asn Phe
485      490      495
Leu His Arg Asp Leu Ala Ala Arg Asn Cys Met Leu Arg Asp Asp Met
500      505      510

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200265_406WO_SEQUENCE_LISTING.TXT

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Thr Val Cys Val Ala Asp Phe Gly Leu Ser Lys Lys Ile Tyr Ser Gly
    515                520                525
Asp Tyr Tyr Arg Gln Gly Arg Ile Ala Lys Met Pro Val Lys Trp Ile
    530                535                540
Ala Ile Glu Ser Leu Ala Asp Arg Val Tyr Thr Ser Lys Ser Asp Val
    545                550                555                560
Trp Ala Phe Gly Val Thr Met Trp Glu Ile Thr Thr Arg Gly Met Thr
    565                570                575
Pro Tyr Pro Gly Val Gln Asn His Glu Met Tyr Asp Tyr Leu Leu His
    580                585                590
Gly His Arg Leu Lys Gln Pro Glu Asp Cys Leu Asp Glu Leu Tyr Asp
    595                600                605
Ile Met Tyr Ser Cys Trp Ser Ala Asp Pro Leu Asp Arg Pro Thr Phe
    610                615                620
Ser Val Leu Arg Leu Gln Leu Glu Lys Leu Ser Glu Ser Leu Pro Asp
    625                630                635                640
Ala Gln Asp Lys Glu Ser Ile Ile Tyr Ile Asn Thr Gln Leu Leu Glu
    645                650                655
Ser Cys Glu Gly Ile Ala Asn Gly Pro Ser Leu Thr Gly Leu Asp Met
    660                665                670
Asn Ile Asp Pro Asp Ser Ile Ile Ala Ser Cys Thr Pro Gly Ala Ala
    675                680                685
Val Ser Val Val Thr Ala Glu Val His Glu Asn Asn Leu Arg Glu Glu
    690                695                700
Arg Tyr Ile Leu Asn Gly Gly Asn Glu Glu Trp Glu Asp Val Ser Ser
    705                710                715                720
Thr Pro Phe Ala Ala Val Thr Pro Glu Lys Asp Gly Val Leu Pro Glu
    725                730                735
Asp Arg Leu Thr Lys Asn Gly Val Ser Trp Ser His His Ser Thr Leu
    740                745                750
Pro Leu Gly Ser Pro Ser Pro Asp Glu Leu Leu Phe Val Asp Asp Ser
    755                760                765
Leu Glu Asp Ser Glu Val Leu Met Ser Trp Arg Arg Arg Gln Arg Arg
    770                775                780
Leu Arg Gly Ala Ser Ser Ala Glu Ala Pro Asp Gly Asp Lys Asp Ala
    785                790                795                800
Pro Glu Pro Leu Asp Lys Val Ile Ile Leu Ser Pro Gly Ile Ser Asp
    805                810                815
Ala Thr Ala Pro Ala Trp Pro Pro Pro Gly Glu Asp Pro Gly Thr Thr
    820                825                830
Pro Pro Gly His Ser Val Pro Val Pro Ala Thr Glu Leu Gly Ser Thr
    835                840                845
Glu Leu Val Thr Thr Lys Thr Ala Gly Pro Glu Gln Gln
    850                855                860

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<210> 138

<211> 828

<212> PRT

200265_406WO_SEQUENCE_LISTING.TXT

<213> Artificial Sequence

<220>

<223> CER94, amino acids 1-22 are signal peptide

<400> 138

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

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200265 406W0 SEQUENCE LISTING.TXT

Ile	Glu	Leu	Thr	Leu	Gln	Ser	Leu	Gly	Val	Ser	Glu	Glu	Leu	Gln	Asn
			340					345					350		
Lys	Leu	Glu	Asp	Val	Val	Ile	Asp	Arg	Asn	Leu	Leu	Val	Leu	Gly	Lys
		355					360					365			
Val	Leu	Gly	Glu	Gly	Glu	Phe	Gly	Ser	Val	Met	Glu	Gly	Asn	Leu	Lys
		370				375					380				
Gln	Glu	Asp	Gly	Thr	Ser	Gln	Lys	Val	Ala	Val	Lys	Thr	Met	Lys	Leu
385					390					395				400	
Asp	Asn	Phe	Ser	Gln	Arg	Glu	Ile	Glu	Glu	Phe	Leu	Ser	Glu	Ala	Ala
			405						410					415	
Cys	Met	Lys	Asp	Phe	Asn	His	Pro	Asn	Val	Ile	Arg	Leu	Leu	Gly	Val
		420						425				430			
Cys	Ile	Glu	Leu	Ser	Ser	Gln	Gly	Ile	Pro	Lys	Pro	Met	Val	Ile	Leu
		435					440					445			
Pro	Phe	Met	Lys	Tyr	Gly	Asp	Leu	His	Thr	Phe	Leu	Leu	Tyr	Ser	Arg
		450				455					460				
Leu	Asn	Thr	Gly	Pro	Lys	Tyr	Ile	His	Leu	Gln	Thr	Leu	Leu	Lys	Phe
465					470					475				480	
Met	Met	Asp	Ile	Ala	Gln	Gly	Met	Glu	Tyr	Leu	Ser	Asn	Arg	Asn	Phe
			485						490					495	
Leu	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Cys	Met	Leu	Arg	Asp	Asp	Met
		500						505					510		
Thr	Val	Cys	Val	Ala	Asp	Phe	Gly	Leu	Ser	Lys	Lys	Ile	Tyr	Ser	Gly
		515					520					525			
Asp	Tyr	Tyr	Arg	Gln	Gly	Arg	Ile	Ala	Lys	Met	Pro	Val	Lys	Trp	Ile
		530				535					540				
Ala	Ile	Glu	Ser	Leu	Ala	Asp	Arg	Val	Tyr	Thr	Ser	Lys	Ser	Asp	Val
545					550					555				560	
Trp	Ala	Phe	Gly	Val	Thr	Met	Trp	Glu	Ile	Thr	Thr	Arg	Gly	Met	Thr
			565						570					575	
Pro	Tyr	Pro	Gly	Val	Gln	Asn	His	Glu	Met	Tyr	Asp	Tyr	Leu	Leu	His
			580					585					590		
Gly	His	Arg	Leu	Lys	Gln	Pro	Glu	Asp	Cys	Leu	Asp	Glu	Leu	Tyr	Asp
		595					600					605			
Ile	Met	Tyr	Ser	Cys	Trp	Ser	Ala	Asp	Pro	Leu	Asp	Arg	Pro	Thr	Phe
		610				615					620				
Ser	Val	Leu	Arg	Leu	Gln	Leu	Glu	Lys	Leu	Ser	Glu	Ser	Leu	Pro	Asp
625					630					635				640	
Ala	Gln	Asp	Lys	Glu	Ser	Ile	Ile	Tyr	Ile	Asn	Thr	Gln	Leu	Leu	Glu
			645						650					655	
Ser	Cys	Glu	Gly	Ile	Ala	Asn	Gly	Pro	Ser	Leu	Thr	Gly	Leu	Asp	Met
		660						665					670		
Asn	Ile	Asp	Pro	Asp	Ser	Ile	Ile	Ala	Ser	Cys	Thr	Pro	Gly	Ala	Ala
		675					680					685			
Val	Ser														

200265_406WO_SEQUENCE_LISTING.TXT

Thr	Pro	Phe	Ala	Ala	Val	Thr	Pro	Glu	Lys	Asp	Gly	Val	Leu	Pro	Glu
			725					730					735		
Asp	Arg	Leu	Thr	Lys	Asn	Gly	Val	Ser	Trp	Ser	His	His	Ser	Thr	Leu
		740						745					750		
Pro	Leu	Gly	Ser	Pro	Ser	Pro	Asp	Glu	Leu	Leu	Phe	Val	Asp	Asp	Ser
		755					760					765			
Leu	Glu	Asp	Ser	Glu	Val	Leu	Met	Tyr	Phe	Leu	Gly	Arg	Leu	Val	Pro
	770					775					780				
Arg	Gly	Arg	Gly	Ala	Ala	Glu	Ala	Ala	Thr	Arg	Lys	Gln	Arg	Ile	Thr
785				790					795						800
Glu	Thr	Glu	Ser	Pro	Tyr	Gln	Glu	Leu	Gln	Gly	Gln	Arg	Ser	Asp	Val
			805					810						815	
Tyr	Ser	Asp	Leu	Asn	Thr	Gln	Arg	Pro	Tyr	Tyr	Lys				
		820						825							

<210> 139

<211> 821

<212> PRT

<213> Artificial Sequence

<220>

<223> CER95, amino acids 1-22 are signal peptide

<400> 139

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

200265_406WO_SEQUENCE_LISTING.TXT

Ser	Thr	Thr	Pro	Gly	Ser	Phe	Ser	Gln	Glu	Thr	Thr	Lys	Gly	Ser	Ala	195	200	205
Phe	Thr	Thr	Glu	Ser	Glu	Thr	Leu	Pro	Ala	Ser	Asn	His	Ser	Gln	Arg	210	215	220
Ser	Met	Met	Thr	Ile	Ser	Thr	Asp	Ile	Ala	Val	Leu	Arg	Pro	Thr	Gly	225	230	235
Ser	Asn	Pro	Gly	Ile	Leu	Pro	Ser	Thr	Ser	Gln	Leu	Thr	Thr	Gln	Lys	245	250	255
Thr	Thr	Leu	Thr	Thr	Ser	Glu	Ser	Leu	Gln	Lys	Thr	Thr	Lys	Ser	His	260	265	270
Gln	Ile	Asn	Ser	Arg	Gln	Thr	Ile	Leu	Ile	Ile	Ala	Cys	Cys	Val	Gly	275	280	285
Phe	Val	Leu	Met	Val	Leu	Leu	Phe	Leu	Ala	Phe	Leu	Ala	Leu	Arg	Arg	290	295	300
Arg	Val	Gln	Glu	Thr	Lys	Phe	Gly	Gly	Ala	Phe	Ser	Glu	Glu	Asp	Ser	305	310	315
Gln	Leu	Val	Val	Asn	Tyr	Arg	Ala	Lys	Lys	Ser	Phe	Cys	Arg	Arg	Ala	325	330	335
Ile	Glu	Leu	Thr	Leu	Gln	Ser	Leu	Gly	Val	Ser	Glu	Glu	Leu	Gln	Asn	340	345	350
Lys	Leu	Glu	Asp	Val	Val	Ile	Asp	Arg	Asn	Leu	Leu	Val	Leu	Gly	Lys	355	360	365
Val	Leu	Gly	Glu	Gly	Glu	Phe	Gly	Ser	Val	Met	Glu	Gly	Asn	Leu	Lys	370	375	380
Gln	Glu	Asp	Gly	Thr	Ser	Gln	Lys	Val	Ala	Val	Lys	Thr	Met	Lys	Leu	385	390	395
Asp	Asn	Phe	Ser	Gln	Arg	Glu	Ile	Glu	Glu	Phe	Leu	Ser	Glu	Ala	Ala	405	410	415
Cys	Met	Lys	Asp	Phe	Asn	His	Pro	Asn	Val	Ile	Arg	Leu	Leu	Gly	Val	420	425	430
Cys	Ile	Glu	Leu	Ser	Ser	Gln	Gly	Ile	Pro	Lys	Pro	Met	Val	Ile	Leu	435	440	445
Pro	Phe	Met	Lys	Tyr	Gly	Asp	Leu	His	Thr	Phe	Leu	Leu	Tyr	Ser	Arg	450	455	460
Leu	Asn	Thr	Gly	Pro	Lys	Tyr	Ile	His	Leu	Gln	Thr	Leu	Leu	Lys	Phe	465	470	475
Met	Met	Asp	Ile	Ala	Gln	Gly	Met	Glu	Tyr	Leu	Ser	Asn	Arg	Asn	Phe	485	490	495
Leu	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Cys	Met	Leu	Arg	Asp	Asp	Met	500	505	510
Thr	Val	Cys	Val	Ala	Asp	Phe	Gly	Leu	Ser	Lys	Lys	Ile	Tyr	Ser	Gly	515	520	525
Asp	Tyr	Tyr	Arg	Gln	Gly	Arg	Ile	Ala	Lys	Met	Pro	Val	Lys	Trp	Ile	530	535	540
Ala	Ile	Glu	Ser	Leu	Ala	Asp	Arg	Val	Tyr	Thr	Ser	Lys	Ser	Asp	Val	545	550	555
Trp	Ala	Phe	Gly	Val	Thr	Met	Trp	Glu	Ile	Thr	Thr	Arg	Gly	Met	Thr	565	570	575

200265_406W0_SEQUENCE_LISTING.TXT

```

Pro Tyr Pro Gly Val Gln Asn His Glu Met Tyr Asp Tyr Leu Leu His
580                    585                    590
Gly His Arg Leu Lys Gln Pro Glu Asp Cys Leu Asp Glu Leu Tyr Asp
595                    600                    605
Ile Met Tyr Ser Cys Trp Ser Ala Asp Pro Leu Asp Arg Pro Thr Phe
610                    615                    620
Ser Val Leu Arg Leu Gln Leu Glu Lys Leu Ser Glu Ser Leu Pro Asp
625                    630                    635                    640
Ala Gln Asp Lys Glu Ser Ile Ile Tyr Ile Asn Thr Gln Leu Leu Glu
645                    650                    655
Ser Cys Glu Gly Ile Ala Asn Gly Pro Ser Leu Thr Gly Leu Asp Met
660                    665                    670
Asn Ile Asp Pro Asp Ser Ile Ile Ala Ser Cys Thr Pro Gly Ala Ala
675                    680                    685
Val Ser Val Val Thr Ala Glu Val His Glu Asn Asn Leu Arg Glu Glu
690                    695                    700
Arg Tyr Ile Leu Asn Gly Gly Asn Glu Glu Trp Glu Asp Val Ser Ser
705                    710                    715                    720
Thr Pro Phe Ala Ala Val Thr Pro Glu Lys Asp Gly Val Leu Pro Glu
725                    730                    735
Asp Arg Leu Thr Lys Asn Gly Val Ser Trp Ser His His Ser Thr Leu
740                    745                    750
Pro Leu Gly Ser Pro Ser Pro Asp Glu Leu Leu Phe Val Asp Asp Ser
755                    760                    765
Leu Glu Asp Ser Glu Val Leu Met Asp Ser Lys Ala Gly Met Glu Glu
770                    775                    780
Asp His Thr Tyr Glu Gly Leu Asp Ile Asp Gln Thr Ala Thr Tyr Glu
785                    790                    795                    800
Asp Ile Val Thr Leu Arg Thr Gly Glu Val Lys Trp Ser Val Gly Glu
805                    810                    815
His Pro Gly Gln Glu
820

```

<210> 140

<211> 862

<212> PRT

<213> Artificial Sequence

<220>

<223> CER96, amino acids 1-22 are signal peptide

<400> 140

```

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

```

200265_406WO_SEQUENCE_LISTING.TXT

```

Arg Asn Ser Met Cys Trp Gly Lys Gly Ser Cys Pro Asn Ser Lys Cys
 50      55      60
Asn Ala Glu Leu Leu Arg Thr Asp Gly Thr Arg Ile Ile Ser Arg Lys
 65      70      75      80
Ser Thr Lys Tyr Thr Leu Leu Gly Lys Val Gln Phe Gly Glu Val Ser
      85      90      95
Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr Cys Cys
      100      105      110
Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn Val Arg
      115      120      125
Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr Thr Thr
      130      135      140
Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
 145      150      155      160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
      165      170      175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
      180      185      190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
      195      200      205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
 210      215      220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
 225      230      235      240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
      245      250      255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
      260      265      270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
      275      280      285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Ala Leu Arg Arg
 290      295      300
Arg Val Gln Glu Thr Lys Phe Gly Gly Ala Phe Ser Glu Glu Asp Ser
 305      310      315      320
Gln Leu Val Val Asn Tyr Arg Ala Lys Lys Ser Phe Cys Arg Arg Ala
      325      330      335
Ile Glu Leu Thr Leu Gln Ser Leu Gly Val Ser Glu Glu Leu Gln Asn
      340      345      350
Lys Leu Glu Asp Val Val Ile Asp Arg Asn Leu Leu Val Leu Gly Lys
      355      360      365
Val Leu Gly Glu Gly Glu Phe Gly Ser Val Met Glu Gly Asn Leu Lys
 370      375      380
Gln Glu Asp Gly Thr Ser Gln Lys Val Ala Val Lys Thr Met Lys Leu
 385      390      395      400
Asp Asn Phe Ser Gln Arg Glu Ile Glu Glu Phe Leu Ser Glu Ala Ala
      405      410      415
Cys Met Lys Asp Phe Asn His Pro Asn Val Ile Arg Leu Leu Gly Val
 420      425      430

```

200265_406WO_SEQUENCE_LISTING.TXT

Cys Ile Glu Leu Ser Ser Gln Gly Ile Pro Lys Pro Met Val Ile Leu
 435 440 445
 Pro Phe Met Lys Tyr Gly Asp Leu His Thr Phe Leu Leu Tyr Ser Arg
 450 455 460
 Leu Asn Thr Gly Pro Lys Tyr Ile His Leu Gln Thr Leu Leu Lys Phe
 465 470 475 480
 Met Met Asp Ile Ala Gln Gly Met Glu Tyr Leu Ser Asn Arg Asn Phe
 485 490 495
 Leu His Arg Asp Leu Ala Ala Arg Asn Cys Met Leu Arg Asp Asp Met
 500 505 510
 Thr Val Cys Val Ala Asp Phe Gly Leu Ser Lys Lys Ile Tyr Ser Gly
 515 520 525
 Asp Tyr Tyr Arg Gln Gly Arg Ile Ala Lys Met Pro Val Lys Trp Ile
 530 535 540
 Ala Ile Glu Ser Leu Ala Asp Arg Val Tyr Thr Ser Lys Ser Asp Val
 545 550 555 560
 Trp Ala Phe Gly Val Thr Met Trp Glu Ile Thr Thr Arg Gly Met Thr
 565 570 575
 Pro Tyr Pro Gly Val Gln Asn His Glu Met Tyr Asp Tyr Leu Leu His
 580 585 590
 Gly His Arg Leu Lys Gln Pro Glu Asp Cys Leu Asp Glu Leu Tyr Asp
 595 600 605
 Ile Met Tyr Ser Cys Trp Ser Ala Asp Pro Leu Asp Arg Pro Thr Phe
 610 615 620
 Ser Val Leu Arg Leu Gln Leu Glu Lys Leu Ser Glu Ser Leu Pro Asp
 625 630 635 640
 Ala Gln Asp Lys Glu Ser Ile Ile Tyr Ile Asn Thr Gln Leu Leu Glu
 645 650 655
 Ser Cys Glu Gly Ile Ala Asn Gly Pro Ser Leu Thr Gly Leu Asp Met
 660 665 670
 Asn Ile Asp Pro Asp Ser Ile Ile Ala Ser Cys Thr Pro Gly Ala Ala
 675 680 685
 Val Ser Val Val Thr Ala Glu Val His Glu Asn Asn Leu Arg Glu Glu
 690 695 700
 Arg Tyr Ile Leu Asn Gly Gly Asn Glu Glu Trp Glu Asp Val Ser Ser
 705 710 715 720
 Thr Pro Phe Ala Ala Val Thr Pro Glu Lys Asp Gly Val Leu Pro Glu
 725 730 735
 Asp Arg Leu Thr Lys Asn Gly Val Ser Trp Ser His His Ser Thr Leu
 740 745 750
 Pro Leu Gly Ser Pro Ser Pro Asp Glu Leu Leu Phe Val Asp Asp Ser
 755 760 765
 Leu Glu Asp Ser Glu Val Leu Met Leu Trp Asn Lys Lys Arg Met Arg
 770 775 780
 Gly Pro Gly Lys Asp Pro Thr Arg Lys Cys Pro Asp Pro Arg Ser Ala
 785 790 795 800
 Ser Ser Pro Lys Gln His Pro Ser Glu Ser Val Tyr Thr Ala Leu Gln
 805 810 815

200265_406WO_SEQUENCE_LISTING.TXT

Arg	Arg	Glu	Thr	Glu	Val	Tyr	Ala	Cys	Ile	Glu	Asn	Glu	Asp	Gly	Ser
			820					825					830		
Ser	Pro	Thr	Ala	Lys	Gln	Ser	Pro	Leu	Ser	Gln	Glu	Arg	Pro	His	Arg
		835					840					845			
Phe	Glu	Asp	Asp	Gly	Glu	Leu	Asn	Leu	Val	Tyr	Glu	Asn	Leu		
	850					855					860				

<210> 141

<211> 774

<212> PRT

<213> Artificial Sequence

<220>

<223> CER97, amino acids 1-22 are signal peptide

<400> 141

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

200265_406WO_SEQUENCE_LISTING.TXT

```

Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
260 265 270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
275 280 285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu His Arg Arg Lys
290 295 300
Lys Glu Thr Arg Tyr Gly Glu Val Phe Glu Pro Thr Val Glu Arg Gly
305 310 315 320
Glu Leu Val Val Arg Tyr Arg Val Arg Lys Ser Tyr Ser Arg Arg Thr
325 330 335
Thr Glu Ala Thr Leu Asn Ser Leu Gly Ile Ser Glu Glu Leu Lys Glu
340 345 350
Lys Leu Arg Asp Val Met Val Asp Arg His Lys Val Ala Leu Gly Lys
355 360 365
Thr Leu Gly Glu Gly Glu Phe Gly Ala Val Met Glu Gly Gln Leu Asn
370 375 380
Gln Asp Asp Ser Ile Leu Lys Val Ala Val Lys Thr Met Lys Ile Ala
385 390 395 400
Ile Cys Thr Arg Ser Glu Leu Glu Asp Phe Leu Ser Glu Ala Val Cys
405 410 415
Met Lys Glu Phe Asp His Pro Asn Val Met Arg Leu Ile Gly Val Cys
420 425 430
Phe Gln Gly Ser Glu Arg Glu Ser Phe Pro Ala Pro Val Val Ile Leu
435 440 445
Pro Phe Met Lys His Gly Asp Leu His Ser Phe Leu Leu Tyr Ser Arg
450 455 460
Leu Gly Asp Gln Pro Val Tyr Leu Pro Thr Gln Met Leu Val Lys Phe
465 470 475 480
Met Ala Asp Ile Ala Ser Gly Met Glu Tyr Leu Ser Thr Lys Arg Phe
485 490 495
Ile His Arg Asp Leu Ala Ala Arg Asn Cys Met Leu Asn Glu Asn Met
500 505 510
Ser Val Cys Val Ala Asp Phe Gly Leu Ser Lys Lys Ile Tyr Asn Gly
515 520 525
Asp Tyr Tyr Arg Gln Gly Arg Ile Ala Lys Met Pro Val Lys Trp Ile
530 535 540
Ala Ile Glu Ser Leu Ala Asp Arg Val Tyr Thr Ser Lys Ser Asp Val
545 550 555 560
Trp Ser Phe Gly Val Thr Met Trp Glu Ile Ala Thr Arg Gly Gln Thr
565 570 575
Pro Tyr Pro Gly Val Glu Asn Ser Glu Ile Tyr Asp Tyr Leu Arg Gln
580 585 590
Gly Asn Arg Leu Lys Gln Pro Ala Asp Cys Leu Asp Gly Leu Tyr Ala
595 600 605
Leu Met Ser Arg Cys Trp Glu Leu Asn Pro Gln Asp Arg Pro Ser Phe
610 615 620
Thr Glu Leu Arg Glu Asp Leu Glu Asn Thr Leu Lys Ala Leu Pro Pro
625 630 635 640

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200265_406WO_SEQUENCE_LISTING.TXT

Ala Gln Glu Pro Asp Glu Ile Leu Tyr Val Asn Met Asp Glu Gly Gly
645 650 655
Gly Tyr Pro Glu Pro Pro Gly Ala Ala Gly Gly Ala Asp Pro Pro Thr
660 665 670
Gln Pro Asp Pro Lys Asp Ser Cys Ser Cys Leu Thr Ala Ala Glu Val
675 680 685
His Pro Ala Gly Arg Tyr Val Leu Cys Pro Ser Thr Thr Pro Ser Pro
690 695 700
Ala Gln Pro Ala Asp Arg Gly Ser Pro Ala Ala Pro Gly Gln Glu Asp
705 710 715 720
Gly Ala Tyr Phe Leu Gly Arg Leu Val Pro Arg Gly Arg Gly Ala Ala
725 730 735
Glu Ala Ala Thr Arg Lys Gln Arg Ile Thr Glu Thr Glu Ser Pro Tyr
740 745 750
Gln Glu Leu Gln Gly Gln Arg Ser Asp Val Tyr Ser Asp Leu Asn Thr
755 760 765
Gln Arg Pro Tyr Tyr Lys
770

<210> 142

<211> 767

<212> PRT

<213> Artificial Sequence

<220>

<223> CER98, amino acids 1-22 are signal peptide

<400> 142

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

200265_406WO_SEQUENCE_LISTING.TXT

```

Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
165 170 175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
180 185 190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
195 200 205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
210 215 220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
225 230 235 240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
245 250 255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
260 265 270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
275 280 285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu His Arg Arg Lys
290 295 300
Lys Glu Thr Arg Tyr Gly Glu Val Phe Glu Pro Thr Val Glu Arg Gly
305 310 315 320
Glu Leu Val Val Arg Tyr Arg Val Arg Lys Ser Tyr Ser Arg Arg Thr
325 330 335
Thr Glu Ala Thr Leu Asn Ser Leu Gly Ile Ser Glu Glu Leu Lys Glu
340 345 350
Lys Leu Arg Asp Val Met Val Asp Arg His Lys Val Ala Leu Gly Lys
355 360 365
Thr Leu Gly Glu Gly Glu Phe Gly Ala Val Met Glu Gly Gln Leu Asn
370 375 380
Gln Asp Asp Ser Ile Leu Lys Val Ala Val Lys Thr Met Lys Ile Ala
385 390 395 400
Ile Cys Thr Arg Ser Glu Leu Glu Asp Phe Leu Ser Glu Ala Val Cys
405 410 415
Met Lys Glu Phe Asp His Pro Asn Val Met Arg Leu Ile Gly Val Cys
420 425 430
Phe Gln Gly Ser Glu Arg Glu Ser Phe Pro Ala Pro Val Val Ile Leu
435 440 445
Pro Phe Met Lys His Gly Asp Leu His Ser Phe Leu Leu Tyr Ser Arg
450 455 460
Leu Gly Asp Gln Pro Val Tyr Leu Pro Thr Gln Met Leu Val Lys Phe
465 470 475 480
Met Ala Asp Ile Ala Ser Gly Met Glu Tyr Leu Ser Thr Lys Arg Phe
485 490 495
Ile His Arg Asp Leu Ala Ala Arg Asn Cys Met Leu Asn Glu Asn Met
500 505 510
Ser Val Cys Val Ala Asp Phe Gly Leu Ser Lys Lys Ile Tyr Asn Gly
515 520 525
Asp Tyr Tyr Arg Gln Gly Arg Ile Ala Lys Met Pro Val Lys Trp Ile
530 535 540

```

200265_406WO_SEQUENCE_LISTING.TXT

```

Ala Ile Glu Ser Leu Ala Asp Arg Val Tyr Thr Ser Lys Ser Asp Val
545          550          555          560
Trp Ser Phe Gly Val Thr Met Trp Glu Ile Ala Thr Arg Gly Gln Thr
          565          570          575
Pro Tyr Pro Gly Val Glu Asn Ser Glu Ile Tyr Asp Tyr Leu Arg Gln
          580          585          590
Gly Asn Arg Leu Lys Gln Pro Ala Asp Cys Leu Asp Gly Leu Tyr Ala
          595          600          605
Leu Met Ser Arg Cys Trp Glu Leu Asn Pro Gln Asp Arg Pro Ser Phe
        610          615          620
Thr Glu Leu Arg Glu Asp Leu Glu Asn Thr Leu Lys Ala Leu Pro Pro
625          630          635          640
Ala Gln Glu Pro Asp Glu Ile Leu Tyr Val Asn Met Asp Glu Gly Gly
          645          650          655
Gly Tyr Pro Glu Pro Pro Gly Ala Ala Gly Gly Ala Asp Pro Pro Thr
          660          665          670
Gln Pro Asp Pro Lys Asp Ser Cys Ser Cys Leu Thr Ala Ala Glu Val
          675          680          685
His Pro Ala Gly Arg Tyr Val Leu Cys Pro Ser Thr Thr Pro Ser Pro
        690          695          700
Ala Gln Pro Ala Asp Arg Gly Ser Pro Ala Ala Pro Gly Gln Glu Asp
705          710          715          720
Gly Ala Asp Ser Lys Ala Gly Met Glu Glu Asp His Thr Tyr Glu Gly
          725          730          735
Leu Asp Ile Asp Gln Thr Ala Thr Tyr Glu Asp Ile Val Thr Leu Arg
          740          745          750
Thr Gly Glu Val Lys Trp Ser Val Gly Glu His Pro Gly Gln Glu
          755          760          765

```

<210> 143

<211> 808

<212> PRT

<213> Artificial Sequence

<220>

<223> CER99, amino acids 1-22 are signal peptide

<400> 143

```

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

```

200265_406WO_SEQUENCE_LISTING.TXT

```

Ser Thr Lys Tyr Thr Leu Leu Gly Lys Val Gln Phe Gly Glu Val Ser
      85                      90                      95
Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr Cys Cys
      100                      105                      110
Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn Val Arg
      115                      120                      125
Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr Thr Thr
      130                      135                      140
Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
      145                      150                      155                      160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
      165                      170                      175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
      180                      185                      190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
      195                      200                      205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
      210                      215                      220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
      225                      230                      235                      240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
      245                      250                      255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
      260                      265                      270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
      275                      280                      285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu His Arg Arg Lys
      290                      295                      300
Lys Glu Thr Arg Tyr Gly Glu Val Phe Glu Pro Thr Val Glu Arg Gly
      305                      310                      315                      320
Glu Leu Val Val Arg Tyr Arg Val Arg Lys Ser Tyr Ser Arg Arg Thr
      325                      330                      335
Thr Glu Ala Thr Leu Asn Ser Leu Gly Ile Ser Glu Glu Leu Lys Glu
      340                      345                      350
Lys Leu Arg Asp Val Met Val Asp Arg His Lys Val Ala Leu Gly Lys
      355                      360                      365
Thr Leu Gly Glu Gly Glu Phe Gly Ala Val Met Glu Gly Gln Leu Asn
      370                      375                      380
Gln Asp Asp Ser Ile Leu Lys Val Ala Val Lys Thr Met Lys Ile Ala
      385                      390                      395                      400
Ile Cys Thr Arg Ser Glu Leu Glu Asp Phe Leu Ser Glu Ala Val Cys
      405                      410                      415
Met Lys Glu Phe Asp His Pro Asn Val Met Arg Leu Ile Gly Val Cys
      420                      425                      430
Phe Gln Gly Ser Glu Arg Glu Ser Phe Pro Ala Pro Val Val Ile Leu
      435                      440                      445
Pro Phe Met Lys His Gly Asp Leu His Ser Phe Leu Leu Tyr Ser Arg
      450                      455                      460

```

200265_406WO_SEQUENCE_LISTING.TXT

```

Leu Gly Asp Gln Pro Val Tyr Leu Pro Thr Gln Met Leu Val Lys Phe
465                               475                               480
Met Ala Asp Ile Ala Ser Gly Met Glu Tyr Leu Ser Thr Lys Arg Phe
                               485                               495
Ile His Arg Asp Leu Ala Ala Arg Asn Cys Met Leu Asn Glu Asn Met
                               500                               510
Ser Val Cys Val Ala Asp Phe Gly Leu Ser Lys Lys Ile Tyr Asn Gly
                               515                               525
Asp Tyr Tyr Arg Gln Gly Arg Ile Ala Lys Met Pro Val Lys Trp Ile
                               530                               540
Ala Ile Glu Ser Leu Ala Asp Arg Val Tyr Thr Ser Lys Ser Asp Val
545                               550                               560
Trp Ser Phe Gly Val Thr Met Trp Glu Ile Ala Thr Arg Gly Gln Thr
                               565                               575
Pro Tyr Pro Gly Val Glu Asn Ser Glu Ile Tyr Asp Tyr Leu Arg Gln
                               580                               590
Gly Asn Arg Leu Lys Gln Pro Ala Asp Cys Leu Asp Gly Leu Tyr Ala
                               595                               605
Leu Met Ser Arg Cys Trp Glu Leu Asn Pro Gln Asp Arg Pro Ser Phe
610                               615                               620
Thr Glu Leu Arg Glu Asp Leu Glu Asn Thr Leu Lys Ala Leu Pro Pro
625                               630                               640
Ala Gln Glu Pro Asp Glu Ile Leu Tyr Val Asn Met Asp Glu Gly Gly
                               645                               655
Gly Tyr Pro Glu Pro Pro Gly Ala Ala Gly Gly Ala Asp Pro Pro Thr
                               660                               670
Gln Pro Asp Pro Lys Asp Ser Cys Ser Cys Leu Thr Ala Ala Glu Val
                               675                               685
His Pro Ala Gly Arg Tyr Val Leu Cys Pro Ser Thr Thr Pro Ser Pro
690                               695                               700
Ala Gln Pro Ala Asp Arg Gly Ser Pro Ala Ala Pro Gly Gln Glu Asp
705                               710                               720
Gly Ala Leu Trp Asn Lys Lys Arg Met Arg Gly Pro Gly Lys Asp Pro
                               725                               735
Thr Arg Lys Cys Pro Asp Pro Arg Ser Ala Ser Ser Pro Lys Gln His
740                               745                               750
Pro Ser Glu Ser Val Tyr Thr Ala Leu Gln Arg Arg Glu Thr Glu Val
755                               760                               765
Tyr Ala Cys Ile Glu Asn Glu Asp Gly Ser Ser Pro Thr Ala Lys Gln
770                               775                               780
Ser Pro Leu Ser Gln Glu Arg Pro His Arg Phe Glu Asp Asp Gly Glu
785                               790                               800
Leu Asn Leu Val Tyr Glu Asn Leu
                               805

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<210> 144

<211> 579

<212> PRT

200265_406WO_SEQUENCE_LISTING.TXT

<213> Artificial Sequence

<220>

<223> CER102, amino acids 1-22 are signal peptide

<400> 144

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

200265_406WO_SEQUENCE_LISTING.TXT

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

<210> 145

<211> 538

<212> PRT

<213> Artificial Sequence

<220>

<223> CER103A, amino acids 1-22 are signal peptide

<400> 145

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

200265_406WO_SEQUENCE_LISTING.TXT

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Arg Asn Ser Met Cys Trp Gly Lys Gly Ser Cys Pro Asn Ser Lys Cys
50      55      60
Asn Ala Glu Leu Leu Arg Thr Asp Gly Thr Arg Ile Ile Ser Arg Lys
65      70      75      80
Ser Thr Lys Tyr Thr Leu Leu Gly Lys Val Gln Phe Gly Glu Val Ser
85      90      95
Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr Cys Cys
100     105     110
Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn Val Arg
115     120     125
Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr Thr Thr
130     135     140
Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
145     150     155     160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
165     170     175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
180     185     190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
195     200     205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
210     215     220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
225     230     235     240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
245     250     255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
260     265     270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
275     280     285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu His His Leu Phe
290     295     300
Tyr Trp Asp Val Trp Phe Ile Tyr Asn Val Cys Leu Ala Lys Val Lys
305     310     315     320
Gly Tyr Arg Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile
325     330     335
Ser Tyr Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu
340     345     350
Leu Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu Cys
355     360     365
Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp Asn Leu
370     375     380
Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val Leu Thr Lys
385     390     395     400
Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe Tyr Leu Ala Leu
405     410     415
Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile Ile Phe Ile Leu Leu
420     425     430

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200265_406WO_SEQUENCE_LISTING.TXT

Glu	Pro	Val	Leu	Gln	His	Ser	Gln	Tyr	Leu	Arg	Leu	Arg	Gln	Arg	Ile
		435					440					445			
Cys	Lys	Ser	Ser	Ile	Leu	Gln	Trp	Pro	Asp	Asn	Pro	Lys	Ala	Glu	Gly
	450					455					460				
Leu	Phe	Trp	Gln	Thr	Leu	Arg	Asn	Val	Val	Leu	Thr	Glu	Asn	Asp	Ser
465					470					475					480
Arg	Tyr	Asn	Asn	Met	Tyr	Val	Asp	Ser	Ile	Lys	Gln	Tyr	Asp	Ser	Lys
				485				490						495	
Ala	Gly	Met	Glu	Glu	Asp	His	Thr	Tyr	Glu	Gly	Leu	Asp	Ile	Asp	Gln
			500					505					510		
Thr	Ala	Thr	Tyr	Glu	Asp	Ile	Val	Thr	Leu	Arg	Thr	Gly	Glu	Val	Lys
		515					520					525			
Trp	Ser	Val	Gly	Glu	His	Pro	Gly	Gln	Glu						
	530					535									

<210> 146

<211> 522

<212> PRT

<213> Artificial Sequence

<220>

<223> CER103B, amino acids 1-22 are signal peptide

<400> 146

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

200265_406W0_SEQUENCE_LISTING.TXT

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

<210> 147

<211> 545

<212> PRT

<213> Artificial Sequence

200265_406WO_SEQUENCE_LISTING.TXT

<220>

<223> CER104, amino acids 1-22 are signal peptide

<400> 147

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

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200265_406WO_SEQUENCE_LISTING.TXT

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

<210> 148

<211> 578

<212> PRT

<213> Artificial Sequence

<220>

<223> CER105, amino acids 1-22 are signal peptide

<400> 148

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

200265_406WO_SEQUENCE_LISTING.TXT

Leu	Thr	Ile	Ser	Asn	Thr	Asn	Arg	Gly	Asp	Ser	Gly	Val	Tyr	Cys	Cys	
			100					105					110			
Arg	Ile	Glu	Val	Pro	Gly	Trp	Phe	Asn	Asp	Val	Lys	Lys	Asn	Val	Arg	
		115					120						125			
Leu	Glu	Leu	Arg	Arg	Ala	Thr	Thr	Thr	Lys	Lys	Pro	Thr	Thr	Thr	Thr	
		130					135					140				
Arg	Pro	Thr	Thr	Thr	Pro	Tyr	Val	Thr	Thr	Thr	Thr	Pro	Glu	Leu	Leu	
145					150					155					160	
Pro	Thr	Thr	Val	Met	Thr	Thr	Ser	Val	Leu	Pro	Thr	Thr	Thr	Pro	Pro	
				165					170					175		
Gln	Thr	Leu	Ala	Thr	Thr	Ala	Phe	Ser	Thr	Ala	Val	Thr	Thr	Cys	Pro	
			180					185						190		
Ser	Thr	Thr	Pro	Gly	Ser	Phe	Ser	Gln	Glu	Thr	Thr	Lys	Gly	Ser	Ala	
		195				200						205				
Phe	Thr	Thr	Glu	Ser	Glu	Thr	Leu	Pro	Ala	Ser	Asn	His	Ser	Gln	Arg	
		210				215					220					
Ser	Met	Met	Thr	Ile	Ser	Thr	Asp	Ile	Ala	Val	Leu	Arg	Pro	Thr	Gly	
225					230					235					240	
Ser	Asn	Pro	Gly	Ile	Leu	Pro	Ser	Thr	Ser	Gln	Leu	Thr	Thr	Gln	Lys	
				245					250					255		
Thr	Thr	Leu	Thr	Thr	Ser	Glu	Ser	Leu	Gln	Lys	Thr	Thr	Lys	Ser	His	
		260						265					270			
Gln	Ile	Asn	Ser	Arg	Gln	Thr	Ile	Leu	Ile	Ile	Ala	Cys	Cys	Val	Gly	
		275					280					285				
Phe	Val	Leu	Met	Val	Leu	Leu	Phe	Leu	Ala	Phe	Leu	His	His	Leu	Phe	
		290				295					300					
Tyr	Trp	Asp	Val	Trp	Phe	Ile	Tyr	Asn	Val	Cys	Leu	Ala	Lys	Val	Lys	
305					310					315					320	
Gly	Tyr	Arg	Ser	Leu	Ser	Thr	Ser	Gln	Thr	Phe	Tyr	Asp	Ala	Tyr	Ile	
				325					330					335		
Ser	Tyr	Asp	Thr	Lys	Asp	Ala	Ser	Val	Thr	Asp	Trp	Val	Ile	Asn	Glu	
			340					345					350			
Leu	Arg	Tyr	His	Leu	Glu	Glu	Ser	Arg	Asp	Lys	Asn	Val	Leu	Leu	Cys	
		355					360					365				
Leu	Glu	Glu	Arg	Asp	Trp	Asp	Pro	Gly	Leu	Ala	Ile	Ile	Asp	Asn	Leu	
		370				375					380					
Met	Gln	Ser	Ile	Asn	Gln	Ser	Lys	Lys	Thr	Val	Phe	Val	Leu	Thr	Lys	
385					390					395					400	
Lys	Tyr	Ala	Lys	Ser	Trp	Asn	Phe	Lys	Thr	Ala	Phe	Tyr	Leu	Ala	Leu	
				405					410					415		
Gln	Arg	Leu	Met	Asp	Glu	Asn	Met	Asp	Val	Ile	Ile	Phe	Ile	Leu	Leu	
			420					425					430			
Glu	Pro	Val	Leu	Gln	His	Ser	Gln	Tyr	Leu	Arg	Leu	Arg	Gln	Arg	Ile	
		435					440					445				
Cys	Lys	Ser	Ser	Ile	Leu	Gln	Trp	Pro	Asp	Asn	Pro	Lys	Ala	Glu	Gly	
		450				455					460					
Leu	Phe	Trp	Gln	Thr	Leu	Arg	Asn	Val	Val	Leu	Thr	Glu	Asn	Asp	Ser	
465					470					475					480	

200265_406WO_SEQUENCE_LISTING.TXT

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Arg Tyr Asn Asn Met Tyr Val Asp Ser Ile Lys Gln Tyr Ser Trp Arg
      485                      490                      495
Arg Arg Gln Arg Arg Leu Arg Gly Ala Ser Ser Ala Glu Ala Pro Asp
      500                      505                      510
Gly Asp Lys Asp Ala Pro Glu Pro Leu Asp Lys Val Ile Ile Leu Ser
      515                      520                      525
Pro Gly Ile Ser Asp Ala Thr Ala Pro Ala Trp Pro Pro Pro Gly Glu
      530                      535                      540
Asp Pro Gly Thr Thr Pro Pro Gly His Ser Val Pro Val Pro Ala Thr
      545                      550                      555                      560
Glu Leu Gly Ser Thr Glu Leu Val Thr Thr Lys Thr Ala Gly Pro Glu
      565                      570                      575
Gln Gln

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<210> 149

<211> 579

<212> PRT

<213> Artificial Sequence

<220>

<223> CER106, amino acids 1-22 are signal peptide

<400> 149

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

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200265_406WO_SEQUENCE_LISTING.TXT

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Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
195                200                205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
210                215                220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
225                230                235                240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
245                250                255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
260                265                270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
275                280                285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Leu Trp Asn Lys
290                295                300
Lys Arg Met Arg Gly Pro Gly Lys Asp Pro Thr Arg Lys Cys Pro Asp
305                310                315                320
Pro Arg Ser Ala Ser Ser Pro Lys Gln His Pro Ser Glu Ser Val Tyr
325                330                335
Thr Ala Leu Gln Arg Arg Glu Thr Glu Val Tyr Ala Cys Ile Glu Asn
340                345                350
Glu Asp Gly Ser Ser Pro Thr Ala Lys Gln Ser Pro Leu Ser Gln Glu
355                360                365
Arg Pro His Arg Phe Glu Asp Asp Gly Glu Leu Asn Leu Val Tyr Glu
370                375                380
Asn Leu His His Leu Phe Tyr Trp Asp Val Trp Phe Ile Tyr Asn Val
385                390                395                400
Cys Leu Ala Lys Val Lys Gly Tyr Arg Ser Leu Ser Thr Ser Gln Thr
405                410                415
Phe Tyr Asp Ala Tyr Ile Ser Tyr Asp Thr Lys Asp Ala Ser Val Thr
420                425                430
Asp Trp Val Ile Asn Glu Leu Arg Tyr His Leu Glu Glu Ser Arg Asp
435                440                445
Lys Asn Val Leu Leu Cys Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu
450                455                460
Ala Ile Ile Asp Asn Leu Met Gln Ser Ile Asn Gln Ser Lys Lys Thr
465                470                475                480
Val Phe Val Leu Thr Lys Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr
485                490                495
Ala Phe Tyr Leu Ala Leu Gln Arg Leu Met Asp Glu Asn Met Asp Val
500                505                510
Ile Ile Phe Ile Leu Leu Glu Pro Val Leu Gln His Ser Gln Tyr Leu
515                520                525
Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile Leu Gln Trp Pro Asp
530                535                540
Asn Pro Lys Ala Glu Gly Leu Phe Trp Gln Thr Leu Arg Asn Val Val
545                550                555                560
Leu Thr Glu Asn Asp Ser Arg Tyr Asn Asn Met Tyr Val Asp Ser Ile
565                570                575

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200265_406WO_SEQUENCE_LISTING.TXT

Lys Gln Tyr

<210> 150

<211> 522

<212> PRT

<213> Artificial Sequence

<220>

<223> CER107, amino acids 1-22 are signal peptide

<400> 150

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

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200265_406WO_SEQUENCE_LISTING.TXT

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Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Asp Ser Lys Ala
290                295                300
Gly Met Glu Glu Asp His Thr Tyr Glu Gly Leu Asp Ile Asp Gln Thr
305                310                315                320
Ala Thr Tyr Glu Asp Ile Val Thr Leu His His Leu Phe Tyr Trp Asp
                325                330                335
Val Trp Phe Ile Tyr Asn Val Cys Leu Ala Lys Val Lys Gly Tyr Arg
340                345                350
Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser Tyr Asp
355                360                365
Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu Leu Arg Tyr
370                375                380
His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu Cys Leu Glu Glu
385                390                395                400
Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp Asn Leu Met Gln Ser
                405                410                415
Ile Asn Gln Ser Lys Lys Thr Val Phe Val Leu Thr Lys Lys Tyr Ala
420                425                430
Lys Ser Trp Asn Phe Lys Thr Ala Phe Tyr Leu Ala Leu Gln Arg Leu
435                440                445
Met Asp Glu Asn Met Asp Val Ile Ile Phe Ile Leu Leu Glu Pro Val
450                455                460
Leu Gln His Ser Gln Tyr Leu Arg Leu Arg Gln Arg Ile Cys Lys Ser
465                470                475                480
Ser Ile Leu Gln Trp Pro Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp
485                490                495
Gln Thr Leu Arg Asn Val Val Leu Thr Glu Asn Asp Ser Arg Tyr Asn
500                505                510
Asn Met Tyr Val Asp Ser Ile Lys Gln Tyr
515                520

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<210> 151

<211> 545

<212> PRT

<213> Artificial Sequence

<220>

<223> CER108, amino acids 1-22 are signal peptide

<400> 151

```

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

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200265_406WO_SEQUENCE_LISTING.TXT

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Asn Ala Glu Leu Leu Arg Thr Asp Gly Thr Arg Ile Ile Ser Arg Lys
65      70      75      80
Ser Thr Lys Tyr Thr Leu Leu Gly Lys Val Gln Phe Gly Glu Val Ser
      85      90      95
Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr Cys Cys
      100      105      110
Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn Val Arg
      115      120      125
Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr Thr Thr
      130      135      140
Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
145      150      155      160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
      165      170      175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
      180      185      190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
      195      200      205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
      210      215      220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
225      230      235      240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
      245      250      255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
      260      265      270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
      275      280      285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Tyr Phe Leu Gly
      290      295      300
Arg Leu Val Pro Arg Gly Arg Gly Ala Ala Glu Ala Ala Thr Arg Lys
305      310      315      320
Gln Arg Ile Thr Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln
      325      330      335
Arg Ser Asp Val Tyr Ser Asp Leu Asn Thr Gln Arg Pro Tyr Tyr Lys
      340      345      350
His His Leu Phe Tyr Trp Asp Val Trp Phe Ile Tyr Asn Val Cys Leu
      355      360      365
Ala Lys Val Lys Gly Tyr Arg Ser Leu Ser Thr Ser Gln Thr Phe Tyr
      370      375      380
Asp Ala Tyr Ile Ser Tyr Asp Thr Lys Asp Ala Ser Val Thr Asp Trp
385      390      395      400
Val Ile Asn Glu Leu Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn
      405      410      415
Val Leu Leu Cys Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile
      420      425      430
Ile Asp Asn Leu Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe
      435      440      445

```

200265_406WO_SEQUENCE_LISTING.TXT

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Val Leu Thr Lys Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe
  450                      455                      460
Tyr Leu Ala Leu Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile Ile
465                      470                      475                      480
Phe Ile Leu Leu Glu Pro Val Leu Gln His Ser Gln Tyr Leu Arg Leu
                      485                      490                      495
Arg Gln Arg Ile Cys Lys Ser Ser Ile Leu Gln Trp Pro Asp Asn Pro
  500                      505                      510
Lys Ala Glu Gly Leu Phe Trp Gln Thr Leu Arg Asn Val Val Leu Thr
  515                      520                      525
Glu Asn Asp Ser Arg Tyr Asn Asn Met Tyr Val Asp Ser Ile Lys Gln
  530                      535                      540
Tyr
545

```

<210> 152

<211> 578

<212> PRT

<213> Artificial Sequence

<220>

<223> CER109, amino acids 1-22 are signal peptide

<400> 152

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

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200265_406WO_SEQUENCE_LISTING.TXT

Ser	Thr	Thr	Pro	Gly	Ser	Phe	Ser	Gln	Glu	Thr	Thr	Lys	Gly	Ser	Ala	195	200	205
Phe	Thr	Thr	Glu	Ser	Glu	Thr	Leu	Pro	Ala	Ser	Asn	His	Ser	Gln	Arg	210	215	220
Ser	Met	Met	Thr	Ile	Ser	Thr	Asp	Ile	Ala	Val	Leu	Arg	Pro	Thr	Gly	225	230	235
Ser	Asn	Pro	Gly	Ile	Leu	Pro	Ser	Thr	Ser	Gln	Leu	Thr	Thr	Gln	Lys	245	250	255
Thr	Thr	Leu	Thr	Thr	Ser	Glu	Ser	Leu	Gln	Lys	Thr	Thr	Lys	Ser	His	260	265	270
Gln	Ile	Asn	Ser	Arg	Gln	Thr	Ile	Leu	Ile	Ile	Ala	Cys	Cys	Val	Gly	275	280	285
Phe	Val	Leu	Met	Val	Leu	Leu	Phe	Leu	Ala	Phe	Leu	Ser	Trp	Arg	Arg	290	295	300
Arg	Gln	Arg	Arg	Leu	Arg	Gly	Ala	Ser	Ser	Ala	Glu	Ala	Pro	Asp	Gly	305	310	315
Asp	Lys	Asp	Ala	Pro	Glu	Pro	Leu	Asp	Lys	Val	Ile	Ile	Leu	Ser	Pro	325	330	335
Gly	Ile	Ser	Asp	Ala	Thr	Ala	Pro	Ala	Trp	Pro	Pro	Pro	Gly	Glu	Asp	340	345	350
Pro	Gly	Thr	Pro	Pro	Gly	His	Ser	Val	Pro	Val	Pro	Ala	Thr	Glu		355	360	365
Leu	Gly	Ser	Thr	Glu	Leu	Val	Thr	Thr	Lys	Thr	Ala	Gly	Pro	Glu	Gln	370	375	380
Gln	His	His	Leu	Phe	Tyr	Trp	Asp	Val	Trp	Phe	Ile	Tyr	Asn	Val	Cys	385	390	395
Leu	Ala	Lys	Val	Lys	Gly	Tyr	Arg	Ser	Leu	Ser	Thr	Ser	Gln	Thr	Phe	405	410	415
Tyr	Asp	Ala	Tyr	Ile	Ser	Tyr	Asp	Thr	Lys	Asp	Ala	Ser	Val	Thr	Asp	420	425	430
Trp	Val	Ile	Asn	Glu	Leu	Arg	Tyr	His	Leu	Glu	Glu	Ser	Arg	Asp	Lys	435	440	445
Asn	Val	Leu	Leu	Cys	Leu	Glu	Glu	Arg	Asp	Trp	Asp	Pro	Gly	Leu	Ala	450	455	460
Ile	Ile	Asp	Asn	Leu	Met	Gln	Ser	Ile	Asn	Gln	Ser	Lys	Lys	Thr	Val	465	470	475
Phe	Val	Leu	Thr	Lys	Lys	Tyr	Ala	Lys	Ser	Trp	Asn	Phe	Lys	Thr	Ala	485	490	495
Phe	Tyr	Leu	Ala	Leu	Gln	Arg	Leu	Met	Asp	Glu	Asn	Met	Asp	Val	Ile	500	505	510
Ile	Phe	Ile	Leu	Leu	Glu	Pro	Val	Leu	Gln	His	Ser	Gln	Tyr	Leu	Arg	515	520	525
Leu	Arg	Gln	Arg	Ile	Cys	Lys	Ser	Ser	Ile	Leu	Gln	Trp	Pro	Asp	Asn	530	535	540
Pro	Lys	Ala	Glu	Gly	Leu	Phe	Trp	Gln	Thr	Leu	Arg	Asn	Val	Val	Leu	545	550	555
Thr	Glu	Asn	Asp	Ser	Arg	Tyr	Asn	Asn	Met	Tyr	Val	Asp	Ser	Ile	Lys	565	570	575

200265_406WO_SEQUENCE_LISTING.TXT

Gln Tyr

<210> 153

<211> 626

<212> PRT

<213> Artificial Sequence

<220>

<223> CER110, amino acids 1-22 are signal peptide

<400> 153

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

200265_406WO_SEQUENCE_LISTING.TXT

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Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Met Ser Leu Leu
290                295                300
Asn Cys Glu Asn Ser Cys Gly Ser Ser Gln Ser Glu Ser Asp Cys Cys
305                310                315                320
Val Ala Met Ala Ser Ser Cys Ser Ala Val Thr Lys Asp Asp Ser Val
                325                330                335
Gly Gly Thr Ala Ser Thr Gly Asn Leu Ser Ser Ser Phe Met Glu Glu
                340                345                350
Ile Gln Gly Tyr Asp Val Glu Phe Asp Pro Pro Leu Glu Ser Lys Tyr
                355                360                365
Glu Cys Pro Ile Cys Leu Met Ala Leu Arg Glu Ala Val Gln Thr Pro
                370                375                380
Cys Gly His Arg Phe Cys Lys Ala Cys Ile Ile Lys Ser Ile Arg Asp
385                390                395                400
Ala Gly His Lys Cys Pro Val Asp Asn Glu Ile Leu Leu Glu Asn Gln
                405                410                415
Leu Phe Pro Asp Asn Phe Ala Lys Arg Glu Ile Leu Ser Leu Met Val
                420                425                430
Lys Cys Pro Asn Glu Gly Cys Leu His Lys Met Glu Leu Arg His Leu
                435                440                445
Glu Asp His Gln Ala His Cys Glu Phe Ala Leu Met Asp Cys Pro Gln
                450                455                460
Cys Gln Arg Pro Phe Gln Lys Phe His Ile Asn Ile His Ile Leu Lys
465                470                475                480
Asp Cys Pro Arg Arg Gln Val Ser Cys Asp Asn Cys Ala Ala Ser Met
                485                490                495
Ala Phe Glu Asp Lys Glu Ile His Asp Gln Asn Cys Pro Leu Ala Asn
                500                505                510
Val Ile Cys Glu Tyr Cys Asn Thr Ile Leu Ile Arg Glu Gln Met Pro
                515                520                525
Asn His Tyr Asp Leu Asp Cys Pro Thr Ala Pro Ile Pro Cys Thr Phe
                530                535                540
Ser Thr Phe Gly Cys His Glu Lys Met Gln Arg Asn His Leu Ala Arg
545                550                555                560
His Leu Gln Glu Asn Thr Gln Ser His Met Arg Met Leu Ala Tyr Phe
                565                570                575
Leu Gly Arg Leu Val Pro Arg Gly Arg Gly Ala Ala Glu Ala Ala Thr
                580                585                590
Arg Lys Gln Arg Ile Thr Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln
                595                600                605
Gly Gln Arg Ser Asp Val Tyr Ser Asp Leu Asn Thr Gln Arg Pro Tyr
        610                615                620
Tyr Lys
625

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<210> 154

<211> 619

<212> PRT

<223> CER111A, amino acids 1-22 are signal peptide

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

200265_406WO_SEQUENCE_LISTING.TXT

Gly	Gly	Thr	Ala	Ser	Thr	Gly	Asn	Leu	Ser	Ser	Ser	Phe	Met	Glu	Glu
			340					345					350		
Ile	Gln	Gly	Tyr	Asp	Val	Glu	Phe	Asp	Pro	Pro	Leu	Glu	Ser	Lys	Tyr
		355					360					365			
Glu	Cys	Pro	Ile	Cys	Leu	Met	Ala	Leu	Arg	Glu	Ala	Val	Gln	Thr	Pro
		370				375					380				
Cys	Gly	His	Arg	Phe	Cys	Lys	Ala	Cys	Ile	Ile	Lys	Ser	Ile	Arg	Asp
385					390					395					400
Ala	Gly	His	Lys	Cys	Pro	Val	Asp	Asn	Glu	Ile	Leu	Leu	Glu	Asn	Gln
			405					410						415	
Leu	Phe	Pro	Asp	Asn	Phe	Ala	Lys	Arg	Glu	Ile	Leu	Ser	Leu	Met	Val
			420					425					430		
Lys	Cys	Pro	Asn	Glu	Gly	Cys	Leu	His	Lys	Met	Glu	Leu	Arg	His	Leu
		435				440						445			
Glu	Asp	His	Gln	Ala	His	Cys	Glu	Phe	Ala	Leu	Met	Asp	Cys	Pro	Gln
	450					455					460				
Cys	Gln	Arg	Pro	Phe	Gln	Lys	Phe	His	Ile	Asn	Ile	His	Ile	Leu	Lys
465					470					475					480
Asp	Cys	Pro	Arg	Arg	Gln	Val	Ser	Cys	Asp	Asn	Cys	Ala	Ala	Ser	Met
				485					490					495	
Ala	Phe	Glu	Asp	Lys	Glu	Ile	His	Asp	Gln	Asn	Cys	Pro	Leu	Ala	Asn
			500					505					510		
Val	Ile	Cys	Glu	Tyr	Cys	Asn	Thr	Ile	Leu	Ile	Arg	Glu	Gln	Met	Pro
		515				520						525			
Asn	His	Tyr	Asp	Leu	Asp	Cys	Pro	Thr	Ala	Pro	Ile	Pro	Cys	Thr	Phe
	530					535					540				
Ser	Thr	Phe	Gly	Cys	His	Glu	Lys	Met	Gln	Arg	Asn	His	Leu	Ala	Arg
545				550						555					560
His	Leu	Gln	Glu	Asn	Thr	Gln	Ser	His	Met	Arg	Met	Leu	Ala	Asp	Ser
				565					570					575	
Lys	Ala	Gly	Met	Glu	Glu	Asp	His	Thr	Tyr	Glu	Gly	Leu	Asp	Ile	Asp
		580						585					590		
Gln	Thr	Ala	Thr	Tyr	Glu	Asp	Ile	Val	Thr	Leu	Arg	Thr	Gly	Glu	Val
		595				600						605			
Lys	Trp	Ser	Val	Gly	Glu	His	Pro	Gly	Gln	Glu					
	610					615									

<210> 155

<211> 603

<212> PRT

<213> Artificial Sequence

<220>

<223> CER111B, amino acids 1-22 are signal peptide

<400> 155

Met	Ser	Lys	Gly	Leu	Leu	Leu	Leu	Trp	Leu	Val	Thr	Glu	Leu	Trp	Trp
1				5					10					15	

200265_406WO_SEQUENCE_LISTING.TXT

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Leu Tyr Leu Thr Pro Ala Ala Ser Glu Asp Thr Ile Ile Gly Phe Leu
    20          25          30
Gly Gln Pro Val Thr Leu Pro Cys His Tyr Leu Ser Trp Ser Gln Ser
    35          40          45
Arg Asn Ser Met Cys Trp Gly Lys Gly Ser Cys Pro Asn Ser Lys Cys
    50          55          60
Asn Ala Glu Leu Leu Arg Thr Asp Gly Thr Arg Ile Ile Ser Arg Lys
    65          70          75          80
Ser Thr Lys Tyr Thr Leu Leu Gly Lys Val Gln Phe Gly Glu Val Ser
    85          90          95
Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr Cys Cys
    100          105          110
Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn Val Arg
    115          120          125
Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr Thr Thr
    130          135          140
Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
    145          150          155          160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
    165          170          175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
    180          185          190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
    195          200          205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
    210          215          220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
    225          230          235          240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
    245          250          255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
    260          265          270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
    275          280          285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Met Ser Leu Leu
    290          295          300
Asn Cys Glu Asn Ser Cys Gly Ser Ser Gln Ser Glu Ser Asp Cys Cys
    305          310          315          320
Val Ala Met Ala Ser Ser Cys Ser Ala Val Thr Lys Asp Asp Ser Val
    325          330          335
Gly Gly Thr Ala Ser Thr Gly Asn Leu Ser Ser Ser Phe Met Glu Glu
    340          345          350
Ile Gln Gly Tyr Asp Val Glu Phe Asp Pro Pro Leu Glu Ser Lys Tyr
    355          360          365
Glu Cys Pro Ile Cys Leu Met Ala Leu Arg Glu Ala Val Gln Thr Pro
    370          375          380
Cys Gly His Arg Phe Cys Lys Ala Cys Ile Ile Lys Ser Ile Arg Asp
    385          390          395          400

```

200265_406WO_SEQUENCE_LISTING.TXT

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

<210> 156

<211> 660

<212> PRT

<213> Artificial Sequence

<220>

<223> CER112, amino acids 1-22 are signal peptide

<400> 156

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

200265_406WO_SEQUENCE_LISTING.TXT

```

Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr Cys Cys
100                      105                      110
Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn Val Arg
115                      120                      125
Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr Thr Thr
130                      135                      140
Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
145                      150                      155                      160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
165                      170                      175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
180                      185                      190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
195                      200                      205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
210                      215                      220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
225                      230                      235                      240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
245                      250                      255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
260                      265                      270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
275                      280                      285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Met Ser Leu Leu
290                      295                      300
Asn Cys Glu Asn Ser Cys Gly Ser Ser Gln Ser Glu Ser Asp Cys Cys
305                      310                      315                      320
Val Ala Met Ala Ser Ser Cys Ser Ala Val Thr Lys Asp Asp Ser Val
325                      330                      335
Gly Gly Thr Ala Ser Thr Gly Asn Leu Ser Ser Ser Phe Met Glu Glu
340                      345                      350
Ile Gln Gly Tyr Asp Val Glu Phe Asp Pro Pro Leu Glu Ser Lys Tyr
355                      360                      365
Glu Cys Pro Ile Cys Leu Met Ala Leu Arg Glu Ala Val Gln Thr Pro
370                      375                      380
Cys Gly His Arg Phe Cys Lys Ala Cys Ile Ile Lys Ser Ile Arg Asp
385                      390                      395                      400
Ala Gly His Lys Cys Pro Val Asp Asn Glu Ile Leu Leu Glu Asn Gln
405                      410                      415
Leu Phe Pro Asp Asn Phe Ala Lys Arg Glu Ile Leu Ser Leu Met Val
420                      425                      430
Lys Cys Pro Asn Glu Gly Cys Leu His Lys Met Glu Leu Arg His Leu
435                      440                      445
Glu Asp His Gln Ala His Cys Glu Phe Ala Leu Met Asp Cys Pro Gln
450                      455                      460
Cys Gln Arg Pro Phe Gln Lys Phe His Ile Asn Ile His Ile Leu Lys
465                      470                      475                      480

```

200265_406WO_SEQUENCE_LISTING.TXT

```

Asp Cys Pro Arg Arg Gln Val Ser Cys Asp Asn Cys Ala Ala Ser Met
      485                      490                      495
Ala Phe Glu Asp Lys Glu Ile His Asp Gln Asn Cys Pro Leu Ala Asn
      500                      505                      510
Val Ile Cys Glu Tyr Cys Asn Thr Ile Leu Ile Arg Glu Gln Met Pro
      515                      520                      525
Asn His Tyr Asp Leu Asp Cys Pro Thr Ala Pro Ile Pro Cys Thr Phe
      530                      535                      540
Ser Thr Phe Gly Cys His Glu Lys Met Gln Arg Asn His Leu Ala Arg
      545                      550                      555                      560
His Leu Gln Glu Asn Thr Gln Ser His Met Arg Met Leu Ala Leu Trp
      565                      570                      575
Asn Lys Lys Arg Met Arg Gly Pro Gly Lys Asp Pro Thr Arg Lys Cys
      580                      585                      590
Pro Asp Pro Arg Ser Ala Ser Ser Pro Lys Gln His Pro Ser Glu Ser
      595                      600                      605
Val Tyr Thr Ala Leu Gln Arg Arg Glu Thr Glu Val Tyr Ala Cys Ile
      610                      615                      620
Glu Asn Glu Asp Gly Ser Ser Pro Thr Ala Lys Gln Ser Pro Leu Ser
      625                      630                      635                      640
Gln Glu Arg Pro His Arg Phe Glu Asp Asp Gly Glu Leu Asn Leu Val
      645                      650                      655
Tyr Glu Asn Leu
      660

```

<210> 157

<211> 659

<212> PRT

<213> Artificial Sequence

<220>

<223> CER113, amino acids 1-22 are signal peptide

<400> 157

```

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

```

200265_406WO_SEQUENCE_LISTING.TXT

```

Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn Val Arg
115 120 125
Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr Thr Thr
130 135 140
Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
145 150 155 160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
165 170 175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
180 185 190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
195 200 205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
210 215 220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
225 230 235 240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
245 250 255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
260 265 270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
275 280 285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Met Ser Leu Leu
290 295 300
Asn Cys Glu Asn Ser Cys Gly Ser Ser Gln Ser Glu Ser Asp Cys Cys
305 310 315 320
Val Ala Met Ala Ser Ser Cys Ser Ala Val Thr Lys Asp Asp Ser Val
325 330 335
Gly Gly Thr Ala Ser Thr Gly Asn Leu Ser Ser Ser Phe Met Glu Glu
340 345 350
Ile Gln Gly Tyr Asp Val Glu Phe Asp Pro Pro Leu Glu Ser Lys Tyr
355 360 365
Glu Cys Pro Ile Cys Leu Met Ala Leu Arg Glu Ala Val Gln Thr Pro
370 375 380
Cys Gly His Arg Phe Cys Lys Ala Cys Ile Ile Lys Ser Ile Arg Asp
385 390 395 400
Ala Gly His Lys Cys Pro Val Asp Asn Glu Ile Leu Leu Glu Asn Gln
405 410 415
Leu Phe Pro Asp Asn Phe Ala Lys Arg Glu Ile Leu Ser Leu Met Val
420 425 430
Lys Cys Pro Asn Glu Gly Cys Leu His Lys Met Glu Leu Arg His Leu
435 440 445
Glu Asp His Gln Ala His Cys Glu Phe Ala Leu Met Asp Cys Pro Gln
450 455 460
Cys Gln Arg Pro Phe Gln Lys Phe His Ile Asn Ile His Ile Leu Lys
465 470 475 480
Asp Cys Pro Arg Arg Gln Val Ser Cys Asp Asn Cys Ala Ala Ser Met
485 490 495

```

200265_406WO_SEQUENCE_LISTING.TXT

```

Ala Phe Glu Asp Lys Glu Ile His Asp Gln Asn Cys Pro Leu Ala Asn
500                    505                    510
Val Ile Cys Glu Tyr Cys Asn Thr Ile Leu Ile Arg Glu Gln Met Pro
515                    520                    525
Asn His Tyr Asp Leu Asp Cys Pro Thr Ala Pro Ile Pro Cys Thr Phe
530                    535                    540
Ser Thr Phe Gly Cys His Glu Lys Met Gln Arg Asn His Leu Ala Arg
545                    550                    555                    560
His Leu Gln Glu Asn Thr Gln Ser His Met Arg Met Leu Ala Ser Trp
565                    570                    575
Arg Arg Arg Gln Arg Arg Leu Arg Gly Ala Ser Ser Ala Glu Ala Pro
580                    585                    590
Asp Gly Asp Lys Asp Ala Pro Glu Pro Leu Asp Lys Val Ile Ile Leu
595                    600                    605
Ser Pro Gly Ile Ser Asp Ala Thr Ala Pro Ala Trp Pro Pro Pro Gly
610                    615                    620
Glu Asp Pro Gly Thr Thr Pro Pro Gly His Ser Val Pro Val Pro Ala
625                    630                    635                    640
Thr Glu Leu Gly Ser Thr Glu Leu Val Thr Thr Lys Thr Ala Gly Pro
645                    650                    655
Glu Gln Gln

```

<210> 158

<211> 1050

<212> PRT

<213> Artificial Sequence

<220>

<223> CER114, amino acids 1-22 are signal peptide

<400> 158

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

```


200265_406WO_SEQUENCE_LISTING.TXT

```

Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr Thr Thr
130      135      140
Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
145      150      155      160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
165      170      175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
180      185      190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
195      200      205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
210      215      220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
225      230      235      240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
245      250      255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
260      265      270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
275      280      285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Met Ser Leu Leu
290      295      300
Asn Cys Glu Asn Ser Cys Gly Ser Ser Gln Ser Glu Ser Asp Cys Cys
305      310      315      320
Val Ala Met Ala Ser Ser Cys Ser Ala Val Thr Lys Asp Asp Ser Val
325      330      335
Gly Gly Thr Ala Ser Thr Gly Asn Leu Ser Ser Ser Phe Met Glu Glu
340      345      350
Ile Gln Gly Tyr Asp Val Glu Phe Asp Pro Pro Leu Glu Ser Lys Tyr
355      360      365
Glu Cys Pro Ile Cys Leu Met Ala Leu Arg Glu Ala Val Gln Thr Pro
370      375      380
Cys Gly His Arg Phe Cys Lys Ala Cys Ile Ile Lys Ser Ile Arg Asp
385      390      395      400
Ala Gly His Lys Cys Pro Val Asp Asn Glu Ile Leu Leu Glu Asn Gln
405      410      415
Leu Phe Pro Asp Asn Phe Ala Lys Arg Glu Ile Leu Ser Leu Met Val
420      425      430
Lys Cys Pro Asn Glu Gly Cys Leu His Lys Met Glu Leu Arg His Leu
435      440      445
Glu Asp His Gln Ala His Cys Glu Phe Ala Leu Met Asp Cys Pro Gln
450      455      460
Cys Gln Arg Pro Phe Gln Lys Phe His Ile Asn Ile His Ile Leu Lys
465      470      475      480
Asp Cys Pro Arg Arg Gln Val Ser Cys Asp Asn Cys Ala Ala Ser Met
485      490      495
Ala Phe Glu Asp Lys Glu Ile His Asp Gln Asn Cys Pro Leu Ala Asn
500      505      510

```

200265_406WO_SEQUENCE_LISTING.TXT

Val	Ile	Cys	Glu	Tyr	Cys	Asn	Thr	Ile	Leu	Ile	Arg	Glu	Gln	Met	Pro		
		515					520					525					
Asn	His	Tyr	Asp	Leu	Asp	Cys	Pro	Thr	Ala	Pro	Ile	Pro	Cys	Thr	Phe		
		530				535					540						
Ser	Thr	Phe	Gly	Cys	His	Glu	Lys	Met	Gln	Arg	Asn	His	Leu	Ala	Arg		
545					550					555					560		
His	Leu	Gln	Glu	Asn	Thr	Gln	Ser	His	Met	Arg	Met	Leu	Ala	Ala	Leu		
				565					570						575		
Arg	Arg	Arg	Val	Gln	Glu	Thr	Lys	Phe	Gly	Gly	Ala	Phe	Ser	Glu	Glu		
			580					585					590				
Asp	Ser	Gln	Leu	Val	Val	Asn	Tyr	Arg	Ala	Lys	Lys	Ser	Phe	Cys	Arg		
		595				600						605					
Arg	Ala	Ile	Glu	Leu	Thr	Leu	Gln	Ser	Leu	Gly	Val	Ser	Glu	Glu	Leu		
	610					615					620						
Gln	Asn	Lys	Leu	Glu	Asp	Val	Val	Ile	Asp	Arg	Asn	Leu	Leu	Val	Leu		
625					630					635					640		
Gly	Lys	Val	Leu	Gly	Glu	Gly	Glu	Phe	Gly	Ser	Val	Met	Glu	Gly	Asn		
				645					650						655		
Leu	Lys	Gln	Glu	Asp	Gly	Thr	Ser	Gln	Lys	Val	Ala	Val	Lys	Thr	Met		
			660					665						670			
Lys	Leu	Asp	Asn	Phe	Ser	Gln	Arg	Glu	Ile	Glu	Glu	Phe	Leu	Ser	Glu		
		675					680					685					
Ala	Ala	Cys	Met	Lys	Asp	Phe	Asn	His	Pro	Asn	Val	Ile	Arg	Leu	Leu		
	690					695					700						
Gly	Val	Cys	Ile	Glu	Leu	Ser	Ser	Gln	Gly	Ile	Pro	Lys	Pro	Met	Val		
705					710					715					720		
Ile	Leu	Pro	Phe	Met	Lys	Tyr	Gly	Asp	Leu	His	Thr	Phe	Leu	Leu	Tyr		
				725				730							735		
Ser	Arg	Leu	Asn	Thr	Gly	Pro	Lys	Tyr	Ile	His	Leu	Gln	Thr	Leu	Leu		
		740					745						750				
Lys	Phe	Met	Met	Asp	Ile	Ala	Gln	Gly	Met	Glu	Tyr	Leu	Ser	Asn	Arg		
		755					760					765					
Asn	Phe	Leu	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Cys	Met	Leu	Arg	Asp		
	770					775					780						
Asp	Met	Thr	Val	Cys	Val	Ala	Asp	Phe	Gly	Leu	Ser	Lys	Lys	Ile	Tyr		
785					790					795					800		
Ser	Gly	Asp	Tyr	Tyr	Arg	Gln	Gly	Arg	Ile	Ala	Lys	Met	Pro	Val	Lys		
				805					810						815		
Trp	Ile	Ala	Ile	Glu	Ser	Leu	Ala	Asp	Arg	Val	Tyr	Thr	Ser	Lys	Ser		
			820					825						830			
Asp	Val	Trp	Ala	Phe	Gly	Val	Thr	Met	Trp	Glu	Ile	Thr	Thr	Arg	Gly		
		835					840							845			
Met	Thr	Pro	Tyr	Pro	Gly	Val	Gln	Asn	His	Glu	Met	Tyr	Asp	Tyr	Leu		
	850					855					860						
Leu	His	Gly	His	Arg	Leu	Lys	Gln	Pro	Glu	Asp	Cys	Leu	Asp	Glu	Leu		
865					870					875					880		
Tyr	Asp	Ile	Met	Tyr	Ser	Cys	Trp	Ser	Ala	Asp	Pro	Leu	Asp	Arg	Pro		
				885					890						895		

200265_406WO_SEQUENCE_LISTING.TXT

```

Thr Phe Ser Val Leu Arg Leu Gln Leu Glu Lys Leu Ser Glu Ser Leu
900                      905                      910
Pro Asp Ala Gln Asp Lys Glu Ser Ile Ile Tyr Ile Asn Thr Gln Leu
915                      920                      925
Leu Glu Ser Cys Glu Gly Ile Ala Asn Gly Pro Ser Leu Thr Gly Leu
930                      935                      940
Asp Met Asn Ile Asp Pro Asp Ser Ile Ile Ala Ser Cys Thr Pro Gly
945                      950                      955                      960
Ala Ala Val Ser Val Val Thr Ala Glu Val His Glu Asn Asn Leu Arg
965                      970                      975
Glu Glu Arg Tyr Ile Leu Asn Gly Gly Asn Glu Glu Trp Glu Asp Val
980                      985                      990
Ser Ser Thr Pro Phe Ala Ala Val Thr Pro Glu Lys Asp Gly Val Leu
995                      1000                     1005
Pro Glu Asp Arg Leu Thr Lys Asn Gly Val Ser Trp Ser His His Ser
1010                     1015                     1020
Thr Leu Pro Leu Gly Ser Pro Ser Pro Asp Glu Leu Leu Phe Val Asp
1025                     1030                     1035                     1040
Asp Ser Leu Glu Asp Ser Glu Val Leu Met
1045                     1050

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<210> 159

<211> 1050

<212> PRT

<213> Artificial Sequence

<220>

<223> CER115, amino acids 1-22 are signal peptide

<400> 159

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

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200265_406WO_SEQUENCE_LISTING.TXT

```

Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
145          150          155          160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
          165          170          175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
          180          185          190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
          195          200          205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
          210          215          220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
225          230          235          240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
          245          250          255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
          260          265          270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
          275          280          285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Ala Leu Arg Arg
          290          295          300
Arg Val Gln Glu Thr Lys Phe Gly Gly Ala Phe Ser Glu Glu Asp Ser
305          310          315          320
Gln Leu Val Val Asn Tyr Arg Ala Lys Lys Ser Phe Cys Arg Arg Ala
          325          330          335
Ile Glu Leu Thr Leu Gln Ser Leu Gly Val Ser Glu Glu Leu Gln Asn
          340          345          350
Lys Leu Glu Asp Val Val Ile Asp Arg Asn Leu Leu Val Leu Gly Lys
          355          360          365
Val Leu Gly Glu Gly Glu Phe Gly Ser Val Met Glu Gly Asn Leu Lys
          370          375          380
Gln Glu Asp Gly Thr Ser Gln Lys Val Ala Val Lys Thr Met Lys Leu
385          390          395          400
Asp Asn Phe Ser Gln Arg Glu Ile Glu Glu Phe Leu Ser Glu Ala Ala
          405          410          415
Cys Met Lys Asp Phe Asn His Pro Asn Val Ile Arg Leu Leu Gly Val
          420          425          430
Cys Ile Glu Leu Ser Ser Gln Gly Ile Pro Lys Pro Met Val Ile Leu
          435          440          445
Pro Phe Met Lys Tyr Gly Asp Leu His Thr Phe Leu Leu Tyr Ser Arg
          450          455          460
Leu Asn Thr Gly Pro Lys Tyr Ile His Leu Gln Thr Leu Leu Lys Phe
465          470          475          480
Met Met Asp Ile Ala Gln Gly Met Glu Tyr Leu Ser Asn Arg Asn Phe
          485          490          495
Leu His Arg Asp Leu Ala Ala Arg Asn Cys Met Leu Arg Asp Asp Met
          500          505          510
Thr Val Cys Val Ala Asp Phe Gly Leu Ser Lys Lys Ile Tyr Ser Gly
          515          520          525

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200265_406WO_SEQUENCE_LISTING.TXT

```

Asp Tyr Tyr Arg Gln Gly Arg Ile Ala Lys Met Pro Val Lys Trp Ile
530                    535                    540
Ala Ile Glu Ser Leu Ala Asp Arg Val Tyr Thr Ser Lys Ser Asp Val
545                    550                    555                    560
Trp Ala Phe Gly Val Thr Met Trp Glu Ile Thr Thr Arg Gly Met Thr
565                    570                    575
Pro Tyr Pro Gly Val Gln Asn His Glu Met Tyr Asp Tyr Leu Leu His
580                    585                    590
Gly His Arg Leu Lys Gln Pro Glu Asp Cys Leu Asp Glu Leu Tyr Asp
595                    600                    605
Ile Met Tyr Ser Cys Trp Ser Ala Asp Pro Leu Asp Arg Pro Thr Phe
610                    615                    620
Ser Val Leu Arg Leu Gln Leu Glu Lys Leu Ser Glu Ser Leu Pro Asp
625                    630                    635                    640
Ala Gln Asp Lys Glu Ser Ile Ile Tyr Ile Asn Thr Gln Leu Leu Glu
645                    650                    655
Ser Cys Glu Gly Ile Ala Asn Gly Pro Ser Leu Thr Gly Leu Asp Met
660                    665                    670
Asn Ile Asp Pro Asp Ser Ile Ile Ala Ser Cys Thr Pro Gly Ala Ala
675                    680                    685
Val Ser Val Val Thr Ala Glu Val His Glu Asn Asn Leu Arg Glu Glu
690                    695                    700
Arg Tyr Ile Leu Asn Gly Gly Asn Glu Glu Trp Glu Asp Val Ser Ser
705                    710                    715                    720
Thr Pro Phe Ala Ala Val Thr Pro Glu Lys Asp Gly Val Leu Pro Glu
725                    730                    735
Asp Arg Leu Thr Lys Asn Gly Val Ser Trp Ser His His Ser Thr Leu
740                    745                    750
Pro Leu Gly Ser Pro Ser Pro Asp Glu Leu Leu Phe Val Asp Asp Ser
755                    760                    765
Leu Glu Asp Ser Glu Val Leu Met Met Ser Leu Leu Asn Cys Glu Asn
770                    775                    780
Ser Cys Gly Ser Ser Gln Ser Glu Ser Asp Cys Cys Val Ala Met Ala
785                    790                    795                    800
Ser Ser Cys Ser Ala Val Thr Lys Asp Asp Ser Val Gly Gly Thr Ala
805                    810                    815
Ser Thr Gly Asn Leu Ser Ser Ser Phe Met Glu Glu Ile Gln Gly Tyr
820                    825                    830
Asp Val Glu Phe Asp Pro Pro Leu Glu Ser Lys Tyr Glu Cys Pro Ile
835                    840                    845
Cys Leu Met Ala Leu Arg Glu Ala Val Gln Thr Pro Cys Gly His Arg
850                    855                    860
Phe Cys Lys Ala Cys Ile Ile Lys Ser Ile Arg Asp Ala Gly His Lys
865                    870                    875                    880
Cys Pro Val Asp Asn Glu Ile Leu Leu Glu Asn Gln Leu Phe Pro Asp
885                    890                    895
Asn Phe Ala Lys Arg Glu Ile Leu Ser Leu Met Val Lys Cys Pro Asn
900                    905                    910

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200265_406WO_SEQUENCE_LISTING.TXT

Glu	Gly	Cys	Leu	His	Lys	Met	Glu	Leu	Arg	His	Leu	Glu	Asp	His	Gln
		915					920					925			
Ala	His	Cys	Glu	Phe	Ala	Leu	Met	Asp	Cys	Pro	Gln	Cys	Gln	Arg	Pro
		930					935					940			
Phe	Gln	Lys	Phe	His	Ile	Asn	Ile	His	Ile	Leu	Lys	Asp	Cys	Pro	Arg
945					950					955					960
Arg	Gln	Val	Ser	Cys	Asp	Asn	Cys	Ala	Ala	Ser	Met	Ala	Phe	Glu	Asp
				965					970					975	
Lys	Glu	Ile	His	Asp	Gln	Asn	Cys	Pro	Leu	Ala	Asn	Val	Ile	Cys	Glu
			980					985					990		
Tyr	Cys	Asn	Thr	Ile	Leu	Ile	Arg	Glu	Gln	Met	Pro	Asn	His	Tyr	Asp
		995					1000					1005			
Leu	Asp	Cys	Pro	Thr	Ala	Pro	Ile	Pro	Cys	Thr	Phe	Ser	Thr	Phe	Gly
	1010					1015					1020				
Cys	His	Glu	Lys	Met	Gln	Arg	Asn	His	Leu	Ala	Arg	His	Leu	Gln	Glu
1025					1030				1035						1040
Asn	Thr	Gln	Ser	His	Met	Arg	Met	Leu	Ala						
				1045					1050						

<210> 160

<211> 767

<212> PRT

<213> Artificial Sequence

<220>

<223> CER116, amino acids 1-22 are signal peptide

<400> 160

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

200265_406WO_SEQUENCE_LISTING.TXT

Pro	Thr	Thr	Val	Met	Thr	Thr	Ser	Val	Leu	Pro	Thr	Thr	Thr	Pro	Pro
				165					170					175	
Gln	Thr	Leu	Ala	Thr	Thr	Ala	Phe	Ser	Thr	Ala	Val	Thr	Thr	Cys	Pro
			180					185						190	
Ser	Thr	Thr	Pro	Gly	Ser	Phe	Ser	Gln	Glu	Thr	Thr	Lys	Gly	Ser	Ala
			195				200					205			
Phe	Thr	Thr	Glu	Ser	Glu	Thr	Leu	Pro	Ala	Ser	Asn	His	Ser	Gln	Arg
	210					215					220				
Ser	Met	Met	Thr	Ile	Ser	Thr	Asp	Ile	Ala	Val	Leu	Arg	Pro	Thr	Gly
225					230					235					240
Ser	Asn	Pro	Gly	Ile	Leu	Pro	Ser	Thr	Ser	Gln	Leu	Thr	Thr	Gln	Lys
				245					250						255
Thr	Thr	Leu	Thr	Thr	Ser	Glu	Ser	Leu	Gln	Lys	Thr	Thr	Lys	Ser	His
			260					265						270	
Gln	Ile	Asn	Ser	Arg	Gln	Thr	Ile	Leu	Ile	Ile	Ala	Cys	Cys	Val	Gly
		275					280					285			
Phe	Val	Leu	Met	Val	Leu	Leu	Phe	Leu	Ala	Phe	Leu	Met	Ser	Leu	Leu
	290					295					300				
Asn	Cys	Glu	Asn	Ser	Cys	Gly	Ser	Ser	Gln	Ser	Glu	Ser	Asp	Cys	Cys
305					310					315					320
Val	Ala	Met	Ala	Ser	Ser	Cys	Ser	Ala	Val	Thr	Lys	Asp	Asp	Ser	Val
				325					330					335	
Gly	Gly	Thr	Ala	Ser	Thr	Gly	Asn	Leu	Ser	Ser	Ser	Phe	Met	Glu	Glu
			340				345						350		
Ile	Gln	Gly	Tyr	Asp	Val	Glu	Phe	Asp	Pro	Pro	Leu	Glu	Ser	Lys	Tyr
		355					360					365			
Glu	Cys	Pro	Ile	Cys	Leu	Met	Ala	Leu	Arg	Glu	Ala	Val	Gln	Thr	Pro
	370					375					380				
Cys	Gly	His	Arg	Phe	Cys	Lys	Ala	Cys	Ile	Ile	Lys	Ser	Ile	Arg	Asp
385					390					395					400
Ala	Gly	His	Lys	Cys	Pro	Val	Asp	Asn	Glu	Ile	Leu	Leu	Glu	Asn	Gln
				405					410					415	
Leu	Phe	Pro	Asp	Asn	Phe	Ala	Lys	Arg	Glu	Ile	Leu	Ser	Leu	Met	Val
			420					425					430		
Lys	Cys	Pro	Asn	Glu	Gly	Cys	Leu	His	Lys	Met	Glu	Leu	Arg	His	Leu
		435					440					445			
Glu	Asp	His	Gln	Ala	His	Cys	Glu	Phe	Ala	Leu	Met	Asp	Cys	Pro	Gln
	450					455					460				
Cys	Gln	Arg	Pro	Phe	Gln	Lys	Phe	His	Ile	Asn	Ile	His	Ile	Leu	Lys
465					470					475					480
Asp	Cys	Pro	Arg	Arg	Gln	Val	Ser	Cys	Asp	Asn	Cys	Ala	Ala	Ser	Met
				485					490					495	
Ala	Phe	Glu	Asp	Lys	Glu	Ile	His	Asp	Gln	Asn	Cys	Pro	Leu	Ala	Asn
			500					505					510		
Val	Ile	Cys	Glu	Tyr	Cys	Asn	Thr	Ile	Leu	Ile	Arg	Glu	Gln	Met	Pro
		515					520					525			
Asn	His	Tyr	Asp	Leu	Asp	Cys	Pro	Thr	Ala	Pro	Ile	Pro	Cys	Thr	Phe
	530					535					540				

200265_406WO_SEQUENCE_LISTING.TXT

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Ser Thr Phe Gly Cys His Glu Lys Met Gln Arg Asn His Leu Ala Arg
545                    550                    555                    560
His Leu Gln Glu Asn Thr Gln Ser His Met Arg Met Leu Ala His His
                    565                    570                    575
Leu Phe Tyr Trp Asp Val Trp Phe Ile Tyr Asn Val Cys Leu Ala Lys
                    580                    585                    590
Val Lys Gly Tyr Arg Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala
                    595                    600                    605
Tyr Ile Ser Tyr Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile
        610                    615                    620
Asn Glu Leu Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu
625                    630                    635                    640
Leu Cys Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp
                    645                    650                    655
Asn Leu Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val Leu
                    660                    665                    670
Thr Lys Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe Tyr Leu
                    675                    680                    685
Ala Leu Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile Ile Phe Ile
        690                    695                    700
Leu Leu Glu Pro Val Leu Gln His Ser Gln Tyr Leu Arg Leu Arg Gln
705                    710                    715                    720
Arg Ile Cys Lys Ser Ser Ile Leu Gln Trp Pro Asp Asn Pro Lys Ala
                    725                    730                    735
Glu Gly Leu Phe Trp Gln Thr Leu Arg Asn Val Val Leu Thr Glu Asn
                    740                    745                    750
Asp Ser Arg Tyr Asn Asn Met Tyr Val Asp Ser Ile Lys Gln Tyr
                    755                    760                    765

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<210> 161

<211> 767

<212> PRT

<213> Artificial Sequence

<220>

<223> CER117, amino acids 1-22 are signal peptide

<400> 161

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

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200265_406WO_SEQUENCE_LISTING.TXT

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Ser Thr Lys Tyr Thr Leu Leu Gly Lys Val Gln Phe Gly Glu Val Ser
      85                      90                      95
Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr Cys Cys
      100                      105                      110
Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn Val Arg
      115                      120                      125
Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr Thr Thr
      130                      135                      140
Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
      145                      150                      155                      160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
      165                      170                      175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
      180                      185                      190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
      195                      200                      205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
      210                      215                      220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
      225                      230                      235                      240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
      245                      250                      255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
      260                      265                      270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
      275                      280                      285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu His His Leu Phe
      290                      295                      300
Tyr Trp Asp Val Trp Phe Ile Tyr Asn Val Cys Leu Ala Lys Val Lys
      305                      310                      315                      320
Gly Tyr Arg Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile
      325                      330                      335
Ser Tyr Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu
      340                      345                      350
Leu Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu Cys
      355                      360                      365
Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp Asn Leu
      370                      375                      380
Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val Leu Thr Lys
      385                      390                      395                      400
Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe Tyr Leu Ala Leu
      405                      410                      415
Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile Ile Phe Ile Leu Leu
      420                      425                      430
Glu Pro Val Leu Gln His Ser Gln Tyr Leu Arg Leu Arg Gln Arg Ile
      435                      440                      445
Cys Lys Ser Ser Ile Leu Gln Trp Pro Asp Asn Pro Lys Ala Glu Gly
      450                      455                      460

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200265_406WO_SEQUENCE_LISTING.TXT

Leu	Phe	Trp	Gln	Thr	Leu	Arg	Asn	Val	Val	Leu	Thr	Glu	Asn	Asp	Ser	465	470	475	480
Arg	Tyr	Asn	Asn	Met	Tyr	Val	Asp	Ser	Ile	Lys	Gln	Tyr	Met	Ser	Leu	485	490	495	
Leu	Asn	Cys	Glu	Asn	Ser	Cys	Gly	Ser	Ser	Gln	Ser	Glu	Ser	Asp	Cys	500	505	510	
Cys	Val	Ala	Met	Ala	Ser	Ser	Cys	Ser	Ala	Val	Thr	Lys	Asp	Asp	Ser	515	520	525	
Val	Gly	Gly	Thr	Ala	Ser	Thr	Gly	Asn	Leu	Ser	Ser	Ser	Phe	Met	Glu	530	535	540	
Glu	Ile	Gln	Gly	Tyr	Asp	Val	Glu	Phe	Asp	Pro	Pro	Leu	Glu	Ser	Lys	545	550	555	560
Tyr	Glu	Cys	Pro	Ile	Cys	Leu	Met	Ala	Leu	Arg	Glu	Ala	Val	Gln	Thr	565	570	575	
Pro	Cys	Gly	His	Arg	Phe	Cys	Lys	Ala	Cys	Ile	Ile	Lys	Ser	Ile	Arg	580	585	590	
Asp	Ala	Gly	His	Lys	Cys	Pro	Val	Asp	Asn	Glu	Ile	Leu	Leu	Glu	Asn	595	600	605	
Gln	Leu	Phe	Pro	Asp	Asn	Phe	Ala	Lys	Arg	Glu	Ile	Leu	Ser	Leu	Met	610	615	620	
Val	Lys	Cys	Pro	Asn	Glu	Gly	Cys	Leu	His	Lys	Met	Glu	Leu	Arg	His	625	630	635	640
Leu	Glu	Asp	His	Gln	Ala	His	Cys	Glu	Phe	Ala	Leu	Met	Asp	Cys	Pro	645	650	655	
Gln	Cys	Gln	Arg	Pro	Phe	Gln	Lys	Phe	His	Ile	Asn	Ile	His	Ile	Leu	660	665	670	
Lys	Asp	Cys	Pro	Arg	Arg	Gln	Val	Ser	Cys	Asp	Asn	Cys	Ala	Ala	Ser	675	680	685	
Met	Ala	Phe	Glu	Asp	Lys	Glu	Ile	His	Asp	Gln	Asn	Cys	Pro	Leu	Ala	690	695	700	
Asn	Val	Ile	Cys	Glu	Tyr	Cys	Asn	Thr	Ile	Leu	Ile	Arg	Glu	Gln	Met	705	710	715	720
Pro	Asn	His	Tyr	Asp	Leu	Asp	Cys	Pro	Thr	Ala	Pro	Ile	Pro	Cys	Thr	725	730	735	
Phe	Ser	Thr	Phe	Gly	Cys	His	Glu	Lys	Met	Gln	Arg	Asn	His	Leu	Ala	740	745	750	
Arg	His	Leu	Gln	Glu	Asn	Thr	Gln	Ser	His	Met	Arg	Met	Leu	Ala		755	760	765	

<210> 162

<211> 571

<212> PRT

<213> Artificial Sequence

<220>

<223> CER118, amino acids 1-22 are signal peptide

<400> 162

200265_406WO_SEQUENCE_LISTING.TXT

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Met Ser Lys Gly Leu Leu Leu Leu Trp Leu Val Thr Glu Leu Trp Trp
 1          5          10          15
Leu Tyr Leu Thr Pro Ala Ala Ser Glu Asp Thr Ile Ile Gly Phe Leu
 20          25          30
Gly Gln Pro Val Thr Leu Pro Cys His Tyr Leu Ser Trp Ser Gln Ser
 35          40          45
Arg Asn Ser Met Cys Trp Gly Lys Gly Ser Cys Pro Asn Ser Lys Cys
 50          55          60
Asn Ala Glu Leu Leu Arg Thr Asp Gly Thr Arg Ile Ile Ser Arg Lys
 65          70          75          80
Ser Thr Lys Tyr Thr Leu Leu Gly Lys Val Gln Phe Gly Glu Val Ser
 85          90          95
Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr Cys Cys
100          105          110
Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn Val Arg
115          120          125
Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr Thr Thr
130          135          140
Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
145          150          155          160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
165          170          175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
180          185          190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
195          200          205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
210          215          220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
225          230          235          240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
245          250          255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
260          265          270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
275          280          285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Ser Tyr Leu Asp
290          295          300
Leu Pro Trp Tyr Leu Arg Met Val Cys Gln Trp Thr Gln Thr Arg Arg
305          310          315          320
Arg Ala Arg Asn Ile Pro Leu Glu Glu Leu Gln Arg Asn Leu Gln Phe
325          330          335
His Ala Phe Ile Ser Tyr Ser Gly His Asp Ser Phe Trp Val Lys Asn
340          345          350
Glu Leu Leu Pro Asn Leu Glu Lys Glu Gly Met Gln Ile Cys Leu His
355          360          365
Glu Arg Asn Phe Val Pro Gly Lys Ser Ile Val Glu Asn Ile Ile Thr
370          375          380

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200265_406WO_SEQUENCE_LISTING.TXT

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

<210> 163

<211> 514

<212> PRT

<213> Artificial Sequence

<220>

<223> CER119B, amino acids 1-22 are signal peptide

<400> 163

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

200265_406WO_SEQUENCE_LISTING.TXT

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Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn Val Arg
    115                120                125
Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr Thr Thr
    130                135                140
Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
    145                150                155                160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
    165                170                175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
    180                185                190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
    195                200                205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
    210                215                220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
    225                230                235                240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
    245                250                255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
    260                265                270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
    275                280                285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Ser Tyr Leu Asp
    290                295                300
Leu Pro Trp Tyr Leu Arg Met Val Cys Gln Trp Thr Gln Thr Arg Arg
    305                310                315                320
Arg Ala Arg Asn Ile Pro Leu Glu Glu Leu Gln Arg Asn Leu Gln Phe
    325                330                335
His Ala Phe Ile Ser Tyr Ser Gly His Asp Ser Phe Trp Val Lys Asn
    340                345                350
Glu Leu Leu Pro Asn Leu Glu Lys Glu Gly Met Gln Ile Cys Leu His
    355                360                365
Glu Arg Asn Phe Val Pro Gly Lys Ser Ile Val Glu Asn Ile Ile Thr
    370                375                380
Cys Ile Glu Lys Ser Tyr Lys Ser Ile Phe Val Leu Ser Pro Asn Phe
    385                390                395                400
Val Gln Ser Glu Trp Cys His Tyr Glu Leu Tyr Phe Ala His His Asn
    405                410                415
Leu Phe His Glu Gly Ser Asn Ser Leu Ile Leu Ile Leu Leu Glu Pro
    420                425                430
Ile Pro Gln Tyr Ser Ile Pro Ser Ser Tyr His Lys Leu Lys Ser Leu
    435                440                445
Met Ala Arg Arg Thr Tyr Leu Glu Trp Pro Lys Glu Lys Ser Lys Arg
    450                455                460
Gly Leu Phe Trp Ala Asn Leu Arg Ala Ala Ile Asn Ile Lys Leu Thr
    465                470                475                480
Glu Gln Ala Lys Lys Asp Ser Lys Ala Gly Met Glu Glu Asp His Thr
    485                490                495

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200265_406WO_SEQUENCE_LISTING.TXT

Tyr Glu Gly Leu Asp Ile Asp Gln Thr Ala Thr Tyr Glu Asp Ile Val
 500 505 510
 Thr Leu

<210> 164

<211> 537

<212> PRT

<213> Artificial Sequence

<220>

<223> CER120, amino acids 1-22 are signal peptide

<400> 164

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

200265_406WO_SEQUENCE_LISTING.TXT

Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
 275 280 285
 Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Ser Tyr Leu Asp
 290 295 300
 Leu Pro Trp Tyr Leu Arg Met Val Cys Gln Trp Thr Gln Thr Arg Arg
 305 310 315 320
 Arg Ala Arg Asn Ile Pro Leu Glu Glu Leu Gln Arg Asn Leu Gln Phe
 325 330 335
 His Ala Phe Ile Ser Tyr Ser Gly His Asp Ser Phe Trp Val Lys Asn
 340 345 350
 Glu Leu Leu Pro Asn Leu Glu Lys Glu Gly Met Gln Ile Cys Leu His
 355 360 365
 Glu Arg Asn Phe Val Pro Gly Lys Ser Ile Val Glu Asn Ile Ile Thr
 370 375 380
 Cys Ile Glu Lys Ser Tyr Lys Ser Ile Phe Val Leu Ser Pro Asn Phe
 385 390 395 400
 Val Gln Ser Glu Trp Cys His Tyr Glu Leu Tyr Phe Ala His His Asn
 405 410 415
 Leu Phe His Glu Gly Ser Asn Ser Leu Ile Leu Ile Leu Leu Glu Pro
 420 425 430
 Ile Pro Gln Tyr Ser Ile Pro Ser Tyr His Lys Leu Lys Ser Leu
 435 440 445
 Met Ala Arg Arg Thr Tyr Leu Glu Trp Pro Lys Glu Lys Ser Lys Arg
 450 455 460
 Gly Leu Phe Trp Ala Asn Leu Arg Ala Ala Ile Asn Ile Lys Leu Thr
 465 470 475 480
 Glu Gln Ala Lys Lys Tyr Phe Leu Gly Arg Leu Val Pro Arg Gly Arg
 485 490 495
 Gly Ala Ala Glu Ala Ala Thr Arg Lys Gln Arg Ile Thr Glu Thr Glu
 500 505 510
 Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg Ser Asp Val Tyr Ser Asp
 515 520 525
 Leu Asn Thr Gln Arg Pro Tyr Tyr Lys
 530 535

<210> 165

<211> 759

<212> PRT

<213> Artificial Sequence

<220>

<223> CER121, amino acids 1-22 are signal peptide

<400> 165

Met Ser Lys Gly Leu Leu Leu Leu Trp Leu Val Thr Glu Leu Trp Trp
 1 5 10 15
 Leu Tyr Leu Thr Pro Ala Ala Ser Glu Asp Thr Ile Ile Gly Phe Leu
 20 25 30

200265_406W0_SEQUENCE_LISTING.TXT

Gly 35	Gln	Pro 35	Val	Thr	Leu	Pro 40	Cys 40	His	Tyr	Leu	Ser 45	Trp 45	Ser	Gln	Ser
Arg 50	Asn	Ser	Met	Cys	Trp	Gly 55	Lys	Gly	Ser	Cys 60	Pro	Asn	Ser	Lys	Cys
Asn 65	Ala	Glu	Leu	Leu	Arg 70	Thr	Asp	Gly	Thr	Arg 75	Ile	Ile	Ser	Arg	Lys 80
Ser	Thr	Lys	Tyr	Thr 85	Leu	Leu	Gly	Lys	Val 90	Gln	Phe	Gly	Glu	Val 95	Ser
Leu	Thr	Ile	Ser 100	Asn	Thr	Asn	Arg	Gly 105	Asp	Ser	Gly	Val	Tyr 110	Cys	Cys
Arg	Ile	Glu 115	Val	Pro	Gly	Trp	Phe 120	Asn	Asp	Val	Lys	Lys 125	Asn	Val	Arg
Leu	Glu 130	Leu	Arg	Arg	Ala	Thr 135	Thr	Thr	Lys	Lys	Pro 140	Thr	Thr	Thr	Thr
Arg 145	Pro	Thr	Thr	Thr	Pro 150	Tyr	Val	Thr	Thr	Thr	Thr 155	Pro	Glu	Leu	Leu 160
Pro	Thr	Thr	Val	Met 165	Thr	Thr	Ser	Val	Leu	Pro	Thr 170	Thr	Thr	Pro 175	Pro
Gln	Thr	Leu	Ala 180	Thr	Thr	Ala	Phe 185	Ser	Thr	Ala	Val	Thr 190	Thr	Cys	Pro
Ser	Thr	Thr 195	Pro	Gly	Ser	Phe 200	Ser	Gln	Glu	Thr	Thr 205	Lys	Gly	Ser	Ala
Phe	Thr 210	Thr	Glu	Ser	Glu	Thr 215	Leu	Pro	Ala	Ser	Asn 220	His	Ser	Gln	Arg
Ser 225	Met	Met	Thr	Ile	Ser 230	Thr	Asp	Ile	Ala	Val 235	Leu	Arg	Pro	Thr	Gly 240
Ser	Asn	Pro	Gly	Ile 245	Leu	Pro	Ser	Thr	Ser	Gln 250	Leu	Thr	Thr	Gln 255	Lys
Thr	Thr	Leu	Thr 260	Thr	Ser	Glu	Ser	Leu 265	Gln	Lys	Thr	Thr 270	Lys	Ser	His
Gln	Ile	Asn 275	Ser	Arg	Gln	Thr	Ile 280	Leu	Ile	Ile	Ala 285	Cys	Cys	Val	Gly
Phe	Val 290	Leu	Met	Val	Leu	Leu 295	Phe	Leu	Ala	Phe	Leu 300	Ser	Tyr	Leu	Asp
Leu 305	Pro	Trp	Tyr	Leu	Arg 310	Met	Val	Cys	Gln	Trp 315	Thr	Gln	Thr	Arg	Arg 320
Arg	Ala	Arg	Asn 325	Ile	Pro	Leu	Glu	Glu	Leu 330	Gln	Arg	Asn	Leu	Gln 335	Phe
His	Ala	Phe	Ile 340	Ser	Tyr	Ser	Gly	His 345	Asp	Ser	Phe	Trp	Val 350	Lys	Asn
Glu	Leu	Leu 355	Pro	Asn	Leu	Glu	Lys 360	Glu	Gly	Met	Gln	Ile 365	Cys	Leu	His
Glu	Arg 370	Asn	Phe	Val	Pro	Gly 375	Lys	Ser	Ile	Val	Glu 380	Asn	Ile	Ile	Thr
Cys 385	Ile	Glu	Lys	Ser	Tyr 390	Lys	Ser	Ile	Phe	Val 395	Leu	Ser	Pro	Asn	Phe 400
Val	Gln	Ser	Glu	Trp 405	Cys	His	Tyr	Glu	Leu	Tyr 410	Phe	Ala	His	His 415	Asn

200265_406WO_SEQUENCE_LISTING.TXT

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Leu Phe His Glu Gly Ser Asn Ser Leu Ile Leu Ile Leu Leu Glu Pro
420                               425                               430
Ile Pro Gln Tyr Ser Ile Pro Ser Ser Tyr His Lys Leu Lys Ser Leu
435                               440                               445
Met Ala Arg Arg Thr Tyr Leu Glu Trp Pro Lys Glu Lys Ser Lys Arg
450                               455                               460
Gly Leu Phe Trp Ala Asn Leu Arg Ala Ala Ile Asn Ile Lys Leu Thr
465                               470                               475                               480
Glu Gln Ala Lys Lys Met Ser Leu Leu Asn Cys Glu Asn Ser Cys Gly
485                               490                               495
Ser Ser Gln Ser Glu Ser Asp Cys Cys Val Ala Met Ala Ser Ser Cys
500                               505                               510
Ser Ala Val Thr Lys Asp Asp Ser Val Gly Gly Thr Ala Ser Thr Gly
515                               520                               525
Asn Leu Ser Ser Ser Phe Met Glu Glu Ile Gln Gly Tyr Asp Val Glu
530                               535                               540
Phe Asp Pro Pro Leu Glu Ser Lys Tyr Glu Cys Pro Ile Cys Leu Met
545                               550                               555                               560
Ala Leu Arg Glu Ala Val Gln Thr Pro Cys Gly His Arg Phe Cys Lys
565                               570                               575
Ala Cys Ile Ile Lys Ser Ile Arg Asp Ala Gly His Lys Cys Pro Val
580                               585                               590
Asp Asn Glu Ile Leu Leu Glu Asn Gln Leu Phe Pro Asp Asn Phe Ala
595                               600                               605
Lys Arg Glu Ile Leu Ser Leu Met Val Lys Cys Pro Asn Glu Gly Cys
610                               615                               620
Leu His Lys Met Glu Leu Arg His Leu Glu Asp His Gln Ala His Cys
625                               630                               635                               640
Glu Phe Ala Leu Met Asp Cys Pro Gln Cys Gln Arg Pro Phe Gln Lys
645                               650                               655
Phe His Ile Asn Ile His Ile Leu Lys Asp Cys Pro Arg Arg Gln Val
660                               665                               670
Ser Cys Asp Asn Cys Ala Ala Ser Met Ala Phe Glu Asp Lys Glu Ile
675                               680                               685
His Asp Gln Asn Cys Pro Leu Ala Asn Val Ile Cys Glu Tyr Cys Asn
690                               695                               700
Thr Ile Leu Ile Arg Glu Gln Met Pro Asn His Tyr Asp Leu Asp Cys
705                               710                               715                               720
Pro Thr Ala Pro Ile Pro Cys Thr Phe Ser Thr Phe Gly Cys His Glu
725                               730                               735
Lys Met Gln Arg Asn His Leu Ala Arg His Leu Gln Glu Asn Thr Gln
740                               745                               750
Ser His Met Arg Met Leu Ala
755

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<210> 166

<211> 113

<212> PRT

200265_406WO_SEQUENCE_LISTING.TXT

<213> Homo sapiens

<220>

<223> wildtype CD3zeta signaling domain

<400> 166

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

```

<210> 167

<211> 112

<212> PRT

<213> Homo sapiens

<220>

<223> variant CD3zeta signaling domain

<400> 167

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

```

<210> 168

200265_406W0_SEQUENCE_LISTING.TXT

<211> 42

<212> PRT

<213> Homo sapiens

<220>

<223> 4-1BB costimulatory signaling domain

<400> 168

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

<210> 169

<211> 41

<212> PRT

<213> Homo sapiens

<220>

<223> CD28 costimulatory signaling domain variant,
L186G/L187G substitutions with positions in
reference to full length protein

<400> 169

Arg	Ser	Lys	Arg	Ser	Arg	Gly	Gly	His	Ser	Asp	Tyr	Met	Asn	Met	Thr
1				5				10						15	
Pro	Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro
			20				25						30		
Pro	Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser							
			35				40								

<210> 170

<211> 41

<212> PRT

<213> Homo sapiens

<220>

<223> wildtype CD28 costimulatory signaling domain

<400> 170

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

200265_406WO_SEQUENCE_LISTING.TXT

<210> 171

<211> 527

<212> PRT

<213> Artificial Sequence

<220>

<223> CER122, amino acids 1-22 are signal peptide

<400> 171

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

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200265_406WO_SEQUENCE_LISTING.TXT

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

<210> 172

<211> 749

<212> PRT

<213> Artificial Sequence

<220>

<223> CER123, amino acids 1-22 are signal peptide

<400> 172

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

200265_406WO_SEQUENCE_LISTING.TXT

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Ser Thr Lys Tyr Thr Leu Leu Gly Lys Val Gln Phe Gly Glu Val Ser
      85                      90                      95
Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr Cys Cys
      100                    105                    110
Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn Val Arg
      115                    120                    125
Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr Thr Thr
      130                    135                    140
Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
      145                    150                    155                    160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
      165                    170                    175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
      180                    185                    190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
      195                    200                    205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
      210                    215                    220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
      225                    230                    235                    240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
      245                    250                    255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
      260                    265                    270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
      275                    280                    285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu His Arg Phe His
      290                    295                    300
Gly Leu Trp Tyr Met Lys Met Met Trp Ala Trp Leu Gln Ala Lys Arg
      305                    310                    315                    320
Lys Pro Arg Lys Ala Pro Ser Arg Asn Ile Cys Tyr Asp Ala Phe Val
      325                    330                    335
Ser Tyr Ser Glu Arg Asp Ala Tyr Trp Val Glu Asn Leu Met Val Gln
      340                    345                    350
Glu Leu Glu Asn Phe Asn Pro Pro Phe Lys Leu Cys Leu His Lys Arg
      355                    360                    365
Asp Phe Ile Pro Gly Lys Trp Ile Ile Asp Asn Ile Ile Asp Ser Ile
      370                    375                    380
Glu Lys Ser His Lys Thr Val Phe Val Leu Ser Glu Asn Phe Val Lys
      385                    390                    395                    400
Ser Glu Trp Cys Lys Tyr Glu Leu Asp Phe Ser His Phe Arg Leu Phe
      405                    410                    415
Asp Glu Asn Asn Asp Ala Ala Ile Leu Ile Leu Leu Glu Pro Ile Glu
      420                    425                    430
Lys Lys Ala Ile Pro Gln Arg Phe Cys Lys Leu Arg Lys Ile Met Asn
      435                    440                    445
Thr Lys Thr Tyr Leu Glu Trp Pro Met Asp Glu Ala Gln Arg Glu Gly
      450                    455                    460

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200265_406WO_SEQUENCE_LISTING.TXT

Phe	Trp	Val	Asn	Leu	Arg	Ala	Ala	Ile	Lys	Ser	Met	Ser	Leu	Leu	Asn
465					470					475					480
Cys	Glu	Asn	Ser	Cys	Gly	Ser	Ser	Gln	Ser	Glu	Ser	Asp	Cys	Cys	Val
				485					490						495
Ala	Met	Ala	Ser	Ser	Cys	Ser	Ala	Val	Thr	Lys	Asp	Asp	Ser	Val	Gly
			500					505						510	
Gly	Thr	Ala	Ser	Thr	Gly	Asn	Leu	Ser	Ser	Ser	Phe	Met	Glu	Glu	Ile
		515					520					525			
Gln	Gly	Tyr	Asp	Val	Glu	Phe	Asp	Pro	Pro	Leu	Glu	Ser	Lys	Tyr	Glu
	530					535					540				
Cys	Pro	Ile	Cys	Leu	Met	Ala	Leu	Arg	Glu	Ala	Val	Gln	Thr	Pro	Cys
545					550					555					560
Gly	His	Arg	Phe	Cys	Lys	Ala	Cys	Ile	Ile	Lys	Ser	Ile	Arg	Asp	Ala
				565						570					575
Gly	His	Lys	Cys	Pro	Val	Asp	Asn	Glu	Ile	Leu	Leu	Glu	Asn	Gln	Leu
			580					585						590	
Phe	Pro	Asp	Asn	Phe	Ala	Lys	Arg	Glu	Ile	Leu	Ser	Leu	Met	Val	Lys
		595					600						605		
Cys	Pro	Asn	Glu	Gly	Cys	Leu	His	Lys	Met	Glu	Leu	Arg	His	Leu	Glu
	610					615					620				
Asp	His	Gln	Ala	His	Cys	Glu	Phe	Ala	Leu	Met	Asp	Cys	Pro	Gln	Cys
625					630					635					640
Gln	Arg	Pro	Phe	Gln	Lys	Phe	His	Ile	Asn	Ile	His	Ile	Leu	Lys	Asp
				645					650						655
Cys	Pro	Arg	Arg	Gln	Val	Ser	Cys	Asp	Asn	Cys	Ala	Ala	Ser	Met	Ala
			660					665						670	
Phe	Glu	Asp	Lys	Glu	Ile	His	Asp	Gln	Asn	Cys	Pro	Leu	Ala	Asn	Val
		675					680						685		
Ile	Cys	Glu	Tyr	Cys	Asn	Thr	Ile	Leu	Ile	Arg	Glu	Gln	Met	Pro	Asn
	690					695					700				
His	Tyr	Asp	Leu	Asp	Cys	Pro	Thr	Ala	Pro	Ile	Pro	Cys	Thr	Phe	Ser
705					710					715					720
Thr	Phe	Gly	Cys	His	Glu	Lys	Met	Gln	Arg	Asn	His	Leu	Ala	Arg	His
				725					730						735
Leu	Gln	Glu	Asn	Thr	Gln	Ser	His	Met	Arg	Met	Leu	Ala			
			740					745							

<210> 173

<211> 561

<212> PRT

<213> Artificial Sequence

<220>

<223> CER124, amino acids 1-22 are signal peptide

<400> 173

Met	Ser	Lys	Gly	Leu	Leu	Leu	Leu	Trp	Leu	Val	Thr	Glu	Leu	Trp	Trp
1				5					10					15	

200265_406WO_SEQUENCE_LISTING.TXT

Leu	Tyr	Leu	Thr	Pro	Ala	Ala	Ser	Glu	Asp	Thr	Ile	Ile	Gly	Phe	Leu
			20					25					30		
Gly	Gln	Pro	Val	Thr	Leu	Pro	Cys	His	Tyr	Leu	Ser	Trp	Ser	Gln	Ser
		35					40					45			
Arg	Asn	Ser	Met	Cys	Trp	Gly	Lys	Gly	Ser	Cys	Pro	Asn	Ser	Lys	Cys
	50					55					60				
Asn	Ala	Glu	Leu	Leu	Arg	Thr	Asp	Gly	Thr	Arg	Ile	Ile	Ser	Arg	Lys
65					70					75					80
Ser	Thr	Lys	Tyr	Thr	Leu	Leu	Gly	Lys	Val	Gln	Phe	Gly	Glu	Val	Ser
			85						90					95	
Leu	Thr	Ile	Ser	Asn	Thr	Asn	Arg	Gly	Asp	Ser	Gly	Val	Tyr	Cys	Cys
			100					105					110		
Arg	Ile	Glu	Val	Pro	Gly	Trp	Phe	Asn	Asp	Val	Lys	Lys	Asn	Val	Arg
		115					120					125			
Leu	Glu	Leu	Arg	Arg	Ala	Thr	Thr	Thr	Lys	Lys	Pro	Thr	Thr	Thr	Thr
	130					135					140				
Arg	Pro	Thr	Thr	Thr	Pro	Tyr	Val	Thr	Thr	Thr	Thr	Pro	Glu	Leu	Leu
145					150					155					160
Pro	Thr	Thr	Val	Met	Thr	Thr	Ser	Val	Leu	Pro	Thr	Thr	Thr	Pro	Pro
				165					170					175	
Gln	Thr	Leu	Ala	Thr	Thr	Ala	Phe	Ser	Thr	Ala	Val	Thr	Thr	Cys	Pro
			180				185						190		
Ser	Thr	Thr	Pro	Gly	Ser	Phe	Ser	Gln	Glu	Thr	Thr	Lys	Gly	Ser	Ala
		195				200						205			
Phe	Thr	Thr	Glu	Ser	Glu	Thr	Leu	Pro	Ala	Ser	Asn	His	Ser	Gln	Arg
	210					215					220				
Ser	Met	Met	Thr	Ile	Ser	Thr	Asp	Ile	Ala	Val	Leu	Arg	Pro	Thr	Gly
225					230					235					240
Ser	Asn	Pro	Gly	Ile	Leu	Pro	Ser	Thr	Ser	Gln	Leu	Thr	Thr	Gln	Lys
			245						250					255	
Thr	Thr	Leu	Thr	Thr	Ser	Glu	Ser	Leu	Gln	Lys	Thr	Thr	Lys	Ser	His
		260						265					270		
Gln	Ile	Asn	Ser	Arg	Gln	Thr	Ile	Leu	Ile	Ile	Ala	Cys	Cys	Val	Gly
		275					280					285			
Phe	Val	Leu	Met	Val	Leu	Leu	Phe	Leu	Ala	Phe	Leu	His	Arg	Phe	His
	290					295					300				
Gly	Leu	Trp	Tyr	Met	Lys	Met	Met	Trp	Ala	Trp	Leu	Gln	Ala	Lys	Arg
305					310					315					320
Lys	Pro	Arg	Lys	Ala	Pro	Ser	Arg	Asn	Ile	Cys	Tyr	Asp	Ala	Phe	Val
			325						330					335	
Ser	Tyr	Ser	Glu	Arg	Asp	Ala	Tyr	Trp	Val	Glu	Asn	Leu	Met	Val	Gln
		340					345						350		
Glu	Leu	Glu	Asn	Phe	Asn	Pro	Pro	Phe	Lys	Leu	Cys	Leu	His	Lys	Arg
		355					360					365			
Asp	Phe	Ile	Pro	Gly	Lys	Trp	Ile	Ile	Asp	Asn	Ile	Ile	Asp	Ser	Ile
	370					375					380				
Glu	Lys	Ser	His	Lys	Thr	Val	Phe	Val	Leu	Ser	Glu	Asn	Phe	Val	Lys
385					390					395					400

200265_406WO_SEQUENCE_LISTING.TXT

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

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<210> 174

<211> 520

<212> PRT

<213> Artificial Sequence

<220>

<223> CER125A, amino acids 1-22 are signal peptide

<400> 174

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

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200265_406WO_SEQUENCE_LISTING.TXT

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Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr Thr Thr
130      135      140
Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
145      150      155      160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
      165      170      175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
      180      185      190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
      195      200      205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
      210      215      220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
      225      230      235      240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
      245      250      255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
      260      265      270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
      275      280      285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu His Arg Phe His
      290      295      300
Gly Leu Trp Tyr Met Lys Met Met Trp Ala Trp Leu Gln Ala Lys Arg
      305      310      315      320
Lys Pro Arg Lys Ala Pro Ser Arg Asn Ile Cys Tyr Asp Ala Phe Val
      325      330      335
Ser Tyr Ser Glu Arg Asp Ala Tyr Trp Val Glu Asn Leu Met Val Gln
      340      345      350
Glu Leu Glu Asn Phe Asn Pro Pro Phe Lys Leu Cys Leu His Lys Arg
      355      360      365
Asp Phe Ile Pro Gly Lys Trp Ile Ile Asp Asn Ile Ile Asp Ser Ile
      370      375      380
Glu Lys Ser His Lys Thr Val Phe Val Leu Ser Glu Asn Phe Val Lys
      385      390      395      400
Ser Glu Trp Cys Lys Tyr Glu Leu Asp Phe Ser His Phe Arg Leu Phe
      405      410      415
Asp Glu Asn Asn Asp Ala Ala Ile Leu Ile Leu Leu Glu Pro Ile Glu
      420      425      430
Lys Lys Ala Ile Pro Gln Arg Phe Cys Lys Leu Arg Lys Ile Met Asn
      435      440      445
Thr Lys Thr Tyr Leu Glu Trp Pro Met Asp Glu Ala Gln Arg Glu Gly
      450      455      460
Phe Trp Val Asn Leu Arg Ala Ala Ile Lys Ser Asp Ser Lys Ala Gly
      465      470      475      480
Met Glu Glu Asp His Thr Tyr Glu Gly Leu Asp Ile Asp Gln Thr Ala
      485      490      495
Thr Tyr Glu Asp Ile Val Thr Leu Arg Thr Gly Glu Val Lys Trp Ser
      500      505      510

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200265_406WO_SEQUENCE_LISTING.TXT

Val Gly Glu His Pro Gly Gln Glu
 515 520

<210> 175

<211> 504

<212> PRT

<213> Artificial Sequence

<220>

<223> CER125B, amino acids 1-22 are signal peptide

<400> 175

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

200265_406WO_SEQUENCE_LISTING.TXT

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

<210> 176

<211> 1108

<212> PRT

<213> Artificial Sequence

<220>

<223> CER5_T2A_HPVI16 E7 TCR tandem expression cassette

<400> 176

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

200265_406WO_SEQUENCE_LISTING.TXT

```

Ser Thr Lys Tyr Thr Leu Leu Gly Lys Val Gln Phe Gly Glu Val Ser
      85                      90                      95
Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr Cys Cys
      100                      105                      110
Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn Val Arg
      115                      120                      125
Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr Thr Thr
      130                      135                      140
Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
      145                      150                      155                      160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
      165                      170                      175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
      180                      185                      190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
      195                      200                      205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
      210                      215                      220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
      225                      230                      235                      240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
      245                      250                      255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
      260                      265                      270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
      275                      280                      285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Lys Phe Tyr Phe
      290                      295                      300
His Leu Met Leu Leu Ala Gly Cys Ile Lys Tyr Gly Arg Gly Glu Asn
      305                      310                      315                      320
Ile Tyr Asp Ala Phe Val Ile Tyr Ser Ser Gln Asp Glu Asp Trp Val
      325                      330                      335
Arg Asn Glu Leu Val Lys Asn Leu Glu Glu Gly Val Pro Pro Phe Gln
      340                      345                      350
Leu Cys Leu His Tyr Arg Asp Phe Ile Pro Gly Val Ala Ile Ala Ala
      355                      360                      365
Asn Ile Ile His Glu Gly Phe His Lys Ser Arg Lys Val Ile Val Val
      370                      375                      380
Val Ser Gln His Phe Ile Gln Ser Arg Trp Cys Ile Phe Glu Tyr Glu
      385                      390                      395                      400
Ile Ala Gln Thr Trp Gln Phe Leu Ser Ser Arg Ala Gly Ile Ile Phe
      405                      410                      415
Ile Val Leu Gln Lys Val Glu Lys Thr Leu Leu Arg Gln Gln Val Glu
      420                      425                      430
Leu Tyr Arg Leu Leu Ser Arg Asn Thr Tyr Leu Glu Trp Glu Asp Ser
      435                      440                      445
Val Leu Gly Arg His Ile Phe Trp Arg Arg Leu Arg Lys Ala Leu Leu
      450                      455                      460

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200265_406WO_SEQUENCE_LISTING.TXT

```

Asp Gly Lys Ser Trp Asn Pro Glu Gly Thr Val Gly Thr Gly Cys Asn
465                               470           475           480
Trp Gln Glu Ala Thr Ser Ile Leu Glu Gly Gly Gly Glu Gly Arg Gly
                               485           490           495
Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala
                               500           505           510
Pro Gly Leu Leu Cys Trp Ala Leu Leu Cys Leu Leu Gly Ala Gly Leu
                               515           520           525
Val Asp Ala Gly Val Thr Gln Ser Pro Thr His Leu Ile Lys Thr Arg
                               530           535           540
Gly Gln Gln Val Thr Leu Arg Cys Ser Pro Lys Ser Gly His Asp Thr
545                               550           555           560
Val Ser Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Gln Phe Ile Phe
                               565           570           575
Gln Tyr Tyr Glu Glu Glu Glu Arg Gln Arg Gly Asn Phe Pro Asp Arg
                               580           585           590
Phe Ser Gly His Gln Phe Pro Asn Tyr Ser Ser Glu Leu Asn Val Asn
                               595           600           605
Ala Leu Leu Leu Gly Asp Ser Ala Leu Tyr Leu Cys Ala Ser Ser Leu
610                               615           620
Gly Trp Arg Gly Gly Arg Tyr Asn Glu Gln Phe Phe Gly Pro Gly Thr
625                               630           635           640
Arg Leu Thr Val Leu Glu Asp Leu Arg Asn Val Thr Pro Pro Lys Val
                               645           650           655
Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala
                               660           665           670
Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu
675                               680           685
Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Cys Thr Asp
690                               695           700
Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg
705                               710           715           720
Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg
                               725           730           735
Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu
740                               745           750
Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly
755                               760           765
Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr Gln Gln Gly Val Leu
770                               775           780
Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr
785                               790           795           800
Ala Val Leu Val Ser Thr Leu Val Val Met Ala Met Val Lys Arg Lys
                               805           810           815
Asn Ser Arg Ala Lys Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu
820                               825           830
Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Trp Gly
835                               840           845

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200265_406WO_SEQUENCE_LISTING.TXT

```

Val Phe Leu Leu Tyr Val Ser Met Lys Met Gly Gly Thr Thr Gly Gln
 850      855      860
Asn Ile Asp Gln Pro Thr Glu Met Thr Ala Thr Glu Gly Ala Ile Val
865      870      875      880
Gln Ile Asn Cys Thr Tyr Gln Thr Ser Gly Phe Asn Gly Leu Phe Trp
      885      890      895
Tyr Gln Gln His Ala Gly Glu Ala Pro Thr Phe Leu Ser Tyr Asn Val
 900      905      910
Leu Asp Gly Leu Glu Glu Lys Gly Arg Phe Ser Ser Phe Leu Ser Arg
 915      920      925
Ser Lys Gly Tyr Ser Tyr Leu Leu Leu Lys Glu Leu Gln Met Lys Asp
 930      935      940
Ser Ala Ser Tyr Leu Cys Ala Ser Val Asp Gly Asn Asn Arg Leu Ala
945      950      955      960
Phe Gly Lys Gly Asn Gln Val Val Val Ile Pro Asn Ile Gln Asn Pro
      965      970      975
Glu Pro Ala Val Tyr Gln Leu Lys Asp Pro Arg Ser Gln Asp Ser Thr
      980      985      990
Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln Ile Asn Val Pro Lys Thr
      995      1000      1005
Met Glu Ser Gly Thr Phe Ile Thr Asp Lys Cys Val Leu Asp Met Lys
1010      1015      1020
Ala Met Asp Ser Lys Ser Asn Gly Ala Ile Ala Trp Ser Asn Gln Thr
1025      1030      1035      1040
Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu Thr Asn Ala Thr Tyr Pro
      1045      1050      1055
Ser Ser Asp Val Pro Cys Asp Ala Thr Leu Thr Glu Lys Ser Phe Glu
      1060      1065      1070
Thr Asp Met Asn Leu Asn Phe Gln Asn Leu Leu Val Ile Val Leu Arg
      1075      1080      1085
Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg
      1090      1095      1100
Leu Trp Ser Ser
1105

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<210> 177

<211> 1119

<212> PRT

<213> Artificial Sequence

<220>

<223> CER19 _T2A_HP16 E7 TCR tandem expression cassette

<400> 177

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Met Ser Lys Gly Leu Leu Leu Leu Trp Leu Val Thr Glu Leu Trp Trp
 1      5      10      15
Leu Tyr Leu Thr Pro Ala Ala Ser Glu Asp Thr Ile Ile Gly Phe Leu
      20      25      30

```

200265_406W0_SEQUENCE_LISTING.TXT

Gly 35	Gln	Pro 35	Val	Thr	Leu	Pro 40	Cys 40	His	Tyr	Leu	Ser 45	Trp 45	Ser	Gln	Ser
Arg 50	Asn	Ser	Met	Cys	Trp	Gly 55	Lys	Gly	Ser	Cys 60	Pro	Asn	Ser	Lys	Cys
Asn 65	Ala	Glu	Leu	Leu	Arg 70	Thr	Asp	Gly	Thr	Arg 75	Ile	Ile	Ser	Arg	Lys 80
Ser	Thr	Lys	Tyr	Thr 85	Leu	Leu	Gly	Lys	Val 90	Gln	Phe	Gly	Glu	Val 95	Ser
Leu	Thr	Ile	Ser 100	Asn	Thr	Asn	Arg	Gly 105	Asp	Ser	Gly	Val	Tyr 110	Cys	Cys
Arg	Ile	Glu 115	Val	Pro	Gly	Trp	Phe 120	Asn	Asp	Val	Lys	Lys 125	Asn	Val	Arg
Leu	Glu 130	Leu	Arg	Arg	Ala	Thr 135	Thr	Thr	Lys	Lys	Pro 140	Thr	Thr	Thr	Thr
Arg 145	Pro	Thr	Thr	Thr	Pro 150	Tyr	Val	Thr	Thr	Thr	Thr 155	Pro	Glu	Leu	Leu 160
Pro	Thr	Thr	Val	Met 165	Thr	Thr	Ser	Val	Leu 170	Pro	Thr	Thr	Thr	Pro 175	Pro
Gln	Thr	Leu	Ala 180	Thr	Thr	Ala	Phe 185	Ser	Thr	Ala	Val	Thr 190	Thr	Cys	Pro
Ser	Thr	Thr 195	Pro	Gly	Ser	Phe 200	Ser	Gln	Glu	Thr	Thr 205	Lys	Gly	Ser	Ala
Phe	Thr 210	Thr	Glu	Ser	Glu	Thr 215	Leu	Pro	Ala	Ser	Asn 220	His	Ser	Gln	Arg
Ser 225	Met	Met	Thr	Ile	Ser 230	Thr	Asp	Ile	Ala	Val 235	Leu	Arg	Pro	Thr	Gly 240
Ser	Asn	Pro	Gly	Ile 245	Leu	Pro	Ser	Thr	Ser 250	Gln	Leu	Thr	Thr	Gln 255	Lys
Thr	Thr	Leu	Thr 260	Thr	Ser	Glu	Ser	Leu 265	Gln	Lys	Thr	Thr 270	Lys	Ser	His
Gln	Ile	Asn 275	Ser	Arg	Gln	Thr	Ile 280	Leu	Ile	Ile	Ala 285	Cys	Cys	Val	Gly
Phe	Val 290	Leu	Met	Val	Leu	Leu 295	Phe	Leu	Ala	Phe 300	Leu	Thr	Lys	Phe	Arg
Gly 305	Phe	Cys	Phe	Ile	Cys 310	Tyr	Lys	Thr	Ala	Gln 315	Arg	Leu	Val	Phe	Lys
Asp	His	Pro	Gln 325	Gly	Thr	Glu	Pro	Asp 330	Met	Tyr	Lys	Tyr	Asp 335	Ala	Tyr
Leu	Cys	Phe	Ser 340	Ser	Lys	Asp	Phe 345	Thr	Trp	Val	Gln	Asn 350	Ala	Leu	Leu
Lys	His	Leu 355	Asp	Thr	Gln	Tyr	Ser 360	Asp	Gln	Asn	Arg 365	Phe	Asn	Leu	Cys
Phe	Glu 370	Glu	Arg	Asp	Phe	Val 375	Pro	Gly	Glu	Asn 380	Arg	Ile	Ala	Asn	Ile
Gln 385	Asp	Ala	Ile	Trp	Asn 390	Ser	Arg	Lys	Ile	Val 395	Cys	Leu	Val	Ser	Arg
His	Phe	Leu	Arg	Asp 405	Gly	Trp	Cys	Leu	Glu 410	Ala	Phe	Ser	Tyr	Ala 415	Gln

200265_406WO_SEQUENCE_LISTING.TXT

Gly	Arg	Cys	Leu	Ser	Asp	Leu	Asn	Ser	Ala	Leu	Ile	Met	Val	Val	Val	420	425	430
Gly	Ser	Leu	Ser	Gln	Tyr	Gln	Leu	Met	Lys	His	Gln	Ser	Ile	Arg	Gly	435	440	445
Phe	Val	Gln	Lys	Gln	Gln	Tyr	Leu	Arg	Trp	Pro	Glu	Asp	Phe	Gln	Asp	450	455	460
Val	Gly	Trp	Phe	Leu	His	Lys	Leu	Ser	Gln	Gln	Ile	Leu	Lys	Lys	Glu	465	470	475
Lys	Glu	Lys	Lys	Lys	Asp	Asn	Asn	Ile	Pro	Leu	Gln	Thr	Val	Ala	Thr	485	490	495
Ile	Ser	Leu	Glu	Gly	Gly	Gly	Glu	Gly	Arg	Gly	Ser	Leu	Leu	Thr	Cys	500	505	510
Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Ala	Pro	Gly	Leu	Leu	Cys	515	520	525
Trp	Ala	Leu	Leu	Cys	Leu	Leu	Gly	Ala	Gly	Leu	Val	Asp	Ala	Gly	Val	530	535	540
Thr	Gln	Ser	Pro	Thr	His	Leu	Ile	Lys	Thr	Arg	Gly	Gln	Gln	Val	Thr	545	550	555
Leu	Arg	Cys	Ser	Pro	Lys	Ser	Gly	His	Asp	Thr	Val	Ser	Trp	Tyr	Gln	565	570	575
Gln	Ala	Leu	Gly	Gln	Gly	Pro	Gln	Phe	Ile	Phe	Gln	Tyr	Tyr	Glu	Glu	580	585	590
Glu	Glu	Arg	Gln	Arg	Gly	Asn	Phe	Pro	Asp	Arg	Phe	Ser	Gly	His	Gln	595	600	605
Phe	Pro	Asn	Tyr	Ser	Ser	Glu	Leu	Asn	Val	Asn	Ala	Leu	Leu	Leu	Gly	610	615	620
Asp	Ser	Ala	Leu	Tyr	Leu	Cys	Ala	Ser	Ser	Leu	Gly	Trp	Arg	Gly	Gly	625	630	635
Arg	Tyr	Asn	Glu	Gln	Phe	Phe	Gly	Pro	Gly	Thr	Arg	Leu	Thr	Val	Leu	645	650	655
Glu	Asp	Leu	Arg	Asn	Val	Thr	Pro	Pro	Lys	Val	Ser	Leu	Phe	Glu	Pro	660	665	670
Ser	Lys	Ala	Glu	Ile	Ala	Asn	Lys	Gln	Lys	Ala	Thr	Leu	Val	Cys	Leu	675	680	685
Ala	Arg	Gly	Phe	Phe	Pro	Asp	His	Val	Glu	Leu	Ser	Trp	Trp	Val	Asn	690	695	700
Gly	Lys	Glu	Val	His	Ser	Gly	Val	Cys	Thr	Asp	Pro	Gln	Ala	Tyr	Lys	705	710	715
Glu	Ser	Asn	Tyr	Ser	Tyr	Cys	Leu	Ser	Ser	Arg	Leu	Arg	Val	Ser	Ala	725	730	735
Thr	Phe	Trp	His	Asn	Pro	Arg	Asn	His	Phe	Arg	Cys	Gln	Val	Gln	Phe	740	745	750
His	Gly	Leu	Ser	Glu	Glu	Asp	Lys	Trp	Pro	Glu	Gly	Ser	Pro	Lys	Pro	755	760	765
Val	Thr	Gln	Asn	Ile	Ser	Ala	Glu	Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	770	775	780
Ile	Thr	Ser	Ala	Ser	Tyr	Gln	Gln	Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	785	790	795
																		800

200265_406WO_SEQUENCE_LISTING.TXT

Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser
 805 810 815
 Thr Leu Val Val Met Ala Met Val Lys Arg Lys Asn Ser Arg Ala Lys
 820 825 830
 Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly
 835 840 845
 Asp Val Glu Glu Asn Pro Gly Pro Met Trp Gly Val Phe Leu Leu Tyr
 850 855 860
 Val Ser Met Lys Met Gly Gly Thr Thr Gly Gln Asn Ile Asp Gln Pro
 865 870 875 880
 Thr Glu Met Thr Ala Thr Glu Gly Ala Ile Val Gln Ile Asn Cys Thr
 885 890 895
 Tyr Gln Thr Ser Gly Phe Asn Gly Leu Phe Trp Tyr Gln Gln His Ala
 900 905 910
 Gly Glu Ala Pro Thr Phe Leu Ser Tyr Asn Val Leu Asp Gly Leu Glu
 915 920 925
 Glu Lys Gly Arg Phe Ser Ser Phe Leu Ser Arg Ser Lys Gly Tyr Ser
 930 935 940
 Tyr Leu Leu Leu Lys Glu Leu Gln Met Lys Asp Ser Ala Ser Tyr Leu
 945 950 955 960
 Cys Ala Ser Val Asp Gly Asn Asn Arg Leu Ala Phe Gly Lys Gly Asn
 965 970 975
 Gln Val Val Val Ile Pro Asn Ile Gln Asn Pro Glu Pro Ala Val Tyr
 980 985 990
 Gln Leu Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr
 995 1000 1005
 Asp Phe Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr
 1010 1015 1020
 Phe Ile Thr Asp Lys Cys Val Leu Asp Met Lys Ala Met Asp Ser Lys
 1025 1030 1035 1040
 Ser Asn Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln
 1045 1050 1055
 Asp Ile Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro
 1060 1065 1070
 Cys Asp Ala Thr Leu Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu
 1075 1080 1085
 Asn Phe Gln Asn Leu Leu Val Ile Val Leu Arg Ile Leu Leu Leu Lys
 1090 1095 1100
 Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
 1105 1110 1115

<210> 178

<211> 1114

<212> PRT

<213> Artificial Sequence

<220>

<223> CER21_T2A_HP16 E7 TCR tandem expression cassette

200265_406WO_SEQUENCE_LISTING.TXT

<400> 178

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Met Ser Lys Gly Leu Leu Leu Leu Trp Leu Val Thr Glu Leu Trp Trp
 1          5          10          15
Leu Tyr Leu Thr Pro Ala Ala Ser Glu Asp Thr Ile Ile Gly Phe Leu
 20          25          30
Gly Gln Pro Val Thr Leu Pro Cys His Tyr Leu Ser Trp Ser Gln Ser
 35          40          45
Arg Asn Ser Met Cys Trp Gly Lys Gly Ser Cys Pro Asn Ser Lys Cys
 50          55          60
Asn Ala Glu Leu Leu Arg Thr Asp Gly Thr Arg Ile Ile Ser Arg Lys
 65          70          75          80
Ser Thr Lys Tyr Thr Leu Leu Gly Lys Val Gln Phe Gly Glu Val Ser
 85          90          95
Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr Cys Cys
100          105          110
Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn Val Arg
115          120          125
Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr Thr Thr
130          135          140
Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
145          150          155          160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
165          170          175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
180          185          190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
195          200          205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
210          215          220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
225          230          235          240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
245          250          255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
260          265          270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
275          280          285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu His His Leu Phe
290          295          300
Tyr Trp Asp Val Trp Phe Ile Tyr Asn Val Cys Leu Ala Lys Val Lys
305          310          315          320
Gly Tyr Arg Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile
325          330          335
Ser Tyr Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu
340          345          350
Leu Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu Cys
355          360          365

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200265_406WO_SEQUENCE_LISTING.TXT

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Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp Asn Leu
370                      375                      380
Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val Leu Thr Lys
385                      390                      395                      400
Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe Tyr Leu Ala Leu
405                      410                      415
Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile Ile Phe Ile Leu Leu
420                      425                      430
Glu Pro Val Leu Gln His Ser Gln Tyr Leu Arg Leu Arg Gln Arg Ile
435                      440                      445
Cys Lys Ser Ser Ile Leu Gln Trp Pro Asp Asn Pro Lys Ala Glu Gly
450                      455                      460
Leu Phe Trp Gln Thr Leu Arg Asn Val Val Leu Thr Glu Asn Asp Ser
465                      470                      475                      480
Arg Tyr Asn Asn Met Tyr Val Asp Ser Ile Lys Gln Tyr Leu Glu Gly
485                      490                      495
Gly Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu
500                      505                      510
Asn Pro Gly Pro Met Ala Pro Gly Leu Leu Cys Trp Ala Leu Leu Cys
515                      520                      525
Leu Leu Gly Ala Gly Leu Val Asp Ala Gly Val Thr Gln Ser Pro Thr
530                      535                      540
His Leu Ile Lys Thr Arg Gly Gln Gln Val Thr Leu Arg Cys Ser Pro
545                      550                      555                      560
Lys Ser Gly His Asp Thr Val Ser Trp Tyr Gln Gln Ala Leu Gly Gln
565                      570                      575
Gly Pro Gln Phe Ile Phe Gln Tyr Tyr Glu Glu Glu Glu Arg Gln Arg
580                      585                      590
Gly Asn Phe Pro Asp Arg Phe Ser Gly His Gln Phe Pro Asn Tyr Ser
595                      600                      605
Ser Glu Leu Asn Val Asn Ala Leu Leu Leu Gly Asp Ser Ala Leu Tyr
610                      615                      620
Leu Cys Ala Ser Ser Leu Gly Trp Arg Gly Gly Arg Tyr Asn Glu Gln
625                      630                      635                      640
Phe Phe Gly Pro Gly Thr Arg Leu Thr Val Leu Glu Asp Leu Arg Asn
645                      650                      655
Val Thr Pro Pro Lys Val Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile
660                      665                      670
Ala Asn Lys Gln Lys Ala Thr Leu Val Cys Leu Ala Arg Gly Phe Phe
675                      680                      685
Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His
690                      695                      700
Ser Gly Val Cys Thr Asp Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser
705                      710                      715                      720
Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp His Asn
725                      730                      735
Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe His Gly Leu Ser Glu
740                      745                      750

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200265_406WO_SEQUENCE_LISTING.TXT

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Glu Asp Lys Trp Pro Glu Gly Ser Pro Lys Pro Val Thr Gln Asn Ile
755 760 765
Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser
770 775 780
Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu
785 790 795 800
Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Thr Leu Val Val Met
805 810 815
Ala Met Val Lys Arg Lys Asn Ser Arg Ala Lys Arg Ser Gly Ser Gly
820 825 830
Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn
835 840 845
Pro Gly Pro Met Trp Gly Val Phe Leu Leu Tyr Val Ser Met Lys Met
850 855 860
Gly Gly Thr Thr Gly Gln Asn Ile Asp Gln Pro Thr Glu Met Thr Ala
865 870 875 880
Thr Glu Gly Ala Ile Val Gln Ile Asn Cys Thr Tyr Gln Thr Ser Gly
885 890 895
Phe Asn Gly Leu Phe Trp Tyr Gln Gln His Ala Gly Glu Ala Pro Thr
900 905 910
Phe Leu Ser Tyr Asn Val Leu Asp Gly Leu Glu Glu Lys Gly Arg Phe
915 920 925
Ser Ser Phe Leu Ser Arg Ser Lys Gly Tyr Ser Tyr Leu Leu Leu Lys
930 935 940
Glu Leu Gln Met Lys Asp Ser Ala Ser Tyr Leu Cys Ala Ser Val Asp
945 950 955 960
Gly Asn Asn Arg Leu Ala Phe Gly Lys Gly Asn Gln Val Val Val Ile
965 970 975
Pro Asn Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp Pro
980 985 990
Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln
995 1000 1005
Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp Lys
1010 1015 1020
Cys Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile
1025 1030 1035 1040
Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu
1045 1050 1055
Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp Ala Thr Leu
1060 1065 1070
Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu
1075 1080 1085
Leu Val Ile Val Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn
1090 1095 1100
Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
1105 1110

```

<210> 179

200265_406WO_SEQUENCE_LISTING.TXT

<211> 1007

<212> PRT

<213> Artificial Sequence

<220>

<223> CER_25_T2A_HPVI6 E7 TCR tandem expression cassette

<400> 179

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

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200265_406WO_SEQUENCE_LISTING.TXT

```

Pro Arg Ser Ala Ser Ser Pro Lys Gln His Pro Ser Glu Ser Val Tyr
      325                      330                      335
Thr Ala Leu Gln Arg Arg Glu Thr Glu Val Tyr Ala Cys Ile Glu Asn
      340                      345                      350
Glu Asp Gly Ser Ser Pro Thr Ala Lys Gln Ser Pro Leu Ser Gln Glu
      355                      360                      365
Arg Pro His Arg Phe Glu Asp Asp Gly Glu Leu Asn Leu Val Tyr Glu
      370                      375                      380
Asn Leu Leu Glu Gly Gly Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys
      385                      390                      395                      400
Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Pro Gly Leu Leu Cys
      405                      410                      415
Trp Ala Leu Leu Cys Leu Leu Gly Ala Gly Leu Val Asp Ala Gly Val
      420                      425                      430
Thr Gln Ser Pro Thr His Leu Ile Lys Thr Arg Gly Gln Gln Val Thr
      435                      440                      445
Leu Arg Cys Ser Pro Lys Ser Gly His Asp Thr Val Ser Trp Tyr Gln
      450                      455                      460
Gln Ala Leu Gly Gln Gly Pro Gln Phe Ile Phe Gln Tyr Tyr Glu Glu
      465                      470                      475                      480
Glu Glu Arg Gln Arg Gly Asn Phe Pro Asp Arg Phe Ser Gly His Gln
      485                      490                      495
Phe Pro Asn Tyr Ser Ser Glu Leu Asn Val Asn Ala Leu Leu Leu Gly
      500                      505                      510
Asp Ser Ala Leu Tyr Leu Cys Ala Ser Ser Leu Gly Trp Arg Gly Gly
      515                      520                      525
Arg Tyr Asn Glu Gln Phe Phe Gly Pro Gly Thr Arg Leu Thr Val Leu
      530                      535                      540
Glu Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser Leu Phe Glu Pro
      545                      550                      555                      560
Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr Leu Val Cys Leu
      565                      570                      575
Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn
      580                      585                      590
Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro Gln Ala Tyr Lys
      595                      600                      605
Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala
      610                      615                      620
Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe
      625                      630                      635                      640
His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly Ser Pro Lys Pro
      645                      650                      655
Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly
      660                      665                      670
Ile Thr Ser Ala Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu
      675                      680                      685
Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser
      690                      695                      700

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200265_406WO_SEQUENCE_LISTING.TXT

```

Thr Leu Val Val Met Ala Met Val Lys Arg Lys Asn Ser Arg Ala Lys
705              710              715              720
Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly
              725              730              735
Asp Val Glu Glu Asn Pro Gly Pro Met Trp Gly Val Phe Leu Leu Tyr
              740              745              750
Val Ser Met Lys Met Gly Gly Thr Thr Gly Gln Asn Ile Asp Gln Pro
              755              760              765
Thr Glu Met Thr Ala Thr Glu Gly Ala Ile Val Gln Ile Asn Cys Thr
              770              775              780
Tyr Gln Thr Ser Gly Phe Asn Gly Leu Phe Trp Tyr Gln Gln His Ala
785              790              795              800
Gly Glu Ala Pro Thr Phe Leu Ser Tyr Asn Val Leu Asp Gly Leu Glu
              805              810              815
Glu Lys Gly Arg Phe Ser Ser Phe Leu Ser Arg Ser Lys Gly Tyr Ser
              820              825              830
Tyr Leu Leu Leu Lys Glu Leu Gln Met Lys Asp Ser Ala Ser Tyr Leu
              835              840              845
Cys Ala Ser Val Asp Gly Asn Asn Arg Leu Ala Phe Gly Lys Gly Asn
850              855              860
Gln Val Val Val Ile Pro Asn Ile Gln Asn Pro Glu Pro Ala Val Tyr
865              870              875              880
Gln Leu Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr
              885              890              895
Asp Phe Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr
              900              905              910
Phe Ile Thr Asp Lys Cys Val Leu Asp Met Lys Ala Met Asp Ser Lys
              915              920              925
Ser Asn Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln
930              935              940
Asp Ile Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro
945              950              955              960
Cys Asp Ala Thr Leu Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu
              965              970              975
Asn Phe Gln Asn Leu Leu Val Ile Val Leu Arg Ile Leu Leu Leu Lys
              980              985              990
Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
              995              1000              1005

```

<210> 180

<211> 1096

<212> PRT

<213> Artificial Sequence

<220>

<223> CER_27_T2A_HPV E7 TCR tandem expression cassette

<400> 180

200265_406WO_SEQUENCE_LISTING.TXT

Met	Ser	Lys	Gly	Leu	Leu	Leu	Leu	Trp	Leu	Val	Thr	Glu	Leu	Trp	Trp	1	5	10	15
Leu	Tyr	Leu	Thr	Pro	Ala	Ala	Ser	Glu	Asp	Thr	Ile	Ile	Gly	Phe	Leu	20	25	30	
Gly	Gln	Pro	Val	Thr	Leu	Pro	Cys	His	Tyr	Leu	Ser	Trp	Ser	Gln	Ser	35	40	45	
Arg	Asn	Ser	Met	Cys	Trp	Gly	Lys	Gly	Ser	Cys	Pro	Asn	Ser	Lys	Cys	50	55	60	
Asn	Ala	Glu	Leu	Leu	Arg	Thr	Asp	Gly	Thr	Arg	Ile	Ile	Ser	Arg	Lys	65	70	75	80
Ser	Thr	Lys	Tyr	Thr	Leu	Leu	Gly	Lys	Val	Gln	Phe	Gly	Glu	Val	Ser	85	90	95	
Leu	Thr	Ile	Ser	Asn	Thr	Asn	Arg	Gly	Asp	Ser	Gly	Val	Tyr	Cys	Cys	100	105	110	
Arg	Ile	Glu	Val	Pro	Gly	Trp	Phe	Asn	Asp	Val	Lys	Lys	Asn	Val	Arg	115	120	125	
Leu	Glu	Leu	Arg	Arg	Ala	Thr	Thr	Thr	Lys	Lys	Pro	Thr	Thr	Thr	Thr	130	135	140	
Arg	Pro	Thr	Thr	Thr	Pro	Tyr	Val	Thr	Thr	Thr	Thr	Pro	Glu	Leu	Leu	145	150	155	160
Pro	Thr	Thr	Val	Met	Thr	Thr	Ser	Val	Leu	Pro	Thr	Thr	Thr	Pro	Pro	165	170	175	
Gln	Thr	Leu	Ala	Thr	Thr	Ala	Phe	Ser	Thr	Ala	Val	Thr	Thr	Cys	Pro	180	185	190	
Ser	Thr	Thr	Pro	Gly	Ser	Phe	Ser	Gln	Glu	Thr	Thr	Lys	Gly	Ser	Ala	195	200	205	
Phe	Thr	Thr	Glu	Ser	Glu	Thr	Leu	Pro	Ala	Ser	Asn	His	Ser	Gln	Arg	210	215	220	
Ser	Met	Met	Thr	Ile	Ser	Thr	Asp	Ile	Ala	Val	Leu	Arg	Pro	Thr	Gly	225	230	235	240
Ser	Asn	Pro	Gly	Ile	Leu	Pro	Ser	Thr	Ser	Gln	Leu	Thr	Thr	Gln	Lys	245	250	255	
Thr	Thr	Leu	Thr	Thr	Ser	Glu	Ser	Leu	Gln	Lys	Thr	Thr	Lys	Ser	His	260	265	270	
Gln	Ile	Asn	Ser	Arg	Gln	Thr	Ile	Leu	Ile	Ile	Ala	Cys	Cys	Val	Gly	275	280	285	
Phe	Val	Leu	Met	Val	Leu	Leu	Phe	Leu	Ala	Phe	Leu	His	Arg	Phe	His	290	295	300	
Gly	Leu	Trp	Tyr	Met	Lys	Met	Met	Trp	Ala	Trp	Leu	Gln	Ala	Lys	Arg	305	310	315	320
Lys	Pro	Arg	Lys	Ala	Pro	Ser	Arg	Asn	Ile	Cys	Tyr	Asp	Ala	Phe	Val	325	330	335	
Ser	Tyr	Ser	Glu	Arg	Asp	Ala	Tyr	Trp	Val	Glu	Asn	Leu	Met	Val	Gln	340	345	350	
Glu	Leu	Glu	Asn	Phe	Asn	Pro	Pro	Phe	Lys	Leu	Cys	Leu	His	Lys	Arg	355	360	365	
Asp	Phe	Ile	Pro	Gly	Lys	Trp	Ile	Ile	Asp	Asn	Ile	Ile	Asp	Ser	Ile	370	375	380	

200265_406WO_SEQUENCE_LISTING.TXT

Glu	Lys	Ser	His	Lys	Thr	Val	Phe	Val	Leu	Ser	Glu	Asn	Phe	Val	Lys	385	390	395	400
Ser	Glu	Trp	Cys	Lys	Tyr	Glu	Leu	Asp	Phe	Ser	His	Phe	Arg	Leu	Phe	405	410	415	
Asp	Glu	Asn	Asn	Asp	Ala	Ala	Ile	Leu	Ile	Leu	Leu	Glu	Pro	Ile	Glu	420	425	430	
Lys	Lys	Ala	Ile	Pro	Gln	Arg	Phe	Cys	Lys	Leu	Arg	Lys	Ile	Met	Asn	435	440	445	
Thr	Lys	Thr	Tyr	Leu	Glu	Trp	Pro	Met	Asp	Glu	Ala	Gln	Arg	Glu	Gly	450	455	460	
Phe	Trp	Val	Asn	Leu	Arg	Ala	Ala	Ile	Lys	Ser	Leu	Glu	Gly	Gly	Gly	465	470	475	480
Glu	Gly	Arg	Gly	Ser	Leu	Leu	Thr	Cys	Gly	Asp	Val	Glu	Glu	Asn	Pro	485	490	495	
Gly	Pro	Met	Ala	Pro	Gly	Leu	Leu	Cys	Trp	Ala	Leu	Leu	Cys	Leu	Leu	500	505	510	
Gly	Ala	Gly	Leu	Val	Asp	Ala	Gly	Val	Thr	Gln	Ser	Pro	Thr	His	Leu	515	520	525	
Ile	Lys	Thr	Arg	Gly	Gln	Gln	Val	Thr	Leu	Arg	Cys	Ser	Pro	Lys	Ser	530	535	540	
Gly	His	Asp	Thr	Val	Ser	Trp	Tyr	Gln	Gln	Ala	Leu	Gly	Gln	Gly	Pro	545	550	555	560
Gln	Phe	Ile	Phe	Gln	Tyr	Tyr	Glu	Glu	Glu	Glu	Arg	Gln	Arg	Gly	Asn	565	570	575	
Phe	Pro	Asp	Arg	Phe	Ser	Gly	His	Gln	Phe	Pro	Asn	Tyr	Ser	Ser	Glu	580	585	590	
Leu	Asn	Val	Asn	Ala	Leu	Leu	Leu	Gly	Asp	Ser	Ala	Leu	Tyr	Leu	Cys	595	600	605	
Ala	Ser	Ser	Leu	Gly	Trp	Arg	Gly	Gly	Arg	Tyr	Asn	Glu	Gln	Phe	Phe	610	615	620	
Gly	Pro	Gly	Thr	Arg	Leu	Thr	Val	Leu	Glu	Asp	Leu	Arg	Asn	Val	Thr	625	630	635	640
Pro	Pro	Lys	Val	Ser	Leu	Phe	Glu	Pro	Ser	Lys	Ala	Glu	Ile	Ala	Asn	645	650	655	
Lys	Gln	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ala	Arg	Gly	Phe	Phe	Pro	Asp	660	665	670	
His	Val	Glu	Leu	Ser	Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	675	680	685	
Val	Cys	Thr	Asp	Pro	Gln	Ala	Tyr	Lys	Glu	Ser	Asn	Tyr	Ser	Tyr	Cys	690	695	700	
Leu	Ser	Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	His	Asn	Pro	Arg	705	710	715	720
Asn	His	Phe	Arg	Cys	Gln	Val	Gln	Phe	His	Gly	Leu	Ser	Glu	Glu	Asp	725	730	735	
Lys	Trp	Pro	Glu	Gly	Ser	Pro	Lys	Pro	Val	Thr	Gln	Asn	Ile	Ser	Ala	740	745	750	
Glu	Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Ile	Thr	Ser	Ala	Ser	Tyr	Gln	755	760	765	

200265 406W0 SEQUENCE LISTING.TXT

Gln 770	Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys
Ala 785	Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Thr	Leu	Val	Val	Met	Ala	Met
Val	Lys	Arg	Lys	Asn	Ser	Arg	Ala	Lys	Arg	Ser	Gly	Ser	Gly	Ala	Thr
Asn	Phe	Ser	Leu	Leu	Lys	Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly
Pro	Met	Trp	Gly	Val	Phe	Leu	Leu	Tyr	Val	Ser	Met	Lys	Met	Gly	Gly
Thr	Thr	Gly	Gln	Asn	Ile	Asp	Gln	Pro	Thr	Glu	Met	Thr	Ala	Thr	Glu
Gly	Ala	Ile	Val	Gln	Ile	Asn	Cys	Thr	Tyr	Gln	Thr	Ser	Gly	Phe	Asn
Gly	Leu	Phe	Trp	Tyr	Gln	Gln	His	Ala	Gly	Glu	Ala	Pro	Thr	Phe	Leu
Ser	Tyr	Asn	Val	Leu	Asp	Gly	Leu	Glu	Lys	Gly	Arg	Phe	Ser	Ser	
Phe	Leu	Ser	Arg	Ser	Lys	Gly	Tyr	Ser	Tyr	Leu	Leu	Leu	Lys	Glu	Leu
Gln	Met	Lys	Asp	Ser	Ala	Ser	Tyr	Leu	Cys	Ala	Ser	Val	Asp	Gly	Asn
Asn	Arg	Leu	Ala	Phe	Gly	Lys	Gly	Asn	Gln	Val	Val	Val	Ile	Pro	Asn
Ile	Gln	Asn	Pro	Glu	Pro	Ala	Val	Tyr	Gln	Leu	Lys	Asp	Pro	Arg	Ser
Gln	Asp	Ser	Thr	Leu	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Ile	Asn
Val	Pro	Lys	Thr	Met	Glu	Ser	Gly	Thr	Phe	Ile	Thr	Asp	Lys	Cys	Val
Leu	Asp	Met	Lys	Ala	Met	Asp	Ser	Lys	Ser	Asn	Gly	Ala	Ile	Ala	Trp
Ser	Asn	Gln	Thr	Ser	Phe	Thr	Cys	Gln	Asp	Ile	Phe	Lys	Glu	Thr	Asn
Ala	Thr	Tyr	Pro	Ser	Ser	Asp	Val	Pro	Cys	Asp	Ala	Thr	Leu	Thr	Glu
Lys	Ser	Phe	Glu	Thr	Asp	Met	Asn	Leu	Asn	Phe	Gln	Asn	Leu	Leu	Val
Ile	Val	Leu	Arg	Ile	Leu	Leu	Leu	Lys	Val	Ala	Gly	Phe	Asn	Leu	Leu
Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser								

<210> 181

<211> 1195

<212> PRT

<213> Artificial Sequence

200265_406WO_SEQUENCE_LISTING.TXT

<220>

<223> CER_29_T2A_HPVI6 E7 TCR tandem expression cassette

<400> 181

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

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200265_406WO_SEQUENCE_LISTING.TXT

```

Ile Gln Gly Tyr Asp Val Glu Phe Asp Pro Pro Leu Glu Ser Lys Tyr
    355                      360                      365
Glu Cys Pro Ile Cys Leu Met Ala Leu Arg Glu Ala Val Gln Thr Pro
    370                      375                      380
Cys Gly His Arg Phe Cys Lys Ala Cys Ile Ile Lys Ser Ile Arg Asp
385                      390                      395                      400
Ala Gly His Lys Cys Pro Val Asp Asn Glu Ile Leu Leu Glu Asn Gln
    405                      410                      415
Leu Phe Pro Asp Asn Phe Ala Lys Arg Glu Ile Leu Ser Leu Met Val
    420                      425                      430
Lys Cys Pro Asn Glu Gly Cys Leu His Lys Met Glu Leu Arg His Leu
    435                      440                      445
Glu Asp His Gln Ala His Cys Glu Phe Ala Leu Met Asp Cys Pro Gln
    450                      455                      460
Cys Gln Arg Pro Phe Gln Lys Phe His Ile Asn Ile His Ile Leu Lys
465                      470                      475                      480
Asp Cys Pro Arg Arg Gln Val Ser Cys Asp Asn Cys Ala Ala Ser Met
    485                      490                      495
Ala Phe Glu Asp Lys Glu Ile His Asp Gln Asn Cys Pro Leu Ala Asn
    500                      505                      510
Val Ile Cys Glu Tyr Cys Asn Thr Ile Leu Ile Arg Glu Gln Met Pro
    515                      520                      525
Asn His Tyr Asp Leu Asp Cys Pro Thr Ala Pro Ile Pro Cys Thr Phe
    530                      535                      540
Ser Thr Phe Gly Cys His Glu Lys Met Gln Arg Asn His Leu Ala Arg
545                      550                      555                      560
His Leu Gln Glu Asn Thr Gln Ser His Met Arg Met Leu Ala Leu Glu
    565                      570                      575
Gly Gly Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu
    580                      585                      590
Glu Asn Pro Gly Pro Met Ala Pro Gly Leu Leu Cys Trp Ala Leu Leu
    595                      600                      605
Cys Leu Leu Gly Ala Gly Leu Val Asp Ala Gly Val Thr Gln Ser Pro
    610                      615                      620
Thr His Leu Ile Lys Thr Arg Gly Gln Gln Val Thr Leu Arg Cys Ser
625                      630                      635                      640
Pro Lys Ser Gly His Asp Thr Val Ser Trp Tyr Gln Gln Ala Leu Gly
    645                      650                      655
Gln Gly Pro Gln Phe Ile Phe Gln Tyr Tyr Glu Glu Glu Glu Arg Gln
    660                      665                      670
Arg Gly Asn Phe Pro Asp Arg Phe Ser Gly His Gln Phe Pro Asn Tyr
    675                      680                      685
Ser Ser Glu Leu Asn Val Asn Ala Leu Leu Leu Gly Asp Ser Ala Leu
    690                      695                      700
Tyr Leu Cys Ala Ser Ser Leu Gly Trp Arg Gly Gly Arg Tyr Asn Glu
705                      710                      715                      720
Gln Phe Phe Gly Pro Gly Thr Arg Leu Thr Val Leu Glu Asp Leu Arg
    725                      730                      735

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200265_406WO_SEQUENCE_LISTING.TXT

```

Asn Val Thr Pro Pro Lys Val Ser Leu Phe Glu Pro Ser Lys Ala Glu
740 745 750
Ile Ala Asn Lys Gln Lys Ala Thr Leu Val Cys Leu Ala Arg Gly Phe
755 760 765
Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val
770 775 780
His Ser Gly Val Cys Thr Asp Pro Gln Ala Tyr Lys Glu Ser Asn Tyr
785 790 795 800
Ser Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp His
805 810 815
Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe His Gly Leu Ser
820 825 830
Glu Glu Asp Lys Trp Pro Glu Gly Ser Pro Lys Pro Val Thr Gln Asn
835 840 845
Ile Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Ile Thr Ser Ala
850 855 860
Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu
865 870 875 880
Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Thr Leu Val Val
885 890 895
Met Ala Met Val Lys Arg Lys Asn Ser Arg Ala Lys Arg Ser Gly Ser
900 905 910
Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu
915 920 925
Asn Pro Gly Pro Met Trp Gly Val Phe Leu Leu Tyr Val Ser Met Lys
930 935 940
Met Gly Gly Thr Thr Gly Gln Asn Ile Asp Gln Pro Thr Glu Met Thr
945 950 955 960
Ala Thr Glu Gly Ala Ile Val Gln Ile Asn Cys Thr Tyr Gln Thr Ser
965 970 975
Gly Phe Asn Gly Leu Phe Trp Tyr Gln Gln His Ala Gly Glu Ala Pro
980 985 990
Thr Phe Leu Ser Tyr Asn Val Leu Asp Gly Leu Glu Glu Lys Gly Arg
995 1000 1005
Phe Ser Ser Phe Leu Ser Arg Ser Lys Gly Tyr Ser Tyr Leu Leu Leu
1010 1015 1020
Lys Glu Leu Gln Met Lys Asp Ser Ala Ser Tyr Leu Cys Ala Ser Val
1025 1030 1035 1040
Asp Gly Asn Asn Arg Leu Ala Phe Gly Lys Gly Asn Gln Val Val Val
1045 1050 1055
Ile Pro Asn Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp
1060 1065 1070
Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser
1075 1080 1085
Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp
1090 1095 1100
Lys Cys Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala
1105 1110 1115 1120

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200265_406WO_SEQUENCE_LISTING.TXT

Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys
1125 1130 1135
Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp Ala Thr
1140 1145 1150
Leu Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn
1155 1160 1165
Leu Leu Val Ile Val Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe
1170 1175 1180
Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
1185 1190 1195

<210> 182

<211> 1195

<212> PRT

<213> Artificial Sequence

<220>

<223> CER_31_T2A_HP16 E7 TCR tandem expression cassette

<400> 182

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

200265_406WO_SEQUENCE_LISTING.TXT

```

Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
225                230                235                240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
                245                250                255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
                260                265                270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
                275                280                285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Met Glu Ser Ser
                290                295                300
Lys Lys Met Asp Ser Pro Gly Ala Leu Gln Thr Asn Pro Pro Leu Lys
305                310                315                320
Leu His Thr Asp Arg Ser Ala Gly Thr Pro Val Phe Val Pro Glu Gln
                325                330                335
Gly Gly Tyr Lys Glu Lys Phe Val Lys Thr Val Glu Asp Lys Tyr Lys
                340                345                350
Cys Glu Lys Cys His Leu Val Leu Cys Ser Pro Lys Gln Thr Glu Cys
                355                360                365
Gly His Arg Phe Cys Glu Ser Cys Met Ala Ala Leu Leu Ser Ser Ser
                370                375                380
Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Val Lys Asp Lys Val
385                390                395                400
Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala Leu Gln Ile Tyr
                405                410                415
Cys Arg Asn Glu Ser Arg Gly Cys Ala Glu Gln Leu Met Leu Gly His
                420                425                430
Leu Leu Val His Leu Lys Asn Asp Cys His Phe Glu Glu Leu Pro Cys
                435                440                445
Val Arg Pro Asp Cys Lys Glu Lys Val Leu Arg Lys Asp Leu Arg Asp
                450                455                460
His Val Glu Lys Ala Cys Lys Tyr Arg Glu Ala Thr Cys Ser His Cys
465                470                475                480
Lys Ser Gln Val Pro Met Ile Ala Leu Gln Lys His Glu Asp Thr Asp
                485                490                495
Cys Pro Cys Val Val Val Ser Cys Pro His Lys Cys Ser Val Gln Thr
                500                505                510
Leu Leu Arg Ser Glu Leu Ser Ala His Leu Ser Glu Cys Val Asn Ala
                515                520                525
Pro Ser Thr Cys Ser Phe Lys Arg Tyr Gly Cys Val Phe Gln Gly Thr
                530                535                540
Asn Gln Gln Ile Lys Ala His Glu Ala Ser Ser Ala Val Gln His Val
545                550                555                560
Asn Leu Leu Lys Glu Trp Ser Asn Ser Leu Glu Lys Lys Val Leu Glu
                565                570                575
Gly Gly Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu
                580                585                590
Glu Asn Pro Gly Pro Met Ala Pro Gly Leu Leu Cys Trp Ala Leu Leu
                595                600                605

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200265_406WO_SEQUENCE_LISTING.TXT

Cys	Leu	Leu	Gly	Ala	Gly	Leu	Val	Asp	Ala	Gly	Val	Thr	Gln	Ser	Pro	610	615	620
Thr	His	Leu	Ile	Lys	Thr	Arg	Gly	Gln	Gln	Val	Thr	Leu	Arg	Cys	Ser	625	630	635
Pro	Lys	Ser	Gly	His	Asp	Thr	Val	Ser	Trp	Tyr	Gln	Gln	Ala	Leu	Gly	645	650	655
Gln	Gly	Pro	Gln	Phe	Ile	Phe	Gln	Tyr	Glu	Glu	Glu	Glu	Arg	Gln		660	665	670
Arg	Gly	Asn	Phe	Pro	Asp	Arg	Phe	Ser	Gly	His	Gln	Phe	Pro	Asn	Tyr	675	680	685
Ser	Ser	Glu	Leu	Asn	Val	Asn	Ala	Leu	Leu	Leu	Gly	Asp	Ser	Ala	Leu	690	695	700
Tyr	Leu	Cys	Ala	Ser	Ser	Leu	Gly	Trp	Arg	Gly	Gly	Arg	Tyr	Asn	Glu	705	710	715
Gln	Phe	Phe	Gly	Pro	Gly	Thr	Arg	Leu	Thr	Val	Leu	Glu	Asp	Leu	Arg	725	730	735
Asn	Val	Thr	Pro	Pro	Lys	Val	Ser	Leu	Phe	Glu	Pro	Ser	Lys	Ala	Glu	740	745	750
Ile	Ala	Asn	Lys	Gln	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ala	Arg	Gly	Phe	755	760	765
Phe	Pro	Asp	His	Val	Glu	Leu	Ser	Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	770	775	780
His	Ser	Gly	Val	Cys	Thr	Asp	Pro	Gln	Ala	Tyr	Lys	Glu	Ser	Asn	Tyr	785	790	795
Ser	Tyr	Cys	Leu	Ser	Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	His	805	810	815
Asn	Pro	Arg	Asn	His	Phe	Arg	Cys	Gln	Val	Gln	Phe	His	Gly	Leu	Ser	820	825	830
Glu	Glu	Asp	Lys	Trp	Pro	Glu	Gly	Ser	Pro	Lys	Pro	Val	Thr	Gln	Asn	835	840	845
Ile	Ser	Ala	Glu	Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Ile	Thr	Ser	Ala	850	855	860
Ser	Tyr	Gln	Gln	Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	865	870	875
Leu	Gly	Lys	Ala	Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Thr	Leu	Val	Val	885	890	895
Met	Ala	Met	Val	Lys	Arg	Lys	Asn	Ser	Arg	Ala	Lys	Arg	Ser	Gly	Ser	900	905	910
Gly	Ala	Thr	Asn	Phe	Ser	Leu	Leu	Lys	Gln	Ala	Gly	Asp	Val	Glu	Glu	915	920	925
Asn	Pro	Gly	Pro	Met	Trp	Gly	Val	Phe	Leu	Leu	Tyr	Val	Ser	Met	Lys	930	935	940
Met	Gly	Gly	Thr	Thr	Gly	Gln	Asn	Ile	Asp	Gln	Pro	Thr	Glu	Met	Thr	945	950	955
Ala	Thr	Glu	Gly	Ala	Ile	Val	Gln	Ile	Asn	Cys	Thr	Tyr	Gln	Thr	Ser	965	970	975
Gly	Phe	Asn	Gly	Leu	Phe	Trp	Tyr	Gln	Gln	His	Ala	Gly	Glu	Ala	Pro	980	985	990

200265_406WO_SEQUENCE_LISTING.TXT

```

Thr Phe Leu Ser Tyr Asn Val Leu Asp Gly Leu Glu Glu Lys Gly Arg
  995                1000                1005
Phe Ser Ser Phe Leu Ser Arg Ser Lys Gly Tyr Ser Tyr Leu Leu Leu
 1010                1015                1020
Lys Glu Leu Gln Met Lys Asp Ser Ala Ser Tyr Leu Cys Ala Ser Val
1025                1030                1035                1040
Asp Gly Asn Asn Arg Leu Ala Phe Gly Lys Gly Asn Gln Val Val Val
      1045                1050                1055
Ile Pro Asn Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp
      1060                1065                1070
Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser
      1075                1080                1085
Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp
      1090                1095                1100
Lys Cys Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala
1105                1110                1115                1120
Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys
      1125                1130                1135
Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp Ala Thr
      1140                1145                1150
Leu Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn
      1155                1160                1165
Leu Leu Val Ile Val Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe
      1170                1175                1180
Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
1185                1190                1195

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<210> 183

<211> 530

<212> PRT

<213> Artificial Sequence

<220>

<223> CER119A, amino acids 1-22 are signal peptide

<400> 183

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

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200265_406WO_SEQUENCE_LISTING.TXT

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Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr Cys Cys
100                      105                      110
Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn Val Arg
115                      120                      125
Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr Thr Thr
130                      135                      140
Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
145                      150                      155                      160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
165                      170                      175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
180                      185                      190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
195                      200                      205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
210                      215                      220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
225                      230                      235                      240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
245                      250                      255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
260                      265                      270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
275                      280                      285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Ser Tyr Leu Asp
290                      295                      300
Leu Pro Trp Tyr Leu Arg Met Val Cys Gln Trp Thr Gln Thr Arg Arg
305                      310                      315                      320
Arg Ala Arg Asn Ile Pro Leu Glu Glu Leu Gln Arg Asn Leu Gln Phe
325                      330                      335
His Ala Phe Ile Ser Tyr Ser Gly His Asp Ser Phe Trp Val Lys Asn
340                      345                      350
Glu Leu Leu Pro Asn Leu Glu Lys Glu Gly Met Gln Ile Cys Leu His
355                      360                      365
Glu Arg Asn Phe Val Pro Gly Lys Ser Ile Val Glu Asn Ile Ile Thr
370                      375                      380
Cys Ile Glu Lys Ser Tyr Lys Ser Ile Phe Val Leu Ser Pro Asn Phe
385                      390                      395                      400
Val Gln Ser Glu Trp Cys His Tyr Glu Leu Tyr Phe Ala His His Asn
405                      410                      415
Leu Phe His Glu Gly Ser Asn Ser Leu Ile Leu Ile Leu Leu Glu Pro
420                      425                      430
Ile Pro Gln Tyr Ser Ile Pro Ser Ser Tyr His Lys Leu Lys Ser Leu
435                      440                      445
Met Ala Arg Arg Thr Tyr Leu Glu Trp Pro Lys Glu Lys Ser Lys Arg
450                      455                      460
Gly Leu Phe Trp Ala Asn Leu Arg Ala Ala Ile Asn Ile Lys Leu Thr
465                      470                      475                      480

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200265_406WO_SEQUENCE_LISTING.TXT

Glu Gln Ala Lys Lys Asp Ser Lys Ala Gly Met Glu Glu Asp His Thr
485 490 495
Tyr Glu Gly Leu Asp Ile Asp Gln Thr Ala Thr Tyr Glu Asp Ile Val
500 505 510
Thr Leu Arg Thr Gly Glu Val Lys Trp Ser Val Gly Glu His Pro Gly
515 520 525
Gln Glu
530

<210> 184

<211> 778

<212> PRT

<213> Artificial Sequence

<220>

<223> CER126, amino acids 1-22 are signal peptide

<400> 184

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

200265_406WO_SEQUENCE_LISTING.TXT

Ser	Asn	Pro	Gly	Ile	Leu	Pro	Ser	Thr	Ser	Gln	Leu	Thr	Thr	Gln	Lys
				245					250					255	
Thr	Thr	Leu	Thr	Thr	Ser	Glu	Ser	Leu	Gln	Lys	Thr	Thr	Lys	Ser	His
				260				265					270		
Gln	Ile	Asn	Ser	Arg	Gln	Thr	Ile	Leu	Ile	Ile	Ala	Cys	Cys	Val	Gly
		275					280				285				
Phe	Val	Leu	Met	Val	Leu	Leu	Phe	Leu	Ala	Phe	Leu	His	Arg	Phe	His
	290					295					300				
Gly	Leu	Trp	Tyr	Met	Lys	Met	Met	Trp	Ala	Trp	Leu	Gln	Ala	Lys	Arg
305					310				315						320
Lys	Pro	Arg	Lys	Ala	Pro	Ser	Arg	Asn	Ile	Cys	Tyr	Asp	Ala	Phe	Val
				325				330						335	
Ser	Tyr	Ser	Glu	Arg	Asp	Ala	Tyr	Trp	Val	Glu	Asn	Leu	Met	Val	Gln
			340					345					350		
Glu	Leu	Glu	Asn	Phe	Asn	Pro	Pro	Phe	Lys	Leu	Cys	Leu	His	Lys	Arg
		355					360					365			
Asp	Phe	Ile	Pro	Gly	Lys	Trp	Ile	Ile	Asp	Asn	Ile	Ile	Asp	Ser	Ile
	370					375					380				
Glu	Lys	Ser	His	Lys	Thr	Val	Phe	Val	Leu	Ser	Glu	Asn	Phe	Val	Lys
385					390					395					400
Ser	Glu	Trp	Cys	Lys	Tyr	Glu	Leu	Asp	Phe	Ser	His	Phe	Arg	Leu	Phe
			405					410						415	
Asp	Glu	Asn	Asn	Asp	Ala	Ala	Ile	Leu	Ile	Leu	Leu	Glu	Pro	Ile	Glu
			420					425					430		
Lys	Lys	Ala	Ile	Pro	Gln	Arg	Phe	Cys	Lys	Leu	Arg	Lys	Ile	Met	Asn
		435					440					445			
Thr	Lys	Thr	Tyr	Leu	Glu	Trp	Pro	Met	Asp	Glu	Ala	Gln	Arg	Glu	Gly
	450					455					460				
Phe	Trp	Val	Asn	Leu	Arg	Ala	Ala	Ile	Lys	Ser	Met	Ala	Ala	Ala	Ser
465					470					475					480
Val	Thr	Pro	Pro	Gly	Ser	Leu	Glu	Leu	Leu	Gln	Pro	Gly	Phe	Ser	Lys
				485					490					495	
Thr	Leu	Leu	Gly	Thr	Lys	Leu	Glu	Ala	Lys	Tyr	Leu	Cys	Ser	Ala	Cys
			500					505					510		
Arg	Asn	Val	Leu	Arg	Arg	Pro	Phe	Gln	Ala	Gln	Cys	Gly	His	Arg	Tyr
		515					520					525			
Cys	Ser	Phe	Cys	Leu	Ala	Ser	Ile	Leu	Ser	Ser	Gly	Pro	Gln	Asn	Cys
	530					535					540				
Ala	Ala	Cys	Val	His	Glu	Gly	Ile	Tyr	Glu	Glu	Gly	Ile	Ser	Ile	Leu
545					550					555					560
Glu	Ser	Ser	Ser	Ala	Phe	Pro	Asp	Asn	Ala	Ala	Arg	Arg	Glu	Val	Glu
				565					570					575	
Ser	Leu	Pro	Ala	Val	Cys	Pro	Ser	Asp	Gly	Cys	Thr	Trp	Lys	Gly	Thr
			580					585					590		
Leu	Lys	Glu	Tyr	Glu	Ser	Cys	His	Glu	Gly	Arg	Cys	Pro	Leu	Met	Leu
		595					600					605			
Thr	Glu	Cys	Pro	Ala	Cys	Lys	Gly	Leu	Val	Arg	Leu	Gly	Glu	Lys	Glu
	610					615					620				

200265_406WO_SEQUENCE_LISTING.TXT

```

Arg His Leu Glu His Glu Cys Pro Glu Arg Ser Leu Ser Cys Arg His
625                               630 635                               640
Cys Arg Ala Pro Cys Cys Gly Ala Asp Val Lys Ala His His Glu Val
                               645 650                               655
Cys Pro Lys Phe Pro Leu Thr Cys Asp Gly Cys Gly Lys Lys Lys Ile
660                               665 670
Pro Arg Glu Lys Phe Gln Asp His Val Lys Thr Cys Gly Lys Cys Arg
675                               680 685
Val Pro Cys Arg Phe His Ala Ile Gly Cys Leu Glu Thr Val Glu Gly
690                               695 700
Glu Lys Gln Gln Glu His Glu Val Gln Trp Leu Arg Glu His Leu Ala
705                               710 715                               720
Met Leu Leu Ser Ser Val Leu Glu Ala Lys Pro Leu Leu Gly Asp Gln
725                               730 735
Ser His Ala Gly Ser Glu Leu Leu Gln Arg Cys Glu Ser Leu Glu Lys
740                               745 750
Lys Thr Ala Thr Phe Glu Asn Ile Val Cys Val Leu Asn Arg Glu Val
755                               760 765
Glu Arg Val Ala Met Thr Ala Glu Ala Cys
770                               775

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<210> 185

<211> 778

<212> PRT

<213> Artificial Sequence

<220>

<223> CER127, amino acids 1-22 are signal peptide

<400> 185

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

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200265_406WO_SEQUENCE_LISTING.TXT

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Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu Leu Leu
145          150          155          160
Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr Pro Pro
          165          170          175
Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr Cys Pro
          180          185          190
Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly Ser Ala
          195          200          205
Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser Gln Arg
          210          215          220
Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro Thr Gly
225          230          235          240
Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr Gln Lys
          245          250          255
Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys Ser His
          260          265          270
Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys Val Gly
          275          280          285
Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Met Ala Ala Ala
          290          295          300
Ser Val Thr Pro Pro Gly Ser Leu Glu Leu Leu Gln Pro Gly Phe Ser
305          310          315          320
Lys Thr Leu Leu Gly Thr Lys Leu Glu Ala Lys Tyr Leu Cys Ser Ala
          325          330          335
Cys Arg Asn Val Leu Arg Arg Pro Phe Gln Ala Gln Cys Gly His Arg
          340          345          350
Tyr Cys Ser Phe Cys Leu Ala Ser Ile Leu Ser Ser Gly Pro Gln Asn
          355          360          365
Cys Ala Ala Cys Val His Glu Gly Ile Tyr Glu Glu Gly Ile Ser Ile
          370          375          380
Leu Glu Ser Ser Ser Ala Phe Pro Asp Asn Ala Ala Arg Arg Glu Val
385          390          395          400
Glu Ser Leu Pro Ala Val Cys Pro Ser Asp Gly Cys Thr Trp Lys Gly
          405          410          415
Thr Leu Lys Glu Tyr Glu Ser Cys His Glu Gly Arg Cys Pro Leu Met
          420          425          430
Leu Thr Glu Cys Pro Ala Cys Lys Gly Leu Val Arg Leu Gly Glu Lys
          435          440          445
Glu Arg His Leu Glu His Glu Cys Pro Glu Arg Ser Leu Ser Cys Arg
          450          455          460
His Cys Arg Ala Pro Cys Cys Gly Ala Asp Val Lys Ala His His Glu
465          470          475          480
Val Cys Pro Lys Phe Pro Leu Thr Cys Asp Gly Cys Gly Lys Lys Lys
          485          490          495
Ile Pro Arg Glu Lys Phe Gln Asp His Val Lys Thr Cys Gly Lys Cys
          500          505          510
Arg Val Pro Cys Arg Phe His Ala Ile Gly Cys Leu Glu Thr Val Glu
          515          520          525

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200265_406WO_SEQUENCE_LISTING.TXT

Gly	Glu	Lys	Gln	Gln	Glu	His	Glu	Val	Gln	Trp	Leu	Arg	Glu	His	Leu
530						535					540				
Ala	Met	Leu	Leu	Ser	Ser	Val	Leu	Glu	Ala	Lys	Pro	Leu	Leu	Gly	Asp
545					550					555					560
Gln	Ser	His	Ala	Gly	Ser	Glu	Leu	Leu	Gln	Arg	Cys	Glu	Ser	Leu	Glu
			565						570					575	
Lys	Lys	Thr	Ala	Thr	Phe	Glu	Asn	Ile	Val	Cys	Val	Leu	Asn	Arg	Glu
		580				585						590			
Val	Glu	Arg	Val	Ala	Met	Thr	Ala	Glu	Ala	Cys	His	Arg	Phe	His	Gly
	595					600					605				
Leu	Trp	Tyr	Met	Lys	Met	Met	Trp	Ala	Trp	Leu	Gln	Ala	Lys	Arg	Lys
610					615					620					
Pro	Arg	Lys	Ala	Pro	Ser	Arg	Asn	Ile	Cys	Tyr	Asp	Ala	Phe	Val	Ser
625					630					635					640
Tyr	Ser	Glu	Arg	Asp	Ala	Tyr	Trp	Val	Glu	Asn	Leu	Met	Val	Gln	Glu
			645						650					655	
Leu	Glu	Asn	Phe	Asn	Pro	Pro	Phe	Lys	Leu	Cys	Leu	His	Lys	Arg	Asp
		660					665						670		
Phe	Ile	Pro	Gly	Lys	Trp	Ile	Ile	Asp	Asn	Ile	Ile	Asp	Ser	Ile	Glu
	675					680						685			
Lys	Ser	His	Lys	Thr	Val	Phe	Val	Leu	Ser	Glu	Asn	Phe	Val	Lys	Ser
690					695					700					
Glu	Trp	Cys	Lys	Tyr	Glu	Leu	Asp	Phe	Ser	His	Phe	Arg	Leu	Phe	Asp
705					710					715					720
Glu	Asn	Asn	Asp	Ala	Ala	Ile	Leu	Ile	Leu	Leu	Glu	Pro	Ile	Glu	Lys
			725						730					735	
Lys	Ala	Ile	Pro	Gln	Arg	Phe	Cys	Lys	Leu	Arg	Lys	Ile	Met	Asn	Thr
		740					745						750		
Lys	Thr	Tyr	Leu	Glu	Trp	Pro	Met	Asp	Glu	Ala	Gln	Arg	Glu	Gly	Phe
	755					760						765			
Trp	Val	Asn	Leu	Arg	Ala	Ala	Ile	Lys	Ser						
770						775									

<210> 186

<211> 796

<212> PRT

<213> Artificial Sequence

<220>

<223> CER128, amino acids 1-22 are signal peptide

<400> 186

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

200265_406WO_SEQUENCE_LISTING.TXT

Arg	Asn	Ser	Met	Cys	Trp	Gly	Lys	Gly	Ser	Cys	Pro	Asn	Ser	Lys	Cys
50						55				60					
Asn	Ala	Glu	Leu	Leu	Arg	Thr	Asp	Gly	Thr	Arg	Ile	Ile	Ser	Arg	Lys
65					70					75					80
Ser	Thr	Lys	Tyr	Thr	Leu	Leu	Gly	Lys	Val	Gln	Phe	Gly	Glu	Val	Ser
				85					90					95	
Leu	Thr	Ile	Ser	Asn	Thr	Asn	Arg	Gly	Asp	Ser	Gly	Val	Tyr	Cys	Cys
			100					105					110		
Arg	Ile	Glu	Val	Pro	Gly	Trp	Phe	Asn	Asp	Val	Lys	Lys	Asn	Val	Arg
	115						120					125			
Leu	Glu	Leu	Arg	Arg	Ala	Thr	Thr	Thr	Lys	Lys	Pro	Thr	Thr	Thr	Thr
	130					135					140				
Arg	Pro	Thr	Thr	Thr	Pro	Tyr	Val	Thr	Thr	Thr	Thr	Pro	Glu	Leu	Leu
145					150					155					160
Pro	Thr	Thr	Val	Met	Thr	Thr	Ser	Val	Leu	Pro	Thr	Thr	Thr	Pro	Pro
				165					170					175	
Gln	Thr	Leu	Ala	Thr	Thr	Ala	Phe	Ser	Thr	Ala	Val	Thr	Thr	Cys	Pro
			180					185					190		
Ser	Thr	Thr	Pro	Gly	Ser	Phe	Ser	Gln	Glu	Thr	Thr	Lys	Gly	Ser	Ala
		195				200						205			
Phe	Thr	Thr	Glu	Ser	Glu	Thr	Leu	Pro	Ala	Ser	Asn	His	Ser	Gln	Arg
	210					215					220				
Ser	Met	Met	Thr	Ile	Ser	Thr	Asp	Ile	Ala	Val	Leu	Arg	Pro	Thr	Gly
225					230					235					240
Ser	Asn	Pro	Gly	Ile	Leu	Pro	Ser	Thr	Ser	Gln	Leu	Thr	Thr	Gln	Lys
				245					250					255	
Thr	Thr	Leu	Thr	Thr	Ser	Glu	Ser	Leu	Gln	Lys	Thr	Thr	Lys	Ser	His
			260					265					270		
Gln	Ile	Asn	Ser	Arg	Gln	Thr	Ile	Leu	Ile	Ile	Ala	Cys	Cys	Val	Gly
	275						280					285			
Phe	Val	Leu	Met	Val	Leu	Leu	Phe	Leu	Ala	Phe	Leu	Met	Ala	Ala	Ala
	290					295					300				
Ser	Val	Thr	Pro	Pro	Gly	Ser	Leu	Glu	Leu	Leu	Gln	Pro	Gly	Phe	Ser
305					310					315					320
Lys	Thr	Leu	Leu	Gly	Thr	Lys	Leu	Glu	Ala	Lys	Tyr	Leu	Cys	Ser	Ala
				325					330					335	
Cys	Arg	Asn	Val	Leu	Arg	Arg	Pro	Phe	Gln	Ala	Gln	Cys	Gly	His	Arg
			340					345					350		
Tyr	Cys	Ser	Phe	Cys	Leu	Ala	Ser	Ile	Leu	Ser	Ser	Gly	Pro	Gln	Asn
		355					360					365			
Cys	Ala	Ala	Cys	Val	His	Glu	Gly	Ile	Tyr	Glu	Glu	Gly	Ile	Ser	Ile
	370					375					380				
Leu	Glu	Ser	Ser	Ser	Ala	Phe	Pro	Asp	Asn	Ala	Ala	Arg	Arg	Glu	Val
385					390					395					400
Glu	Ser	Leu	Pro	Ala	Val	Cys	Pro	Ser	Asp	Gly	Cys	Thr	Trp	Lys	Gly
				405					410					415	
Thr	Leu	Lys	Glu	Tyr	Glu	Ser	Cys	His	Glu	Gly	Arg	Cys	Pro	Leu	Met
			420					425					430		

200265_406WO_SEQUENCE_LISTING.TXT

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Leu Thr Glu Cys Pro Ala Cys Lys Gly Leu Val Arg Leu Gly Glu Lys
    435                      440                      445
Glu Arg His Leu Glu His Glu Cys Pro Glu Arg Ser Leu Ser Cys Arg
    450                      455                      460
His Cys Arg Ala Pro Cys Cys Gly Ala Asp Val Lys Ala His His Glu
465                      470                      475                      480
Val Cys Pro Lys Phe Pro Leu Thr Cys Asp Gly Cys Gly Lys Lys Lys
    485                      490                      495
Ile Pro Arg Glu Lys Phe Gln Asp His Val Lys Thr Cys Gly Lys Cys
    500                      505                      510
Arg Val Pro Cys Arg Phe His Ala Ile Gly Cys Leu Glu Thr Val Glu
    515                      520                      525
Gly Glu Lys Gln Gln Glu His Glu Val Gln Trp Leu Arg Glu His Leu
    530                      535                      540
Ala Met Leu Leu Ser Ser Val Leu Glu Ala Lys Pro Leu Leu Gly Asp
545                      550                      555                      560
Gln Ser His Ala Gly Ser Glu Leu Leu Gln Arg Cys Glu Ser Leu Glu
    565                      570                      575
Lys Lys Thr Ala Thr Phe Glu Asn Ile Val Cys Val Leu Asn Arg Glu
    580                      585                      590
Val Glu Arg Val Ala Met Thr Ala Glu Ala Cys His His Leu Phe Tyr
    595                      600                      605
Trp Asp Val Trp Phe Ile Tyr Asn Val Cys Leu Ala Lys Val Lys Gly
    610                      615                      620
Tyr Arg Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser
625                      630                      635                      640
Tyr Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu Leu
    645                      650                      655
Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu Cys Leu
    660                      665                      670
Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp Asn Leu Met
    675                      680                      685
Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val Leu Thr Lys Lys
    690                      695                      700
Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe Tyr Leu Ala Leu Gln
705                      710                      715                      720
Arg Leu Met Asp Glu Asn Met Asp Val Ile Ile Phe Ile Leu Leu Glu
    725                      730                      735
Pro Val Leu Gln His Ser Gln Tyr Leu Arg Leu Arg Gln Arg Ile Cys
    740                      745                      750
Lys Ser Ser Ile Leu Gln Trp Pro Asp Asn Pro Lys Ala Glu Gly Leu
    755                      760                      765
Phe Trp Gln Thr Leu Arg Asn Val Val Leu Thr Glu Asn Asp Ser Arg
    770                      775                      780
Tyr Asn Asn Met Tyr Val Asp Ser Ile Lys Gln Tyr
785                      790                      795

```

<210> 187

200265_406WO_SEQUENCE_LISTING.TXT

<211> 796

<212> PRT

<213> Artificial Sequence

<220>

<223> CER129, amino acids 1-22 are signal peptide

<400> 187

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

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200265_406WO_SEQUENCE_LISTING.TXT

Gly Tyr Arg Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile
 325 330 335
 Ser Tyr Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu
 340 345 350
 Leu Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu Cys
 355 360 365
 Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp Asn Leu
 370 375 380
 Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val Leu Thr Lys
 385 390 395 400
 Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe Tyr Leu Ala Leu
 405 410 415
 Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile Ile Phe Ile Leu Leu
 420 425 430
 Glu Pro Val Leu Gln His Ser Gln Tyr Leu Arg Leu Arg Gln Arg Ile
 435 440 445
 Cys Lys Ser Ser Ile Leu Gln Trp Pro Asp Asn Pro Lys Ala Glu Gly
 450 455 460
 Leu Phe Trp Gln Thr Leu Arg Asn Val Val Leu Thr Glu Asn Asp Ser
 465 470 475 480
 Arg Tyr Asn Asn Met Tyr Val Asp Ser Ile Lys Gln Tyr Met Ala Ala
 485 490 495
 Ala Ser Val Thr Pro Pro Gly Ser Leu Glu Leu Leu Gln Pro Gly Phe
 500 505 510
 Ser Lys Thr Leu Leu Gly Thr Lys Leu Glu Ala Lys Tyr Leu Cys Ser
 515 520 525
 Ala Cys Arg Asn Val Leu Arg Arg Pro Phe Gln Ala Gln Cys Gly His
 530 535 540
 Arg Tyr Cys Ser Phe Cys Leu Ala Ser Ile Leu Ser Ser Gly Pro Gln
 545 550 555 560
 Asn Cys Ala Ala Cys Val His Glu Gly Ile Tyr Glu Glu Gly Ile Ser
 565 570 575
 Ile Leu Glu Ser Ser Ser Ala Phe Pro Asp Asn Ala Ala Arg Arg Glu
 580 585 590
 Val Glu Ser Leu Pro Ala Val Cys Pro Ser Asp Gly Cys Thr Trp Lys
 595 600 605
 Gly Thr Leu Lys Glu Tyr Glu Ser Cys His Glu Gly Arg Cys Pro Leu
 610 615 620
 Met Leu Thr Glu Cys Pro Ala Cys Lys Gly Leu Val Arg Leu Gly Glu
 625 630 635 640
 Lys Glu Arg His Leu Glu His Glu Cys Pro Glu Arg Ser Leu Ser Cys
 645 650 655
 Arg His Cys Arg Ala Pro Cys Cys Gly Ala Asp Val Lys Ala His His
 660 665 670
 Glu Val Cys Pro Lys Phe Pro Leu Thr Cys Asp Gly Cys Gly Lys Lys
 675 680 685
 Lys Ile Pro Arg Glu Lys Phe Gln Asp His Val Lys Thr Cys Gly Lys
 690 695 700

200265_406WO_SEQUENCE_LISTING.TXT

Cys	Arg	Val	Pro	Cys	Arg	Phe	His	Ala	Ile	Gly	Cys	Leu	Glu	Thr	Val
705					710					715					720
Glu	Gly	Glu	Lys	Gln	Gln	Glu	His	Glu	Val	Gln	Trp	Leu	Arg	Glu	His
				725					730						735
Leu	Ala	Met	Leu	Leu	Ser	Ser	Val	Leu	Glu	Ala	Lys	Pro	Leu	Leu	Gly
				740					745						750
Asp	Gln	Ser	His	Ala	Gly	Ser	Glu	Leu	Leu	Gln	Arg	Cys	Glu	Ser	Leu
		755					760					765			
Glu	Lys	Lys	Thr	Ala	Thr	Phe	Glu	Asn	Ile	Val	Cys	Val	Leu	Asn	Arg
	770					775					780				
Glu	Val	Glu	Arg	Val	Ala	Met	Thr	Ala	Glu	Ala	Cys				
785						790					795				

<210> 188

<211> 504

<212> PRT

<213> Artificial Sequence

<220>

<223> hCER21

<400> 188

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

200265_406WO_SEQUENCE_LISTING.TXT

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

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<210> 189

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> hCER29

<400> 189

200265_406WO_SEQUENCE_LISTING.TXT

Glu	Thr	Val	Val	Thr	Glu	Val	Leu	Gly	His	Arg	Val	Thr	Leu	Pro	Cys
1				5				10					15		
Leu	Tyr	Ser	Ser	Trp	Ser	His	Asn	Ser	Asn	Ser	Met	Cys	Trp	Gly	Lys
			20				25					30			
Asp	Gln	Cys	Pro	Tyr	Ser	Gly	Cys	Lys	Glu	Ala	Leu	Ile	Arg	Thr	Asp
		35				40					45				
Gly	Met	Arg	Val	Thr	Ser	Arg	Lys	Ser	Ala	Lys	Tyr	Arg	Leu	Gln	Gly
50					55				60						
Thr	Ile	Pro	Arg	Gly	Asp	Val	Ser	Leu	Thr	Ile	Leu	Asn	Pro	Ser	Glu
65				70					75					80	
Ser	Asp	Ser	Gly	Val	Tyr	Cys	Cys	Arg	Ile	Glu	Val	Pro	Gly	Trp	Phe
			85					90					95		
Asn	Asp	Val	Lys	Ile	Asn	Val	Arg	Leu	Asn	Leu	Gln	Arg	Ala	Ser	Thr
		100					105					110			
Thr	Thr	His	Arg	Thr	Ala	Thr	Thr	Thr	Thr	Arg	Arg	Thr	Thr	Thr	Thr
		115					120					125			
Ser	Pro	Thr	Thr	Thr	Arg	Gln	Met	Thr	Thr	Thr	Pro	Ala	Ala	Leu	Pro
		130				135					140				
Thr	Thr	Val	Val	Thr	Thr	Pro	Asp	Leu	Thr	Thr	Gly	Thr	Pro	Leu	Gln
145					150				155					160	
Met	Thr	Thr	Ile	Ala	Val	Phe	Thr	Thr	Ala	Asn	Thr	Cys	Leu	Ser	Leu
			165				170						175		
Thr	Pro	Ser	Thr	Leu	Pro	Glu	Glu	Ala	Thr	Gly	Leu	Leu	Thr	Pro	Glu
			180				185					190			
Pro	Ser	Lys	Glu	Gly	Pro	Ile	Leu	Thr	Ala	Glu	Ser	Glu	Thr	Val	Leu
		195				200					205				
Pro	Ser	Asp	Ser	Trp	Ser	Ser	Val	Glu	Ser	Thr	Ser	Ala	Asp	Thr	Val
		210				215				220					
Leu	Leu	Thr	Ser	Lys	Glu	Ser	Lys	Val	Trp	Asp	Leu	Pro	Ser	Thr	Ser
225				230						235				240	
His	Val	Ser	Met	Trp	Lys	Thr	Ser	Asp	Ser	Val	Ser	Ser	Pro	Gln	Pro
			245					250					255		
Gly	Ala	Ser	Asp	Thr	Ala	Val	Pro	Glu	Gln	Asn	Lys	Thr	Thr	Lys	Thr
			260				265					270			
Gly	Gln	Met	Asp	Gly	Ile	Pro	Met	Ser	Met	Lys	Asn	Glu	Met	Pro	Ile
		275				280					285				
Ser	Gln	Leu	Leu	Met	Ile	Ile	Ala	Pro	Ser	Leu	Gly	Phe	Val	Leu	Phe
		290			295					300					
Ala	Leu	Phe	Val	Ala	Phe	Leu	Met	Ser	Leu	Leu	Asn	Cys	Glu	Asn	Ser
305				310					315					320	
Cys	Gly	Ser	Ser	Gln	Ser	Glu	Ser	Asp	Cys	Cys	Val	Ala	Met	Ala	Ser
			325					330					335		
Ser	Cys	Ser	Ala	Val	Thr	Lys	Asp	Asp	Ser	Val	Gly	Gly	Thr	Ala	Ser
			340				345					350			
Thr	Gly	Asn	Leu	Ser	Ser	Ser	Phe	Met	Glu	Glu	Ile	Gln	Gly	Tyr	Asp
		355				360					365				
Val	Glu	Phe	Asp	Pro	Pro	Leu	Glu	Ser	Lys	Tyr	Glu	Cys	Pro	Ile	Cys
		370				375					380				

200265_406WO_SEQUENCE_LISTING.TXT

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

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<210> 190

<211> 556

<212> PRT

<213> Artificial Sequence

<220>

<223> hCER104

<400> 190

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

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200265_406WO_SEQUENCE_LISTING.TXT

Asn	Asp	Val	Lys	Ile	Asn	Val	Arg	Leu	Asn	Leu	Gln	Arg	Ala	Ser	Thr
			100					105					110		
Thr	Thr	His	Arg	Thr	Ala	Thr	Thr	Thr	Thr	Arg	Arg	Thr	Thr	Thr	Thr
		115					120					125			
Ser	Pro	Thr	Thr	Thr	Arg	Gln	Met	Thr	Thr	Thr	Pro	Ala	Ala	Leu	Pro
	130					135					140				
Thr	Thr	Val	Val	Thr	Thr	Pro	Asp	Leu	Thr	Thr	Gly	Thr	Pro	Leu	Gln
145					150					155					160
Met	Thr	Thr	Ile	Ala	Val	Phe	Thr	Thr	Ala	Asn	Thr	Cys	Leu	Ser	Leu
			165						170					175	
Thr	Pro	Ser	Thr	Leu	Pro	Glu	Glu	Ala	Thr	Gly	Leu	Leu	Thr	Pro	Glu
			180					185						190	
Pro	Ser	Lys	Glu	Gly	Pro	Ile	Leu	Thr	Ala	Glu	Ser	Glu	Thr	Val	Leu
		195					200					205			
Pro	Ser	Asp	Ser	Trp	Ser	Ser	Val	Glu	Ser	Thr	Ser	Ala	Asp	Thr	Val
	210					215					220				
Leu	Leu	Thr	Ser	Lys	Glu	Ser	Lys	Val	Trp	Asp	Leu	Pro	Ser	Thr	Ser
225					230					235					240
His	Val	Ser	Met	Trp	Lys	Thr	Ser	Asp	Ser	Val	Ser	Ser	Pro	Gln	Pro
			245						250					255	
Gly	Ala	Ser	Asp	Thr	Ala	Val	Pro	Glu	Gln	Asn	Lys	Thr	Thr	Lys	Thr
			260					265					270		
Gly	Gln	Met	Asp	Gly	Ile	Pro	Met	Ser	Met	Lys	Asn	Glu	Met	Pro	Ile
		275					280					285			
Ser	Gln	Leu	Leu	Met	Ile	Ile	Ala	Pro	Ser	Leu	Gly	Phe	Val	Leu	Phe
	290					295					300				
Ala	Leu	Phe	Val	Ala	Phe	Leu	His	His	Leu	Phe	Tyr	Trp	Asp	Val	Trp
305					310					315					320
Phe	Ile	Tyr	Asn	Val	Cys	Leu	Ala	Lys	Val	Lys	Gly	Tyr	Arg	Ser	Leu
			325						330					335	
Ser	Thr	Ser	Gln	Thr	Phe	Tyr	Asp	Ala	Tyr	Ile	Ser	Tyr	Asp	Thr	Lys
			340					345					350		
Asp	Ala	Ser	Val	Thr	Asp	Trp	Val	Ile	Asn	Glu	Leu	Arg	Tyr	His	Leu
		355					360					365			
Glu	Glu	Ser	Arg	Asp	Lys	Asn	Val	Leu	Leu	Cys	Leu	Glu	Glu	Arg	Asp
	370					375					380				
Trp	Asp	Pro	Gly	Leu	Ala	Ile	Ile	Asp	Asn	Leu	Met	Gln	Ser	Ile	Asn
385					390					395					400
Gln	Ser	Lys	Lys	Thr	Val	Phe	Val	Leu	Thr	Lys	Lys	Tyr	Ala	Lys	Ser
			405						410					415	
Trp	Asn	Phe	Lys	Thr	Ala	Phe	Tyr	Leu	Ala	Leu	Gln	Arg	Leu	Met	Asp
			420					425					430		
Glu	Asn	Met	Asp	Val	Ile	Ile	Phe	Ile	Leu	Leu	Glu	Pro	Val	Leu	Gln
		435					440					445			
His	Ser	Gln	Tyr	Leu	Arg	Leu	Arg	Gln	Arg	Ile	Cys	Lys	Ser	Ser	Ile
	450					455					460				
Leu	Gln	Trp	Pro	Asp	Asn	Pro	Lys	Ala	Glu	Gly	Leu	Phe	Trp	Gln	Thr
465					470					475					480

200265_406WO_SEQUENCE_LISTING.TXT

Leu Arg Asn Val Val Leu Thr Glu Asn Asp Ser Arg Tyr Asn Asn Met
485 490 495
Tyr Val Asp Ser Ile Lys Gln Tyr Tyr Phe Leu Gly Arg Leu Val Pro
500 505 510
Arg Gly Arg Gly Ala Ala Glu Ala Ala Thr Arg Lys Gln Arg Ile Thr
515 520 525
Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg Ser Asp Val
530 535 540
Tyr Ser Asp Leu Asn Thr Gln Arg Pro Tyr Tyr Lys
545 550 555

<210> 191

<211> 778

<212> PRT

<213> Artificial Sequence

<220>

<223> hCER116

<400> 191

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

200265_406WO_SEQUENCE_LISTING.TXT

Leu	Leu	Thr	Ser	Lys	Glu	Ser	Lys	Val	Trp	Asp	Leu	Pro	Ser	Thr	Ser	225	230	235	240
His	Val	Ser	Met	Trp	Lys	Thr	Ser	Asp	Ser	Val	Ser	Ser	Pro	Gln	Pro	245	250	255	
Gly	Ala	Ser	Asp	Thr	Ala	Val	Pro	Glu	Gln	Asn	Lys	Thr	Thr	Lys	Thr	260	265	270	
Gly	Gln	Met	Asp	Gly	Ile	Pro	Met	Ser	Met	Lys	Asn	Glu	Met	Pro	Ile	275	280	285	
Ser	Gln	Leu	Leu	Met	Ile	Ile	Ala	Pro	Ser	Leu	Gly	Phe	Val	Leu	Phe	290	295	300	
Ala	Leu	Phe	Val	Ala	Phe	Leu	Met	Ser	Leu	Leu	Asn	Cys	Glu	Asn	Ser	305	310	315	320
Cys	Gly	Ser	Ser	Gln	Ser	Glu	Ser	Asp	Cys	Cys	Val	Ala	Met	Ala	Ser	325	330	335	
Ser	Cys	Ser	Ala	Val	Thr	Lys	Asp	Asp	Ser	Val	Gly	Gly	Thr	Ala	Ser	340	345	350	
Thr	Gly	Asn	Leu	Ser	Ser	Ser	Phe	Met	Glu	Glu	Ile	Gln	Gly	Tyr	Asp	355	360	365	
Val	Glu	Phe	Asp	Pro	Pro	Leu	Glu	Ser	Lys	Tyr	Glu	Cys	Pro	Ile	Cys	370	375	380	
Leu	Met	Ala	Leu	Arg	Glu	Ala	Val	Gln	Thr	Pro	Cys	Gly	His	Arg	Phe	385	390	395	400
Cys	Lys	Ala	Cys	Ile	Ile	Lys	Ser	Ile	Arg	Asp	Ala	Gly	His	Lys	Cys	405	410	415	
Pro	Val	Asp	Asn	Glu	Ile	Leu	Leu	Glu	Asn	Gln	Leu	Phe	Pro	Asp	Asn	420	425	430	
Phe	Ala	Lys	Arg	Glu	Ile	Leu	Ser	Leu	Met	Val	Lys	Cys	Pro	Asn	Glu	435	440	445	
Gly	Cys	Leu	His	Lys	Met	Glu	Leu	Arg	His	Leu	Glu	Asp	His	Gln	Ala	450	455	460	
His	Cys	Glu	Phe	Ala	Leu	Met	Asp	Cys	Pro	Gln	Cys	Gln	Arg	Pro	Phe	465	470	475	480
Gln	Lys	Phe	His	Ile	Asn	Ile	His	Ile	Leu	Lys	Asp	Cys	Pro	Arg	Arg	485	490	495	
Gln	Val	Ser	Cys	Asp	Asn	Cys	Ala	Ala	Ser	Met	Ala	Phe	Glu	Asp	Lys	500	505	510	
Glu	Ile	His	Asp	Gln	Asn	Cys	Pro	Leu	Ala	Asn	Val	Ile	Cys	Glu	Tyr	515	520	525	
Cys	Asn	Thr	Ile	Leu	Ile	Arg	Glu	Gln	Met	Pro	Asn	His	Tyr	Asp	Leu	530	535	540	
Asp	Cys	Pro	Thr	Ala	Pro	Ile	Pro	Cys	Thr	Phe	Ser	Thr	Phe	Gly	Cys	545	550	555	560
His	Glu	Lys	Met	Gln	Arg	Asn	His	Leu	Ala	Arg	His	Leu	Gln	Glu	Asn	565	570	575	
Thr	Gln	Ser	His	Met	Arg	Met	Leu	Ala	His	His	Leu	Phe	Tyr	Trp	Asp	580	585	590	
Val	Trp	Phe	Ile	Tyr	Asn	Val	Cys	Leu	Ala	Lys	Val	Lys	Gly	Tyr	Arg	595	600	605	

200265_406WO_SEQUENCE_LISTING.TXT

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Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser Tyr Asp
610 615 620
Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu Leu Arg Tyr
625 630 635 640
His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu Cys Leu Glu Glu
645 650 655
Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp Asn Leu Met Gln Ser
660 665 670
Ile Asn Gln Ser Lys Lys Thr Val Phe Val Leu Thr Lys Lys Tyr Ala
675 680 685
Lys Ser Trp Asn Phe Lys Thr Ala Phe Tyr Leu Ala Leu Gln Arg Leu
690 695 700
Met Asp Glu Asn Met Asp Val Ile Ile Phe Ile Leu Leu Glu Pro Val
705 710 715 720
Leu Gln His Ser Gln Tyr Leu Arg Leu Arg Gln Arg Ile Cys Lys Ser
725 730 735
Ser Ile Leu Gln Trp Pro Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp
740 745 750
Gln Thr Leu Arg Asn Val Val Leu Thr Glu Asn Asp Ser Arg Tyr Asn
755 760 765
Asn Met Tyr Val Asp Ser Ile Lys Gln Tyr
770 775

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<210> 192

<211> 778

<212> PRT

<213> Artificial Sequence

<220>

<223> hCER117

<400> 192

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

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200265_406WO_SEQUENCE_LISTING.TXT

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Ser Pro Thr Thr Thr Arg Gln Met Thr Thr Thr Pro Ala Ala Leu Pro
130      135      140
Thr Thr Val Val Thr Thr Pro Asp Leu Thr Thr Gly Thr Pro Leu Gln
145      150      155      160
Met Thr Thr Ile Ala Val Phe Thr Thr Ala Asn Thr Cys Leu Ser Leu
165      170      175
Thr Pro Ser Thr Leu Pro Glu Glu Ala Thr Gly Leu Leu Thr Pro Glu
180      185      190
Pro Ser Lys Glu Gly Pro Ile Leu Thr Ala Glu Ser Glu Thr Val Leu
195      200      205
Pro Ser Asp Ser Trp Ser Ser Val Glu Ser Thr Ser Ala Asp Thr Val
210      215      220
Leu Leu Thr Ser Lys Glu Ser Lys Val Trp Asp Leu Pro Ser Thr Ser
225      230      235      240
His Val Ser Met Trp Lys Thr Ser Asp Ser Val Ser Ser Pro Gln Pro
245      250      255
Gly Ala Ser Asp Thr Ala Val Pro Glu Gln Asn Lys Thr Thr Lys Thr
260      265      270
Gly Gln Met Asp Gly Ile Pro Met Ser Met Lys Asn Glu Met Pro Ile
275      280      285
Ser Gln Leu Leu Met Ile Ile Ala Pro Ser Leu Gly Phe Val Leu Phe
290      295      300
Ala Leu Phe Val Ala Phe Leu His His Leu Phe Tyr Trp Asp Val Trp
305      310      315      320
Phe Ile Tyr Asn Val Cys Leu Ala Lys Val Lys Gly Tyr Arg Ser Leu
325      330      335
Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser Tyr Asp Thr Lys
340      345      350
Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu Leu Arg Tyr His Leu
355      360      365
Glu Glu Ser Arg Asp Lys Asn Val Leu Leu Cys Leu Glu Glu Arg Asp
370      375      380
Trp Asp Pro Gly Leu Ala Ile Ile Asp Asn Leu Met Gln Ser Ile Asn
385      390      395      400
Gln Ser Lys Lys Thr Val Phe Val Leu Thr Lys Lys Tyr Ala Lys Ser
405      410      415
Trp Asn Phe Lys Thr Ala Phe Tyr Leu Ala Leu Gln Arg Leu Met Asp
420      425      430
Glu Asn Met Asp Val Ile Ile Phe Ile Leu Leu Glu Pro Val Leu Gln
435      440      445
His Ser Gln Tyr Leu Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile
450      455      460
Leu Gln Trp Pro Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp Gln Thr
465      470      475      480
Leu Arg Asn Val Val Leu Thr Glu Asn Asp Ser Arg Tyr Asn Asn Met
485      490      495
Tyr Val Asp Ser Ile Lys Gln Tyr Met Ser Leu Leu Asn Cys Glu Asn
500      505      510

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200265_406WO_SEQUENCE_LISTING.TXT

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Ser Cys Gly Ser Ser Gln Ser Glu Ser Asp Cys Cys Val Ala Met Ala
  515                      520                      525
Ser Ser Cys Ser Ala Val Thr Lys Asp Asp Ser Val Gly Gly Thr Ala
  530                      535                      540
Ser Thr Gly Asn Leu Ser Ser Ser Phe Met Glu Glu Ile Gln Gly Tyr
545                      550                      555                      560
Asp Val Glu Phe Asp Pro Pro Leu Glu Ser Lys Tyr Glu Cys Pro Ile
  565                      570                      575
Cys Leu Met Ala Leu Arg Glu Ala Val Gln Thr Pro Cys Gly His Arg
  580                      585                      590
Phe Cys Lys Ala Cys Ile Ile Lys Ser Ile Arg Asp Ala Gly His Lys
  595                      600                      605
Cys Pro Val Asp Asn Glu Ile Leu Leu Glu Asn Gln Leu Phe Pro Asp
  610                      615                      620
Asn Phe Ala Lys Arg Glu Ile Leu Ser Leu Met Val Lys Cys Pro Asn
625                      630                      635                      640
Glu Gly Cys Leu His Lys Met Glu Leu Arg His Leu Glu Asp His Gln
  645                      650                      655
Ala His Cys Glu Phe Ala Leu Met Asp Cys Pro Gln Cys Gln Arg Pro
  660                      665                      670
Phe Gln Lys Phe His Ile Asn Ile His Ile Leu Lys Asp Cys Pro Arg
  675                      680                      685
Arg Gln Val Ser Cys Asp Asn Cys Ala Ala Ser Met Ala Phe Glu Asp
  690                      695                      700
Lys Glu Ile His Asp Gln Asn Cys Pro Leu Ala Asn Val Ile Cys Glu
705                      710                      715                      720
Tyr Cys Asn Thr Ile Leu Ile Arg Glu Gln Met Pro Asn His Tyr Asp
  725                      730                      735
Leu Asp Cys Pro Thr Ala Pro Ile Pro Cys Thr Phe Ser Thr Phe Gly
  740                      745                      750
Cys His Glu Lys Met Gln Arg Asn His Leu Ala Arg His Leu Gln Glu
  755                      760                      765
Asn Thr Gln Ser His Met Arg Met Leu Ala
  770                      775

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<210> 193

<211> 538

<212> PRT

<213> Artificial Sequence

<220>

<223> hCER122

<400> 193

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Glu Thr Val Val Thr Glu Val Leu Gly His Arg Val Thr Leu Pro Cys
  1                      5                      10                      15
Leu Tyr Ser Ser Trp Ser His Asn Ser Asn Ser Met Cys Trp Gly Lys
  20                      25                      30

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200265_406WO_SEQUENCE_LISTING.TXT

Asp	Gln	Cys	Pro	Tyr	Ser	Gly	Cys	Lys	Glu	Ala	Leu	Ile	Arg	Thr	Asp		
		35					40					45					
Gly	Met	Arg	Val	Thr	Ser	Arg	Lys	Ser	Ala	Lys	Tyr	Arg	Leu	Gln	Gly		
	50					55					60						
Thr	Ile	Pro	Arg	Gly	Asp	Val	Ser	Leu	Thr	Ile	Leu	Asn	Pro	Ser	Glu		
65					70					75					80		
Ser	Asp	Ser	Gly	Val	Tyr	Cys	Cys	Arg	Ile	Glu	Val	Pro	Gly	Trp	Phe		
			85					90					95				
Asn	Asp	Val	Lys	Ile	Asn	Val	Arg	Leu	Asn	Leu	Gln	Arg	Ala	Ser	Thr		
			100					105					110				
Thr	Thr	His	Arg	Thr	Ala	Thr	Thr	Thr	Thr	Arg	Arg	Thr	Thr	Thr	Thr		
		115					120						125				
Ser	Pro	Thr	Thr	Thr	Arg	Gln	Met	Thr	Thr	Thr	Pro	Ala	Ala	Leu	Pro		
	130					135						140					
Thr	Thr	Val	Val	Thr	Thr	Pro	Asp	Leu	Thr	Thr	Gly	Thr	Pro	Leu	Gln		
145					150						155				160		
Met	Thr	Thr	Ile	Ala	Val	Phe	Thr	Thr	Ala	Asn	Thr	Cys	Leu	Ser	Leu		
				165					170						175		
Thr	Pro	Ser	Thr	Leu	Pro	Glu	Glu	Ala	Thr	Gly	Leu	Leu	Thr	Pro	Glu		
			180					185						190			
Pro	Ser	Lys	Glu	Gly	Pro	Ile	Leu	Thr	Ala	Glu	Ser	Glu	Thr	Val	Leu		
	195					200						205					
Pro	Ser	Asp	Ser	Trp	Ser	Ser	Val	Glu	Ser	Thr	Ser	Ala	Asp	Thr	Val		
	210					215					220						
Leu	Leu	Thr	Ser	Lys	Glu	Ser	Lys	Val	Trp	Asp	Leu	Pro	Ser	Thr	Ser		
225					230					235					240		
His	Val	Ser	Met	Trp	Lys	Thr	Ser	Asp	Ser	Val	Ser	Ser	Pro	Gln	Pro		
			245					250						255			
Gly	Ala	Ser	Asp	Thr	Ala	Val	Pro	Glu	Gln	Asn	Lys	Thr	Thr	Lys	Thr		
		260						265					270				
Gly	Gln	Met	Asp	Gly	Ile	Pro	Met	Ser	Met	Lys	Asn	Glu	Met	Pro	Ile		
		275					280					285					
Ser	Gln	Leu	Leu	Met	Ile	Ile	Ala	Pro	Ser	Leu	Gly	Phe	Val	Leu	Phe		
	290					295					300						
Ala	Leu	Phe	Val	Ala	Phe	Leu	His	Arg	Phe	His	Gly	Leu	Trp	Tyr	Met		
305					310					315					320		
Lys	Met	Met	Trp	Ala	Trp	Leu	Gln	Ala	Lys	Arg	Lys	Pro	Arg	Lys	Ala		
			325					330						335			
Pro	Ser	Arg	Asn	Ile	Cys	Tyr	Asp	Ala	Phe	Val	Ser	Tyr	Ser	Glu	Arg		
			340				345						350				
Asp	Ala	Tyr	Trp	Val	Glu	Asn	Leu	Met	Val	Gln	Glu	Leu	Glu	Asn	Phe		
	355					360						365					
Asn	Pro	Pro	Phe	Lys	Leu	Cys	Leu	His	Lys	Arg	Asp	Phe	Ile	Pro	Gly		
	370					375					380						
Lys	Trp	Ile	Ile	Asp	Asn	Ile	Ile	Asp	Ser	Ile	Glu	Lys	Ser	His	Lys		
385					390					395					400		
Thr	Val	Phe	Val	Leu	Ser	Glu	Asn	Phe	Val	Lys	Ser	Glu	Trp	Cys	Lys		
			405						410					415			

200265_406WO_SEQUENCE_LISTING.TXT

Tyr Glu Leu Asp Phe Ser His Phe Arg Leu Phe Asp Glu Asn Asn Asp
420 425 430
Ala Ala Ile Leu Ile Leu Leu Glu Pro Ile Glu Lys Lys Ala Ile Pro
435 440 445
Gln Arg Phe Cys Lys Leu Arg Lys Ile Met Asn Thr Lys Thr Tyr Leu
450 455 460
Glu Trp Pro Met Asp Glu Ala Gln Arg Glu Gly Phe Trp Val Asn Leu
465 470 475 480
Arg Ala Ala Ile Lys Ser Tyr Phe Leu Gly Arg Leu Val Pro Arg Gly
485 490 495
Arg Gly Ala Ala Glu Ala Ala Thr Arg Lys Gln Arg Ile Thr Glu Thr
500 505 510
Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg Ser Asp Val Tyr Ser
515 520 525
Asp Leu Asn Thr Gln Arg Pro Tyr Tyr Lys
530 535

<210> 194

<211> 760

<212> PRT

<213> Artificial Sequence

<220>

<223> hCER123

<400> 194

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

200265_406WO_SEQUENCE_LISTING.TXT

Thr	Pro	Ser	Thr	Leu	Pro	Glu	Glu	Ala	Thr	Gly	Leu	Leu	Thr	Pro	Glu	180	185	190
Pro	Ser	Lys	Glu	Gly	Pro	Ile	Leu	Thr	Ala	Glu	Ser	Glu	Thr	Val	Leu	195	200	205
Pro	Ser	Asp	Ser	Trp	Ser	Ser	Val	Glu	Ser	Thr	Ser	Ala	Asp	Thr	Val	210	215	220
Leu	Leu	Thr	Ser	Lys	Glu	Ser	Lys	Val	Trp	Asp	Leu	Pro	Ser	Thr	Ser	225	230	235
His	Val	Ser	Met	Trp	Lys	Thr	Ser	Asp	Ser	Val	Ser	Ser	Pro	Gln	Pro	245	250	255
Gly	Ala	Ser	Asp	Thr	Ala	Val	Pro	Glu	Gln	Asn	Lys	Thr	Thr	Lys	Thr	260	265	270
Gly	Gln	Met	Asp	Gly	Ile	Pro	Met	Ser	Met	Lys	Asn	Glu	Met	Pro	Ile	275	280	285
Ser	Gln	Leu	Leu	Met	Ile	Ile	Ala	Pro	Ser	Leu	Gly	Phe	Val	Leu	Phe	290	295	300
Ala	Leu	Phe	Val	Ala	Phe	Leu	His	Arg	Phe	His	Gly	Leu	Trp	Tyr	Met	305	310	315
Lys	Met	Met	Trp	Ala	Trp	Leu	Gln	Ala	Lys	Arg	Lys	Pro	Arg	Lys	Ala	325	330	335
Pro	Ser	Arg	Asn	Ile	Cys	Tyr	Asp	Ala	Phe	Val	Ser	Tyr	Ser	Glu	Arg	340	345	350
Asp	Ala	Tyr	Trp	Val	Glu	Asn	Leu	Met	Val	Gln	Glu	Leu	Glu	Asn	Phe	355	360	365
Asn	Pro	Pro	Phe	Lys	Leu	Cys	Leu	His	Lys	Arg	Asp	Phe	Ile	Pro	Gly	370	375	380
Lys	Trp	Ile	Ile	Asp	Asn	Ile	Ile	Asp	Ser	Ile	Glu	Lys	Ser	His	Lys	385	390	395
Thr	Val	Phe	Val	Leu	Ser	Glu	Asn	Phe	Val	Lys	Ser	Glu	Trp	Cys	Lys	405	410	415
Tyr	Glu	Leu	Asp	Phe	Ser	His	Phe	Arg	Leu	Phe	Asp	Glu	Asn	Asn	Asp	420	425	430
Ala	Ala	Ile	Leu	Ile	Leu	Leu	Glu	Pro	Ile	Glu	Lys	Lys	Ala	Ile	Pro	435	440	445
Gln	Arg	Phe	Cys	Lys	Leu	Arg	Lys	Ile	Met	Asn	Thr	Lys	Thr	Tyr	Leu	450	455	460
Glu	Trp	Pro	Met	Asp	Glu	Ala	Gln	Arg	Glu	Gly	Phe	Trp	Val	Asn	Leu	465	470	475
Arg	Ala	Ala	Ile	Lys	Ser	Met	Ser	Leu	Leu	Asn	Cys	Glu	Asn	Ser	Cys	485	490	495
Gly	Ser	Ser	Gln	Ser	Glu	Ser	Asp	Cys	Cys	Val	Ala	Met	Ala	Ser	Ser	500	505	510
Cys	Ser	Ala	Val	Thr	Lys	Asp	Asp	Ser	Val	Gly	Gly	Thr	Ala	Ser	Thr	515	520	525
Gly	Asn	Leu	Ser	Ser	Ser	Phe	Met	Glu	Glu	Ile	Gln	Gly	Tyr	Asp	Val	530	535	540
Glu	Phe	Asp	Pro	Pro	Leu	Glu	Ser	Lys	Tyr	Glu	Cys	Pro	Ile	Cys	Leu	545	550	555

200265_406WO_SEQUENCE_LISTING.TXT

```

Met Ala Leu Arg Glu Ala Val Gln Thr Pro Cys Gly His Arg Phe Cys
      565                      570                      575
Lys Ala Cys Ile Ile Lys Ser Ile Arg Asp Ala Gly His Lys Cys Pro
      580                      585                      590
Val Asp Asn Glu Ile Leu Leu Glu Asn Gln Leu Phe Pro Asp Asn Phe
      595                      600                      605
Ala Lys Arg Glu Ile Leu Ser Leu Met Val Lys Cys Pro Asn Glu Gly
      610                      615                      620
Cys Leu His Lys Met Glu Leu Arg His Leu Glu Asp His Gln Ala His
      625                      630                      635                      640
Cys Glu Phe Ala Leu Met Asp Cys Pro Gln Cys Gln Arg Pro Phe Gln
      645                      650                      655
Lys Phe His Ile Asn Ile His Ile Leu Lys Asp Cys Pro Arg Arg Gln
      660                      665                      670
Val Ser Cys Asp Asn Cys Ala Ala Ser Met Ala Phe Glu Asp Lys Glu
      675                      680                      685
Ile His Asp Gln Asn Cys Pro Leu Ala Asn Val Ile Cys Glu Tyr Cys
      690                      695                      700
Asn Thr Ile Leu Ile Arg Glu Gln Met Pro Asn His Tyr Asp Leu Asp
      705                      710                      715                      720
Cys Pro Thr Ala Pro Ile Pro Cys Thr Phe Ser Thr Phe Gly Cys His
      725                      730                      735
Glu Lys Met Gln Arg Asn His Leu Ala Arg His Leu Gln Glu Asn Thr
      740                      745                      750
Gln Ser His Met Arg Met Leu Ala
      755                      760

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<210> 195

<211> 789

<212> PRT

<213> Artificial Sequence

<220>

<223> hCER126

<400> 195

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

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Asn	Asp	Val	Lys	Ile	Asn	Val	Arg	Leu	Asn	Leu	Gln	Arg	Ala	Ser	Thr
			100					105					110		
Thr	Thr	His	Arg	Thr	Ala	Thr	Thr	Thr	Thr	Arg	Arg	Thr	Thr	Thr	Thr
		115					120					125			
Ser	Pro	Thr	Thr	Thr	Arg	Gln	Met	Thr	Thr	Thr	Pro	Ala	Ala	Leu	Pro
	130					135					140				
Thr	Thr	Val	Val	Thr	Thr	Pro	Asp	Leu	Thr	Thr	Gly	Thr	Pro	Leu	Gln
145					150					155					160
Met	Thr	Thr	Ile	Ala	Val	Phe	Thr	Thr	Ala	Asn	Thr	Cys	Leu	Ser	Leu
			165						170					175	
Thr	Pro	Ser	Thr	Leu	Pro	Glu	Glu	Ala	Thr	Gly	Leu	Leu	Thr	Pro	Glu
			180					185						190	
Pro	Ser	Lys	Glu	Gly	Pro	Ile	Leu	Thr	Ala	Glu	Ser	Glu	Thr	Val	Leu
		195					200					205			
Pro	Ser	Asp	Ser	Trp	Ser	Ser	Val	Glu	Ser	Thr	Ser	Ala	Asp	Thr	Val
	210					215					220				
Leu	Leu	Thr	Ser	Lys	Glu	Ser	Lys	Val	Trp	Asp	Leu	Pro	Ser	Thr	Ser
225					230					235					240
His	Val	Ser	Met	Trp	Lys	Thr	Ser	Asp	Ser	Val	Ser	Ser	Pro	Gln	Pro
			245						250					255	
Gly	Ala	Ser	Asp	Thr	Ala	Val	Pro	Glu	Gln	Asn	Lys	Thr	Thr	Lys	Thr
			260					265					270		
Gly	Gln	Met	Asp	Gly	Ile	Pro	Met	Ser	Met	Lys	Asn	Glu	Met	Pro	Ile
		275					280					285			
Ser	Gln	Leu	Leu	Met	Ile	Ile	Ala	Pro	Ser	Leu	Gly	Phe	Val	Leu	Phe
	290					295					300				
Ala	Leu	Phe	Val	Ala	Phe	Leu	His	Arg	Phe	His	Gly	Leu	Trp	Tyr	Met
305					310					315					320
Lys	Met	Met	Trp	Ala	Trp	Leu	Gln	Ala	Lys	Arg	Lys	Pro	Arg	Lys	Ala
			325						330					335	
Pro	Ser	Arg	Asn	Ile	Cys	Tyr	Asp	Ala	Phe	Val	Ser	Tyr	Ser	Glu	Arg
			340					345						350	
Asp	Ala	Tyr	Trp	Val	Glu	Asn	Leu	Met	Val	Gln	Glu	Leu	Glu	Asn	Phe
		355					360					365			
Asn	Pro	Pro	Phe	Lys	Leu	Cys	Leu	His	Lys	Arg	Asp	Phe	Ile	Pro	Gly
	370					375					380				
Lys	Trp	Ile	Ile	Asp	Asn	Ile	Ile	Asp	Ser	Ile	Glu	Lys	Ser	His	Lys
385					390					395					400
Thr	Val	Phe	Val	Leu	Ser	Glu	Asn	Phe	Val	Lys	Ser	Glu	Trp	Cys	Lys
			405						410					415	
Tyr	Glu	Leu	Asp	Phe	Ser	His	Phe	Arg	Leu	Phe	Asp	Glu	Asn	Asn	Asp
			420					425					430		
Ala	Ala	Ile	Leu	Ile	Leu	Leu	Glu	Pro	Ile	Glu	Lys	Lys	Ala	Ile	Pro
		435					440					445			
Gln	Arg	Phe	Cys	Lys	Leu	Arg	Lys	Ile	Met	Asn	Thr	Lys	Thr	Tyr	Leu
	450					455					460				
Glu	Trp	Pro	Met	Asp	Glu	Ala	Gln	Arg	Glu	Gly	Phe	Trp	Val	Asn	Leu
465					470					475					480

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Arg Ala Ala Ile Lys Ser Met Ala Ala Ala Ser Val Thr Pro Pro Gly
485                               490           495
Ser Leu Glu Leu Leu Gln Pro Gly Phe Ser Lys Thr Leu Leu Gly Thr
500                               505           510
Lys Leu Glu Ala Lys Tyr Leu Cys Ser Ala Cys Arg Asn Val Leu Arg
515                               520           525
Arg Pro Phe Gln Ala Gln Cys Gly His Arg Tyr Cys Ser Phe Cys Leu
530                               535           540
Ala Ser Ile Leu Ser Ser Gly Pro Gln Asn Cys Ala Ala Cys Val His
545                               550           555           560
Glu Gly Ile Tyr Glu Glu Gly Ile Ser Ile Leu Glu Ser Ser Ser Ala
565                               570           575
Phe Pro Asp Asn Ala Ala Arg Arg Glu Val Glu Ser Leu Pro Ala Val
580                               585           590
Cys Pro Ser Asp Gly Cys Thr Trp Lys Gly Thr Leu Lys Glu Tyr Glu
595                               600           605
Ser Cys His Glu Gly Arg Cys Pro Leu Met Leu Thr Glu Cys Pro Ala
610                               615           620
Cys Lys Gly Leu Val Arg Leu Gly Glu Lys Glu Arg His Leu Glu His
625                               630           635           640
Glu Cys Pro Glu Arg Ser Leu Ser Cys Arg His Cys Arg Ala Pro Cys
645                               650           655
Cys Gly Ala Asp Val Lys Ala His His Glu Val Cys Pro Lys Phe Pro
660                               665           670
Leu Thr Cys Asp Gly Cys Gly Lys Lys Lys Ile Pro Arg Glu Lys Phe
675                               680           685
Gln Asp His Val Lys Thr Cys Gly Lys Cys Arg Val Pro Cys Arg Phe
690                               695           700
His Ala Ile Gly Cys Leu Glu Thr Val Glu Gly Glu Lys Gln Gln Glu
705                               710           715           720
His Glu Val Gln Trp Leu Arg Glu His Leu Ala Met Leu Leu Ser Ser
725                               730           735
Val Leu Glu Ala Lys Pro Leu Leu Gly Asp Gln Ser His Ala Gly Ser
740                               745           750
Glu Leu Leu Gln Arg Cys Glu Ser Leu Glu Lys Lys Thr Ala Thr Phe
755                               760           765
Glu Asn Ile Val Cys Val Leu Asn Arg Glu Val Glu Arg Val Ala Met
770                               775           780
Thr Ala Glu Ala Cys
785

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